Table S7 - RNA-seq expression of *K. pneumoniae* KP6870155 coculture biofilms with *A. baumannii* AB6870155 in SLMM versus KP6870155 monoculture biofilms grown in SLMM

locus_tag	gene	log2FoldChange	padj	product	eC_number	eggnog_gene	eggnog_product
MNLKPGEA_	MNLKPGEA	7.136858658	9.28E-101	hypothetical protein	NA	0	acetyltransferase
MNLKPGEA_	folP_2	6.27902491	6.50E-106	Dihydropteroate synthas	2.5.1.15	folP	Catalyzes the condensation of pa
MNLKPGEA_	adh	5.374565901	7.06E-52	Aldehyde dehydrogenase	1.2.1.3	acoD	belongs to the aldehyde dehydrc
MNLKPGEA_	pspG	4.654700312	1.31E-21	Phage shock protein G	NA	pspG	Phage Shock Protein G
MNLKPGEA_	yccU	4.64161323	8.75E-208	putative protein YccU	NA	yccU	CoA-binding protein
MNLKPGEA_	MNLKPGEA	4.562028466	1.38E-19	hypothetical protein	NA	0	0
MNLKPGEA_	yohC	4.27183438	2.94E-116	Inner membrane protein	NA	yohC	Membrane
MNLKPGEA_	MNLKPGEA	3.702460158	1.70E-32	hypothetical protein	NA	0	Protein of unknown function (DU
MNLKPGEA_	emrE	3.680786096	2.59E-30	Multidrug transporter Er	NA	0	Small Multidrug Resistance prot
MNLKPGEA_	MNLKPGEA	3.53474057	1.94E-21	hypothetical protein	NA	0	Inhibitor of glucose uptake trans
MNLKPGEA_	mntS	3.330416907	3.38E-33	Small protein MntS	NA	0	0
MNLKPGEA_	yccX	3.293692864	NA	Acylphosphatase	3.6.1.7	acyP	Belongs to the acylphosphatase
MNLKPGEA_	rlmI	3.234545353	4.58E-34	Ribosomal RNA large su	2.1.1.191	rlmI	Specifically methylates the cytos
MNLKPGEA_	yjaB	3.228165582	7.00E-27	Peptidyl-lysine N-acetylt	2.3.1.-	yjaB	Acetyltransferase
MNLKPGEA_	sodC	3.188213862	6.53E-30	Superoxide dismutase [C	1.15.1.1	sodC	Destroys radicals which are norr
MNLKPGEA_	MNLKPGEA	3.151057642	2.11E-33	hypothetical protein	NA	ypfN	Uncharacterised protein family (
MNLKPGEA_	MNLKPGEA	3.062165983	1.11E-33	hypothetical protein	NA	0	Activator of Hsp90 ATPase 1 fam
MNLKPGEA_	MNLKPGEA	3.034466712	0.00040439	hypothetical protein	NA	Z012_054	acetyltransferase
MNLKPGEA_	pspA_2	3.018830201	8.28E-20	Phage shock protein A	NA	pspA	Phage shock protein A
MNLKPGEA_	norV	2.985060946	3.96E-05	Anaerobic nitric oxide re	NA	norV	uses NADH to detoxify nitric oxic
MNLKPGEA_	mcbA	2.93281651	2.47E-12	putative protein McbA	NA	mcbA	colanic acid metabolic process
MNLKPGEA_	higB-2	2.925037286	3.82E-12	Toxin HigB-2	NA	0	Cytotoxic translational repressor
MNLKPGEA_	iolE_2	2.915426348	NA	Inosose dehydratase	4.2.1.44	0	AP endonuclease
MNLKPGEA_	MNLKPGEA	2.882686043	1.25E-10	hypothetical protein	NA	0	Domain of unknown function (DU
MNLKPGEA_	MNLKPGEA	2.882229157	NA	IS6 family transposase IS	NA	0	Transposase IS66 family

MNLKPGEA_ norW_1	2.828035105	5.58E-05	Nitric oxide reductase Fl	1.18.1.-	norW	One of at least two accessory pr
MNLKPGEA_ fic	2.802916313	1.48E-14	putative protein adenyly	2.7.7.-	fic	cell filamentation protein Fic
MNLKPGEA_ slp	2.785884153	3.65E-38	Outer membrane protei	NA	yeaY	Outer Membrane Lipoprotein
MNLKPGEA_ ybjM	2.759376634	NA	Inner membrane protein	NA	ybjM	Putative inner membrane protei
MNLKPGEA_ fdoH	2.756440643	1.27E-06	Formate dehydrogenase	NA	fdoH	formate dehydrogenase
MNLKPGEA_ MNLKPGEA	2.747477812	8.86E-55	hypothetical protein	NA	yeaQ	transglycosylase associated prot
MNLKPGEA_ livJ_1	2.721140074	0.00137559	Leu/Ile/Val-binding prot	NA	livJ	With LivFGHM is involved in the
MNLKPGEA_ yedI	2.719238193	6.16E-12	Inner membrane protein	NA	yedI	protein conserved in bacteria
MNLKPGEA_ mdtA_2	2.698725853	0.00024268	Multidrug resistance pro	NA	0	Belongs to the membrane fusio
MNLKPGEA_ qorA	2.689630775	8.07E-19	Quinone oxidoreductase	1.6.5.5	qor	COG0604 NADPH quinone reduc
MNLKPGEA_ uspB	2.680477512	4.82E-24	Universal stress protein	NA	uspB	ppGpp-dependent, membrane a
MNLKPGEA_ MNLKPGEA	2.676517276	8.37E-12	hypothetical protein	NA	yodD	Protein of unknown function (DU
MNLKPGEA_ MNLKPGEA	2.643462146	1.04E-11	hypothetical protein	NA	0	Belongs to the purine-cytosine p
MNLKPGEA_ yeaR_2	2.636509087	NA	putative protein YeaR	NA	0	protein domain, possibly involve
MNLKPGEA_ yedK_2	2.629582507	2.89E-08	SOS response-associate	3.4.-.-	yedK	Belongs to the SOS response-as
MNLKPGEA_ MNLKPGEA	2.619075279	2.18E-10	hypothetical protein	NA	0	0
MNLKPGEA_ fliY_2	2.597191208	4.81E-20	L-cystine-binding protein	NA	fliY	Belongs to the bacterial solute-b
MNLKPGEA_ MNLKPGEA	2.545246364	9.17E-06	hypothetical protein	NA	0	0
MNLKPGEA_ ilvH	2.498326283	2.35E-22	Acetolactate synthase is	2.2.1.6	ilvH	acetolactate synthase
MNLKPGEA_ yhcO	2.489029105	2.14E-11	putative protein YhcO	NA	yhcO	inhibitor
MNLKPGEA_ MNLKPGEA	2.488336657	5.86E-21	hypothetical protein	NA	yacL	Belongs to the UPF0231 family
MNLKPGEA_ MNLKPGEA	2.468138643	1.35E-06	hypothetical protein	NA	0	Protein of unknown function (DU
MNLKPGEA_ pspB	2.454858006	1.04E-11	Phage shock protein B	NA	pspB	Phage shock protein B
MNLKPGEA_ ant1	2.442302863	2.19E-15	Streptomycin 3''-adenyly	2.7.7.47	aadA4	Domain of unknown function (DU
MNLKPGEA_ MNLKPGEA	2.442046433	1.26E-09	hypothetical protein	NA	yebG	protein conserved in bacteria
MNLKPGEA_ MNLKPGEA	2.435018664	0.00338691	hypothetical protein	NA	#N/A	#N/A
MNLKPGEA_ pspD	2.409568294	9.43E-07	Phage shock protein D	NA	pspD	Phage Shock Protein
MNLKPGEA_ pncC_3	2.402720531	2.27E-16	Nicotinamide-nucleotide	3.5.1.42	ydeJ	Competence-damaged protein
MNLKPGEA_ menA	2.398504189	4.55E-23	1,4-dihydroxy-2-naphtho	2.5.1.74	menA	Belongs to the MenA family. Typ
MNLKPGEA_ MNLKPGEA	2.394367904	5.01E-06	hypothetical protein	NA	bhsA_1	Protein of unknown function (DU

MNLKPGEA_	tatE	2.375970265	5.71E-07	Sec-independent protein	NA	tatE	Part of the twin-arginine translo
MNLKPGEA_	MNLKPGEA	2.365039372	NA	hypothetical protein	NA	0	tail collar domain protein
MNLKPGEA_	MNLKPGEA	2.344682041	2.17E-07	hypothetical protein	NA	ydhL	Fe-S protein
MNLKPGEA_	ssb	2.338273176	7.88E-28	Single-stranded DNA-bir	NA	ssb	Plays an important role in DNA r
MNLKPGEA_	MNLKPGEA	2.335905942	4.18E-09	hypothetical protein	NA	capB	Cold-Shock Protein
MNLKPGEA_	MNLKPGEA	2.331266011	NA	hypothetical protein	NA	0	Type VI secretion system protein
MNLKPGEA_	MNLKPGEA	2.331266011	NA	hypothetical protein	NA	#N/A	#N/A
MNLKPGEA_	nadX	2.331266011	NA	L-aspartate dehydrogena	1.4.1.21	nadX	Specifically catalyzes the NAD o
MNLKPGEA_	fdoI	2.324693493	4.44E-15	Formate dehydrogenase	NA	fdoI	formate dehydrogenase
MNLKPGEA_	MNLKPGEA	2.321111827	3.25E-05	hypothetical protein	NA	rafY	Porin-like glycoporin RafY
MNLKPGEA_	gltR_1	2.31721249	0.00188257	HTH-type transcriptional	NA	0	LysR substrate binding domain
MNLKPGEA_	aspT_1	2.311268897	2.41E-09	Aspartate/alanine antipo	NA	yidE	transport protein
MNLKPGEA_	yhfG	2.294848851	3.02E-05	putative protein YhfG	NA	yhfG	Protein of unknown function (DU
MNLKPGEA_	ybiI_2	2.284750966	2.14E-19	putative protein YbiI	NA	ybiI	DnaK suppressor protein
MNLKPGEA_	MNLKPGEA	2.283384023	0.00220565	hypothetical protein	NA	hopD	Cleaves type-4 fimbrial leader se
MNLKPGEA_	phnG	2.279827385	NA	Alpha-D-ribose 1-methyl	2.7.8.37	phnG	Phosphonate C-P lyase system p
MNLKPGEA_	rhaR_3	2.27435063	3.11E-05	HTH-type transcriptional	NA	pobR	transcriptional regulator
MNLKPGEA_	MNLKPGEA	2.263760601	NA	hypothetical protein	NA	0	(twin-arginine translocation) pat
MNLKPGEA_	MNLKPGEA	2.249519127	NA	hypothetical protein	NA	0	secretion activating protein
MNLKPGEA_	cynR_1	2.246560756	1.63E-07	HTH-type transcriptional	NA	yfeR	transcriptional regulator
MNLKPGEA_	pspC	2.245491282	4.48E-09	Phage shock protein C	NA	pspC	phage shock protein C
MNLKPGEA_	MNLKPGEA	2.243276772	4.03E-11	hypothetical protein	NA	0	0
MNLKPGEA_	epsL	2.242240845	NA	Type II secretion system	NA	gspL	involved in a type II secretion sys
MNLKPGEA_	ydbM	2.242240845	NA	Putative acyl-CoA dehydı	1.3.99.-	0	acyl-CoA dehydrogenase
MNLKPGEA_	MNLKPGEA	2.23982369	NA	hypothetical protein	NA	ygdB	Protein of unknown function (DU
MNLKPGEA_	pgpC	2.236939171	7.85E-09	Phosphatidylglycerophos	3.1.3.27	yfhB	HAD superfamily (Subfamily IF)
MNLKPGEA_	MNLKPGEA	2.22002875	2.01E-12	hypothetical protein	NA	0	0
MNLKPGEA_	bglH_2	2.195829512	2.62E-05	Cryptic outer membrane	NA	bglH	PFAM porin LamB type
MNLKPGEA_	dctA_2	2.194938404	0.00048361	C4-dicarboxylate transpo	NA	gltP	Belongs to the dicarboxylate am
MNLKPGEA_	gamA	2.193432222	0.00903224	putative glucosamine-6-	3.5.99.6	yieK	glucosamine-6-phosphate deam

MNLKPGEA_ gci	2.192830886	0.00029219	D-galactarolactone cyclo	5.5.1.27	0	Belongs to the mandelate racem
MNLKPGEA_ nlpA	2.19153587	NA	Lipoprotein 28	NA	metQ	Belongs to the nlpA lipoprotein f
MNLKPGEA_ cutC	2.161983996	6.01E-16	Copper homeostasis pro	NA	cutC	Participates in the control of cop
MNLKPGEA_ MNLKPGEA	2.157477256	4.23E-05	hypothetical protein	NA	lrpC	AsnC family transcriptional regu
MNLKPGEA_ tauA	2.153442679	NA	Taurine-binding periplas	NA	tauA	taurine ABC transporter
MNLKPGEA_ obgE	2.151832679	4.61E-12	GTPase ObgE/CgtA	3.6.5.-	obg	An essential GTPase which binds
MNLKPGEA_ uspE	2.148735577	2.03E-24	Universal stress protein	NA	uspE	universal stress protein
MNLKPGEA_ dapA_2	2.141243956	0.01499852	4-hydroxy-tetrahydrodipi	4.3.3.7	dapA3	Belongs to the DapA family
MNLKPGEA_ MNLKPGEA	2.12914614	NA	hypothetical protein	NA	0	transcriptional regulator
MNLKPGEA_ MNLKPGEA	2.126386566	1.51E-06	hypothetical protein	NA	0	LysM domain
MNLKPGEA_ ureB	2.120931357	NA	Urease subunit beta	3.5.1.5	ureB	Belongs to the urease beta subu
MNLKPGEA_ ybaY	2.117301542	1.63E-08	putative lipoprotein YbaY	NA	ybaY	protein conserved in bacteria
MNLKPGEA_ tpa	2.114449978	NA	Taurine--pyruvate aminc	2.6.1.77	0	Belongs to the class-III pyridoxal
MNLKPGEA_ acrR_1	2.104844842	NA	HTH-type transcriptional	NA	envR	acrEF envCD operon
MNLKPGEA_ chaB	2.100380466	1.28E-19	Putative cation transport	NA	chaB	Cation transport regulator
MNLKPGEA_ yphA	2.087447751	5.32E-12	Inner membrane protein	NA	yphA	SURF4 family
MNLKPGEA_ pbpG	2.083737125	1.88E-09	D-alanyl-D-alanine endo	3.4.21.-	pbpG	Belongs to the peptidase S11 fa
MNLKPGEA_ MNLKPGEA	2.082563588	0.00022844	hypothetical protein	NA	yhcN	Protein of unknown function (DU
MNLKPGEA_ rbsC_6	2.076216802	0.01833863	Ribose import permease	NA	0	Branched-chain amino acid trans
MNLKPGEA_ yvqK	2.065348552	NA	Corrinoid adenosyltransf	2.5.1.17	meaD	adenosyltransferase
MNLKPGEA_ pfkA	2.064753488	2.18E-22	ATP-dependent 6-phospl	2.7.1.11	pfkA	Catalyzes the phosphorylation of
MNLKPGEA_ yedK_1	2.064709389	2.42E-13	SOS response-associate	3.4.-.-	yedK	SOS response associated peptida
MNLKPGEA_ cybC	2.064286067	3.04E-19	Soluble cytochrome b562	NA	cybC	Cytochrome b(562)
MNLKPGEA_ ycbB	2.064144608	5.51E-17	putative L,D-transpeptida	2.-.-.-	ycbB	protein conserved in bacteria
MNLKPGEA_ MNLKPGEA	2.062660578	7.73E-08	hypothetical protein	NA	#N/A	#N/A
MNLKPGEA_ aptA_2	2.06222392	0.02989629	Apulose-4-phosphate tra	2.2.1.-	tktB	Transketolase
MNLKPGEA_ yccJ	2.058422239	1.14E-07	putative protein YccJ	NA	yccJ	YccJ-like protein
MNLKPGEA_ sauU	2.055943972	NA	putative sulfoacetate tra	NA	sauU	Major Facilitator Superfamily
MNLKPGEA_ trxC	2.050830736	1.91E-07	Thioredoxin 2	1.8.1.8	trxC	Thioredoxin
MNLKPGEA_ moaE	2.050824426	0.0054781	Molybdopterin synthase	2.8.1.12	moaE	Molybdopterin converting factor

MNLKPGEA_ dcp	2.050491911	4.50E-16	Dipeptidyl carboxypeptid	3.4.15.5	dcp	PFAM peptidase M3A and M3B,
MNLKPGEA_ MNLKPGEA	2.045770252	NA	hypothetical protein	NA	0	transcriptional regulator
MNLKPGEA_ MNLKPGEA	2.040194107	1.98E-13	hypothetical protein	NA	yczG	transcriptional regulator
MNLKPGEA_ sufA	2.040075496	2.66E-11	Protein SufA	NA	sufA	Is able to transfer iron-sulfur clu
MNLKPGEA_ MNLKPGEA	2.040056629	2.54E-25	hypothetical protein	NA	0	RelE family toxin-antitoxin syste
MNLKPGEA_ cof	2.031241536	4.42E-12	HMP-PP phosphatase	3.6.1.-	cof	Catalyzes the hydrolysis of 4-am
MNLKPGEA_ livF_1	2.028632965	0.01381004	High-affinity branched-cl	NA	livF	Branched-chain amino acid trans
MNLKPGEA_ osmE	2.027156021	2.54E-09	Osmotically-inducible pu	NA	osmE	activator of ntr-like gene proteir
MNLKPGEA_ dsrB	2.026662768	9.65E-09	Protein DsrB	NA	dsrB	Dextransucrase DSRB
MNLKPGEA_ MNLKPGEA	2.025695406	6.37E-18	hypothetical protein	NA	prkA	Serine Protein Kinase
MNLKPGEA_ yciE_1	2.023866281	1.80E-07	Protein YciE	NA	yciE	protein conserved in bacteria
MNLKPGEA_ pgtP	2.018752398	8.15E-05	Phosphoglycerate transp	NA	glpT	transporter
MNLKPGEA_ mngR_1	2.011147413	4.78E-09	Mannosyl-D-glycerate tr	NA	yidP	transcriptional regulator
MNLKPGEA_ hspQ	2.008916461	2.73E-10	Heat shock protein HspQ	NA	hspQ	Involved in the degradation of ce
MNLKPGEA_ MNLKPGEA	2.006837021	1.95E-06	hypothetical protein	NA	ycfJ	Outer Membrane Lipoprotein
MNLKPGEA_ mqo_1	1.995018304	3.18E-28	Malate:quinone oxidorec	1.1.5.4	mqo	malate quinone oxidoreductase
MNLKPGEA_ pabA	1.993958122	0.01776619	Aminodeoxychorismate s	2.6.1.85	trpG	anthranilate synthase
MNLKPGEA_ ttuD	1.992781174	6.77E-07	Putative hydroxypyruvate	1.1.1.81	ttuD	Hydroxypyruvate reductase
MNLKPGEA_ abaF_2	1.98471412	NA	Fosfomycin resistance pı	NA	shiA	Major facilitator superfamily
MNLKPGEA_ MNLKPGEA	1.984173872	2.36E-08	hypothetical protein	NA	yggN	Protein of unknown function (DU
MNLKPGEA_ hyuC	1.97528798	NA	N-carbamoyl-L-amino-ac	3.5.1.87	amaB_2	the allantoate amidohydrolase f
MNLKPGEA_ nlhH	1.974215654	5.51E-17	Carboxylesterase NlhH	3.1.1.1	aes	alpha/beta hydrolase fold
MNLKPGEA_ ispH	1.959382941	2.16E-05	4-hydroxy-3-methylbut-2	1.17.7.4	ispH	Catalyzes the conversion of 1-hy
MNLKPGEA_ pyrF	1.959017413	0.00181717	Orotidine 5'-phosphate d	4.1.1.23	pyrF	Catalyzes the decarboxylation of
MNLKPGEA_ rob_1	1.958810402	0.01055064	Right origin-binding prot	NA	0	sequence-specific DNA binding
MNLKPGEA_ wecG	1.958566247	0.01457965	UDP-N-acetyl-D-mannos	2.4.1.180	rffM	Catalyzes the synthesis of Und-P
MNLKPGEA_ MNLKPGEA	1.951070795	0.0006178	hypothetical protein	NA	creA	protein conserved in bacteria
MNLKPGEA_ nagB	1.939555827	6.09E-18	Glucosamine-6-phospha	3.5.99.6	nagB	Catalyzes the reversible isomeri
MNLKPGEA_ ytbE	1.938311792	3.28E-09	putative oxidoreductase	1.-.-.-	0	reductase
MNLKPGEA_ cho	1.933901316	1.96E-06	Excinuclease cho	3.1.25.-	cho	Nuclease subunit of the excinucl

MNLKPGEA_	MNLKPGEA	1.925933676	NA	hypothetical protein	NA	0	0
MNLKPGEA_	tatA	1.921873453	4.12E-13	Sec-independent protein	NA	tatA	Part of the twin-arginine translo
MNLKPGEA_	glgS_1	1.91558609	6.63E-11	Surface composition reg	NA	0	response to butan-1-ol
MNLKPGEA_	phoH	1.910714271	2.01E-06	Protein PhoH	NA	phoH	phosphate starvation-inducible p
MNLKPGEA_	MNLKPGEA	1.900144521	6.14E-14	hypothetical protein	NA	doc	Death ON curing protein
MNLKPGEA_	fliY_6	1.894981523	7.55E-05	L-cystine-binding protein	NA	0	extracellular solute-binding prot
MNLKPGEA_	fucP_2	1.890013319	0.00284631	L-fucose-proton symport	NA	fucP	transporter
MNLKPGEA_	garK_2	1.880594809	5.39E-09	Glycerate 2-kinase	2.7.1.165	glxK	Belongs to the glycerate kinase
MNLKPGEA_	slyB	1.87855912	2.53E-09	Outer membrane lipopro	NA	slyB	Outer Membrane Lipoprotein
MNLKPGEA_	MNLKPGEA	1.876897342	2.44E-14	hypothetical protein	NA	yeaH	Belongs to the UPF0229 family
MNLKPGEA_	proP_2	1.870953291	2.72E-17	Proline/betaine transpor	NA	proP	transporter
MNLKPGEA_	MNLKPGEA	1.867641401	0.00626229	hypothetical protein	NA	ycaP	Membrane
MNLKPGEA_	fumB	1.863763869	0.00028188	Fumarate hydratase clas	4.2.1.2	fumA	Catalyzes the reversible hydratic
MNLKPGEA_	fabG_10	1.863608168	0.02355927	3-oxoacyl-[acyl-carrier-p	1.1.1.100	0	Dehydrogenases with different s
MNLKPGEA_	MNLKPGEA	1.860770164	1.33E-22	hypothetical protein	NA	yqaE	homolog of Blt101
MNLKPGEA_	MNLKPGEA	1.854827107	5.65E-08	hypothetical protein	NA	yjdI	Divergent 4Fe-4S mono-cluster
MNLKPGEA_	bhsA_1	1.848294769	3.88E-06	Multiple stress resistanc	NA	bhsA	Multiple stress resistance protei
MNLKPGEA_	yhdT	1.847854782	NA	putative membrane prot	NA	yhdT	Membrane
MNLKPGEA_	MNLKPGEA	1.846882262	4.42E-12	hypothetical protein	NA	ycgN	Belongs to the UPF0260 family
MNLKPGEA_	chaC	1.845004035	1.46E-12	Glutathione-specific gan	4.3.2.7	chaC	Catalyzes the cleavage of glutat
MNLKPGEA_	MNLKPGEA	1.843924955	6.72E-08	hypothetical protein	NA	0	Fimbrial protein
MNLKPGEA_	MNLKPGEA	1.84050873	0.00029948	hypothetical protein	NA	0	0
MNLKPGEA_	MNLKPGEA	1.84021742	4.38E-11	hypothetical protein	NA	#N/A	#N/A
MNLKPGEA_	chbG	1.838389232	0.01116591	Chitooligosaccharide dea	3.5.1.105	chbG	Involved in the degradation of ch
MNLKPGEA_	MNLKPGEA	1.834611058	1.36E-10	hypothetical protein	NA	ysaB	YsaB-like lipoprotein
MNLKPGEA_	MNLKPGEA	1.829997689	0.00010684	hypothetical protein	NA	0	oxidized base lesion DNA N-glyc
MNLKPGEA_	hosA	1.827102359	3.84E-07	Transcriptional regulator	NA	hosA	Transcriptional regulator
MNLKPGEA_	MNLKPGEA	1.824744754	0.04541966	hypothetical protein	NA	YPO1157	conserved protein
MNLKPGEA_	yciH	1.821455711	4.34E-08	putative protein YciH	NA	yciH	Translation Initiation Factor
MNLKPGEA_	ecpE_2	1.820198378	0.00044549	putative fimbrial chaper	NA	0	Part of the ecpRABCDE operon,

MNLKPGEA_	yibH_1	1.819687703	0.00059535	Inner membrane protein	NA	yibH	secretion protein HlyD family
MNLKPGEA_	sufC	1.810953104	2.95E-12	putative ATP-dependent	NA	sufC	FeS assembly ATPase SufC
MNLKPGEA_	ycgZ	1.806601257	0.00288975	putative two-component	NA	ycgZ	Two-component-system connec
MNLKPGEA_	MNLKPGEA	1.803252771	6.20E-05	putative protein	NA	0	Hydrolases of the alpha beta sup
MNLKPGEA_	MNLKPGEA	1.801260163	3.05E-07	hypothetical protein	NA	yiiS	Protein of unknown function (DU
MNLKPGEA_	MNLKPGEA	1.793148623	0.00651653	hypothetical protein	NA	0	0
MNLKPGEA_	fabG_2	1.791682157	1.06E-05	3-oxoacyl-[acyl-carrier-p	1.1.1.100	MA20_35	Belongs to the short-chain dehyd
MNLKPGEA_	MNLKPGEA	1.789771511	0.00045055	hypothetical protein	NA	0	Prophage CP4-57 regulatory prot
MNLKPGEA_	bluF_2	1.786822584	3.79E-06	Blue light- and temperat	NA	ycgF	EAL domain
MNLKPGEA_	mltF_3	1.785293851	1.41E-05	Membrane-bound lytic n	4.2.2.-	0	Murein-degrading enzyme that d
MNLKPGEA_	MNLKPGEA	1.777476684	NA	hypothetical protein	NA	0	Phosphoenolpyruvate-dependent
MNLKPGEA_	MNLKPGEA	1.773022909	NA	IS1 family transposase IS	NA	insB	cog cog1662
MNLKPGEA_	MNLKPGEA	1.772429419	NA	hypothetical protein	NA	0	0
MNLKPGEA_	MNLKPGEA	1.771609981	0.00546024	hypothetical protein	NA	0	tautomerase
MNLKPGEA_	MNLKPGEA	1.769507122	0.0017404	hypothetical protein	NA	0	ACT domain protein
MNLKPGEA_	MNLKPGEA	1.769376781	1.12E-05	hypothetical protein	NA	yybR_1	transcriptional regulator
MNLKPGEA_	mntB_2	1.769297381	6.72E-08	Manganese transport sy	NA	sitC	iron transport system membran
MNLKPGEA_	glnQ_1	1.767612321	NA	Glutamine transport ATP	3.6.3.-	livG	Part of the ABC transporter com
MNLKPGEA_	metJ	1.766483812	1.06E-09	Met repressor	NA	metJ	This regulatory protein, when co
MNLKPGEA_	MNLKPGEA	1.765731668	NA	hypothetical protein	NA	0	Prophage CP4-57 regulatory prot
MNLKPGEA_	MNLKPGEA	1.764902285	0.00329611	hypothetical protein	NA	#N/A	#N/A
MNLKPGEA_	fabD_1	1.751960525	NA	Malonyl CoA-acyl carrier	2.3.1.39	mdcH	malonyl CoA-acyl carrier protein
MNLKPGEA_	btuD_5	1.746031942	NA	Vitamin B12 import ATP	7.6.2.8	0	(ABC) transporter
MNLKPGEA_	MNLKPGEA	1.744682652	3.98E-10	hypothetical protein	NA	yjgA	Belongs to the UPF0307 family
MNLKPGEA_	soxR	1.743711454	0.00557917	Redox-sensitive transcri	NA	soxR	redox-sensitive transcriptional a
MNLKPGEA_	mglA_2	1.742791607	NA	Galactose/methyl galact	7.5.2.11	mglA_3	(ABC) transporter
MNLKPGEA_	MNLKPGEA	1.742400322	0.00334239	hypothetical protein	NA	0	Glutathione-dependent formald
MNLKPGEA_	nadR	1.738306727	2.51E-18	Trifunctional NAD biosyr	NA	nadR	transcriptional regulator
MNLKPGEA_	aptB_2	1.729861181	1.95E-06	Apulose-4-phosphate tra	2.2.1.-	dxs_2	Transketolase
MNLKPGEA_	tauD	1.725368182	NA	Alpha-ketoglutarate-dep	1.14.11.17	tauD	taurine catabolism dioxygenase

MNLKPGEA_	rbsK_3	1.721054577	9.56E-07	Ribokinase	2.7.1.15	0	PfkB domain protein
MNLKPGEA_	rhaT	1.718565987	1.45E-11	L-rhamnose-proton sym	NA	rhaT	Uptake of L-rhamnose across th
MNLKPGEA_	ssuA_3	1.715573868	NA	Putative aliphatic sulfon	NA	ssuA	ABC transporter
MNLKPGEA_	MNLKPGEA	1.715235561	NA	hypothetical protein	NA	0	COG1028 Dehydrogenases with
MNLKPGEA_	def	1.710466113	7.14E-07	Peptide deformylase	3.5.1.88	def	Removes the formyl group from
MNLKPGEA_	MNLKPGEA	1.708265594	0.00011169	hypothetical protein	NA	ydcK	COG1208 Nucleoside-diphospha
MNLKPGEA_	butA	1.7031305	0.00012157	Diacetyl reductase [(S)-a	1.1.1.304	0	Dehydrogenases with different s
MNLKPGEA_	MNLKPGEA	1.702677004	4.31E-07	hypothetical protein	NA	ybjD	ATP-dependent endonuclease of
MNLKPGEA_	pnuC	1.702218314	8.05E-13	Nicotinamide riboside tr	NA	pnuC	nicotinamide mononucleotide tr
MNLKPGEA_	cbdB	1.700243113	NA	2-halobenzoate 1,2-diox	1.14.12.13	benB	COG5517 Small subunit of phen
MNLKPGEA_	MNLKPGEA	1.696198296	0.00875532	hypothetical protein	NA	0	Acetyltransferase (GNAT) doma
MNLKPGEA_	ybdK	1.696126031	5.26E-07	Putative glutamate--cyst	6.3.2.2	ybdK	ATP-dependent carboxylate-ami
MNLKPGEA_	MNLKPGEA	1.694715435	0.00103555	Putative cytokinin ribosic	3.2.2.-	VM57_08	Belongs to the LOG family
MNLKPGEA_	ygbN	1.692617625	0.00048077	Inner membrane perme	NA	ygbN	Gluconate
MNLKPGEA_	mntB_3	1.690196573	7.23E-07	Manganese transport sy	NA	sitB	(ABC) transporter
MNLKPGEA_	fhuF	1.689470271	4.64E-11	Ferric iron reductase pro	NA	fhuF	Iron reductase
MNLKPGEA_	yjdJ	1.688198444	1.67E-08	putative protein YjdJ	NA	yjdJ	GCN5-related N-acetyl-transfera
MNLKPGEA_	MNLKPGEA	1.683379256	0.00237653	hypothetical protein	NA	0	0
MNLKPGEA_	lptB_1	1.681262998	0.01792575	Lipopolysaccharide expo	3.6.3.-	livG	Part of the ABC transporter com
MNLKPGEA_	ecpD	1.67837389	NA	Fimbria adhesin EcpD	NA	yagW	Part of the ecpRABCDE operon,
MNLKPGEA_	ubiX	1.676019034	0.00043163	Flavin prenyltransferase	2.5.1.129	ubiX	Flavin prenyltransferase that cat
MNLKPGEA_	glgX	1.674070504	3.04E-14	Glycogen debranching e	3.2.1.196	glgX	Belongs to the glycosyl hydrolas
MNLKPGEA_	MNLKPGEA	1.671441514	0.05307825	hypothetical protein	NA	yjiJ	Major facilitator Superfamily
MNLKPGEA_	MNLKPGEA	1.665762673	0.05484874	hypothetical protein	NA	kdgF	PFAM Cupin 2, conserved barrel
MNLKPGEA_	MNLKPGEA	1.664799994	3.30E-06	hypothetical protein	NA	yjjZ	Protein of unknown function (DU
MNLKPGEA_	ygaV	1.653763659	0.01751832	putative HTH-type transc	NA	ygaV	transcriptional regulator
MNLKPGEA_	rplO	1.653632017	3.25E-05	50S ribosomal protein L1	NA	rplO	binds to the 23S rRNA
MNLKPGEA_	MNLKPGEA	1.652781107	0.00351013	hypothetical protein	NA	ybjK	transcriptional regulator
MNLKPGEA_	MNLKPGEA	1.648797671	5.21E-07	putative signaling protei	NA	0	Diguanylate cyclase
MNLKPGEA_	ybhR_1	1.648165653	2.72E-05	putative multidrug ABC t	NA	ybhS	ABC-type multidrug transport sy

MNLKPGEA_ davD	1.641513683	0.03514029	Glutarate-semialdehyde	1.2.1.-	gabD	belongs to the aldehyde dehydrc
MNLKPGEA_ lexA_3	1.641322448	1.05E-06	LexA repressor	3.4.21.88	lexA	Represses a number of genes in
MNLKPGEA_ MNLKPGEA	1.640018071	0.00260562	hypothetical protein	NA	0	Protein involved in biological_pr
MNLKPGEA_ lamB_4	1.636909061	0.02000482	Maltoporin	NA	lamB	involved in the transport of malt
MNLKPGEA_ MNLKPGEA	1.636789691	4.12E-06	hypothetical protein	NA	0	0
MNLKPGEA_ MNLKPGEA	1.633540565	8.23E-08	hypothetical protein	NA	ydfF	transcriptional regulator
MNLKPGEA_ yaiY	1.629985065	NA	Inner membrane protein	NA	yaiY	Protein of unknown function (DU
MNLKPGEA_ gudP_3	1.626954434	0.00029905	putative glucarate transp	NA	0	transporter
MNLKPGEA_ ydiK	1.624464379	4.79E-09	Putative transport protei	NA	ydiK	ydiK promoter presents a PurR s
MNLKPGEA_ MNLKPGEA	1.624297267	2.25E-06	hypothetical protein	NA	0	Antitoxin component of a toxin-a
MNLKPGEA_ arnE	1.620760082	NA	putative 4-amino-4-deox	NA	arnE	Translocates 4-amino-4-deoxy-L
MNLKPGEA_ frmA	1.617457896	5.56E-05	S-(hydroxymethyl)glutatl	1.1.1.284	frmA	Belongs to the zinc-containing a
MNLKPGEA_ MNLKPGEA	1.611029466	0.00028229	hypothetical protein	NA	bcsD	cellulose synthase
MNLKPGEA_ kdgT	1.610815155	NA	2-keto-3-deoxygluconate	NA	0	The 2-keto-3-deoxygluconate pe
MNLKPGEA_ uspG_3	1.607934846	4.24E-08	Universal stress protein	NA	uspG	Belongs to the universal stress p
MNLKPGEA_ yfcD	1.604845163	2.62E-05	putative Nudix hydrolase	3.6.-.-	yfcD	NUDIX hydrolase
MNLKPGEA_ MNLKPGEA	1.598511492	NA	hypothetical protein	NA	#N/A	#N/A
MNLKPGEA_ MNLKPGEA	1.597968556	0.00706607	hypothetical protein	NA	0	PTS sugar transporter
MNLKPGEA_ MNLKPGEA	1.596690066	0.00686177	hypothetical protein	NA	yghX	Dienelactone hydrolase
MNLKPGEA_ MNLKPGEA	1.583038907	7.16E-15	hypothetical protein	NA	#N/A	#N/A
MNLKPGEA_ bolA	1.582693551	1.39E-10	DNA-binding transcriptic	NA	bolA	Belongs to the BolA IbaG family
MNLKPGEA_ asd_1	1.5817091	2.05E-06	Aspartate-semialdehyde	1.2.1.11	asd	Catalyzes the NADPH-dependent
MNLKPGEA_ sorB_2	1.575450491	0.06394261	PTS system sorbose-spe	2.7.1.206	0	PTS system sorbose subfamily II
MNLKPGEA_ MNLKPGEA	1.572279189	0.12011791	hypothetical protein	NA	0	0
MNLKPGEA_ menD	1.565411406	2.93E-09	2-succinyl-5-enolpyruvyl-	2.2.1.9	menD	Catalyzes the thiamine diphosph
MNLKPGEA_ MNLKPGEA	1.56495557	1.39E-05	hypothetical protein	NA	yjdC	Transcriptional regulator
MNLKPGEA_ moaA	1.557588046	0.00021206	GTP 3',8-cyclase	4.1.99.22	moaA	Catalyzes the cyclization of GTP
MNLKPGEA_ livK	1.556710948	0.03956751	Leucine-specific-binding	NA	livK	With LivFGHM is involved in the
MNLKPGEA_ ycjX	1.553896844	3.21E-06	putative protein YcjX	NA	ycjX	COG3106 Predicted ATPase
MNLKPGEA_ btuB	1.553450245	0.01381004	Vitamin B12 transporter	NA	btuB	Involved in the active translocati

MNLKPGEA_	ynfD	1.553199836	7.22E-13	putative protein YnfD	NA	ynfD	membrane
MNLKPGEA_	yciV	1.546451608	1.16E-06	5'-3' exoribonuclease	3.1.13.-	trpH	Metal-dependent phosphoestera
MNLKPGEA_	nupG	1.545145307	1.65E-06	Nucleoside permease Nu	NA	nupG	Broad-specificity transporter of
MNLKPGEA_	MNLKPGEA	1.542653588	0.106317	hypothetical protein	NA	0	Bacteriophage HK97-gp10, putat
MNLKPGEA_	zwf	1.542347655	1.11E-06	Glucose-6-phosphate 1-(	1.1.1.49	zwf	Catalyzes the oxidation of glucos
MNLKPGEA_	MNLKPGEA	1.539000677	0.04056612	hypothetical protein	NA	0	0
MNLKPGEA_	ganB	1.536487142	0.00706607	Arabinogalactan endo-be	3.2.1.89	ganB	Arabinogalactan endo-beta-1,4-
MNLKPGEA_	eutC_2	1.534297854	0.01554006	Ethanolamine ammonia-	4.3.1.7	eutC	Belongs to the EutC family
MNLKPGEA_	MNLKPGEA	1.531183338	0.00912115	hypothetical protein	NA	ybbK	Purine nucleoside phosphorylase
MNLKPGEA_	bglA_2	1.53101967	0.08517452	6-phospho-beta-glucosic	3.2.1.86	celA	Belongs to the glycosyl hydrolas
MNLKPGEA_	MNLKPGEA	1.530052527	3.88E-06	IS1595 family transposa	NA	folA	Key enzyme in folate metabolisr
MNLKPGEA_	MNLKPGEA	1.529567672	NA	hypothetical protein	NA	#N/A	#N/A
MNLKPGEA_	pdxY	1.526793557	1.14E-07	Pyridoxal kinase PdxY	2.7.1.35	pdxY	Pyridoxal kinase involved in the s
MNLKPGEA_	MNLKPGEA	1.525943514	NA	hypothetical protein	NA	0	Glycine-rich SFCGS
MNLKPGEA_	uxuA_2	1.520658539	0.00108332	Mannonate dehydratase	4.2.1.8	uxuA	Catalyzes the dehydration of D-r
MNLKPGEA_	yhhA	1.520461614	0.00035749	putative protein YhhA	NA	yhhA	Protein of unknown function (DU
MNLKPGEA_	MNLKPGEA	1.518445893	NA	hypothetical protein	NA	0	Putative 3TM holin, Phage_holin
MNLKPGEA_	pld1	1.518445893	NA	Pyridoxal 4-dehydrogena	1.1.1.107	0	Aldo Keto reductase
MNLKPGEA_	MNLKPGEA	1.516249708	0.00020215	hypothetical protein	NA	ychH	cellular response to cadmium io
MNLKPGEA_	dnaQ	1.515344536	1.59E-07	DNA polymerase III subu	2.7.7.7	dnaQ	DNA polymerase III is a complex
MNLKPGEA_	moaF	1.513799708	NA	Protein MoaF	NA	moaF	MoaF C-terminal domain
MNLKPGEA_	msrP	1.512136535	0.00461898	Protein-methionine-sulfo	1.8.5.-	msrP	Part of the MsrPQ system that r
MNLKPGEA_	MNLKPGEA	1.509795741	5.31E-12	hypothetical protein	NA	#N/A	#N/A
MNLKPGEA_	rsmA	1.509531253	4.00E-08	Ribosomal RNA small su	2.1.1.182	ksgA	Specifically dimethylates two ac
MNLKPGEA_	dmlR_17	1.509138025	0.06608956	HTH-type transcriptional	NA	0	transcriptional regulator
MNLKPGEA_	kdpA	1.507946143	NA	Potassium-transporting A	NA	kdpA	Part of the high-affinity ATP-driv
MNLKPGEA_	fdoG_2	1.507881424	0.02965223	Formate dehydrogenase	1.17.1.9	fdoG	Belongs to the prokaryotic molyl
MNLKPGEA_	livH_3	1.504945955	3.05E-06	High-affinity branched-cl	NA	livH	Belongs to the binding-protein-d
MNLKPGEA_	tmcA	1.503441667	0.00113772	tRNA(Met) cytidine acet	2.3.1.193	tmcA	Catalyzes the formation of N(4)-
MNLKPGEA_	dapL	1.499238504	0.04546623	LL-diaminopimelate ami	2.6.1.83	0	Aminotransferase class I and II

MNLKPGEA_	lsrD_2	1.496941999	0.08806507	Autoinducer 2 import sy	NA	lsrD_1	Branched-chain amino acid tran
MNLKPGEA_	argP_3	1.49479921	NA	HTH-type transcriptional	NA	0	transcriptional regulator
MNLKPGEA_	MNLKPGEA	1.492788559	NA	hypothetical protein	NA	gpW	Baseplate assembly protein
MNLKPGEA_	MNLKPGEA	1.482421483	0.10745078	hypothetical protein	NA	#N/A	#N/A
MNLKPGEA_	gcd	1.480393215	7.73E-05	Quinoprotein glucose de	1.1.5.2	gcd	Dehydrogenase
MNLKPGEA_	rbsC_1	1.478739713	0.00179018	Ribose import permease	NA	0	Belongs to the binding-protein-d
MNLKPGEA_	dadA_2	1.476855039	0.00313443	D-amino acid dehydroge	1.4.99.-	dadA2	D-amino acid dehydrogenase
MNLKPGEA_	dhaB	1.473086396	NA	Glycerol dehydratase lar	4.2.1.30	dhaB	Dehydratase large subunit
MNLKPGEA_	MNLKPGEA	1.472754508	5.19E-07	hypothetical protein	NA	aroM	AroM protein
MNLKPGEA_	xynR_2	1.469733624	0.03602655	HTH-type transcriptional	NA	mhpR	transcriptional regulator
MNLKPGEA_	MNLKPGEA	1.466479965	NA	hypothetical protein	NA	0	Membrane
MNLKPGEA_	MNLKPGEA	1.465771033	4.05E-05	hypothetical protein	NA	ycjF	UPF0283 membrane protein
MNLKPGEA_	gstB_3	1.463515535	0.03128456	Glutathione S-transferas	2.5.1.18	yliJ	Glutathione S-Transferase
MNLKPGEA_	dapE	1.463179014	5.31E-08	Succinyl-diaminopimelat	3.5.1.18	dapE	Catalyzes the hydrolysis of N-suc
MNLKPGEA_	pphA	1.463068892	0.00056302	Serine/threonine-protein	3.1.3.16	pphA	Serine Threonine protein
MNLKPGEA_	yhaH	1.460946327	4.67E-08	Inner membrane protein	NA	yhaH	Membrane
MNLKPGEA_	ydjE	1.457555636	0.09003704	Inner membrane metabo	NA	0	Sugar (and other) transporter
MNLKPGEA_	psiE	1.457455551	4.05E-06	Protein PsiE	NA	psiE	Protein PsiE homolog
MNLKPGEA_	MNLKPGEA	1.45619348	0.00152452	Extracellular exo-alpha-(	3.2.1.55	abf2	Belongs to the glycosyl hydrolas
MNLKPGEA_	lsrG	1.450096723	0.01776619	(4S)-4-hydroxy-5-phosph	5.3.1.32	lsrG	Involved in the degradation of pl
MNLKPGEA_	MNLKPGEA	1.448560853	NA	hypothetical protein	NA	0	ABC-type nitrate sulfonate bicar
MNLKPGEA_	ytfE	1.448560853	NA	Iron-sulfur cluster repair	NA	ytfE	Di-iron-containing protein involv
MNLKPGEA_	srlB_2	1.448495859	NA	PTS system glucitol/sorb	NA	0	PTS system glucitol/sorbitol-spe
MNLKPGEA_	gudD	1.44613436	0.00255621	Glucarate dehydratase	4.2.1.40	gudD	Belongs to the mandelate racem
MNLKPGEA_	MNLKPGEA	1.442161349	NA	hypothetical protein	NA	0	COG3678 P pilus assembly Cpx s
MNLKPGEA_	MNLKPGEA	1.442110343	1.46E-11	hypothetical protein	NA	0	0
MNLKPGEA_	MNLKPGEA	1.440697191	NA	hypothetical protein	NA	0	HlyD family secretion protein
MNLKPGEA_	dmlR_12	1.437096557	NA	HTH-type transcriptional	NA	0	transcriptional regulator
MNLKPGEA_	ulaA_1	1.435905706	0.15011301	Ascorbate-specific PTS s	NA	ulaA	transporter subunit
MNLKPGEA_	yibL	1.43470649	1.51E-08	putative protein YibL	NA	yibL	Protein of unknown function (DU

MNLKPGEA_ fdoG_1	1.434437794	6.06E-06	Formate dehydrogenase	1.17.1.9	fdnG	Sulfate ABC transporter substrat
MNLKPGEA_ ydcV_1	1.434284145	2.06E-05	Inner membrane ABC tra	NA	ydcV	ABC transporter (permease)
MNLKPGEA_ pmrD	1.432100705	0.11311848	Signal transduction prote	NA	pmrD	Polymyxin resistance protein Pm
MNLKPGEA_ ubiK	1.431394845	1.05E-06	Ubiquinone biosynthesis	NA	yqiC	protein conserved in bacteria
MNLKPGEA_ lhpD	1.431096134	0.09489446	Delta(1)-pyrroline-2-carb	1.5.1.21	allD	Belongs to the LDH2 MDH2 oxid
MNLKPGEA_ rutE	1.431046329	NA	putative malonic semiald	1.1.1.298	rutE	May reduce toxic product malon
MNLKPGEA_ ynjF	1.43018848	0.0322141	Inner membrane protein	NA	ynjF	Belongs to the CDP-alcohol phos
MNLKPGEA_ MNLKPGEA	1.429009984	8.07E-08	hypothetical protein	NA	0	0
MNLKPGEA_ MNLKPGEA	1.42837283	0.00047412	hypothetical protein	NA	yiaF	exported protein
MNLKPGEA_ norG_1	1.426320503	4.43E-05	HTH-type transcriptional	NA	0	Transcriptional regulator
MNLKPGEA_ tauR	1.425960049	NA	HTH-type transcriptional	NA	0	Transcriptional regulators contai
MNLKPGEA_ MNLKPGEA	1.425014386	1.27E-05	ISNCY family transposas	NA	0	Transposase
MNLKPGEA_ mlaA	1.422816902	4.42E-12	Intermembrane phospho	NA	vacJ	Lipoprotein
MNLKPGEA_ MNLKPGEA	1.417332708	NA	hypothetical protein	NA	pduK	BMC
MNLKPGEA_ MNLKPGEA	1.417332708	NA	hypothetical protein	NA	0	N-acetyltransferase
MNLKPGEA_ sfsA	1.415708886	2.26E-06	Sugar fermentation stim	NA	sfsA	Belongs to the SfsA family
MNLKPGEA_ relB	1.415634141	0.00029336	Antitoxin RelB	NA	relB	bifunctional antitoxin of the RelE
MNLKPGEA_ MNLKPGEA	1.415373533	0.02441751	hypothetical protein	NA	0	0
MNLKPGEA_ MNLKPGEA	1.41464177	0.01781782	hypothetical protein	NA	0	0
MNLKPGEA_ MNLKPGEA	1.414096618	1.08E-06	hypothetical protein	NA	fcy21	Belongs to the purine-cytosine p
MNLKPGEA_ axe1-6A	1.41270485	0.00059782	Carbohydrate acetyl este	NA	yieL	Belongs to the glycosyl hydrolas
MNLKPGEA_ pduE_1	1.412351573	NA	Propanediol dehydratase	4.2.1.28	pduE	Dehydratase Small Subunit
MNLKPGEA_ yhdG	1.412129231	0.00263918	putative amino acid perr	NA	eat	amino acid
MNLKPGEA_ ttdT	1.412000098	0.09943911	L-tartrate/succinate anti	NA	ttdT	PFAM Sodium sulphate symport
MNLKPGEA_ glnP_2	1.411246209	NA	putative glutamine ABC	NA	glnP	(ABC) transporter
MNLKPGEA_ MNLKPGEA	1.410229968	NA	hypothetical protein	NA	phnE	Phosphonate ABC transporter
MNLKPGEA_ sufD	1.409788324	2.28E-05	FeS cluster assembly pro	NA	sufD	FeS assembly protein SufD
MNLKPGEA_ yhbE	1.409457934	0.00066007	putative inner membran	NA	yhbE	Permeases of the drug metaboli
MNLKPGEA_ sufB	1.406953562	2.56E-09	FeS cluster assembly pro	NA	sufB	FeS assembly protein SufB
MNLKPGEA_ dsdX_1	1.406318757	NA	D-serine transporter Dsd	NA	dsdX	Gluconate

MNLKPGEA_	ribA	1.403827039	0.01923371	GTP cyclohydrolase-2	3.5.4.25	ribA	Catalyzes the conversion of GTP
MNLKPGEA_	osmB	1.403502314	0.00065844	Osmotically-inducible lip	NA	osmB	Lipoprotein
MNLKPGEA_	sbnD_2	1.400151435	0.01952357	Staphyloferrin B transpo	NA	mdtG	Major facilitator Superfamily
MNLKPGEA_	menI	1.399574768	0.11385609	1,4-dihydroxy-2-naphtho	3.1.2.28	menI	Catalyzes the hydrolysis of 1,4-d
MNLKPGEA_	MNLKPGEA	1.399519926	9.43E-07	hypothetical protein	NA	bssR	disruption of this gene in Escher
MNLKPGEA_	aidB	1.397621156	3.76E-06	Putative acyl-CoA dehydı	1.3.99.-	aidB	acyl-CoA dehydrogenase
MNLKPGEA_	cmpR_2	1.395655935	0.00347372	HTH-type transcriptional	NA	yeiE	transcriptional regulator
MNLKPGEA_	MNLKPGEA	1.393846931	0.21923061	hypothetical protein	NA	#N/A	#N/A
MNLKPGEA_	dppD_1	1.388813786	0.08240801	Dipeptide transport ATP-	NA	dppD	Belongs to the ABC transporter s
MNLKPGEA_	ydcO	1.388809396	NA	Inner membrane protein	NA	ydcO	protein involved in benzoate me
MNLKPGEA_	pqiC	1.388619458	2.61E-06	Intermembrane transpor	NA	ymbA	protein conserved in bacteria
MNLKPGEA_	nupX	1.388544047	0.00483084	Putative nucleoside pern	NA	nupX	Belongs to the concentrative nuc
MNLKPGEA_	MNLKPGEA	1.388397808	4.05E-05	hypothetical protein	NA	#N/A	#N/A
MNLKPGEA_	arsR2	1.387821119	0.13552919	Arsenic resistance transc	NA	arsR	transcriptional regulator
MNLKPGEA_	rhtB_2	1.387535627	0.04775858	Homoserine/homoserine	NA	rhtB	efflux protein
MNLKPGEA_	bglJ	1.386996368	0.20748569	Transcriptional activator	NA	bglJ	transcriptional
MNLKPGEA_	gloC	1.385545426	0.05573951	Hydroxyacylglutathione h	3.1.2.6	ycbL	COG0491 Zn-dependent hydrola
MNLKPGEA_	MNLKPGEA	1.384058105	4.16E-06	putative periplasmic iror	NA	sitA	Belongs to the bacterial solute-b
MNLKPGEA_	MNLKPGEA	1.382722425	0.00058931	hypothetical protein	NA	#N/A	#N/A
MNLKPGEA_	fabG_5	1.381985327	0.10348362	3-oxoacyl-[acyl-carrier-p	1.1.1.100	0	short-chain dehydrogenase
MNLKPGEA_	MNLKPGEA	1.380978777	6.20E-05	hypothetical protein	NA	#N/A	#N/A
MNLKPGEA_	epsF_1	1.377484955	NA	Type II secretion system	NA	gspF	general secretion pathway prote
MNLKPGEA_	MNLKPGEA	1.377484955	NA	hypothetical protein	NA	#N/A	#N/A
MNLKPGEA_	MNLKPGEA	1.376938609	0.04998991	hypothetical protein	NA	yafS	Methyl-transferase
MNLKPGEA_	acnA	1.372633666	0.00018828	Aconitate hydratase A	4.2.1.3	acnA	Catalyzes the isomerization of ci
MNLKPGEA_	amtB	1.372424571	0.03592371	Ammonia channel	NA	amtB	Ammonium transporter
MNLKPGEA_	yfiF	1.371918955	0.00040956	putative tRNA/rRNA me	2.1.1.-	yfiF	Belongs to the class IV-like SAM
MNLKPGEA_	MNLKPGEA	1.370227192	0.00948678	hypothetical protein	NA	0	0
MNLKPGEA_	cusB	1.36957804	NA	Cation efflux system pro	NA	cusB	Belongs to the membrane fusion
MNLKPGEA_	MNLKPGEA	1.368123261	0.00160972	hypothetical protein	NA	0	0

MNLKPGEA_ glpR_2	1.368017507	0.0037802	Glycerol-3-phosphate re	NA	0	Transcriptional Regulator, DeoR
MNLKPGEA_ phnN	1.367993558	0.00105676	Ribose 1,5-bisphosphate	2.7.4.23	phnN	Catalyzes the phosphorylation of
MNLKPGEA_ MNLKPGEA	1.36766209	0.02612784	hypothetical protein	NA	0	serine threonine protein kinase
MNLKPGEA_ MNLKPGEA	1.365203957	0.11500926	hypothetical protein	NA	0	DoxX family
MNLKPGEA_ MNLKPGEA	1.363598417	3.71E-05	hypothetical protein	NA	ybeL	Zinc-ribbon containing domain
MNLKPGEA_ speA	1.363525086	3.51E-09	Biosynthetic arginine de	4.1.1.19	speA	Catalyzes the biosynthesis of ag
MNLKPGEA_ MNLKPGEA	1.363321785	0.1727474	hypothetical protein	NA	#N/A	#N/A
MNLKPGEA_ otsB	1.361367055	4.84E-05	Trehalose-6-phosphate p	3.1.3.12	otsB	Removes the phosphate from tr
MNLKPGEA_ MNLKPGEA	1.356418331	NA	hypothetical protein	NA	0	Domain of unknown function (DU
MNLKPGEA_ chbC	1.355605131	NA	PTS system N,N'-diacety	NA	celB	The phosphoenolpyruvate-deper
MNLKPGEA_ klcA_2	1.353939944	1.49E-10	Antirestriction protein Kl	NA	0	Antirestriction protein
MNLKPGEA_ pfkB	1.351502823	9.17E-07	ATP-dependent 6-phospl	2.7.1.11	pfkB	belongs to the carbohydrate kina
MNLKPGEA_ oxyR_2	1.351373547	6.93E-05	Hydrogen peroxide-induc	NA	oxyR_3	transcriptional regulator
MNLKPGEA_ yjfF	1.34971449	0.07855486	Inner membrane ABC tra	NA	yjfF	Belongs to the binding-protein-d
MNLKPGEA_ rbsA_4	1.349044159	NA	Ribose import ATP-bindi	7.5.2.7	rbsA	import. Responsible for energy c
MNLKPGEA_ ydgJ_1	1.347662659	0.00112891	putative oxidoreductase	1.-.-.-	ydgJ	oxidoreductase
MNLKPGEA_ MNLKPGEA	1.347061116	0.08374568	hypothetical protein	NA	yjcE	NhaP-type Na H and K H antiport
MNLKPGEA_ rluC	1.346949752	9.94E-05	Ribosomal large subunit	5.4.99.24	rluC	Responsible for synthesis of pse
MNLKPGEA_ MNLKPGEA	1.34467429	NA	IS3 family transposase IS	NA	0	Transposase and inactivated der
MNLKPGEA_ rffG	1.343707525	0.00108108	dTDP-glucose 4,6-dehydr	4.2.1.46	rffG	Belongs to the NAD(P)-depender
MNLKPGEA_ MNLKPGEA	1.343095721	7.43E-06	hypothetical protein	NA	katN	Mn-containing catalase
MNLKPGEA_ MNLKPGEA	1.342140848	NA	hypothetical protein	NA	#N/A	#N/A
MNLKPGEA_ phrB	1.340052716	0.00017159	Deoxyribodipyrimidine pl	4.1.99.3	phrB	Belongs to the DNA photolyase f
MNLKPGEA_ rraA	1.338989476	1.67E-06	Regulator of ribonucleas	NA	rraA	Catalyzes the aldol cleavage of 4
MNLKPGEA_ grxD	1.336198503	0.00072632	Glutaredoxin 4	NA	grxD	Belongs to the glutaredoxin fam
MNLKPGEA_ clpS	1.336001146	9.48E-09	ATP-dependent Clp prote	NA	clpS	Involved in the modulation of th
MNLKPGEA_ dgcP	1.333108391	2.82E-06	Diguanylate cyclase DgcI	2.7.7.65	yeaP	Diguanylate cyclase
MNLKPGEA_ ydfZ	1.332853603	0.00014165	Putative selenoprotein Y	NA	ydfZ_1	selenium-binding protein YdfZ
MNLKPGEA_ MNLKPGEA	1.331603227	8.54E-05	hypothetical protein	NA	0	transcriptional regulator
MNLKPGEA_ ynfE_1	1.330860813	NA	Putative dimethyl sulfoxi	1.8.99.-	ynfE	Belongs to the prokaryotic molyb

MNLKPGEA_ MNLKPGEA	1.330495666	4.64E-07	hypothetical protein	NA	0	Phage Mu protein F like protein
MNLKPGEA_ kgtP_1	1.330401219	0.01347212	Alpha-ketoglutarate per	NA	kgtP	transporter
MNLKPGEA_ gcvA_2	1.326857751	NA	Glycine cleavage system	NA	gcvA	transcriptional regulator
MNLKPGEA_ uxuA_1	1.323944101	0.02988465	Mannonate dehydratase	4.2.1.8	uxuA	Catalyzes the dehydration of D-r
MNLKPGEA_ ybeM	1.323875163	0.00020215	Deaminated glutathione	3.5.1.128	ybeM	Nitrilase cyanide hydratase and
MNLKPGEA_ cpoB	1.323659667	2.75E-07	Cell division coordinator	NA	cpoB	Mediates coordination of peptid
MNLKPGEA_ putP	1.322207047	0.03445069	Sodium/proline symport	NA	putP	Belongs to the sodium solute sy
MNLKPGEA_ hcaR_1	1.320577064	5.49E-07	Hca operon transcription	NA	ynfL	transcriptional regulator
MNLKPGEA_ csrA	1.32050193	2.41E-07	Carbon storage regulato	NA	csrA	Could accelerate the degradatio
MNLKPGEA_ yfcJ_2	1.319644828	0.04861015	putative MFS-type trans	NA	yajR_1	Major facilitator Superfamily
MNLKPGEA_ MNLKPGEA	1.31916093	0.01788841	hypothetical protein	NA	0	ParD-like antitoxin of type II bac
MNLKPGEA_ yebE	1.310140521	2.09E-05	Inner membrane protein	NA	yebE	Protein of unknown function (DU
MNLKPGEA_ MNLKPGEA	1.309389636	NA	hypothetical protein	NA	#N/A	#N/A
MNLKPGEA_ MNLKPGEA	1.307689812	NA	putative protein	NA	glpQ1	glycerophosphoryl diester phosp
MNLKPGEA_ nudC	1.307252749	6.71E-05	NADH pyrophosphatase	3.6.1.22	nudC	nadh pyrophosphatase
MNLKPGEA_ bioH	1.306323282	NA	Pimeloyl-[acyl-carrier pr	3.1.1.85	bioH	The physiological role of BioH is
MNLKPGEA_ sotB_2	1.306299525	NA	Sugar efflux transporter	NA	0	Major Facilitator Superfamily
MNLKPGEA_ MNLKPGEA	1.3033817	0.00413568	hypothetical protein	NA	0	Caudovirales tail fibre assembly
MNLKPGEA_ lamB_3	1.300893415	NA	Maltoporin	NA	0	maltodextrin transmembrane tr
MNLKPGEA_ MNLKPGEA	1.300696242	0.00016268	hypothetical protein	NA	#N/A	#N/A
MNLKPGEA_ MNLKPGEA	1.298776087	0.00683544	hypothetical protein	NA	yraR	Nucleoside-diphosphate-sugar e
MNLKPGEA_ MNLKPGEA	1.298732838	6.20E-05	hypothetical protein	NA	yfbV	UPF0208 membrane protein
MNLKPGEA_ argE_2	1.298174188	NA	Acetylornithine deacetyl	3.5.1.16	argE	Belongs to the peptidase M20A
MNLKPGEA_ MNLKPGEA	1.296811749	0.00084406	hypothetical protein	NA	0	Protein involved in biological_pr
MNLKPGEA_ yadV_2	1.296531075	NA	putative fimbrial chaper	NA	0	chaperone
MNLKPGEA_ MNLKPGEA	1.295790189	0.08502679	hypothetical protein	NA	MA20_1	decarboxylase
MNLKPGEA_ MNLKPGEA	1.295660824	0.21121518	hypothetical protein	NA	0	0
MNLKPGEA_ sapA	1.294987127	4.48E-06	Peptide transport peripl	NA	sapA	ABC transporter substrate-bindi
MNLKPGEA_ gltI	1.291954384	0.00029058	Glutamate/aspartate im	NA	gltI	ABC-type amino acid transport s
MNLKPGEA_ MNLKPGEA	1.290326194	0.00055237	Endoglucanase	3.2.1.4	celC	Belongs to the glycosyl hydrolas

MNLKPGEA_	lacC_2	1.290014905	0.13707291	Tagatose-6-phosphate ki	2.7.1.144	fruK	belongs to the carbohydrate kina
MNLKPGEA_	MNLKPGEA	1.289498979	0.00153462	hypothetical protein	NA	0	PAAR repeat-containing protein
MNLKPGEA_	acrZ	1.289300236	NA	Multidrug efflux pump a	NA	acrZ	drug transmembrane transporte
MNLKPGEA_	cydB_2	1.288135051	0.00353324	Cytochrome bd-I ubiquin	7.1.1.7	cydB	oxidase subunit
MNLKPGEA_	MNLKPGEA	1.287236473	NA	hypothetical protein	NA	0	luxr family transcriptional regula
MNLKPGEA_	mhpF	1.287157605	NA	Acetaldehyde dehydroge	1.2.1.10	mhpF	Catalyzes the conversion of acet
MNLKPGEA_	ssuE	1.286802661	NA	FMN reductase (NADPH)	1.5.1.38	ssuE	fmn reductase
MNLKPGEA_	MNLKPGEA	1.286528394	NA	hypothetical protein	NA	S	virion morphogenesis protein
MNLKPGEA_	ybdM	1.286070743	NA	putative protein YbdM	NA	ybdM	ParB-like nuclease domain
MNLKPGEA_	MNLKPGEA	1.284899453	NA	hypothetical protein	NA	0	protein conserved in bacteria
MNLKPGEA_	exuT_1	1.284580369	0.10677635	Hexuronate transporter	NA	0	Major facilitator superfamily
MNLKPGEA_	MNLKPGEA	1.28393333	NA	hypothetical protein	NA	0	NAD FAD-binding protein
MNLKPGEA_	yejG	1.282288175	0.01213962	putative protein YejG	NA	yejG	YejG-like protein
MNLKPGEA_	yjjQ	1.281230416	NA	Putative transcription fa	NA	yjjQ	regulator
MNLKPGEA_	rbsC_3	1.281113818	NA	Ribose import permease	NA	rbsC_3	Belongs to the binding-protein-d
MNLKPGEA_	MNLKPGEA	1.280250874	NA	hypothetical protein	NA	0	outer membrane
MNLKPGEA_	ugpQ	1.274818891	NA	Glycerophosphodiester p	3.1.4.46	ugpQ	glycerophosphoryl diester phosp
MNLKPGEA_	pmbA	1.274163075	1.16E-05	Metalloprotease PmbA	3.4.-.-	pmbA	Protease involved in proteolytic
MNLKPGEA_	MNLKPGEA	1.273677059	5.57E-06	hypothetical protein	NA	higA-2	Helix-turn-helix domain
MNLKPGEA_	MNLKPGEA	1.273514421	0.16800891	hypothetical protein	NA	0	0
MNLKPGEA_	MNLKPGEA	1.273338048	0.00689195	hypothetical protein	NA	0	Hemin uptake protein
MNLKPGEA_	erpA	1.271761454	1.49E-10	Iron-sulfur cluster inserti	NA	erpA	iron--sulfur cluster insertion prot
MNLKPGEA_	MNLKPGEA	1.270239822	0.01733249	hypothetical protein	NA	ypeC	Protein of unknown function (DU
MNLKPGEA_	umuC_5	1.269543961	0.11456291	Protein UmuC	NA	umuC	DNA polymerase
MNLKPGEA_	MNLKPGEA	1.26628738	NA	hypothetical protein	NA	#N/A	#N/A
MNLKPGEA_	umuC_4	1.266027697	0.2099743	Protein UmuC	NA	umuC	Binds processed UmuD protein t
MNLKPGEA_	MNLKPGEA	1.265654931	9.17E-06	hypothetical protein	NA	0	0
MNLKPGEA_	MNLKPGEA	1.263685999	0.00045406	hypothetical protein	NA	ats	acetyltransferase
MNLKPGEA_	MNLKPGEA	1.263541104	NA	hypothetical protein	NA	#N/A	#N/A
MNLKPGEA_	frlB_1	1.263533908	0.00052842	Fructosamine deglycase	3.5.-.-	0	SIS domain

MNLKPGEA_ ynfM	1.262933378	0.00039586	Inner membrane transpc	NA	ynfM	Major facilitator Superfamily
MNLKPGEA_ ruvB	1.262302368	5.87E-05	Holliday junction ATP-de	3.6.4.12	ruvB	The RuvA-RuvB complex in the p
MNLKPGEA_ yegT	1.260346135	NA	Putative nucleoside tran	NA	yegT	Broad-specificity transporter of
MNLKPGEA_ sotB_3	1.25952779	0.05241043	sugar efflux transporter	NA	ynfM_3	Major facilitator Superfamily
MNLKPGEA_ scrY_2	1.256187357	0.01006208	Sucrose porin	NA	0	Maltoporin (phage lambda and r
MNLKPGEA_ MNLKPGEA	1.25444049	0.19033486	hypothetical protein	NA	0	Phosphotransferase System
MNLKPGEA_ wrbA	1.254047976	0.00157527	NAD(P)H dehydrogenase	1.6.5.2	wrbA	Belongs to the WrbA family
MNLKPGEA_ chbA_3	1.251363703	0.07011441	PTS system N,N'-diacety	NA	0	PTS system, Lactose/Cellobiose
MNLKPGEA_ acoR	1.250896032	0.01504851	Acetoin dehydrogenase (	NA	acoR	transcriptional regulator
MNLKPGEA_ MNLKPGEA	1.250130959	NA	hypothetical protein	NA	0	Antioxidant protein with alkyl hy
MNLKPGEA_ yohK_2	1.249959498	NA	Inner membrane protein	NA	lrgB	effector of murein hydrolase
MNLKPGEA_ fdnG_1	1.245613906	0.22191083	Formate dehydrogenase	1.17.5.3	fdnG	Sulfate ABC transporter substrat
MNLKPGEA_ yqgF	1.244617218	0.00042209	Putative pre-16S rRNA n	3.1.-.-	yqgF	Could be a nuclease involved in p
MNLKPGEA_ smvA	1.243783753	NA	Methyl viologen resistan	NA	smvA	Major facilitator superfamily
MNLKPGEA_ MNLKPGEA	1.241172139	NA	hypothetical protein	NA	0	portal protein
MNLKPGEA_ yebV	1.240826508	1.63E-05	putative protein YebV	NA	yebV	Protein of unknown function (DU
MNLKPGEA_ MNLKPGEA	1.240332083	2.66E-07	hypothetical protein	NA	yjgR	ATP-binding protein
MNLKPGEA_ MNLKPGEA	1.238765047	NA	hypothetical protein	NA	0	0
MNLKPGEA_ helD	1.238015635	3.22E-05	DNA helicase IV	3.6.4.12	helD	DNA helicase
MNLKPGEA_ MNLKPGEA	1.235844379	NA	6-deoxy-6-sulfogluconol	3.1.1.99	0	gluconolactonase
MNLKPGEA_ citB_2	1.235069654	0.01467754	Transcriptional regulator	NA	citB	transcriptional regulatory protei
MNLKPGEA_ fdnI	1.231222827	0.00844047	Formate dehydrogenase	NA	fdnI	formate dehydrogenase
MNLKPGEA_ ubiB	1.230096266	7.21E-08	putative protein kinase U	2.7.-.-	ubiB	Is probably a protein kinase regu
MNLKPGEA_ frcA_2	1.229543132	0.00185945	Fructose import ATP-bin	7.5.2.-	0	(ABC) transporter
MNLKPGEA_ rnd	1.228255693	0.1222743	Ribonuclease D	3.1.13.5	rnd	Exonuclease involved in the 3' pr
MNLKPGEA_ fpr	1.227950387	0.03027926	Flavodoxin/ferredoxin--N	1.18.1.2	fpr	COG1018 Flavodoxin reductases
MNLKPGEA_ MNLKPGEA	1.226885846	0.06953784	hypothetical protein	NA	0	Protein of unknown function (DU
MNLKPGEA_ occP	1.225093279	NA	Octopine permease ATP-	NA	0	abc transporter atp-binding prot
MNLKPGEA_ eutB_2	1.223157701	0.00661112	Ethanolamine ammonia-	4.3.1.7	eutB	With EutC catalyzes the formati
MNLKPGEA_ rhaS_12	1.222772906	0.00205652	HTH-type transcriptional	NA	0	transcriptional regulator

MNLKPGEA_	MNLKPGEA	1.2209641	3.80E-08	hypothetical protein	NA	yicC	Stress-induced protein
MNLKPGEA_	yiaW_1	1.219424176	0.00651436	Inner membrane protein	NA	yiaW	Protein of unknown function (DU
MNLKPGEA_	pckA_1	1.218384637	6.09E-08	Phosphoenolpyruvate ca	4.1.1.49	pckA	Involved in the gluconeogenesis.
MNLKPGEA_	mscL	1.216242244	1.17E-07	Large-conductance mecl	NA	mscL	Channel that opens in response t
MNLKPGEA_	sseA	1.215998757	1.46E-05	3-mercaptopyruvate sulf	2.8.1.2	sseA	sulfurtransferase
MNLKPGEA_	nagC_2	1.213547486	9.95E-05	N-acetylglucosamine rep	NA	nagC	Regulates the synthesis of gluco
MNLKPGEA_	treS	1.212740055	0.00159242	Trehalose synthase/amy	3.2.1.1	0	COG0366 Glycosidases
MNLKPGEA_	dmsB_2	1.212225305	NA	Anaerobic dimethyl sulfo	NA	dmsB	reductase chain B
MNLKPGEA_	MNLKPGEA	1.211073756	NA	hypothetical protein	NA	0	(ABC) transporter
MNLKPGEA_	ttuB_4	1.211039552	0.15877339	Putative tartrate transpo	NA	0	Major facilitator superfamily
MNLKPGEA_	polB	1.209082675	7.08E-05	DNA polymerase II	2.7.7.7	polB	DNA polymerase
MNLKPGEA_	ubiA	1.206590882	0.20647218	4-hydroxybenzoate octap	2.5.1.39	ubiA	Catalyzes the prenylation of para
MNLKPGEA_	nqrF	1.206344916	0.00042349	Na(+)-translocating NAD	7.2.1.1	nqrF	NQR complex catalyzes the redu
MNLKPGEA_	nei	1.205980003	NA	Endonuclease 8	3.2.2.-	nei	Involved in base excision repair o
MNLKPGEA_	phoE	1.200764736	0.03293064	Outer membrane porin F	NA	phoE	Belongs to the Gram-negative p
MNLKPGEA_	MNLKPGEA	1.197327013	0.09060046	hypothetical protein	NA	0	response regulator
MNLKPGEA_	ihfA	1.194892579	7.54E-05	Integration host factor su	NA	himA	This protein is one of the two su
MNLKPGEA_	MNLKPGEA	1.19464391	0.0192123	hypothetical protein	NA	acdP	Zn-dependent dipeptidase, micr
MNLKPGEA_	yajO_4	1.192427835	0.00012882	1-deoxyxylulose-5-phosp	1.1.-.-	yajO	Aldo keto reductase
MNLKPGEA_	MNLKPGEA	1.192361489	0.0637612	hypothetical protein	NA	0	Transposase
MNLKPGEA_	phnU	1.192041876	NA	Putative 2-aminoethylph	NA	phnU	Binding-protein-dependent trans
MNLKPGEA_	MNLKPGEA	1.191613157	0.10629982	hypothetical protein	NA	0	extensin
MNLKPGEA_	MNLKPGEA	1.190426923	0.00489408	hypothetical protein	NA	gbuR	transcriptional regulator
MNLKPGEA_	rhaD	1.189278741	NA	Rhamnulose-1-phosphat	4.1.2.19	rhaD	Catalyzes the reversible cleavag
MNLKPGEA_	MNLKPGEA	1.187027233	2.92E-10	hypothetical protein	NA	ecnB	Entericidin EcnA/B family
MNLKPGEA_	MNLKPGEA	1.185524995	0.04169052	hypothetical protein	NA	yjjA	Glycoprotein Receptor
MNLKPGEA_	dcuD	1.184504406	0.00105676	Putative cryptic C4-dicar	NA	dcuC	C4-dicarboxylate
MNLKPGEA_	MNLKPGEA	1.183537935	0.00189994	hypothetical protein	NA	0	0
MNLKPGEA_	hxpA	1.181164243	0.08005385	Hexitol phosphatase A	3.1.3.22	yfbT	Phosphatase
MNLKPGEA_	mdtA_4	1.178739607	0.00125456	Multidrug resistance pro	NA	0	Belongs to the membrane fusion

MNLKPGEA_	MNLKPGEA	1.178589904	0.00078548	hypothetical protein	NA	mpr	SprT-like family
MNLKPGEA_	lysA	1.1765452	0.11428674	Diaminopimelate decarb	4.1.1.20	lysA	Specifically catalyzes the decarb
MNLKPGEA_	uraA	1.176261725	0.01233011	Uracil permease	NA	uraA	Xanthine uracil
MNLKPGEA_	MNLKPGEA	1.17538936	0.00281682	hypothetical protein	NA	0	conserved small protein
MNLKPGEA_	codA_2	1.172596075	NA	Cytosine deaminase	3.5.4.1	codA	cytosine deaminase
MNLKPGEA_	MNLKPGEA	1.172484027	0.01396671	hypothetical protein	NA	#N/A	#N/A
MNLKPGEA_	pgl_2	1.171091011	0.02989287	6-phosphogluconolacton	3.1.1.31	ykgB	COG2706 3-carboxymuconate cy
MNLKPGEA_	lacI_2	1.170425075	0.0012059	Lactose operon represso	NA	lacI	binds specific sites in lac operon
MNLKPGEA_	rbsK_2	1.170150278	0.24861382	Ribokinase	2.7.1.15	rbsK	Catalyzes the phosphorylation of
MNLKPGEA_	tldD	1.169451315	6.48E-09	Metalloprotease TldD	3.4.-.-	tldD	'responsible for the proteolytic r
MNLKPGEA_	MNLKPGEA	1.16869077	0.01945821	hypothetical protein	NA	0	0
MNLKPGEA_	MNLKPGEA	1.168442036	0.20850177	hypothetical protein	NA	0	HNH nucleases
MNLKPGEA_	dsdC_2	1.168112179	0.12850938	HTH-type transcriptional	NA	0	transcriptional regulator
MNLKPGEA_	rob_2	1.166205119	0.00524884	Right origin-binding prot	NA	ykgA	transcriptional regulator
MNLKPGEA_	yshB	1.164462395	0.00091295	putative protein YshB	NA	#N/A	#N/A
MNLKPGEA_	MNLKPGEA	1.163315093	0.0082316	hypothetical protein	NA	#N/A	#N/A
MNLKPGEA_	MNLKPGEA	1.162827026	0.25356654	hypothetical protein	NA	0	Bacterial regulatory proteins, te
MNLKPGEA_	ilvI_1	1.162110254	0.00149054	Acetolactate synthase is	2.2.1.6	0	COG0028 Thiamine pyrophospha
MNLKPGEA_	MNLKPGEA	1.160774977	0.00362492	hypothetical protein	NA	0	0
MNLKPGEA_	ydjA	1.15851875	0.00204857	Putative NAD(P)H nitrore	1.-.-.-	ydjA	Nitroreductase
MNLKPGEA_	nanE	1.157707537	0.01335391	Putative N-acetylmanno	5.1.3.9	nanE	Converts N-acetylmannosamine-
MNLKPGEA_	MNLKPGEA	1.156801751	0.10411839	hypothetical protein	NA	#N/A	#N/A
MNLKPGEA_	lsrR	1.154647313	0.00156657	Transcriptional regulator	NA	lsrR	transcriptional regulator
MNLKPGEA_	MNLKPGEA	1.153884274	0.01846996	hypothetical protein	NA	yiiR	Membrane
MNLKPGEA_	edcC	1.153024187	NA	Phenolic acid decarboxyl	4.1.1.61	vdcC	Decarboxylase involved in the de
MNLKPGEA_	yadV_3	1.153024187	NA	putative fimbrial chaper	NA	0	Pili assembly chaperone PapD, C
MNLKPGEA_	bauC	1.152869257	0.08511045	Putative 3-oxopropanoat	1.2.1.-	mmsA	Methylmalonate-semialdehyde (
MNLKPGEA_	MNLKPGEA	1.152215308	0.06845311	hypothetical protein	NA	0	0
MNLKPGEA_	hpf	1.151144679	0.0005928	Ribosome hibernation pr	NA	hpf	sigma (54) modulation protein
MNLKPGEA_	glgS_2	1.148835089	0.00080721	Surface composition reg	NA	glgS	positive regulation of cellular ca

MNLKPGEA_ nemA	1.14854414	0.2358048	N-ethylmaleimide reduc	1.3.1.-	nemA	nadh flavin
MNLKPGEA_ yofA_1	1.148125636	NA	HTH-type transcriptional	NA	cysL_1	transcriptional regulator
MNLKPGEA_ ygaP	1.14705749	NA	Inner membrane protein	NA	ygaP	SMART Rhodanese domain prot
MNLKPGEA_ fepA_2	1.146971953	0.00913306	Ferrienterobactin recept	NA	fepA	Receptor
MNLKPGEA_ pcaR_2	1.145455658	0.23940281	Pca regulon regulatory p	NA	pcaR	transcriptional regulator
MNLKPGEA_ lptG	1.144910201	0.00159242	Lipopolysaccharide expo	NA	lptG	permease
MNLKPGEA_ MNLKPGEA	1.144865434	3.41E-09	hypothetical protein	NA	#N/A	#N/A
MNLKPGEA_ hdfR_2	1.144255685	0.0367703	HTH-type transcriptional	NA	VPA0331	Transcriptional regulator
MNLKPGEA_ setB	1.143035279	NA	Sugar efflux transporter	NA	setB	Major facilitator Superfamily
MNLKPGEA_ cmpR_3	1.141817473	0.05766792	HTH-type transcriptional	NA	yfiE	Transcriptional regulator
MNLKPGEA_ MNLKPGEA	1.139126245	7.20E-06	hypothetical protein	NA	ytfK	Protein of unknown function (DU
MNLKPGEA_ MNLKPGEA	1.138326725	0.2142873	IS3 family transposase IS	NA	0	Transposase and inactivated der
MNLKPGEA_ MNLKPGEA	1.138241757	0.07977507	hypothetical protein	NA	0	tail assembly chaperone
MNLKPGEA_ dksA	1.137686013	0.00185856	RNA polymerase-binding	NA	dksA	Transcription factor that acts by
MNLKPGEA_ gsiD_2	1.136783975	NA	Glutathione transport sy	NA	gsiD	transport
MNLKPGEA_ MNLKPGEA	1.135787448	NA	hypothetical protein	NA	eutT	Cobalamin adenosyltransferase
MNLKPGEA_ yycE	1.134322046	0.03765872	putative protein YycE	NA	yycE	PFAM Glyoxalase bleomycin resi
MNLKPGEA_ MNLKPGEA	1.132257326	0.10696683	hypothetical protein	NA	yajD	endonuclease
MNLKPGEA_ MNLKPGEA	1.129664401	NA	hypothetical protein	NA	braE	Belongs to the binding-protein-d
MNLKPGEA_ MNLKPGEA	1.12900824	0.00205652	hypothetical protein	NA	0	Acetyltransferase
MNLKPGEA_ relE_1	1.128886008	0.04409263	mRNA interferase toxin	3.1.-.-	relE	Cytotoxic translational repressor
MNLKPGEA_ MNLKPGEA	1.124421589	0.04394148	hypothetical protein	NA	0	0
MNLKPGEA_ glgB	1.123525019	9.11E-05	1,4-alpha-glucan branchi	2.4.1.18	glgB	Catalyzes the formation of the a
MNLKPGEA_ MNLKPGEA	1.122637298	0.18782914	hypothetical protein	NA	#N/A	#N/A
MNLKPGEA_ kefG	1.116257276	0.23339116	Glutathione-regulated p	1.6.5.2	nqo2	NADPH dehydrogenase
MNLKPGEA_ pgpA	1.115930193	0.08374568	Phosphatidylglycerophos	3.1.3.27	pgpA	Lipid phosphatase which dephos
MNLKPGEA_ cbl	1.11591994	0.08005385	HTH-type transcriptional	NA	cbl	transcriptional regulator
MNLKPGEA_ rbsA_2	1.115639486	0.18894956	Ribose import ATP-bindi	7.5.2.7	0	ABC transporter
MNLKPGEA_ fieF	1.114606161	2.44E-05	Ferrous-iron efflux pump	NA	fieF	Belongs to the cation diffusion f
MNLKPGEA_ dcyD	1.113986906	0.00444903	D-cysteine desulfhydrase	4.4.1.15	dcyD	Catalyzes the alpha,beta-elimina

MNLKPGEA_ ecpB	1.113953026	NA	putative fimbrial chaper	NA	ecpB	Part of the ecpRABCDE operon, v
MNLKPGEA_ MNLKPGEA	1.113627763	0.05130677	hypothetical protein	NA	0	transcriptional
MNLKPGEA_ tqsA	1.111799072	0.0004764	AI-2 transport protein Tc	NA	tqsA	permease
MNLKPGEA_ actP_1	1.110191408	NA	Cation/acetate symporte	NA	0	Belongs to the sodium solute sy
MNLKPGEA_ lsrB_2	1.108778092	0.0593724	Autoinducer 2-binding pr	NA	lsrB_2	(ABC) transporter
MNLKPGEA_ araE	1.108252231	NA	Arabinose-proton sympo	NA	araE	Major facilitator Superfamily
MNLKPGEA_ MNLKPGEA	1.108020853	0.03012006	hypothetical protein	NA	#N/A	#N/A
MNLKPGEA_ fimD_2	1.10740253	NA	Outer membrane usher p	NA	0	Usher protein
MNLKPGEA_ yeaX_1	1.105683858	0.1238924	Carnitine monooxygenas	1.14.13.239	vanB	Flavodoxin reductases (Ferredox
MNLKPGEA_ MNLKPGEA	1.103756667	NA	hypothetical protein	NA	0	Fimbrial protein
MNLKPGEA_ treF	1.103744167	0.0018687	Cytoplasmic trehalase	3.2.1.28	treF	Provides the cells with the abilit
MNLKPGEA_ sgrR_2	1.102479167	0.01732696	HTH-type transcriptional	NA	sgrR	Activates the small RNA gene sg
MNLKPGEA_ fdnH	1.10205026	0.19325659	Formate dehydrogenase	NA	fdnH	formate dehydrogenase
MNLKPGEA_ MNLKPGEA	1.100680251	NA	hypothetical protein	NA	yneG	Domain of unknown function (DU
MNLKPGEA_ livH_1	1.100586462	NA	High-affinity branched-c	NA	livH	Belongs to the binding-protein-d
MNLKPGEA_ yegS	1.10041705	0.00165308	putative lipid kinase Yeg	2.7.1.-	yegS	the in vivo substrate is
MNLKPGEA_ erfK	1.099149829	4.76E-05	putative L,D-transpeptid	2.-.-.-	erfK	Catalyzes th removal of D-alanir
MNLKPGEA_ MNLKPGEA	1.097793774	0.0001399	hypothetical protein	NA	0	0
MNLKPGEA_ yggR	1.097500074	NA	putative protein YggR	NA	pilT	twitching motility protein
MNLKPGEA_ fadA	1.096981638	0.00023784	3-ketoacyl-CoA thiolase	2.3.1.16	fadA	Catalyzes the final step of fatty a
MNLKPGEA_ argP_2	1.095397633	0.28928657	HTH-type transcriptional	NA	nac	transcriptional regulator
MNLKPGEA_ hcxA	1.094577772	NA	Hydroxycarboxylate dehy	1.1.1.-	ybdH	Iron-containing alcohol dehydrog
MNLKPGEA_ MNLKPGEA	1.093304482	0.00114473	hypothetical protein	NA	0	Enoyl-(Acyl carrier protein) redu
MNLKPGEA_ rhmA	1.092569501	0.28608192	2-keto-3-deoxy-L-rhamn	4.1.2.53	rhmA	Belongs to the HpcH HpaI aldola
MNLKPGEA_ MNLKPGEA	1.091622601	NA	hypothetical protein	NA	gpJ	baseplate assembly protein
MNLKPGEA_ MNLKPGEA	1.091059149	NA	hypothetical protein	NA	0	Domain of unknown function (DU
MNLKPGEA_ MNLKPGEA	1.090826947	NA	hypothetical protein	NA	0	0
MNLKPGEA_ gmuD_1	1.089732336	0.03421676	6-phospho-beta-glucosic	3.2.1.86	celH	Belongs to the glycosyl hydrolas
MNLKPGEA_ MNLKPGEA	1.087667185	0.03761699	hypothetical protein	NA	0	0
MNLKPGEA_ rsmD	1.085825558	0.03508713	Ribosomal RNA small su	2.1.1.171	rsmD	Specifically methylates the guar

MNLKPGEA_	sapB	1.085721514	0.02382585	Putrescine export systen	NA	sapB	peptide transport system, perme
MNLKPGEA_	MNLKPGEA	1.083204782	0.00948678	hypothetical protein	NA	yjiN	Membrane
MNLKPGEA_	fucI	1.081660391	NA	L-fucose isomerase	5.3.1.25	fucI	Converts the aldose L-fucose int
MNLKPGEA_	hypB	1.079519091	NA	Hydrogenase maturatior	NA	hypB	Hydrogenase accessory protein H
MNLKPGEA_	MNLKPGEA	1.079444264	0.28622319	hypothetical protein	NA	0	0
MNLKPGEA_	MNLKPGEA	1.07912261	NA	hypothetical protein	NA	0	Bacterial alpha-L-rhamnosidase
MNLKPGEA_	MNLKPGEA	1.078940436	0.01176393	hypothetical protein	NA	marC	UPF0056 membrane protein
MNLKPGEA_	MNLKPGEA	1.077740839	NA	hypothetical protein	NA	gpD	late control
MNLKPGEA_	rlmE	1.076000962	0.00012015	Ribosomal RNA large su	2.1.1.166	ftsJ	Specifically methylates the uridi
MNLKPGEA_	MNLKPGEA	1.075335411	0.00185212	hypothetical protein	NA	0	Diguanylate cyclase
MNLKPGEA_	pulD	1.074178834	0.32479671	Secretin PulD	NA	gspD	General Secretion Pathway prot
MNLKPGEA_	nikD	1.07230408	NA	Nickel import ATP-bindir	7.2.2.11	nikD	Part of the ABC transporter com
MNLKPGEA_	MNLKPGEA	1.071721441	NA	hypothetical protein	NA	arsR	transcriptional regulator
MNLKPGEA_	MNLKPGEA	1.069388994	0.0175668	hypothetical protein	NA	0	Phage derived protein Gp49-like
MNLKPGEA_	fbaA_2	1.069101311	0.20861883	putative fructose-bispho	4.1.2.13	0	Aldolase
MNLKPGEA_	MNLKPGEA	1.068814841	NA	hypothetical protein	NA	0	Membrane
MNLKPGEA_	gltC_1	1.067983974	0.16397629	HTH-type transcriptional	NA	allS_3	Transcriptional regulator
MNLKPGEA_	MNLKPGEA	1.067477116	8.10E-05	hypothetical protein	NA	msyB	SecY secA suppressor protein
MNLKPGEA_	astE_2	1.067171136	0.07664422	Succinylglutamate desuc	3.5.1.96	astE	Belongs to the AspA AstE family
MNLKPGEA_	fadD	1.067054564	0.00730926	Long-chain-fatty-acid--C	6.2.1.3	fadD	COG0318 Acyl-CoA synthetases (
MNLKPGEA_	MNLKPGEA	1.064366803	0.00193965	hypothetical protein	NA	0	Diguanylate cyclase
MNLKPGEA_	ureG	1.063934886	0.25930143	Urease accessory protein	NA	ureG	Facilitates the functional incorpo
MNLKPGEA_	MNLKPGEA	1.063875229	0.12299617	hypothetical protein	NA	0	PFAM GCN5-related N-acetyltra
MNLKPGEA_	MNLKPGEA	1.063769154	0.00018807	hypothetical protein	NA	0	0
MNLKPGEA_	dmsA_1	1.062717807	0.14294542	Dimethyl sulfoxide reduc	1.8.5.3	dmsA	Belongs to the prokaryotic molyb
MNLKPGEA_	opuE	1.057022823	NA	Osmoregulated proline t	NA	VVA1143	Belongs to the sodium solute sy
MNLKPGEA_	gabT	1.056709568	0.00523583	4-aminobutyrate aminot	2.6.1.19	gabT	Belongs to the class-III pyridoxal
MNLKPGEA_	MNLKPGEA	1.056105183	0.04361157	hypothetical protein	NA	ygdD	Small membrane protein
MNLKPGEA_	sixA	1.054996571	0.00505999	Phosphohistidine phosph	3.1.3.-	sixA	phosphohistidine phosphatase
MNLKPGEA_	dapB	1.052776949	0.0106095	4-hydroxy-tetrahydrodipi	1.17.1.8	dapB	Catalyzes the conversion of 4-hy

MNLKPGEA_	patA	1.051298784	0.00495727	Putrescine aminotransfe	2.6.1.82	patA	Catalyzes the aminotransferase
MNLKPGEA_	MNLKPGEA	1.050970987	NA	hypothetical protein	NA	#N/A	#N/A
MNLKPGEA_	fhuC_1	1.05021793	NA	Iron(3+)-hydroxamate im	7.2.2.16	fecE	(ABC) transporter
MNLKPGEA_	cat3	1.046379266	0.15381821	Chloramphenicol acetylt	2.3.1.28	cat	This enzyme is an effector of chl
MNLKPGEA_	ygeA	1.046126795	0.08183421	L-aspartate/glutamate-s	5.1.1.13	ygeA	Belongs to the aspartate glutam
MNLKPGEA_	MNLKPGEA	1.045165494	0.2343975	putative transporter	NA	ynfM_2	Major facilitator Superfamily
MNLKPGEA_	alkA	1.044978374	0.16586139	DNA-3-methyladenine gl	3.2.2.21	alkA	3-methyladenine DNA glycosylas
MNLKPGEA_	speD	1.044801189	0.01602154	S-adenosylmethionine d	4.1.1.50	speD	Catalyzes the decarboxylation of
MNLKPGEA_	xerC_3	1.04470216	0.00018288	Tyrosine recombinase Xe	NA	0	Phage integrase family
MNLKPGEA_	MNLKPGEA	1.041655154	0.03023814	hypothetical protein	NA	yeaE	Aldo keto
MNLKPGEA_	cpxP	1.04163506	1.77E-08	Periplasmic protein CpxP	NA	cpxP	Repressor of the Cpx envelope st
MNLKPGEA_	ecoRIIR	1.03843443	9.20E-07	Type-2 restriction enzym	3.1.21.4	0	EcoRII C terminal
MNLKPGEA_	MNLKPGEA	1.037296564	0.08006215	putative protein	NA	Z012_123	Phage terminase large subunit
MNLKPGEA_	malE	1.034411199	0.1207877	Maltose/maltodextrin-bi	NA	malE	Bacterial extracellular solute-bir
MNLKPGEA_	MNLKPGEA	1.032622479	1.15E-05	hypothetical protein	NA	0	transcriptional regulator
MNLKPGEA_	hfq	1.031690028	4.81E-06	RNA-binding protein Hfq	NA	hfq	RNA chaperone that binds small
MNLKPGEA_	pncC_2	1.028138728	0.04736174	Nicotinamide-nucleotide	3.5.1.42	yfaY	Belongs to the CinA family
MNLKPGEA_	pgaC	1.026834151	NA	Poly-beta-1,6-N-acetyl-D	2.4.1.-	pgaC	Poly-beta-1,6-N-acetyl-D-glucosa
MNLKPGEA_	MNLKPGEA	1.026515557	0.31896731	hypothetical protein	NA	livM	Belongs to the binding-protein-d
MNLKPGEA_	rcnA	1.026385827	NA	Nickel/cobalt efflux syst	NA	rcnA	Belongs to the NiCoT transporte
MNLKPGEA_	hns	1.02566889	3.59E-05	DNA-binding protein H-N	NA	hns	Belongs to the histone-like prote
MNLKPGEA_	MNLKPGEA	1.023741424	NA	hypothetical protein	NA	0	Putative inner membrane export
MNLKPGEA_	MNLKPGEA	1.023726588	NA	hypothetical protein	NA	0	0
MNLKPGEA_	MNLKPGEA	1.02328457	NA	hypothetical protein	NA	0	glyoxalase bleomycin resistance
MNLKPGEA_	MNLKPGEA	1.022785269	0.00865625	hypothetical protein	NA	yniB	Membrane
MNLKPGEA_	birA	1.022463099	NA	Bifunctional ligase/repre	6.3.4.15	birA	Acts both as a biotin-- acetyl-CoA
MNLKPGEA_	yhaJ_2	1.02174908	0.0142401	HTH-type transcriptional	NA	yeeY	transcriptional regulator
MNLKPGEA_	gltR_2	1.021706508	NA	HTH-type transcriptional	NA	yneJ	Transcriptional regulator
MNLKPGEA_	hpxW	1.021482171	NA	Oxamate amidohydrolas	3.5.1.126	ggt	Gamma-glutamyltransferase
MNLKPGEA_	MNLKPGEA	1.021231691	3.07E-05	hypothetical protein	NA	0	0

MNLKPGEA_ sfnC	1.01922812	NA	putative FMNH2-depend	1.14.14.-	soxC	acyl-CoA dehydrogenase
MNLKPGEA_ pcaG	1.019127029	0.32571875	Protocatechuate 3,4-dio	1.13.11.3	pcaG	protocatechuate 3,4-dioxygenas
MNLKPGEA_ benM_3	1.018433074	0.0082316	HTH-type transcriptional	NA	0	transcriptional regulator
MNLKPGEA_ MNLKPGEA	1.018417985	0.08136237	Protein virB10	NA	0	Bacterial conjugation TrbI-like p
MNLKPGEA_ yfdC	1.018298919	0.00085055	Inner membrane protein	NA	yfdC	Formate nitrite
MNLKPGEA_ sufS	1.017329112	0.00210287	Cysteine desulfurase	2.8.1.7	sufS	Cysteine desulfurases mobilize t
MNLKPGEA_ mdtA_3	1.016555636	0.01956214	Multidrug resistance pro	NA	ttgA	Belongs to the membrane fusio
MNLKPGEA_ cbs	1.015391328	NA	Putative cystathionine b	4.2.1.22	cbs	Belongs to the cysteine synthase
MNLKPGEA_ MNLKPGEA	1.013269072	0.01494629	hypothetical protein	NA	yheT	hydrolase of the alpha beta-hyd
MNLKPGEA_ MNLKPGEA	1.013142209	NA	hypothetical protein	NA	0	0
MNLKPGEA_ scrK_1	1.012910608	0.33229626	Fructokinase	2.7.1.4	scrK	Belongs to the carbohydrate kin
MNLKPGEA_ MNLKPGEA	1.012794724	0.31705872	hypothetical protein	NA	0	0
MNLKPGEA_ abgT	1.012513753	NA	p-aminobenzoyl-glutam	NA	abgT	transporter
MNLKPGEA_ blc_2	1.012295349	0.01381004	Outer membrane lipopr	NA	blc	Outer Membrane Lipoprotein
MNLKPGEA_ yccA	1.012078078	7.83E-05	Modulator of FtsH prote	NA	yccA	Belongs to the BI1 family
MNLKPGEA_ yqjH	1.011764646	0.19193357	NADPH-dependent ferric	1.16.1.9	yqjH	Siderophore-interacting protein
MNLKPGEA_ MNLKPGEA	1.009666552	0.01698362	hypothetical protein	NA	0	ASCH
MNLKPGEA_ gbuA	1.00920671	0.32563976	Guanidinobutyrase	3.5.3.7	speB	Belongs to the arginase family
MNLKPGEA_ bglF_1	1.008962136	0.13680345	PTS system beta-glucosi	NA	ascF	Phosphotransferase System
MNLKPGEA_ MNLKPGEA	1.008184273	0.20045123	hypothetical protein	NA	0	transcriptional regulator
MNLKPGEA_ MNLKPGEA	1.007852318	0.15978169	hypothetical protein	NA	0	Protein of unknown function (DU
MNLKPGEA_ MNLKPGEA	1.006885906	NA	hypothetical protein	NA	0	protein conserved in bacteria
MNLKPGEA_ hin_3	1.005755212	0.0004546	DNA-invertase hin	NA	0	Resolvase, N terminal domain
MNLKPGEA_ MNLKPGEA	1.004226906	0.0244967	hypothetical protein	NA	0	transcriptional regulator
MNLKPGEA_ mpaA	1.003748687	0.00861585	Murein peptide amidase	3.4.17.-	mpaA	Murein peptide amidase A
MNLKPGEA_ gcvA_4	1.003469573	0.0411687	Glycine cleavage system	NA	0	Glycine cleavage system transcr
MNLKPGEA_ dusA	1.002792786	0.01587157	tRNA-dihydrouridine(20/	1.3.1.-	dusA	Catalyzes the synthesis of 5,6-di
MNLKPGEA_ intA_4	1.002117341	7.28E-06	Prophage integrase IntA	NA	int	Belongs to the 'phage' integrase
MNLKPGEA_ sorC_3	1.000638318	0.35828896	PTS system sorbose-spe	NA	0	PTS system sorbose-specific iic
MNLKPGEA_ MNLKPGEA	1.000386255	0.03185464	hypothetical protein	NA	0	Helix-turn-helix domain

MNLKPGEA_	rbsC_7	1.000223679	NA	Ribose import permease	NA	MA20_14	Belongs to the binding-protein-d
MNLKPGEA_	soxS_2	0.99892836	0.15657111	Regulatory protein SoxS	NA	soxS	transcriptional regulator
MNLKPGEA_	bhsA_2	0.997224053	0.0269546	Multiple stress resistanc	NA	ybiJ	protein involved in
MNLKPGEA_	setA	0.994539483	0.19842458	Sugar efflux transporter	NA	setA	Major facilitator Superfamily
MNLKPGEA_	MNLKPGEA	0.993177893	0.02633288	hypothetical protein	NA	ycgB	SpoVR family
MNLKPGEA_	pulG	0.993100952	NA	Type II secretion system	NA	gspG	General Secretion Pathway prot
MNLKPGEA_	tehA	0.988253693	0.10255658	Tellurite resistance prote	NA	tehA	PFAM C4-dicarboxylate transpor
MNLKPGEA_	rafA	0.987044409	NA	Alpha-galactosidase	3.2.1.22	rafA	alpha-galactosidase
MNLKPGEA_	budC	0.986834499	0.01035454	Diacetyl reductase [(S)-a	1.1.1.304	budC	COG1028 Dehydrogenases with
MNLKPGEA_	MNLKPGEA	0.986375655	0.00022458	hypothetical protein	NA	yebW	Protein of unknown function (DU
MNLKPGEA_	MNLKPGEA	0.986194578	0.01940737	hypothetical protein	NA	yhaL	0
MNLKPGEA_	MNLKPGEA	0.985119644	0.03479944	hypothetical protein	NA	0	0
MNLKPGEA_	MNLKPGEA	0.985016674	0.16824182	hypothetical protein	NA	yhhM	Protein of unknown function (DU
MNLKPGEA_	yafV	0.983200987	0.00844047	Omega-amidase YafV	3.5.1.3	yafV	Hydrolase
MNLKPGEA_	MNLKPGEA	0.981864668	0.26870218	hypothetical protein	NA	0	transcriptional regulator
MNLKPGEA_	phoB	0.981281778	0.00615876	Phosphate regulon trans	NA	phoB	phosphate regulon transcriptiona
MNLKPGEA_	cysQ	0.979370604	0.0058432	3'(2'),5'-bisphosphate nu	3.1.3.7	cysQ	3'(2'),5'-bisphosphate nucleotida
MNLKPGEA_	pqqB	0.978805215	0.08191724	Coenzyme PQQ synthesis	NA	pqqB	May be involved in the transport
MNLKPGEA_	MNLKPGEA	0.977906035	0.02547568	hypothetical protein	NA	ypfH	Phospholipase Carboxylesterase
MNLKPGEA_	map_1	0.976591524	0.05714107	Methionine aminopeptic	3.4.11.18	map_2	Methionine aminopeptidase
MNLKPGEA_	MNLKPGEA	0.975669245	NA	hypothetical protein	NA	urtB	Belongs to the binding-protein-d
MNLKPGEA_	chbA_2	0.975505688	0.21852772	PTS system N,N'-diacety	NA	celC	PTS system, cellobiose-specific I
MNLKPGEA_	MNLKPGEA	0.975033757	0.02000482	hypothetical protein	NA	#N/A	#N/A
MNLKPGEA_	MNLKPGEA	0.974986188	NA	hypothetical protein	NA	0	enzyme of the cupin superfamily
MNLKPGEA_	pdeG	0.972796888	0.01293658	putative cyclic di-GMP p	3.1.4.52	ycgG	Diguanylate phosphodiesterase
MNLKPGEA_	MNLKPGEA	0.972342075	0.13388853	hypothetical protein	NA	0	YfaZ precursor
MNLKPGEA_	MNLKPGEA	0.969699704	2.62E-05	putative ketoamine kina	2.7.1.-	yniA	Fructosamine kinase
MNLKPGEA_	MNLKPGEA	0.968130393	0.00026862	hypothetical protein	NA	yhjY	outer membrane autotransporte
MNLKPGEA_	scoA	0.967826908	NA	putative succinyl-CoA:3-k	2.8.3.5	scoA	COG1788 Acyl CoA acetate 3-ket
MNLKPGEA_	MNLKPGEA	0.967767563	0.13022199	hypothetical protein	NA	arfA	Domain of unknown function

MNLKPGEA_	phnP	0.965754234	0.31370697	Phosphoribosyl 1,2-cyclic	3.1.4.55	phnP	Carbon-phosphorus lyase comple
MNLKPGEA_	chaA	0.963394377	0.00379407	Sodium-potassium/proto	NA	chaA	Calcium Proton
MNLKPGEA_	nepI_2	0.962134291	0.35080154	Purine ribonucleoside ef	NA	nepI	Major facilitator Superfamily
MNLKPGEA_	MNLKPGEA	0.960639741	0.26043881	hypothetical protein	NA	#N/A	#N/A
MNLKPGEA_	dgcQ	0.960435622	0.03950447	putative diguanylate cycl	2.7.7.65	yedQ	Diguanylate cyclase
MNLKPGEA_	uspG_2	0.960287793	0.01923717	Universal stress protein	NA	uspG_1	Required for resistance to DNA-(
MNLKPGEA_	zapA	0.960008946	0.005809	Cell division protein ZapA	NA	zapA	Activator of cell division through
MNLKPGEA_	recA	0.959612974	0.00046079	Protein RecA	NA	recA	Can catalyze the hydrolysis of AT
MNLKPGEA_	fimD_3	0.959128261	NA	Outer membrane usher p	NA	fimD	outer membrane usher protein
MNLKPGEA_	ttuB_3	0.958085532	0.22455143	Putative tartrate transpo	NA	0	Major Facilitator
MNLKPGEA_	mnaT	0.958080612	0.31211369	L-amino acid N-acyltrans	2.3.1.-	yncA	acetyltransferase
MNLKPGEA_	MNLKPGEA	0.957773814	NA	hypothetical protein	NA	0	0
MNLKPGEA_	dgt	0.954954752	0.00050941	Deoxyguanosinetriphosp	3.1.5.1	dgt	dGTPase preferentially hydrolyze
MNLKPGEA_	MNLKPGEA	0.954865764	0.01433537	hypothetical protein	NA	ypfJ	zinc metallopeptidase
MNLKPGEA_	ytfF	0.953752529	0.25405905	Inner membrane protein	NA	ytfF	Permeases of the drug metaboli
MNLKPGEA_	umuD_5	0.952890329	0.01611527	Protein UmuD	3.4.21.-	umuD	Peptidase S24-like
MNLKPGEA_	yajO_2	0.947903921	0.31510114	1-deoxyxylulose-5-phosp	1.1.-.-	0	aldo keto reductase
MNLKPGEA_	ihfB	0.947875038	0.00262451	Integration host factor su	NA	himD	This protein is one of the two su
MNLKPGEA_	bdcA_2	0.947123742	0.16344394	Cyclic-di-GMP-binding bi	NA	0	COG1028 Dehydrogenases with
MNLKPGEA_	narV	0.947072461	0.20060065	Respiratory nitrate reduc	1.7.5.1	narI	nitrate reductase, gamma subur
MNLKPGEA_	bsmA	0.94603546	0.00122967	Lipoprotein BsmA	NA	bsmA	In Escherichia coli, mutation of t
MNLKPGEA_	MNLKPGEA	0.945676029	0.14869967	hypothetical protein	NA	ytcA	Uncharacterised protein family
MNLKPGEA_	metQ_3	0.944806775	0.31896731	putative D-methionine-b	NA	metQ_2	NLPA lipoprotein
MNLKPGEA_	dsbA	0.939931159	0.00117455	Thiol:disulfide interchan	NA	dsbA	Thiol disulfide interchange prote
MNLKPGEA_	mepS_2	0.939838034	0.03514029	Murein DD-endopeptidas	3.4.-.-	nlpC	COG0791 Cell wall-associated hy
MNLKPGEA_	copA	0.937565033	0.05325585	Copper-exporting P-type	7.2.2.8	copA	P-type atpase
MNLKPGEA_	MNLKPGEA	0.937483969	0.43000708	IS6 family transposase IS	NA	0	Transposase IS66 family
MNLKPGEA_	pheT	0.937291293	3.37E-06	Phenylalanine--tRNA liga	6.1.1.20	pheT	Belongs to the phenylalanyl-tRN
MNLKPGEA_	MNLKPGEA	0.936767646	NA	hypothetical protein	NA	0	Protein of unknown function (DU
MNLKPGEA_	MNLKPGEA	0.934702916	0.0081626	hypothetical protein	NA	kguE	Xylose isomerase domain protei

MNLKPGEA_	MNLKPGEA	0.933458192	0.23638322	hypothetical protein	NA	yeiH	Belongs to the UPF0324 family
MNLKPGEA_	MNLKPGEA	0.932545261	0.06529963	hypothetical protein	NA	0	transcriptional
MNLKPGEA_	MNLKPGEA	0.932057813	NA	ISNCY family transposas	NA	0	PFAM Integrase catalytic
MNLKPGEA_	pdxK	0.931876933	0.15759861	Pyridoxine/pyridoxal/pyr	2.7.1.35	pdxK	Pyridoxal kinase involved in the s
MNLKPGEA_	ygcS	0.931594504	NA	Inner membrane metab	NA	ygcS	Major facilitator superfamily
MNLKPGEA_	MNLKPGEA	0.928034529	NA	hypothetical protein	NA	ptxB	Phosphotransferase system, lact
MNLKPGEA_	fimD_7	0.925834992	0.17507042	Outer membrane usher	NA	0	Usher protein
MNLKPGEA_	fecA	0.924603051	0.05216627	Fe(3+) dicitrate transpor	NA	yncD	receptor
MNLKPGEA_	rluB	0.923763388	0.0047737	Ribosomal large subunit	5.4.99.22	rluB	Belongs to the pseudouridine sy
MNLKPGEA_	celA_2	0.923365381	NA	PTS system cellobiose-sp	2.7.1.205	celA	Phosphotransferase System
MNLKPGEA_	cimH	0.922371299	0.22272994	Citrate/malate transport	NA	cimH	Uptake of citrate across the bou
MNLKPGEA_	zntB_2	0.919540308	0.06884793	Zinc transport protein Zr	NA	zntB	Zinc transport protein zntB
MNLKPGEA_	crr	0.919115523	0.00033814	PTS system glucose-spe	NA	crr	pts system
MNLKPGEA_	suhB_3	0.918445408	0.38240071	Inositol-1-monophospha	3.1.3.25	0	inositol monophosphatase
MNLKPGEA_	MNLKPGEA	0.918336637	0.02975297	hypothetical protein	NA	0	Mechanosensitive ion channel
MNLKPGEA_	yibH_2	0.917781259	0.22802842	Inner membrane protein	NA	yiaV	secretion protein HlyD family
MNLKPGEA_	cbpM	0.917155699	0.22679141	Chaperone modulatory p	NA	cbpM	Interacts with CbpA and inhibits
MNLKPGEA_	kbp	0.916404986	0.27296096	Potassium binding prote	NA	ygaU	peptidoglycan-binding protein
MNLKPGEA_	ghrB	0.915609732	0.02412582	Glyoxylate/hydroxypyruv	1.1.1.79	ghrB	Catalyzes the NADPH-dependent
MNLKPGEA_	MNLKPGEA	0.914710423	0.00787343	hypothetical protein	NA	yceA	Belongs to the UPF0176 family
MNLKPGEA_	MNLKPGEA	0.914700763	NA	hypothetical protein	NA	stbD	Antitoxin component of a toxin-a
MNLKPGEA_	dmlR_11	0.909929267	0.22349801	HTH-type transcriptional	NA	0	Transcriptional regulator
MNLKPGEA_	MNLKPGEA	0.909844334	0.02578781	hypothetical protein	NA	pleD	Diguanylate cyclase
MNLKPGEA_	MNLKPGEA	0.909794021	NA	hypothetical protein	NA	0	LVIVD repeat
MNLKPGEA_	ybdO_1	0.909695535	0.04974389	putative HTH-type transc	NA	ybeF	transcriptional regulator
MNLKPGEA_	bcsG	0.909020955	0.11322418	Cellulose biosynthesis pr	NA	bcsG	cellulose synthase operon protei
MNLKPGEA_	topA_1	0.905898201	0.02146523	DNA topoisomerase 1	5.6.2.1	yrdD	dNA topoisomerase
MNLKPGEA_	glnL	0.904740519	0.08339769	Sensory histidine kinase/	2.7.13.3	glnL	Signal transduction histidine kin
MNLKPGEA_	phnT	0.903541031	NA	Putative 2-aminoethylph	NA	phnT	Belongs to the ABC transporter s
MNLKPGEA_	soxS_1	0.903088874	0.27989898	Regulatory protein SoxS	NA	ramA	Transcriptional regulator

MNLKPGEA_	MNLKPGEA	0.901675131	0.00067402	hypothetical protein	NA	#N/A	#N/A
MNLKPGEA_	tesB	0.900707828	0.04383479	Acyl-CoA thioesterase 2	3.1.2.-	tesB	Acyl-CoA thioesterase
MNLKPGEA_	MNLKPGEA	0.900641594	0.2735426	hypothetical protein	NA	0	SIS domain
MNLKPGEA_	rssB	0.8999353	0.01026396	Regulator of RpoS	NA	rssB	Regulates the turnover of the sig
MNLKPGEA_	yqjG	0.899415251	0.17649102	Glutathionyl-hydroquino	1.8.5.7	yqjG	Glutathione S-Transferase
MNLKPGEA_	yfgD	0.899250793	0.06808741	putative protein YfgD	NA	arsC	arsenate reductase
MNLKPGEA_	rspB	0.899114674	0.39170785	Starvation-sensing prote	1.1.1.-	rspB	Dehydrogenase
MNLKPGEA_	selO	0.898903107	0.0495479	Protein adenylyltransfera	2.7.7.-	ydiU	Belongs to the UPF0061 (SELO)
MNLKPGEA_	xylP	0.897638062	0.09336521	Isoprimeverose transpor	NA	0	COG2211 Na melibiose symport
MNLKPGEA_	MNLKPGEA	0.897402549	0.23679913	hypothetical protein	NA	#N/A	#N/A
MNLKPGEA_	hexR_4	0.895045532	0.03479944	HTH-type transcriptional	NA	0	Transcriptional regulator
MNLKPGEA_	malQ	0.894927693	0.00448607	4-alpha-glucanotransfer	2.4.1.25	malQ	4-alpha-glucanotransferase
MNLKPGEA_	sdaA	0.894722358	0.00571449	L-serine dehydratase 1	4.3.1.17	sdaA	l-serine dehydratase
MNLKPGEA_	uspA	0.894535298	0.00336921	Universal stress protein	NA	uspA	Required for resistance to DNA-
MNLKPGEA_	iraM	0.889760627	0.27919693	Anti-adapter protein IraM	NA	iraM	Inhibits RpoS proteolysis by regu
MNLKPGEA_	cdiA	0.887073956	0.09532816	tRNA nuclease CdiA	3.1.-.-	0	Large exoproteins involved in he
MNLKPGEA_	bglA_3	0.886103266	0.27529135	Aryl-phospho-beta-D-glu	3.2.1.86	0	Belongs to the glycosyl hydrolas
MNLKPGEA_	MNLKPGEA	0.885547614	0.13022199	hypothetical protein	NA	0	0
MNLKPGEA_	yfgJ	0.884364919	0.01040123	putative protein YfgJ	NA	yfgJ	bacterial-type flagellum-depend
MNLKPGEA_	aaeA_1	0.883438243	0.10658995	p-hydroxybenzoic acid ef	NA	aaeA	P-hydroxybenzoic acid efflux pur
MNLKPGEA_	cydB_1	0.881556838	NA	Cytochrome bd-I ubiquin	7.1.1.7	cydB	oxidase subunit
MNLKPGEA_	fhlA	0.881508945	0.02225426	Formate hydrogenlyase t	NA	fhlA	transcriptional regulator
MNLKPGEA_	yhjD	0.881027948	0.03945722	Inner membrane protein	NA	yhjD	Membrane
MNLKPGEA_	rlmM	0.880042444	0.05106827	Ribosomal RNA large su	2.1.1.186	rlmM	Belongs to the class I-like SAM-l
MNLKPGEA_	decR	0.87892735	0.04860662	DNA-binding transcriptic	NA	ybaO	transcriptional regulator
MNLKPGEA_	epd	0.878280662	2.34E-05	D-erythrose-4-phosphate	1.2.1.72	epd	Belongs to the glyceraldehyde-3
MNLKPGEA_	lacY	0.876184221	NA	Lactose permease	NA	0	Major facilitator superfamily
MNLKPGEA_	MNLKPGEA	0.876103609	0.07161737	hypothetical protein	NA	Z012_01	Permeases of the drug metaboli
MNLKPGEA_	MNLKPGEA	0.875984334	0.00819883	hypothetical protein	NA	0	0
MNLKPGEA_	MNLKPGEA	0.875012436	0.02418965	hypothetical protein	NA	yajQ	Belongs to the UPF0234 family

MNLKPGEA_	mntH	0.874935725	0.02413276	Divalent metal cation tra	NA	mntH	H( )-stimulated, divalent metal c
MNLKPGEA_	MNLKPGEA	0.873816986	NA	hypothetical protein	NA	phnD	Phosphonate ABC transporter
MNLKPGEA_	MNLKPGEA	0.871687565	0.04967077	hypothetical protein	NA	#N/A	#N/A
MNLKPGEA_	ufaA1	0.871287019	NA	Tuberculostearic acid me	2.1.1.-	cfa	synthase
MNLKPGEA_	rcsB	0.866498381	0.01381683	Transcriptional regulator	NA	rcsB	Component of the Rcs signaling
MNLKPGEA_	MNLKPGEA	0.866122338	NA	hypothetical protein	NA	0	0
MNLKPGEA_	rluA_2	0.865796757	0.25364981	Dual-specificity RNA pse	5.4.99.28	rluA	Responsible for synthesis of pse
MNLKPGEA_	garD	0.865787431	0.1407788	Galactarate dehydratase	4.2.1.42	garD	Catalyzes the dehydration of gal
MNLKPGEA_	rpmE2	0.865562129	0.1443338	50S ribosomal protein L3	NA	rpmE2	Ribosomal protein L31
MNLKPGEA_	ybaB	0.863662355	0.05501012	Nucleoid-associated prot	NA	ybaB	Binds to DNA and alters its conf
MNLKPGEA_	bglT	0.862705431	0.39711642	6-phospho-beta-glucosic	3.2.1.86	celF	Glycoside hydrolase
MNLKPGEA_	MNLKPGEA	0.860960559	NA	hypothetical protein	NA	0	0
MNLKPGEA_	msuD_2	0.860536353	NA	Methanesulfonate monoc	1.14.14.5	ssuD_2	Alkanesulfonate monooxygenase
MNLKPGEA_	arsH	0.860457966	0.31211369	NADPH-dependent FMN	1.-.-.-	arsH	NADPH-dependent FMN reducta
MNLKPGEA_	thiK	0.860122961	0.42028139	Thiamine kinase	2.7.1.89	thiK	Catalyzes the phosphorylation of
MNLKPGEA_	MNLKPGEA	0.859610218	0.06491675	hypothetical protein	NA	yahO	Protein of unknown function (DU
MNLKPGEA_	MNLKPGEA	0.858292268	NA	hypothetical protein	NA	0	Multidrug DMT transporter perm
MNLKPGEA_	uspG_1	0.857872847	0.17664401	Universal stress protein	NA	0	Universal stress protein
MNLKPGEA_	MNLKPGEA	0.85762302	0.31112237	hypothetical protein	NA	0	protein conserved in bacteria
MNLKPGEA_	MNLKPGEA	0.857515571	0.05396559	hypothetical protein	NA	yrdB	Protein of unknown function (DU
MNLKPGEA_	bmr3	0.856838624	NA	Multidrug resistance pro	NA	0	Major facilitator Superfamily
MNLKPGEA_	ydgI	0.856013126	0.03625331	Putative arginine/ornithi	NA	ydgI	Arginine ornithine antiporter
MNLKPGEA_	mntR	0.853175866	0.0154159	Transcriptional regulator	NA	mntR	transcriptional regulator
MNLKPGEA_	csdA	0.853048509	0.17564414	Cysteine desulfurase Csc	2.8.1.7	csdA	Cysteine desulfurases mobilize t
MNLKPGEA_	rrrD	0.853014549	NA	Lysozyme RrrD	3.2.1.17	rrrD	lysozyme
MNLKPGEA_	MNLKPGEA	0.852269927	0.15035623	hypothetical protein	NA	0	type VI secretion protein
MNLKPGEA_	tusB	0.849585671	0.0106282	Protein TusB	NA	tusB	Part of a sulfur-relay system req
MNLKPGEA_	araH	0.848020183	0.16058141	L-arabinose transport sy	NA	araH	Belongs to the binding-protein-d
MNLKPGEA_	MNLKPGEA	0.847733506	0.01733249	hypothetical protein	NA	MA20_06	Prolyl-tRNA synthetase
MNLKPGEA_	ybjG	0.847100403	0.34007142	Putative undecaprenyl-di	3.6.1.27	ybjG	Phosphatase

MNLKPGEA_ fruA_2	0.845152832	0.15869933	PTS system fructose-spe	NA	fruA	PTS system, fructose subfamily,
MNLKPGEA_ lpp1	0.844573339	0.00029905	Major outer membrane l	NA	lpp	Lipoprotein leucine-zipper
MNLKPGEA_ lpoB	0.843631541	0.02926177	Penicillin-binding protein	NA	lpoB	Regulator of peptidoglycan syntl
MNLKPGEA_ arnD	0.843225598	NA	putative 4-deoxy-4-form	3.5.1.-	arnD	Catalyzes the deformylation of 4
MNLKPGEA_ ykgO	0.842999748	0.1821417	50S ribosomal protein L3	NA	rpmJ	Belongs to the bacterial ribosom
MNLKPGEA_ pagP	0.840555779	0.023031	Lipid A palmitoyltransfer	2.3.1.251	pagP	Transfers a palmitate residue fr
MNLKPGEA_ yusV	0.839418639	0.02692244	putative siderophore tra	NA	yusV	(ABC) transporter
MNLKPGEA_ lolA	0.837842124	0.00152452	Outer-membrane lipopro	NA	lolA	Participates in the translocation
MNLKPGEA_ cbiN	0.837562236	NA	Cobalt transport protein	NA	cbiN	Part of the energy-coupling facto
MNLKPGEA_ ltaE	0.836853678	0.03193632	Low specificity L-threoni	4.1.2.48	ltaE	Threonine aldolase
MNLKPGEA_ fumD	0.836322874	0.11996489	Fumarase D	4.2.1.2	ydhZ	fumarate hydratase activity
MNLKPGEA_ bfr	0.835318893	0.0134477	Bacterioferritin	1.16.3.1	bfr	Iron-storage protein, whose ferr
MNLKPGEA_ MNLKPGEA	0.83508925	0.13003502	hypothetical protein	NA	0	Protein involved in oxidoreducta
MNLKPGEA_ hdeB_2	0.834795301	NA	Acid stress chaperone H	NA	hdeB	Required for optimal acid stress
MNLKPGEA_ dnaJ	0.834349932	0.19117668	Chaperone protein DnaJ	NA	dnaJ	ATP binding to DnaK triggers the
MNLKPGEA_ pgk	0.83197841	0.0035624	Phosphoglycerate kinase	2.7.2.3	pgk	Belongs to the phosphoglycerate
MNLKPGEA_ MNLKPGEA	0.827570016	0.00137559	hypothetical protein	NA	ygaC	Protein of unknown function (DU
MNLKPGEA_ sufE	0.826527535	0.05132872	Cysteine desulfuration p	NA	sufE	PFAM Fe-S metabolism associat
MNLKPGEA_ yihI	0.826447933	0.00564197	Der GTPase-activating p	NA	yihI	A GTPase-activating protein (GA
MNLKPGEA_ MNLKPGEA	0.824775857	NA	hypothetical protein	NA	fldX	3-hydroxyisobutyrate dehydroge
MNLKPGEA_ MNLKPGEA	0.824214544	NA	Deacetylase	3.1.1.-	dho	Amidohydrolase family
MNLKPGEA_ MNLKPGEA	0.822706182	0.10986879	IS3 family transposase IS	NA	0	Transposase
MNLKPGEA_ ulaA_4	0.82241756	0.38910762	Ascorbate-specific PTS s	NA	0	protein conserved in bacteria
MNLKPGEA_ MNLKPGEA	0.820828872	NA	hypothetical protein	NA	ypfG	Protein of unknown function (DU
MNLKPGEA_ fadE	0.820168977	0.03193632	Acyl-coenzyme A dehydr	1.3.8.7	fadE	acyl-CoA dehydrogenase
MNLKPGEA_ MNLKPGEA	0.818715174	0.43755908	hypothetical protein	NA	ybdF	YjbR
MNLKPGEA_ ddpA_1	0.818205938	NA	putative D,D-dipeptide-b	NA	0	Extracellular solute-binding prot
MNLKPGEA_ glnQ_3	0.815443085	NA	Glutamine transport ATP	NA	gluA	(ABC) transporter
MNLKPGEA_ MNLKPGEA	0.815432658	0.42944752	IS3 family transposase IS	NA	0	Transposase
MNLKPGEA_ fiu	0.814760637	0.34150115	Catecholate siderophore	NA	fiu	receptor

MNLKPGEA_	MNLKPGEA	0.813700263	0.25498175	hypothetical protein	NA	ybjC	Protein of unknown function (DU
MNLKPGEA_	MNLKPGEA	0.813027394	0.46044305	hypothetical protein	NA	0	Protein of unknown function (DU
MNLKPGEA_	MNLKPGEA	0.812294123	NA	hypothetical protein	NA	0	lytic transglycosylase activity
MNLKPGEA_	MNLKPGEA	0.811739569	0.00787343	IS3 family transposase IS	NA	0	transposase
MNLKPGEA_	hemE	0.811032661	0.06563379	Uroporphyrinogen decarl	4.1.1.37	hemE	Catalyzes the decarboxylation of
MNLKPGEA_	matP	0.810951453	0.02975297	Macrodomain Ter protei	NA	matP	Required for spatial organizatio
MNLKPGEA_	MNLKPGEA	0.810412043	NA	hypothetical protein	NA	eutH	ethanolamine utilization protein
MNLKPGEA_	ywrO	0.810163077	0.29814004	General stress protein 1	1.6.99.-	kefG	Regulatory subunit of a potassiu
MNLKPGEA_	MNLKPGEA	0.80943518	0.07257987	putative protein	NA	yggL	protein conserved in bacteria
MNLKPGEA_	MNLKPGEA	0.807996001	0.01118505	hypothetical protein	NA	yjfN	Protein of unknown function (DU
MNLKPGEA_	MNLKPGEA	0.807858528	0.00199719	hypothetical protein	NA	0	0
MNLKPGEA_	MNLKPGEA	0.804139394	0.17259834	hypothetical protein	NA	0	Membrane
MNLKPGEA_	pflA	0.802434981	0.04553759	Pyruvate formate-lyase 1	1.97.1.4	pflA	Activation of pyruvate formate-l
MNLKPGEA_	MNLKPGEA	0.802272849	NA	hypothetical protein	NA	0	0
MNLKPGEA_	ompR_1	0.800989044	0.03864654	Transcriptional regulator	NA	ompR	Response regulators consisting c
MNLKPGEA_	MNLKPGEA	0.797493917	0.40417243	hypothetical protein	NA	MA20_23	membrane
MNLKPGEA_	MNLKPGEA	0.79746588	NA	hypothetical protein	NA	0	Phage regulatory protein
MNLKPGEA_	ompX	0.796924883	0.00560193	Outer membrane protein	NA	ompX	PFAM virulence-related outer m
MNLKPGEA_	MNLKPGEA	0.795474531	NA	hypothetical protein	NA	0	polarity suppression protein
MNLKPGEA_	edd	0.79534891	0.34838961	Phosphogluconate dehyc	4.2.1.12	edd	Belongs to the IlvD Edd family
MNLKPGEA_	ynhG	0.79444693	0.00146366	putative L,D-transpeptida	2.-.-.-	ycfS	ErfK YbiS YcfS YnhG family prote
MNLKPGEA_	epmC	0.79356237	0.37371869	Elongation factor P hydro	1.14.-.-	yfcM	protein conserved in bacteria
MNLKPGEA_	smg	0.791134303	0.00854843	Protein Smg	NA	smg	Belongs to the Smg family
MNLKPGEA_	paaX	0.790864938	0.01193852	Transcriptional repressor	NA	paaX	phenylacetic acid degradation op
MNLKPGEA_	MNLKPGEA	0.790862469	0.46155005	hypothetical protein	NA	0	terminase
MNLKPGEA_	lsrB_1	0.790095736	0.33176006	Autoinducer 2-binding pr	NA	lsrB	Periplasmic binding protein dom
MNLKPGEA_	yidZ	0.789246047	0.43962659	HTH-type transcriptional	NA	yidZ	HTH-type transcriptional regulat
MNLKPGEA_	MNLKPGEA	0.789021554	0.11471931	Gluconate 2-dehydrogen	1.1.99.3	0	Gluconate 2-dehydrogenase
MNLKPGEA_	hipO_3	0.788992142	0.03922855	Hippurate hydrolase	3.5.1.32	0	amidohydrolase
MNLKPGEA_	astD_3	0.788329812	0.07150654	N-succinylglutamate 5-s	1.2.1.71	astD	Catalyzes the NAD-dependent re

MNLKPGEA_	ydcU	0.787203097	0.23638322	Inner membrane ABC tra	NA	ydcU	ABC transporter (Permease
MNLKPGEA_	xylE	0.786885324	0.38074369	D-xylose-proton symport	NA	0	Major facilitator Superfamily
MNLKPGEA_	frdD	0.78584174	0.22236257	Fumarate reductase sub	NA	frdD	Seems to be involved in the ancl
MNLKPGEA_	MNLKPGEA	0.785443066	0.06898904	hypothetical protein	NA	0	Antitermination protein
MNLKPGEA_	pncA	0.784447733	0.27897433	Nicotinamidase	3.5.1.19	pncA	Nicotinamidase
MNLKPGEA_	mug	0.784202395	0.40080791	G/U mismatch-specific I	3.2.2.28	mug	Excises ethenocytosine and urac
MNLKPGEA_	MNLKPGEA	0.784133501	0.08502679	hypothetical protein	NA	ybhB	PFAM PEBP family protein
MNLKPGEA_	kdgM	0.783586354	0.05508619	Oligogalacturonate-spec	NA	kdgM	oligogalacturonate-specific porir
MNLKPGEA_	benM_2	0.783103403	0.1148752	HTH-type transcriptional	NA	0	transcriptional regulator
MNLKPGEA_	thpA_2	0.782964814	0.35520398	D-threitol-binding protei	NA	mocB	ABC-type sugar transport systen
MNLKPGEA_	relE_2	0.781590973	0.01795809	mRNA interferase toxin	3.1.-.-	stbE	ParE toxin of type II toxin-antito
MNLKPGEA_	MNLKPGEA	0.780281943	0.03182058	hypothetical protein	NA	ynfC	Uncharacterised protein family (
MNLKPGEA_	yohD	0.779695605	0.11488552	Inner membrane protein	NA	yohD	Membrane
MNLKPGEA_	MNLKPGEA	0.778669877	NA	hypothetical protein	NA	0	Xylose isomerase
MNLKPGEA_	smf-1	0.773812183	0.20395915	Major fimbrial subunit S	NA	0	COG3539 P pilus assembly prote
MNLKPGEA_	MNLKPGEA	0.77335816	0.02609313	hypothetical protein	NA	0	Protein of unknown function (DL
MNLKPGEA_	MNLKPGEA	0.770018505	0.44659046	hypothetical protein	NA	ytfH	Transcriptional regulator
MNLKPGEA_	MNLKPGEA	0.769658767	0.09931062	hypothetical protein	NA	0	EAL domain
MNLKPGEA_	MNLKPGEA	0.766359428	0.03193632	hypothetical protein	NA	0	0
MNLKPGEA_	MNLKPGEA	0.765832068	0.37764481	hypothetical protein	NA	0	Transcriptional
MNLKPGEA_	hdfR_1	0.765278941	0.42949565	HTH-type transcriptional	NA	0	transcriptional regulator
MNLKPGEA_	atzE	0.763663864	NA	1-carboxybiuret hydrolas	3.5.1.131	gatA	Allows the formation of correctl
MNLKPGEA_	polA	0.763470878	0.00280389	DNA polymerase I	2.7.7.7	polA	In addition to polymerase activit
MNLKPGEA_	MNLKPGEA	0.763123656	0.35134134	Catechol O-methyltransf	2.1.1.6	mdmC	Methyltransferase domain
MNLKPGEA_	mreD	0.763044119	0.0080514	Rod shape-determining	NA	mreD	Involved in formation of the rod
MNLKPGEA_	MNLKPGEA	0.762961367	0.38090165	hypothetical protein	NA	ycgR	Acts as a flagellar brake, regulat
MNLKPGEA_	xylR	0.761038395	0.17312835	Xylose operon regulatory	NA	xylR	transcriptional regulator
MNLKPGEA_	yrfG	0.760017439	0.06920994	GMP/IMP nucleotidase \	3.1.3.5	yrfG	Hydrolase
MNLKPGEA_	MNLKPGEA	0.758495715	0.23006593	hypothetical protein	NA	0	0
MNLKPGEA_	pdeF	0.75829472	0.27292797	Cyclic di-GMP phosphodi	3.1.4.52	yfgF	cyclic-guanylate-specific phosph

MNLKPGEA_	MNLKPGEA	0.758092008	NA	hypothetical protein	NA	0	baseplate assembly protein
MNLKPGEA_	MNLKPGEA	0.756799053	0.43534581	hypothetical protein	NA	sfsB	transcriptional regulator
MNLKPGEA_	glnH_3	0.754823127	0.36578077	ABC transporter glutami	NA	fliY_2	Belongs to the bacterial solute-b
MNLKPGEA_	dhaM	0.754469531	0.35236174	PEP-dependent dihydrox	2.7.1.121	dhaM	Belongs to the PEP-utilizing enzy
MNLKPGEA_	MNLKPGEA	0.753608496	0.39595886	hypothetical protein	NA	#N/A	#N/A
MNLKPGEA_	oppC	0.751555725	0.35823986	Oligopeptide transport s	NA	oppC	COG1173 ABC-type dipeptide oli
MNLKPGEA_	MNLKPGEA	0.751326184	0.04204192	hypothetical protein	NA	0	0
MNLKPGEA_	ntrC	0.750089714	0.11871087	DNA-binding transcriptic	NA	glnG	COG2204 Response regulator co
MNLKPGEA_	lptF	0.749193829	0.00816415	Lipopolysaccharide expo	NA	lptF	Permease
MNLKPGEA_	malI	0.746701717	0.37797689	Maltose regulon regulat	NA	malI	Transcriptional regulator
MNLKPGEA_	MNLKPGEA	0.746502299	0.43755908	hypothetical protein	NA	0	Protein of unknown function (DU
MNLKPGEA_	MNLKPGEA	0.745745323	NA	hypothetical protein	NA	#N/A	#N/A
MNLKPGEA_	MNLKPGEA	0.744227008	0.43617699	hypothetical protein	NA	#N/A	#N/A
MNLKPGEA_	nodD2_2	0.743970336	0.44003864	Nodulation protein D 2	NA	mexT	transcriptional regulator
MNLKPGEA_	qseG	0.743783281	0.01602154	Quorum-sensing regulat	NA	yfhG	YfhG lipoprotein
MNLKPGEA_	katG	0.742757844	0.01396671	Catalase-peroxidase	1.11.1.21	katG	Bifunctional enzyme with both c
MNLKPGEA_	MNLKPGEA	0.740820875	NA	hypothetical protein	NA	0	Lactoylglutathione lyase and rela
MNLKPGEA_	slyA_2	0.740614377	0.19193357	Transcriptional regulato	NA	0	transcriptional regulator
MNLKPGEA_	MNLKPGEA	0.740067088	NA	hypothetical protein	NA	0	0
MNLKPGEA_	MNLKPGEA	0.739756152	0.11477825	hypothetical protein	NA	0	Acetyltransferase (GNAT) family
MNLKPGEA_	coaE	0.73975061	0.07229634	Dephospho-CoA kinase	2.7.1.24	coaE	Catalyzes the phosphorylation of
MNLKPGEA_	tehB	0.737806384	NA	Tellurite methyltransfera	2.1.1.265	tehB	Tellurite resistance protein TehB
MNLKPGEA_	gltK	0.737270958	0.2810573	Glutamate/aspartate im	NA	gltK	With GltJLPS and GadC for gluta
MNLKPGEA_	yadG	0.736355781	0.20060065	putative ABC transporte	NA	yadG	(ABC) transporter
MNLKPGEA_	nanR	0.735916566	0.04820067	HTH-type transcriptional	NA	yieP	transcriptional regulator
MNLKPGEA_	moaB	0.734144407	0.27385798	Molybdenum cofactor bi	NA	moaB	May be involved in the biosynthe
MNLKPGEA_	oqxB25	0.733863531	0.408996	multidrug efflux RND tra	NA	mexF	Belongs to the resistance-nodula
MNLKPGEA_	MNLKPGEA	0.732011834	0.24099062	hypothetical protein	NA	yjeI	Membrane
MNLKPGEA_	fabG_4	0.731328914	NA	3-oxoacyl-[acyl-carrier-p	1.1.1.100	entA	NAD dependent epimerase/dehy
MNLKPGEA_	rusA	0.731248395	NA	Crossover junction endo	3.1.22.4	rusA	Endonuclease that resolves Holli

MNLKPGEA_	glpR_3	0.730220689	NA	Glycerol-3-phosphate re	NA	ygbI	DeoR C terminal sensor domain
MNLKPGEA_	MNLKPGEA	0.730033077	0.3906211	hypothetical protein	NA	yohJ	UPF0299 membrane protein
MNLKPGEA_	MNLKPGEA	0.72992025	0.49247401	hypothetical protein	NA	yohM	Belongs to the NiCoT transporte
MNLKPGEA_	yeeZ	0.726870982	0.06386009	Protein YeeZ	NA	yeeZ	COG0451 Nucleoside-diphospha
MNLKPGEA_	MNLKPGEA	0.724741895	0.12436211	hypothetical protein	NA	yegH	membrane protein, terc
MNLKPGEA_	MNLKPGEA	0.723004436	0.02813725	hypothetical protein	NA	CI	repressor
MNLKPGEA_	opd	0.721652135	0.2189482	Parathion hydrolase	3.1.8.1	pteR	phosphotriesterase homology pr
MNLKPGEA_	MNLKPGEA	0.721600135	0.06904445	hypothetical protein	NA	0	Protein of unknown function (DU
MNLKPGEA_	fumC	0.72094844	0.11993834	Fumarate hydratase clas	4.2.1.2	fumC	Involved in the TCA cycle. Cataly
MNLKPGEA_	kdgK_1	0.71890274	0.12822164	2-dehydro-3-deoxyglucor	2.7.1.45	kguK	2-dehydro-3-deoxygluconokinase
MNLKPGEA_	abaF_1	0.718798976	0.27371109	Fosfomycin resistance pı	NA	shiA	Major facilitator superfamily
MNLKPGEA_	MNLKPGEA	0.718501626	0.07622399	hypothetical protein	NA	0	peptidylprolyl isomerase
MNLKPGEA_	yrdA_2	0.718132899	0.33705293	Protein YrdA	NA	paaY	Phenylacetic acid degradation pı
MNLKPGEA_	MNLKPGEA	0.714512272	0.07972181	hypothetical protein	NA	dprA	Rossmann fold nucleotide-bindi
MNLKPGEA_	MNLKPGEA	0.712918649	0.39663794	hypothetical protein	NA	0	Phosphodiester glycosidase
MNLKPGEA_	uxaB_1	0.712907684	0.12201449	Altronate oxidoreductase	1.1.1.58	uxaB	Belongs to the mannitol dehydrc
MNLKPGEA_	rnc	0.712744305	0.03193632	Ribonuclease 3	3.1.26.3	rnc	Digests double-stranded RNA. Ir
MNLKPGEA_	mntB_1	0.710493559	0.06884793	Manganese transport sy	NA	sitD	COG1108 ABC-type Mn2 Zn2 tra
MNLKPGEA_	cysC	0.709806694	0.48957215	Adenylyl-sulfate kinase	2.7.1.25	cysC	Catalyzes the synthesis of activa
MNLKPGEA_	arsC_1	0.707409718	NA	Arsenate reductase	1.20.4.1	arsC	arsenate reductase
MNLKPGEA_	ompW	0.705719588	0.0737788	Outer membrane protei	NA	ompW	outer membrane protein W
MNLKPGEA_	alsT	0.705456315	0.16472366	Amino-acid carrier prote	NA	yaaJ	alanine symporter
MNLKPGEA_	MNLKPGEA	0.704756933	0.20468764	hypothetical protein	NA	yhbW	COG2141 Coenzyme F420-deper
MNLKPGEA_	MNLKPGEA	0.703029602	0.51611762	hypothetical protein	NA	0	0
MNLKPGEA_	fusA_2	0.702506608	0.03403717	Elongation factor G	NA	fusA	Catalyzes the GTP-dependent rib
MNLKPGEA_	tmk	0.700371334	0.24793585	Thymidylate kinase	2.7.4.9	tmk	Phosphorylation of dTMP to forn
MNLKPGEA_	MNLKPGEA	0.698276786	0.50730841	hypothetical protein	NA	0	Bacterial toxin 44
MNLKPGEA_	rhaR_2	0.697825444	0.09252067	HTH-type transcriptional	NA	0	helix_turn_helix, arabinose oper
MNLKPGEA_	slyA_3	0.696372499	0.49847787	Transcriptional regulator	NA	slyA	Transcriptional regulator
MNLKPGEA_	aldA	0.695920481	0.4932447	Lactaldehyde dehydroge	1.2.1.22	aldA	belongs to the aldehyde dehydrc

MNLKPGEA_	MNLKPGEA	0.694775317	0.03738712	hypothetical protein	NA	#N/A	#N/A
MNLKPGEA_	MNLKPGEA	0.694329104	0.01494485	hypothetical protein	NA	ydcL	Protein of unknown function (DU
MNLKPGEA_	cysT	0.693064046	0.41750964	Sulfate transport system	NA	cysT	sulfate ABC transporter
MNLKPGEA_	gcvA_3	0.69112877	NA	Glycine cleavage system	NA	gcvA_4	Transcriptional regulator, LysR f
MNLKPGEA_	pduF	0.690773364	0.5700196	Propanediol diffusion fac	NA	glpF	Belongs to the MIP aquaporin (T
MNLKPGEA_	MNLKPGEA	0.690395158	NA	hypothetical protein	NA	0	phage tail tape measure protein
MNLKPGEA_	yacG	0.689861997	0.34032494	DNA gyrase inhibitor Yac	NA	yacG	Inhibits all the catalytic activitie
MNLKPGEA_	MNLKPGEA	0.689553001	0.11859146	hypothetical protein	NA	gstA	Belongs to the GST superfamily
MNLKPGEA_	slyX	0.689085702	0.13910618	Protein SlyX	NA	slyX	Belongs to the SlyX family
MNLKPGEA_	MNLKPGEA	0.688815223	0.52118975	hypothetical protein	NA	#N/A	#N/A
MNLKPGEA_	ytfT	0.688436875	0.45134489	Inner membrane ABC tra	NA	ytfT	Belongs to the binding-protein-d
MNLKPGEA_	MNLKPGEA	0.688244283	0.42784713	hypothetical protein	NA	0	0
MNLKPGEA_	btuD_9	0.687693479	0.48747048	Vitamin B12 import ATP	7.6.2.8	0	Amino Acid
MNLKPGEA_	MNLKPGEA	0.687634485	0.22169083	hypothetical protein	NA	0	Alpha beta hydrolase
MNLKPGEA_	MNLKPGEA	0.686108909	0.04347903	hypothetical protein	NA	ybhP	Endonuclease Exonuclease Phosp
MNLKPGEA_	luxS	0.685967212	0.07377725	S-ribosylhomocysteine ly	4.4.1.21	luxS	Involved in the synthesis of auto
MNLKPGEA_	MNLKPGEA	0.68571165	0.52770422	hypothetical protein	NA	pgaD	PgaD-like protein
MNLKPGEA_	iolS	0.685039773	0.38646682	Aldo-keto reductase IolS	1.1.1.-	0	Aldo keto reductase
MNLKPGEA_	yghU	0.684159646	0.14773363	Disulfide-bond oxidoredu	1.8.4.-	yghU	Belongs to the GST superfamily
MNLKPGEA_	atsB	0.683429646	0.57057789	Anaerobic sulfatase-mat	1.1.99.-	aslB	Radical SAM domain protein
MNLKPGEA_	ulaD	0.683226595	0.56504393	3-keto-L-gulonate-6-pho	4.1.1.85	ulaD	Catalyzes the decarboxylation of
MNLKPGEA_	dcuS	0.682032366	0.26412888	Sensor histidine kinase D	2.7.13.3	dcuS	signal transduction histidine kina
MNLKPGEA_	dinB	0.681888207	0.139726	DNA polymerase IV	2.7.7.7	dinB	Poorly processive, error-prone DI
MNLKPGEA_	umuC_1	0.681111552	0.19290874	Protein UmuC	NA	umuC	DNA polymerase
MNLKPGEA_	bglA_1	0.680667645	0.1299986	6-phospho-beta-glucosic	3.2.1.86	bglA	Belongs to the glycosyl hydrolase
MNLKPGEA_	dgoT_1	0.680339143	0.40777269	D-galactonate transporte	NA	dgoT	Major facilitator superfamily
MNLKPGEA_	iolG_5	0.680331986	NA	Inositol 2-dehydrogenase	1.1.1.369	0	oxidoreductase
MNLKPGEA_	dmoA	0.679684031	NA	Dimethyl-sulfide monoox	1.14.13.131	soxA	COG2141 Coenzyme F420-deper
MNLKPGEA_	osmY_2	0.679282706	0.08549513	Osmotically-inducible pr	NA	osmY	Periplasmic or secreted lipoprote
MNLKPGEA_	fadL	0.677562907	0.06238678	Long-chain fatty acid tra	NA	fadL	long-chain fatty acid transport p

MNLKPGEA_ rppH_1	0.677519491	0.51225084	RNA pyrophosphohydrol	3.6.1.-	0	Belongs to the Nudix hydrolase f
MNLKPGEA_ ydcY	0.676243096	0.07023233	putative protein YdcY	NA	ydcY	Protein of unknown function (DU
MNLKPGEA_ nemR	0.67596755	0.1148752	HTH-type transcriptional	NA	nemR	transcriptional regulator
MNLKPGEA_ fkpB	0.675327102	0.12989878	FKBP-type 16 kDa peptid	5.2.1.8	fkpB	Peptidyl-prolyl cis-trans
MNLKPGEA_ pyrG_1	0.674916498	0.00948459	CTP synthase	6.3.4.2	pyrG	Catalyzes the ATP-dependent an
MNLKPGEA_ fnr	0.674857424	0.02605323	Fumarate and nitrate re	NA	fnr	COG0664 cAMP-binding proteins
MNLKPGEA_ ftsH	0.674812161	0.06410481	ATP-dependent zinc met	3.4.24.-	ftsH	Acts as a processive, ATP-depen
MNLKPGEA_ apaG	0.673492279	0.20781456	Protein ApaG	NA	apaG	protein affecting Mg2 Co2 transp
MNLKPGEA_ MNLKPGEA	0.67321961	0.058033	hypothetical protein	NA	0	Antitoxin component of a toxin-a
MNLKPGEA_ aptB_1	0.67225546	0.27076041	Apulose-4-phosphate tra	2.2.1.-	IV02_097	Transketolase
MNLKPGEA_ MNLKPGEA	0.671497616	0.04046142	hypothetical protein	NA	0	0
MNLKPGEA_ tomB	0.670801144	0.02526801	Hha toxicity modulator T	NA	tomB	Biofilm formation regulator Yba
MNLKPGEA_ ycnE	0.670621925	NA	Putative monooxygenase	1.-.-.-	0	Antibiotic biosynthesis monooxy
MNLKPGEA_ MNLKPGEA	0.670500444	NA	hypothetical protein	NA	traD	Conjugal transfer protein TraG
MNLKPGEA_ cobQ	0.669799312	0.45922526	Cobyric acid synthase	NA	cobQ	Catalyzes amidations at positior
MNLKPGEA_ ycgM	0.667424085	0.16348346	putative protein YcgM	NA	ycgM	COG0179 2-keto-4-pentenoate h
MNLKPGEA_ uhpT	0.666987739	0.2827359	Hexose-6-phosphate:phc	NA	uhpT	PFAM Major facilitator superfan
MNLKPGEA_ arcA	0.666890565	0.10384526	Aerobic respiration contr	NA	arcA	Two component transcriptional r
MNLKPGEA_ ddrA_2	0.666551533	NA	Diol dehydratase-reactiv	NA	pduG	dehydratase
MNLKPGEA_ menH_2	0.666153455	0.56977554	2-succinyl-6-hydroxy-2,4	4.2.99.20	menH	Catalyzes a proton abstraction re
MNLKPGEA_ gntR_1	0.665362028	0.1227923	HTH-type transcriptional	NA	gntR	Transcriptional
MNLKPGEA_ sbnA	0.664447269	0.39582268	N-(2-amino-2-carboxyetl	2.5.1.140	cysK_2	cysteine synthase
MNLKPGEA_ MNLKPGEA	0.66306185	0.06309084	hypothetical protein	NA	#N/A	#N/A
MNLKPGEA_ dtpT	0.661311695	0.05249215	Di-/tripeptide transporte	NA	dtpT	Proton-dependent permease tha
MNLKPGEA_ nusG	0.660870979	0.0111143	Transcription terminatio	NA	nusG	Participates in transcription elor
MNLKPGEA_ zntR	0.659399163	0.1308644	HTH-type transcriptional	NA	zntR	transcriptional regulator
MNLKPGEA_ roxA_1	0.658706347	0.01978674	50S ribosomal protein L1	1.14.11.47	ycfD	Cupin 4 family protein
MNLKPGEA_ lsrD_1	0.656359828	0.58780007	Autoinducer 2 import sys	NA	lsrD	Branched-chain amino acid trans
MNLKPGEA_ yciO	0.655794356	0.09690373	putative protein YciO	NA	yciO	Belongs to the SUA5 family
MNLKPGEA_ adhP_2	0.654109822	0.01231375	Alcohol dehydrogenase,	1.1.1.1	adhP	alcohol dehydrogenase

MNLKPGEA_	dmsA_2	0.654083842	NA	Dimethyl sulfoxide/trime	1.7.2.3	dorA	Belongs to the prokaryotic molyl
MNLKPGEA_	MNLKPGEA	0.653929807	0.52919092	putative protein	NA	0	Hydrolases of the alpha beta sup
MNLKPGEA_	MNLKPGEA	0.653851124	0.17573094	hypothetical protein	NA	0	Protein tyrosine serine phosphat
MNLKPGEA_	MNLKPGEA	0.653804109	0.45605087	hypothetical protein	NA	ybbO	Belongs to the short-chain dehyd
MNLKPGEA_	mrdB	0.653543854	0.43552895	Peptidoglycan glycosyltra	2.4.1.129	mrdB	Peptidoglycan polymerase that i
MNLKPGEA_	MNLKPGEA	0.651832871	0.31025248	hypothetical protein	NA	etfD	Fimbrial protein
MNLKPGEA_	MNLKPGEA	0.651771866	0.0259001	hypothetical protein	NA	0	sequence-specific DNA binding
MNLKPGEA_	marA	0.651103132	0.49630565	Multiple antibiotic resist	NA	marA	Transcriptional activator of gene
MNLKPGEA_	MNLKPGEA	0.649968315	0.11304561	hypothetical protein	NA	0	0
MNLKPGEA_	thiL	0.649667765	0.34840559	Thiamine-monophospha	2.7.4.16	thiL	Catalyzes the ATP-dependent ph
MNLKPGEA_	pgrR_4	0.649648191	0.49448705	HTH-type transcriptional	NA	dmlR_3	Transcriptional regulator
MNLKPGEA_	murQ_2	0.646159247	0.1289742	N-acetylmuramic acid 6-	4.2.1.126	0	Specifically catalyzes the cleava
MNLKPGEA_	nifJ	0.645469602	0.04563195	Pyruvate-flavodoxin oxid	1.2.7.-	nifJ	Oxidoreductase required for the
MNLKPGEA_	lptD	0.645226817	0.04668395	LPS-assembly protein Lp	NA	lptD	Together with LptE, is involved i
MNLKPGEA_	amnD	0.64335905	NA	2-aminomuconate deam	3.5.99.5	0	Translation Initiation Inhibitor Yj
MNLKPGEA_	cynR_6	0.643013771	0.43056525	HTH-type transcriptional	NA	mdcR	Transcriptional regulator
MNLKPGEA_	cusC_2	0.642964555	NA	Cation efflux system pro	NA	cusC	RND efflux system, outer memb
MNLKPGEA_	hypA	0.642964555	NA	Hydrogenase maturation	NA	hypA	Probably plays a role in a hydrog
MNLKPGEA_	hypC	0.642964555	NA	Hydrogenase maturation	NA	hypC	Hydrogenase assembly chaperon
MNLKPGEA_	MNLKPGEA	0.642964555	NA	hypothetical protein	NA	0	Xylose isomerase
MNLKPGEA_	MNLKPGEA	0.642964555	NA	hypothetical protein	NA	0	0
MNLKPGEA_	MNLKPGEA	0.642964555	NA	hypothetical protein	NA	0	Required for the export of heme
MNLKPGEA_	MNLKPGEA	0.642964555	NA	hypothetical protein	NA	0	ergothioneine biosynthetic proce
MNLKPGEA_	MNLKPGEA	0.642964555	NA	hypothetical protein	NA	azlC	branched-chain amino acid
MNLKPGEA_	ugpA_2	0.642964555	NA	sn-glycerol-3-phosphate	NA	MA20_28	Binding-protein-dependent trans
MNLKPGEA_	rsgA	0.638345302	0.03792434	Small ribosomal subunit	3.6.1.-	rsgA	One of several proteins that assi
MNLKPGEA_	clsA	0.636147715	0.26043881	Cardiolipin synthase A	2.7.8.-	cls	Catalyzes the reversible phospha
MNLKPGEA_	malF	0.636030659	0.4494911	Maltose/maltodextrin tr	NA	malF	transport
MNLKPGEA_	MNLKPGEA	0.6352831	0.43591563	hypothetical protein	NA	yeaK	YbaK prolyl-tRNA synthetase ass
MNLKPGEA_	MNLKPGEA	0.633792708	0.47080788	hypothetical protein	NA	yjjU	esterase of the alpha-beta hydro

MNLKPGEA_ thlA_3	0.633245457	0.60220229	Acetyl-CoA acetyltransfe	2.3.1.9	bktB	Catalyzes the final step of fatty a
MNLKPGEA_ prmA	0.633052919	0.07424211	Ribosomal protein L11 m	2.1.1.-	prmA	Ribosomal protein L11 methyltra
MNLKPGEA_ MNLKPGEA	0.633035987	0.17165925	hypothetical protein	NA	ydhS	FAD-NAD(P)-binding
MNLKPGEA_ MNLKPGEA	0.632444001	0.04281818	hypothetical protein	NA	yhhN	membrane
MNLKPGEA_ MNLKPGEA	0.629344509	0.12270721	hypothetical protein	NA	yieE	Phosphopantetheinyl transferase
MNLKPGEA_ frlB_2	0.629282053	0.50319304	Fructosamine deglycase	3.5.-.-	frlB	Glucosamine--fructose-6-phospl
MNLKPGEA_ dhaK_1	0.629174003	0.19464266	Dihydroxyacetone kinase	2.7.1.29	dhaK	Dihydroxyacetone kinase
MNLKPGEA_ MNLKPGEA	0.627566105	0.07206835	hypothetical protein	NA	guaA_2	Glutamine amidotransferase
MNLKPGEA_ MNLKPGEA	0.626520946	0.45231664	hypothetical protein	NA	omp	Membrane
MNLKPGEA_ metQ_1	0.626290711	0.23245251	D-methionine-binding lip	NA	0	Belongs to the NlpA lipoprotein
MNLKPGEA_ proS	0.626141586	0.14527734	Proline--tRNA ligase	6.1.1.15	proS	Catalyzes the attachment of pro
MNLKPGEA_ ddpC_3	0.624836218	NA	putative D,D-dipeptide tr	NA	yddQ	Binding-protein-dependent trans
MNLKPGEA_ dmsB_1	0.624836218	NA	Anaerobic dimethyl sulfo	NA	dmsB	reductase chain B
MNLKPGEA_ lacG_2	0.624836218	NA	Lactose transport system	NA	MA20_28	Binding-protein-dependent trans
MNLKPGEA_ MNLKPGEA	0.624836218	NA	hypothetical protein	NA	#N/A	#N/A
MNLKPGEA_ MNLKPGEA	0.624836218	NA	hypothetical protein	NA	0	protein possibly involved in utiliz
MNLKPGEA_ MNLKPGEA	0.624836218	NA	IS5 family transposase IS	NA	0	ISSoEn1, terminal inverted repea
MNLKPGEA_ MNLKPGEA	0.624836218	NA	3-mercaptopropionate d	1.13.11.-	0	Cysteine dioxygenase type I
MNLKPGEA_ MNLKPGEA	0.624836218	NA	hypothetical protein	NA	0	ISSoEn1, terminal inverted repea
MNLKPGEA_ MNLKPGEA	0.624836218	NA	IS1 family transposase IS	NA	0	cog cog1662
MNLKPGEA_ nikR	0.624836218	NA	Nickel-responsive regula	NA	nikR	Transcriptional repressor of the
MNLKPGEA_ rutC_1	0.624836218	NA	Putative aminoacrylate p	1.-.-.-	0	translation initiation inhibitor, yj
MNLKPGEA_ mtlR	0.624489909	0.25630786	Mannitol operon repress	NA	mtlR	Mannitol repressor
MNLKPGEA_ rffH	0.62443757	0.30502099	Glucose-1-phosphate thy	2.7.7.24	rffH	Catalyzes the formation of dTDP
MNLKPGEA_ mshD	0.623831049	NA	Mycothiol acetyltransfer	2.3.1.189	0	N-acetyltransferase
MNLKPGEA_ curA	0.623464526	0.33944608	NADPH-dependent curcu	1.3.1.-	yncB	nadp-dependent
MNLKPGEA_ cusF	0.622771912	NA	Cation efflux system pro	NA	cusF	Copper binding periplasmic prot
MNLKPGEA_ ddpC_2	0.622771912	NA	putative D,D-dipeptide tr	NA	0	COG1173 ABC-type dipeptide oli
MNLKPGEA_ epsE_1	0.622771912	NA	Type II secretion system	NA	gspE	Type II secretory pathway, ATPas
MNLKPGEA_ fliY_5	0.622771912	NA	L-cystine-binding protein	NA	0	ABC transporter substrate-bindi

MNLKPGEA_	MNLKPGEA	0.622771912	NA	hypothetical protein	NA	pilC	type II secretion system
MNLKPGEA_	MNLKPGEA	0.622771912	NA	hypothetical protein	NA	0	0
MNLKPGEA_	MNLKPGEA	0.622771912	NA	hypothetical protein	NA	0	transcriptional activator, Ogr del
MNLKPGEA_	MNLKPGEA	0.622771912	NA	hypothetical protein	NA	0	COG2801 Transposase and inact
MNLKPGEA_	pduA_2	0.622771912	NA	Propanediol utilization p	NA	pduA	Carbon dioxide concentrating me
MNLKPGEA_	rsxC_1	0.622771912	NA	Ion-translocating oxidore	7.-.-.-	pduS	NADH dehydrogenase
MNLKPGEA_	sgbH	0.622771912	NA	3-keto-L-gulonate-6-pho	4.1.1.85	sgbH	decarboxylase
MNLKPGEA_	dmlR_10	0.622333068	NA	HTH-type transcriptional	NA	0	transcriptional regulator
MNLKPGEA_	pduX	0.619005488	NA	L-threonine kinase	2.7.1.177	pduX	GHMP kinase
MNLKPGEA_	trpS	0.618956092	0.1207877	Tryptophan--tRNA ligase	6.1.1.2	trpS	Tryptophanyl-tRNA synthetase
MNLKPGEA_	yfkN	0.618629653	0.44818779	Trifunctional nucleotide	NA	cpdB	5'-nucleotidase, C-terminal dom
MNLKPGEA_	iscX	0.618571126	0.16414214	Protein IscX	NA	iscX	Iron-sulphur cluster assembly
MNLKPGEA_	celA_3	0.618443227	0.21838429	PTS system cellobiose-sp	2.7.1.205	celA	Phosphotransferase System
MNLKPGEA_	htpX_1	0.617897711	0.05624732	Protease HtpX	3.4.24.-	htpX	Belongs to the peptidase M48B
MNLKPGEA_	alsC	0.617644312	NA	D-allose transport syster	NA	alsC_1	Belongs to the binding-protein-d
MNLKPGEA_	ccmL	0.617644312	NA	Carbon dioxide concentra	NA	pduN	ethanolamine utilization protein
MNLKPGEA_	eutD	0.617644312	NA	Ethanolamine utilization	NA	pta	belongs to the CobB CobQ famil
MNLKPGEA_	hyfA_1	0.617644312	NA	Hydrogenase-4 compone	1.-.-.-	hycB	Formate hydrogenlyase
MNLKPGEA_	livF_4	0.617644312	NA	High-affinity branched-cl	NA	urtD	abc transporter atp-binding prot
MNLKPGEA_	manP	0.617644312	NA	PTS system mannose-sp	NA	manP	PTS system fructose-specific IIB
MNLKPGEA_	MNLKPGEA	0.617644312	NA	hypothetical protein	NA	pduM	propanediol utilization protein
MNLKPGEA_	MNLKPGEA	0.617644312	NA	hypothetical protein	NA	0	0
MNLKPGEA_	MNLKPGEA	0.617644312	NA	hypothetical protein	NA	0	0
MNLKPGEA_	MNLKPGEA	0.617644312	NA	hypothetical protein	NA	0	0
MNLKPGEA_	MNLKPGEA	0.617644312	NA	IS3 family transposase IS	NA	0	Transposase
MNLKPGEA_	MNLKPGEA	0.617644312	NA	hypothetical protein	NA	#N/A	#N/A
MNLKPGEA_	ompR_3	0.615429822	0.30075961	Transcriptional regulator	NA	0	response regulator
MNLKPGEA_	sdaC_2	0.615428917	0.56869985	Serine transporter	NA	0	Serine transporter
MNLKPGEA_	MNLKPGEA	0.615270816	NA	hypothetical protein	NA	0	ABC transporter substrate-bindi
MNLKPGEA_	kdpC	0.615101908	0.4571454	Potassium-transporting A	NA	kdpC	Part of the high-affinity ATP-driv

MNLKPGEA_	yhjR	0.614982631	0.16239411	Protein YhjR	NA	yhjR	Cellulose biosynthesis protein B
MNLKPGEA_	MNLKPGEA	0.614774006	0.03602655	hypothetical protein	NA	yoaC	Domain of unknown function (DU
MNLKPGEA_	MNLKPGEA	0.614657466	0.48394449	hypothetical protein	NA	#N/A	#N/A
MNLKPGEA_	hdfR_3	0.613475993	0.45325725	HTH-type transcriptional	NA	0	transcriptional regulator
MNLKPGEA_	MNLKPGEA	0.612671461	0.5771334	hypothetical protein	NA	lrpC	AsnC family transcriptional regu
MNLKPGEA_	MNLKPGEA	0.611416424	0.56811687	hypothetical protein	NA	0	Transcriptional regulator
MNLKPGEA_	degP	0.61127076	0.00854843	Periplasmic serine endop	3.4.21.107	degP	Belongs to the peptidase S1C fa
MNLKPGEA_	clpB	0.611257216	0.21491423	Chaperone protein ClpB	NA	clpB	Part of a stress-induced multi-ch
MNLKPGEA_	MNLKPGEA	0.609378219	NA	hypothetical protein	NA	0	Fimbrial protein
MNLKPGEA_	MNLKPGEA	0.608532169	0.56096864	hypothetical protein	NA	msaD	tautomerase
MNLKPGEA_	mlrA	0.608042166	0.18130387	HTH-type transcriptional	NA	ycgE	Transcriptional regulator
MNLKPGEA_	yhaK	0.607922719	0.44595243	Pirin-like protein YhaK	NA	yhaK	Belongs to the pirin family
MNLKPGEA_	rpiA	0.605523311	0.38646682	Ribose-5-phosphate isor	5.3.1.6	rpiA	Catalyzes the reversible conversi
MNLKPGEA_	aaeB_2	0.605237068	0.61236584	p-hydroxybenzoic acid ef	NA	ydhK	Fusaric acid resistance protein
MNLKPGEA_	wecA	0.604943375	0.15826306	Undecaprenyl-phosphate	2.7.8.33	wecA	Catalyzes the transfer of the Glc
MNLKPGEA_	puuD	0.604642499	0.42306103	Gamma-glutamyl-gamm	3.5.1.94	puuD	Gamma-glutamyl-gamma-amin
MNLKPGEA_	cdd	0.604525014	0.32439135	Cytidine deaminase	3.5.4.5	cdd	This enzyme scavenges exogeno
MNLKPGEA_	ydhF	0.60442063	0.11645802	Oxidoreductase YdhF	1.-.-.-	ydhF	Aldo Keto reductase
MNLKPGEA_	mntB_4	0.602739071	0.22064543	Manganese transport sy	NA	mntB	(ABC) transporter
MNLKPGEA_	rimP	0.602637045	0.07754222	Ribosome maturation fa	NA	rimP	Required for maturation of 30S
MNLKPGEA_	manZ_1	0.602547805	0.32255724	PTS system mannose-sp	NA	manZ	PTS system mannose fructose s
MNLKPGEA_	rihA	0.601375215	0.29814004	Pyrimidine-specific ribor	3.2.-.-	rihA	Belongs to the IUNH family
MNLKPGEA_	MNLKPGEA	0.59953153	0.41127487	Gluconate 2-dehydrogen	1.1.99.3	0	Choline dehydrogenase and rela
MNLKPGEA_	licC_2	0.598933054	0.31505041	Lichenan permease IIC c	NA	0	The phosphoenolpyruvate-deper
MNLKPGEA_	sutR_2	0.598393725	0.56655267	HTH-type transcriptional	NA	sinR	Transcriptional regulator
MNLKPGEA_	MNLKPGEA	0.59835552	0.50964222	hypothetical protein	NA	0	Integrase core domain
MNLKPGEA_	rhaS_8	0.598106797	0.46104038	HTH-type transcriptional	NA	ftrA	Transcriptional regulator contair
MNLKPGEA_	MNLKPGEA	0.595734637	0.62241488	hypothetical protein	NA	0	alcohol dehydrogenase
MNLKPGEA_	evgA	0.595130642	NA	DNA-binding transcriptic	NA	evgA	response regulator
MNLKPGEA_	kdpD	0.593507596	0.35893225	Sensor protein KdpD	2.7.13.3	kdpD	PhoQ Sensor

MNLKPGEA_	MNLKPGEA	0.592529466	0.06506667	hypothetical protein	NA	0	Protein of unknown function (DU
MNLKPGEA_	cysP	0.592281763	NA	Thiosulfate-binding prot	NA	cysP	Thiosulfate transporter subunit
MNLKPGEA_	MNLKPGEA	0.591689272	0.53286358	hypothetical protein	NA	yjjB	UPF0442 protein
MNLKPGEA_	yfhM	0.591456713	0.18418837	Alpha-2-macroglobulin	NA	yfhM	Large extracellular alpha-helical
MNLKPGEA_	yihV	0.590742229	NA	Sulfofructose kinase	2.7.1.184	0	Phosphorylates 6-deoxy-6-sulfo-
MNLKPGEA_	lon_2	0.590361682	0.25647312	Lon protease	3.4.21.53	lon	ATP-dependent serine protease
MNLKPGEA_	ycgL	0.590252058	0.12989878	Protein YcgL	NA	ycgL	YcgL domain-containing protein
MNLKPGEA_	mtlA	0.589088898	0.22677051	PTS system mannitol-sp	NA	mtlA	PTS system mannitol-specific
MNLKPGEA_	nfsA	0.589085619	0.54464975	Oxygen-insensitive NADI	1.-.-.-	nfsA	Nitroreductase
MNLKPGEA_	rbsC_9	0.588506333	0.40773371	Ribose import permease	NA	rbsC	Belongs to the binding-protein-d
MNLKPGEA_	ubiE	0.588500673	0.28798265	Ubiquinone/menaquinor	2.1.1.163	ubiE	Methyltransferase required for t
MNLKPGEA_	ytfJ	0.588336749	0.08647519	putative protein YtfJ	NA	ytfJ	transcriptional regulator
MNLKPGEA_	yqjD	0.587461201	0.01197544	putative protein YqjD	NA	yqjD	Membrane protein YqjD
MNLKPGEA_	srmB	0.58671083	0.20235647	ATP-dependent RNA heli	3.6.4.13	srmB	DEAD-box RNA helicase involved
MNLKPGEA_	lgoT_4	0.58650808	0.34032494	putative L-galactonate tr	NA	yjjL	Major facilitator superfamily
MNLKPGEA_	yjeH	0.585947856	0.48905029	L-methionine/branched-	NA	yjeH	amino acid
MNLKPGEA_	rpmE	0.58550059	0.16478261	50S ribosomal protein L3	NA	rpmE	Binds the 23S rRNA
MNLKPGEA_	pcaB	0.583084612	0.59460201	3-carboxy-cis,cis-mucona	5.5.1.2	pcaB	3-carboxy-cis,cis-muconate cyclo
MNLKPGEA_	yjjX	0.58077727	0.1488255	Inosine/xanthosine triph	3.6.1.-	yjjX	Phosphatase that hydrolyzes nor
MNLKPGEA_	MNLKPGEA	0.580111505	0.04822839	Epimerase family protei	NA	yfcH	epimerase
MNLKPGEA_	yfiH	0.579859165	0.10923788	Polyphenol oxidase	1.10.3.-	yfiH	Belongs to the multicopper oxida
MNLKPGEA_	MNLKPGEA	0.576750368	NA	hypothetical protein	NA	0	NmrA-like family
MNLKPGEA_	map_2	0.576080928	0.05562269	Methionine aminopeptic	3.4.11.18	map	Methionine aminopeptidase
MNLKPGEA_	ybeY	0.572848659	0.18080894	Endoribonuclease YbeY	3.1.-.-	ybeY	Single strand-specific metallo-en
MNLKPGEA_	MNLKPGEA	0.571127282	0.48603926	hypothetical protein	NA	yheV	nucleic-acid-binding protein con
MNLKPGEA_	ybjP	0.570262806	0.22385713	putative lipoprotein YbjP	NA	ybjP	Induced during stationary phase
MNLKPGEA_	astB_2	0.569879362	0.2261918	N-succinylarginine dihyd	3.5.3.23	astB	Catalyzes the hydrolysis of N(2)-
MNLKPGEA_	cueO	0.569079113	0.3422073	Blue copper oxidase Cue	NA	cueO	Multi-copper
MNLKPGEA_	dacC	0.569046219	0.08617536	D-alanyl-D-alanine carbc	3.4.16.4	dacC	Belongs to the peptidase S11 fa
MNLKPGEA_	fdhD	0.569029497	0.47443455	Sulfur carrier protein FdI	NA	fdhD	Required for formate dehydroge

MNLKPGEA_	MNLKPGEA	0.568779606	NA	hypothetical protein	NA	0	0
MNLKPGEA_	MNLKPGEA	0.567952815	0.31213546	hypothetical protein	NA	0	Belongs to the NiCoT transporte
MNLKPGEA_	MNLKPGEA	0.567869778	NA	hypothetical protein	NA	vasA	Type VI secretion
MNLKPGEA_	adhE_1	0.567611364	NA	Aldehyde-alcohol dehydr	NA	pduQ	alcohol dehydrogenase
MNLKPGEA_	gsiA_1	0.567611364	NA	Glutathione import ATP-	7.4.2.10	0	ATPase activity
MNLKPGEA_	MNLKPGEA	0.567611364	NA	hypothetical protein	NA	0	oxidoreductase
MNLKPGEA_	MNLKPGEA	0.567611364	NA	hypothetical protein	NA	0	0
MNLKPGEA_	MNLKPGEA	0.567611364	NA	hypothetical protein	NA	0	0
MNLKPGEA_	MNLKPGEA	0.567611364	NA	hypothetical protein	NA	yqjZ	Antibiotic biosynthesis monooxy
MNLKPGEA_	nrtA	0.567611364	NA	Nitrate/nitrite binding pı	NA	nasF	COG0715 ABC-type nitrate sulfo
MNLKPGEA_	pduD_1	0.567611364	NA	Propanediol dehydratase	4.2.1.28	0	dehydratase, medium subunit
MNLKPGEA_	aptA_1	0.565600268	NA	Apulose-4-phosphate tra	2.2.1.-	tktB	Transketolase
MNLKPGEA_	gudP_2	0.564920759	0.63884242	putative glucarate transp	NA	0	Major Facilitator Superfamily
MNLKPGEA_	mlc	0.564777424	0.15826306	Protein mlc	NA	mlc	Mlc, controls the expression of g
MNLKPGEA_	gspK	0.564695855	NA	Putative type II secretior	NA	gspK	COG3156 Type II secretory pathv
MNLKPGEA_	MNLKPGEA	0.564695855	NA	hypothetical protein	NA	0	TupA-like ATPgrasp
MNLKPGEA_	MNLKPGEA	0.564695855	NA	hypothetical protein	NA	0	NmrA-like family
MNLKPGEA_	MNLKPGEA	0.564695855	NA	hypothetical protein	NA	0	0
MNLKPGEA_	ssuC_2	0.564695855	NA	Putative aliphatic sulfon	NA	tauC	ABC-type nitrate sulfonate bicar
MNLKPGEA_	MNLKPGEA	0.564406527	0.49605462	hypothetical protein	NA	0	0
MNLKPGEA_	rbsC_10	0.562957924	0.3305496	Ribose import permease	NA	0	Belongs to the binding-protein-c
MNLKPGEA_	intS_1	0.562422634	0.51279028	Prophage integrase IntS	NA	0	Pfam:Arm-DNA-bind_3
MNLKPGEA_	ttuB_1	0.562386274	NA	Putative tartrate transpc	NA	0	Major facilitator superfamily
MNLKPGEA_	madA	0.56225358	NA	Acetyl-S-ACP:malonate /	2.3.1.187	mdcA	Malonate decarboxylase
MNLKPGEA_	MNLKPGEA	0.561534275	NA	hypothetical protein	NA	malF	transport
MNLKPGEA_	hmuU_2	0.560435349	NA	Hemin transport system	NA	0	Belongs to the binding-protein-c
MNLKPGEA_	ygjP	0.559306108	0.65210516	UTP pyrophosphatase	3.6.1.-	ygjP	WLM domain
MNLKPGEA_	metN2	0.558375459	NA	Methionine import ATP-I	3.6.3.-	metN	Part of the ABC transporter com
MNLKPGEA_	hdfR_4	0.558265984	0.64446591	HTH-type transcriptional	NA	0	Transcriptional regulator
MNLKPGEA_	fba	0.556848241	0.54988726	Fructose-bisphosphate a	4.1.2.13	fba	Aldolase

MNLKPGEA_	MNLKPGEA	0.556776054	0.38955838	hypothetical protein	NA	0	Protein of unknown function (DU
MNLKPGEA_	hypE	0.556518216	0.65462721	Carbamoyl dehydratase	4.2.1.-	hypE	hydrogenase expression formati
MNLKPGEA_	yijE	0.555994684	0.52675046	putative cystine transpor	NA	yijE	EamA-like transporter family
MNLKPGEA_	yoaK	0.555455755	0.54610599	putative membrane prot	NA	yoaK	0
MNLKPGEA_	MNLKPGEA	0.55491332	0.30403998	hypothetical protein	NA	0	Protein of unknown function (DU
MNLKPGEA_	MNLKPGEA	0.553399163	0.10629982	hypothetical protein	NA	yhjG	protein involved in outer membr
MNLKPGEA_	zapD	0.552498195	0.35230714	Cell division protein ZapI	NA	zapD	Cell division factor that enhance
MNLKPGEA_	MNLKPGEA	0.552162203	0.61013332	hypothetical protein	NA	0	0
MNLKPGEA_	hyfA_2	0.551085454	NA	Hydrogenase-4 compone	1.-.-.-	hydN	electron transport
MNLKPGEA_	MNLKPGEA	0.549610378	0.44506231	Endo-4-O-sulfatase	3.1.6.-	0	Sulfatase
MNLKPGEA_	ybdZ	0.549545547	NA	Enterobactin biosynthesi	NA	0	PFAM MbtH domain protein
MNLKPGEA_	leuB	0.547873096	0.54925129	3-isopropylmalate dehyc	1.1.1.85	leuB	Catalyzes the oxidation of 3-carb
MNLKPGEA_	MNLKPGEA	0.546999324	NA	hypothetical protein	NA	0	decarboxylase
MNLKPGEA_	fepB	0.546974107	0.13943795	Ferrienterobactin-bindin	NA	fepB	Periplasmic binding protein
MNLKPGEA_	zapB	0.546135481	0.09252067	Cell division protein ZapI	NA	zapB	Non-essential, abundant cell div
MNLKPGEA_	MNLKPGEA	0.544810971	0.5832339	hypothetical protein	NA	0	cellulase activity
MNLKPGEA_	ksdD	0.543010933	NA	3-oxosteroid 1-dehydrog	1.3.99.4	0	Succinate dehydrogenase fumar
MNLKPGEA_	norR_3	0.541386198	0.15308374	Anaerobic nitric oxide re	NA	0	transcriptional regulator
MNLKPGEA_	mdtD	0.541320253	0.32297869	Putative multidrug resist	NA	mdtD	Major facilitator superfamily
MNLKPGEA_	yfeY	0.540226376	0.57593141	putative protein YfeY	NA	yfeY	Protein of unknown function (DU
MNLKPGEA_	MNLKPGEA	0.539689262	0.24111335	hypothetical protein	NA	phnA	Alkylphosphonate utilization ope
MNLKPGEA_	gmuD_2	0.539022832	0.40385959	6-phospho-beta-glucosic	3.2.1.86	0	Belongs to the glycosyl hydrolas
MNLKPGEA_	yjbR	0.538808801	0.44255728	putative protein YjbR	NA	yjbR	protein conserved in bacteria
MNLKPGEA_	MNLKPGEA	0.537782141	0.16361833	hypothetical protein	NA	0	0
MNLKPGEA_	mobA	0.537655097	0.5480161	Molybdenum cofactor gu	2.7.7.77	mobA	Transfers a GMP moiety from G
MNLKPGEA_	fabG_1	0.536489364	NA	3-oxoacyl-[acyl-carrier-p	1.1.1.100	0	short-chain dehydrogenase
MNLKPGEA_	nagA	0.53604501	0.16231334	N-acetylglucosamine-6-p	3.5.1.25	nagA	Belongs to the metallo-depende
MNLKPGEA_	pduC	0.536029482	NA	Propanediol dehydratase	4.2.1.28	pduC	Dehydratase large subunit
MNLKPGEA_	chbA_5	0.534139739	0.08863366	PTS system N,N'-diacety	NA	chbA_4	Phosphotransferase System
MNLKPGEA_	mdtO	0.533597689	NA	Multidrug resistance pro	NA	0	Resistance protein

MNLKPGEA_	MNLKPGEA	0.533250442	0.39913727	hypothetical protein	NA	yjbD	YjbD family (DUF3811)
MNLKPGEA_	ybbJ	0.533224198	0.58165989	Inner membrane protein	NA	ybbJ	Membrane protein implicated ir
MNLKPGEA_	MNLKPGEA	0.531187597	0.13797155	hypothetical protein	NA	0	Antirestriction protein (ArdA)
MNLKPGEA_	MNLKPGEA	0.530994261	0.25013652	hypothetical protein	NA	ydiY	Salt-induced outer membrane pı
MNLKPGEA_	cydA_1	0.529866177	0.30486126	Cytochrome bd ubiquinol	1.10.3.-	cydA	oxidase, subunit
MNLKPGEA_	arnC	0.529320002	0.61713709	Undecaprenyl-phosphate	2.4.2.53	arnC	Catalyzes the transfer of 4-deox
MNLKPGEA_	ftsI_1	0.528149196	0.67169289	Peptidoglycan D,D-transp	3.4.16.4	ftsI	Catalyzes cross-linking of the pe
MNLKPGEA_	yqjA	0.5273488	0.31366494	Inner membrane protein	NA	yqjA	Inner membrane protein yqjA
MNLKPGEA_	MNLKPGEA	0.526414111	0.63568663	hypothetical protein	NA	yncA_3	COG0454 Histone acetyltransfer
MNLKPGEA_	ytfQ	0.526011552	0.35175297	ABC transporter periplas	NA	ytfQ	Periplasmic binding protein LacI
MNLKPGEA_	gshA	0.525165552	0.08796934	Glutamate--cysteine liga	6.3.2.2	gshA	Belongs to the glutamate--cyste
MNLKPGEA_	acpP	0.524036383	0.28961215	Acyl carrier protein	NA	acpP	Carrier of the growing fatty acid
MNLKPGEA_	xylA_1	0.522940581	0.2784927	Xylose isomerase	5.3.1.5	xylA	Belongs to the xylose isomerase
MNLKPGEA_	MNLKPGEA	0.522484717	0.67169289	hypothetical protein	NA	0	Putative inner membrane export
MNLKPGEA_	ycdZ	0.522185883	0.56655267	Inner membrane protein	NA	ycdZ	Protein of unknown function (DU
MNLKPGEA_	secE	0.52099101	0.04204192	Protein translocase subu	NA	secE	Essential subunit of the Sec prot
MNLKPGEA_	MNLKPGEA	0.520724465	0.59460201	hypothetical protein	NA	yraQ	permease
MNLKPGEA_	ygaZ_2	0.519144117	NA	Inner membrane protein	NA	ygaZ	AzlC protein
MNLKPGEA_	MNLKPGEA	0.518501241	0.27850291	hypothetical protein	NA	0	0
MNLKPGEA_	MNLKPGEA	0.517643069	0.50730841	hypothetical protein	NA	rimL	Acetyltransferases including N-a
MNLKPGEA_	MNLKPGEA	0.517618167	0.59747454	hypothetical protein	NA	0	0
MNLKPGEA_	MNLKPGEA	0.517536402	NA	hypothetical protein	NA	0	Binding-protein-dependent trans
MNLKPGEA_	MNLKPGEA	0.51751829	NA	hypothetical protein	NA	yciW	protein conserved in bacteria
MNLKPGEA_	MNLKPGEA	0.517325846	0.63464999	Tn3 family transposase I	NA	tnpA	Transposase
MNLKPGEA_	sotB_1	0.517212736	0.39712786	Sugar efflux transporter	NA	sotB	Major facilitator Superfamily
MNLKPGEA_	pat_1	0.517151132	0.02871059	Peptidyl-lysine N-acetylt	2.3.1.-	yfiQ	Acyl-CoA synthetase (NDP formi
MNLKPGEA_	argE_1	0.516943475	0.48957215	Acetylornithine deacetyla	3.5.1.16	dapE2	Acetylornithine deacetylase
MNLKPGEA_	hyfB	0.516394662	NA	Hydrogenase-4 compone	1.-.-.-	hycC	formate hydrogenlyase subunit 3
MNLKPGEA_	MNLKPGEA	0.5163667	0.44595243	ISNCY family transposas	NA	0	Transposase
MNLKPGEA_	MNLKPGEA	0.516274864	NA	hypothetical protein	NA	yaiI	Belongs to the UPF0178 family

MNLKPGEA_	baeS	0.515908759	NA	Signal transduction histi	2.7.13.3	baeS	PhoQ Sensor
MNLKPGEA_	dhaT	0.515734407	0.6446508	1,3-propanediol dehydro	1.1.1.202	dhaT	alcohol dehydrogenase
MNLKPGEA_	ppnN	0.5153509	0.25456094	Pyrimidine/purine nucle	3.2.2.-	ygdH	Rossmann fold nucleotide-bindi
MNLKPGEA_	msrA	0.515172761	0.04158675	Peptide methionine sulf	1.8.4.11	msrA	Has an important function as a r
MNLKPGEA_	zraR	0.514159494	0.67365142	Transcriptional regulato	NA	zraR	COG2204 Response regulator co
MNLKPGEA_	ygaM	0.512991189	0.14527734	putative protein YgaM	NA	ygaM	ribosome binding
MNLKPGEA_	oprM_3	0.512096681	0.56616033	Outer membrane protei	NA	oprM	membrane
MNLKPGEA_	MNLKPGEA	0.511818111	0.15848137	hypothetical protein	NA	yqeI	Transcriptional regulatory protei
MNLKPGEA_	xylB_2	0.511080308	NA	Xylulose kinase	2.7.1.17	xylB	xylulose kinase
MNLKPGEA_	ygiD	0.510814416	0.43419795	4,5-DOPA dioxygenase e	1.13.11.29	ygiD	dioxygenase
MNLKPGEA_	engB	0.509772435	0.1207877	putative GTP-binding pro	NA	engB	Necessary for normal cell divisic
MNLKPGEA_	amaB_1	0.509744398	NA	N-carbamoyl-L-amino ac	3.5.1.87	amaB	the allantoate amidohydrolase f
MNLKPGEA_	bdcR	0.509729364	NA	HTH-type transcriptional	NA	yjgJ	tetR family
MNLKPGEA_	MNLKPGEA	0.509071509	NA	Zinc-type alcohol dehydr	NA	0	Belongs to the zinc-containing a
MNLKPGEA_	hemL	0.507940219	0.37992681	Glutamate-1-semialdeh	5.4.3.8	hemL	Glutamate-1-semialdehyde ami
MNLKPGEA_	MNLKPGEA	0.507891146	NA	hypothetical protein	NA	#N/A	#N/A
MNLKPGEA_	tktB	0.506915621	0.04851835	Transketolase 2	2.2.1.1	tktA	Catalyzes the transfer of a two-c
MNLKPGEA_	gltC_3	0.505437178	NA	HTH-type transcriptional	NA	0	transcriptional regulator
MNLKPGEA_	MNLKPGEA	0.50509005	0.39318437	hypothetical protein	NA	0	0
MNLKPGEA_	MNLKPGEA	0.504730471	0.29272892	hypothetical protein	NA	0	KilA-N domain
MNLKPGEA_	MNLKPGEA	0.504426481	NA	hypothetical protein	NA	0	Protein of unknown function (DU
MNLKPGEA_	MNLKPGEA	0.503375748	0.408996	hypothetical protein	NA	0	0
MNLKPGEA_	yjiA	0.503115661	0.32746875	P-loop guanosine triphos	3.6.-.-	yjiA	cobalamin synthesis protein
MNLKPGEA_	nhaA_2	0.503062828	0.38014692	Na(+)/H(+) antiporter NI	NA	nhaA	Na( ) H( ) antiporter that extrude
MNLKPGEA_	ves	0.502442109	0.65552295	Protein Ves	NA	ydjR	protein conserved in bacteria
MNLKPGEA_	MNLKPGEA	0.502148501	0.45544669	hypothetical protein	NA	0	glyoxalase bleomycin resistance
MNLKPGEA_	fliY_3	0.502098033	NA	L-cystine-binding protei	NA	0	belongs to the bacterial solute-b
MNLKPGEA_	novR	0.501429293	0.69286427	Decarboxylase NovR	4.1.-.-	fucA	COG0235 Ribulose-5-phosphate
MNLKPGEA_	narJ	0.50114024	NA	Nitrate reductase molyb	NA	narJ	Nitrate reductase
MNLKPGEA_	garK_3	0.500684466	NA	Glycerate 2-kinase	2.7.1.165	0	Belongs to the glycerate kinase

MNLKPGEA_	deoD	0.499887467	0.22151059	Purine nucleoside phosp	2.4.2.1	deoD	Purine nucleoside phosphorylase
MNLKPGEA_	MNLKPGEA	0.499480854	NA	hypothetical protein	NA	0	0
MNLKPGEA_	dppC	0.4989845	NA	Dipeptide transport syste	NA	dppC	PFAM binding-protein-dependen
MNLKPGEA_	proW	0.498896502	NA	Glycine betaine/proline t	NA	proW	ABC-type proline glycine betaine
MNLKPGEA_	degS	0.495132861	0.25390754	Serine endoprotease Deg	3.4.21.107	degS	Belongs to the peptidase S1C fa
MNLKPGEA_	MNLKPGEA	0.494908487	NA	hypothetical protein	NA	0	decarboxylase
MNLKPGEA_	MNLKPGEA	0.494863912	0.16478261	hypothetical protein	NA	0	0
MNLKPGEA_	gltJ_2	0.494237877	NA	Glutamate/aspartate im	NA	gltJ	(ABC) transporter
MNLKPGEA_	MNLKPGEA	0.494237877	NA	hypothetical protein	NA	ytnP	Beta-lactamase
MNLKPGEA_	licH_2	0.493806009	NA	putative 6-phospho-beta	3.2.1.86	chbF	Family 4 glycosyl hydrolase
MNLKPGEA_	comR	0.493766884	0.16578199	HTH-type transcriptional	NA	ycfQ	Transcriptional regulator
MNLKPGEA_	MNLKPGEA	0.492487334	0.43546434	hypothetical protein	NA	0	0
MNLKPGEA_	eamA	0.491567743	0.68384479	putative amino-acid met	NA	eamA	of the drug metabolite transport
MNLKPGEA_	MNLKPGEA	0.491397169	NA	hypothetical protein	NA	#N/A	#N/A
MNLKPGEA_	MNLKPGEA	0.491397169	NA	hypothetical protein	NA	0	Dehydratase medium subunit
MNLKPGEA_	MNLKPGEA	0.491397169	NA	hypothetical protein	NA	0	Domain of unknown function (DU
MNLKPGEA_	MNLKPGEA	0.491397169	NA	hypothetical protein	NA	#N/A	#N/A
MNLKPGEA_	MNLKPGEA	0.491397169	NA	hypothetical protein	NA	#N/A	#N/A
MNLKPGEA_	ompA_2	0.491397169	NA	Outer membrane protein	NA	0	Belongs to the ompA family
MNLKPGEA_	outC	0.491397169	NA	Type II secretion system	NA	gspC	General secretion pathway prote
MNLKPGEA_	MNLKPGEA	0.491285215	0.21067744	hypothetical protein	NA	0	Protein of unknown function (DU
MNLKPGEA_	MNLKPGEA	0.491271328	0.29682534	hypothetical protein	NA	0	conserved protein, contains doul
MNLKPGEA_	MNLKPGEA	0.491233022	0.38671447	hypothetical protein	NA	yebO	YebO-like protein
MNLKPGEA_	ddpF	0.490261365	NA	putative D,D-dipeptide tr	NA	gsiA_3	(ABC) transporter
MNLKPGEA_	MNLKPGEA	0.490261365	NA	IS3 family transposase IS	NA	0	Transposase and inactivated der
MNLKPGEA_	MNLKPGEA	0.490261365	NA	hypothetical protein	NA	0	Phage tail assembly chaperone,
MNLKPGEA_	pduE_2	0.490261365	NA	Propanediol dehydratase	4.2.1.28	pduE	Dehydratase Small Subunit
MNLKPGEA_	yhdJ	0.490261365	NA	DNA adenine methyltrar	2.1.1.72	VP0394	Belongs to the N(4) N(6)-methyl
MNLKPGEA_	queD	0.490011545	0.35048869	6-carboxy-5,6,7,8-tetrah	4.1.2.50	queD	synthase
MNLKPGEA_	cra_2	0.489374419	0.24981206	Catabolite repressor/act	NA	fruR	Transcriptional

MNLKPGEA_	mltF_1	0.488774297	0.65552295	Membrane-bound lytic n	4.2.2.-	pheC	Belongs to the bacterial solute-b
MNLKPGEA_	cca	0.48856845	0.21966067	Multifunctional CCA prot	NA	cca	Catalyzes the addition and repai
MNLKPGEA_	betI_1	0.487939591	NA	HTH-type transcriptional	NA	0	Transcriptional regulator
MNLKPGEA_	fruA_3	0.487867369	0.49653856	PTS system fructose-spe	NA	0	and phosphoenolpyruvate-deper
MNLKPGEA_	ybhL	0.487321038	0.09490295	Inner membrane protein	NA	ybhL	Belongs to the BI1 family
MNLKPGEA_	MNLKPGEA	0.487009787	0.65038236	hypothetical protein	NA	0	Acetyltransferases, including N-
MNLKPGEA_	chiQ	0.486856318	0.3635011	putative lipoprotein ChiC	NA	ybfN	YbfN-like lipoprotein
MNLKPGEA_	dmlR_5	0.486424745	0.68054746	HTH-type transcriptional	NA	ptxR	transcriptional regulator
MNLKPGEA_	menH_3	0.485557961	0.48159085	2-succinyl-6-hydroxy-2,4	4.2.99.20	0	Serine aminopeptidase, S33
MNLKPGEA_	mdh_1	0.485446259	0.24479274	Malate dehydrogenase	1.1.1.37	mdh	Catalyzes the reversible oxidatio
MNLKPGEA_	quiA	0.485164003	0.25356654	Quinate/shikimate dehy	1.1.5.8	quiA	Dehydrogenase
MNLKPGEA_	yjhP	0.48510844	0.66327114	putative protein YjhP	NA	0	Methyltransferase domain
MNLKPGEA_	MNLKPGEA	0.484908292	0.41530145	hypothetical protein	NA	yjeJ	YjeJ-like
MNLKPGEA_	MNLKPGEA	0.484354536	0.15035623	hypothetical protein	NA	0	Toxin YafO, type II toxin-antitoxi
MNLKPGEA_	potA_2	0.48387582	0.37244979	Spermidine/putrescine i	7.6.2.11	ydcT	Part of the ABC transporter com
MNLKPGEA_	ecpE_1	0.483566304	NA	putative fimbrial chaper	NA	ecpE	Part of the ecpRABCDE operon,
MNLKPGEA_	cspC	0.482917907	0.05160114	Cold shock-like protein C	NA	cspC	Cold shock
MNLKPGEA_	rsxG	0.482751256	0.4212445	Ion-translocating oxidore	7.-.-.-	rnfG	Part of a membrane complex in
MNLKPGEA_	moxC	0.482584297	NA	Putative monooxygenase	1.14.-.-	moxC	monooxygenase
MNLKPGEA_	adhP_1	0.48227095	0.27809794	Alcohol dehydrogenase,	1.1.1.1	adhP	alcohol dehydrogenase
MNLKPGEA_	pgrR_10	0.481971271	0.28447198	HTH-type transcriptional	NA	0	transcriptional regulator
MNLKPGEA_	cutD	0.48194319	NA	Choline trimethylamine-	1.97.1.-	ybiY	Pyruvate formate lyase-activatir
MNLKPGEA_	MNLKPGEA	0.48194319	NA	ISNCY family transposas	NA	0	PFAM Integrase catalytic
MNLKPGEA_	pduB	0.48194319	NA	Propanediol utilization p	NA	pduB	may be involved in the formatio
MNLKPGEA_	manZ_3	0.481604278	0.67623958	PTS system mannose-sp	NA	0	PTS mannose transporter subuni
MNLKPGEA_	MNLKPGEA	0.481229352	0.10168254	hypothetical protein	NA	ynfB	Belongs to the UPF0482 family
MNLKPGEA_	astD_1	0.480602575	NA	N-succinylglutamate 5-s	1.2.1.71	pduP	Aldehyde dehydrogenase
MNLKPGEA_	luxA	0.480602575	NA	Alkanal monooxygenase	1.14.14.3	MA20_0(	COG2141 Coenzyme F420-deper
MNLKPGEA_	MNLKPGEA	0.480602575	NA	hypothetical protein	NA	#N/A	#N/A
MNLKPGEA_	rutC_2	0.480602575	NA	Putative aminoacrylate p	1.-.-.-	rutC	May reduce aminoacrylate perac

MNLKPGEA_	MNLKPGEA	0.479524759	NA	hypothetical protein	NA	0	0
MNLKPGEA_	uhpC	0.479524759	NA	Membrane sensor protei	NA	uhpC	transporter
MNLKPGEA_	metQ_2	0.479267054	NA	D-methionine-binding lip	NA	metQ_3	Belongs to the nlpA lipoprotein f
MNLKPGEA_	MNLKPGEA	0.479267054	NA	hypothetical protein	NA	0	type VI secretion protein
MNLKPGEA_	MNLKPGEA	0.479267054	NA	hypothetical protein	NA	0	Type IV VI secretion system
MNLKPGEA_	MNLKPGEA	0.479267054	NA	hypothetical protein	NA	0	PRD domain protein
MNLKPGEA_	MNLKPGEA	0.479267054	NA	hypothetical protein	NA	0	0
MNLKPGEA_	MNLKPGEA	0.478016536	0.46626672	hypothetical protein	NA	#N/A	#N/A
MNLKPGEA_	MNLKPGEA	0.477321367	NA	hypothetical protein	NA	0	0
MNLKPGEA_	MNLKPGEA	0.477321367	NA	hypothetical protein	NA	0	0
MNLKPGEA_	tauB	0.477321367	NA	Taurine import ATP-bind	7.6.2.7	tauB	Part of the ABC transporter com
MNLKPGEA_	yadV_1	0.477321367	NA	putative fimbrial chaper	NA	cupB4	Pili and flagellar-assembly chap
MNLKPGEA_	iolG_4	0.477257348	NA	Inositol 2-dehydrogenase	1.1.1.369	0	oxidoreductase
MNLKPGEA_	mdcC	0.477257348	NA	Malonate decarboxylase	NA	mdcC	Subunit of malonate decarboxyla
MNLKPGEA_	MNLKPGEA	0.477257348	NA	hypothetical protein	NA	#N/A	#N/A
MNLKPGEA_	MNLKPGEA	0.477257348	NA	hypothetical protein	NA	pduT	propanediol utilization protein
MNLKPGEA_	MNLKPGEA	0.477257348	NA	Isoxanthopterin deamina	3.5.4.11	atzB	COG0402 Cytosine deaminase a
MNLKPGEA_	MNLKPGEA	0.477257348	NA	hypothetical protein	NA	fimA	Major pilin protein
MNLKPGEA_	MNLKPGEA	0.477257348	NA	hypothetical protein	NA	0	NMT1-like family
MNLKPGEA_	MNLKPGEA	0.477257348	NA	IS3 family transposase IS	NA	0	Transposase
MNLKPGEA_	MNLKPGEA	0.477257348	NA	IS1 family transposase IS	NA	0	cog cog1662
MNLKPGEA_	MNLKPGEA	0.477257348	NA	hypothetical protein	NA	#N/A	#N/A
MNLKPGEA_	rluA_1	0.477257348	NA	Dual-specificity RNA pse	5.4.99.28	rluA_2	Pseudouridine synthase
MNLKPGEA_	MNLKPGEA	0.477169849	0.25530329	hypothetical protein	NA	0	lactoylglutathione lyase activity
MNLKPGEA_	epsM	0.475934432	NA	Type II secretion system	NA	gspM	involved in a type II secretion sys
MNLKPGEA_	gspH	0.475934432	NA	Putative type II secretior	NA	0	general secretion pathway prote
MNLKPGEA_	MNLKPGEA	0.475934432	NA	hypothetical protein	NA	0	0
MNLKPGEA_	MNLKPGEA	0.475934432	NA	hypothetical protein	NA	0	Type VI secretion lipoprotein, Va
MNLKPGEA_	MNLKPGEA	0.475934432	NA	hypothetical protein	NA	0	Protein of unknown function (DU
MNLKPGEA_	MNLKPGEA	0.475934432	NA	hypothetical protein	NA	0	Protein of unknown function (DU

MNLKPGEA_	MNLKPGEA	0.475934432	NA	hypothetical protein	NA	nucD	lysozyme
MNLKPGEA_	MNLKPGEA	0.475934432	NA	hypothetical protein	NA	0	tail protein x
MNLKPGEA_	MNLKPGEA	0.475934432	NA	hypothetical protein	NA	0	PTS system fructose IIA compon
MNLKPGEA_	MNLKPGEA	0.475934432	NA	hypothetical protein	NA	0	Protein of unknown function (DU
MNLKPGEA_	MNLKPGEA	0.475934432	NA	hypothetical protein	NA	0	PerC transcriptional activator
MNLKPGEA_	rbsC_2	0.475934432	NA	Ribose import permease	NA	0	Belongs to the binding-protein-d
MNLKPGEA_	rhaA	0.475934432	NA	L-rhamnose isomerase	5.3.1.14	rhaA	L-rhamnose isomerase
MNLKPGEA_	ybiS	0.475654259	0.33223224	putative L,D-transpeptid	2.-.-.-	ybiS	ErfK YbiS YcfS YnhG family prote
MNLKPGEA_	metF	0.474161011	0.45706472	5,10-methylenetetrahydr	1.5.1.20	metF	Methylenetetrahydrofolate redu
MNLKPGEA_	yabI_2	0.472856865	0.38963735	Inner membrane protein	NA	yabI	membrane-associated protein
MNLKPGEA_	eutM	0.472633009	NA	Ethanolamine utilization	NA	eutM	BMC domain
MNLKPGEA_	eutN	0.472633009	NA	Ethanolamine utilization	NA	eutN	Ethanolamine utilization protein
MNLKPGEA_	MNLKPGEA	0.472633009	NA	hypothetical protein	NA	#N/A	#N/A
MNLKPGEA_	MNLKPGEA	0.472633009	NA	hypothetical protein	NA	0	Bacteriophage holin family HP1
MNLKPGEA_	MNLKPGEA	0.472633009	NA	hypothetical protein	NA	pilA	Belongs to the N-Me-Phe pilin fa
MNLKPGEA_	phnF	0.472633009	NA	putative transcriptional r	NA	phnF	Transcriptional regulator
MNLKPGEA_	phnK	0.472633009	NA	Putative phosphonates u	NA	phnK	phosphonate C-P lyase system p
MNLKPGEA_	ydjZ	0.472633009	NA	TVP38/TMEM64 family i	NA	ydjZ	TVP38 TMEM64 family inner me
MNLKPGEA_	yecS_3	0.472633009	NA	L-cystine transport syste	NA	0	(ABC) transporter
MNLKPGEA_	metN_1	0.471826273	NA	Methionine import ATP-l	3.6.3.-	0	Part of the ABC transporter com
MNLKPGEA_	MNLKPGEA	0.471826273	NA	hypothetical protein	NA	#N/A	#N/A
MNLKPGEA_	MNLKPGEA	0.471826273	NA	hypothetical protein	NA	0	Terminase, ATPase subunit
MNLKPGEA_	phnV	0.471826273	NA	Putative 2-aminoethylph	NA	phnV	TIGRFAM 2-aminoethylphospho
MNLKPGEA_	rcsC_1	0.470234959	0.53358531	Sensor histidine kinase F	2.7.13.3	evgS	PhoQ Sensor
MNLKPGEA_	malT_1	0.470005619	0.08301768	HTH-type transcriptional	NA	malT	Positively regulates the transcrip
MNLKPGEA_	iolG_2	0.469841274	0.66055687	Inositol 2-dehydrogenase	1.1.1.369	0	oxidoreductase
MNLKPGEA_	gltA_2	0.468011169	NA	Citrate synthase	2.3.3.16	0	Belongs to the citrate synthase f
MNLKPGEA_	malG_1	0.467514206	NA	Maltose/maltodextrin tr	NA	ganQ	transport
MNLKPGEA_	raiA	0.464970838	0.03881724	Ribosome-associated inl	NA	raiA	Sigma 54 modulation protein
MNLKPGEA_	umuD_4	0.46483844	0.57273586	Protein UmuD	3.4.21.-	umuD	Peptidase S24-like

MNLKPGEA_	bglK	0.464216305	NA	Beta-glucoside kinase	2.7.1.85	bglK	ROK family
MNLKPGEA_	fabG_3	0.463023241	NA	3-oxoacyl-[acyl-carrier-p	1.1.1.100	fabG	Belongs to the short-chain dehyd
MNLKPGEA_	MNLKPGEA	0.463011787	0.26623055	hypothetical protein	NA	0	Polysaccharide pyruvyl transfera
MNLKPGEA_	MNLKPGEA	0.462226546	NA	hypothetical protein	NA	livM	Belongs to the binding-protein-d
MNLKPGEA_	appA	0.460764058	0.66502191	Oligopeptide-binding pro	NA	0	ABC transporter substrate-bindi
MNLKPGEA_	rlhA_1	0.460573988	0.61003708	23S rRNA 5-hydroxycytid	NA	yegQ	protease
MNLKPGEA_	MNLKPGEA	0.460540978	0.4530702	hypothetical protein	NA	0	0
MNLKPGEA_	MNLKPGEA	0.460452504	0.15222348	hypothetical protein	NA	0	0
MNLKPGEA_	narI	0.459808263	0.66615114	Respiratory nitrate reduc	1.7.5.1	narI	nitrate reductase, gamma subur
MNLKPGEA_	tsaC	0.459723494	0.51348612	Threonylcarbamoyl-AMP	2.7.7.87	tsaC	Required for the formation of a
MNLKPGEA_	entF	0.458761238	0.36167206	Enterobactin synthase co	2.7.7.-	entF	amino acid activation for nonrib
MNLKPGEA_	pqqD	0.45701262	NA	PqqA binding protein	NA	pqqD	With PqqC converts a biosynthet
MNLKPGEA_	MNLKPGEA	0.455010913	0.43578441	hypothetical protein	NA	0	antiporter activity
MNLKPGEA_	MNLKPGEA	0.453703823	0.57057789	hypothetical protein	NA	ycaQ	protein conserved in bacteria
MNLKPGEA_	iolI	0.453313961	NA	Inosose isomerase	5.3.99.11	iolI	isomerase
MNLKPGEA_	astA_2	0.453020091	0.45216252	Arginine N-succinyltrans	2.3.1.109	astA	arginine N-succinyltransferase
MNLKPGEA_	xerD_2	0.451909925	0.5390143	Tyrosine recombinase Xe	NA	0	Belongs to the 'phage' integrase
MNLKPGEA_	yliI	0.450830791	0.48766522	Aldose sugar dehydroger	1.1.5.-	yliI	glucose sorbosone
MNLKPGEA_	gmuB	0.448579747	NA	PTS system oligo-beta-m	2.7.1.205	0	PTS system, Lactose/Cellobiose
MNLKPGEA_	yabI_1	0.448457716	NA	Inner membrane protein	NA	0	FtsZ-dependent cytokinesis
MNLKPGEA_	narH	0.447927347	0.67612396	Respiratory nitrate reduc	1.7.5.1	narH	nitrate reductase beta subunit
MNLKPGEA_	eno	0.447724432	0.22455143	Enolase	4.2.1.11	eno	Catalyzes the reversible conversi
MNLKPGEA_	dmlR_8	0.4476419	0.32271923	HTH-type transcriptional	NA	0	transcriptional regulator
MNLKPGEA_	chbF	0.447476634	0.71443185	6-phospho-beta-glucosic	3.2.1.86	chbF	Catalyzes the fromation of N-ac
MNLKPGEA_	rbsC_5	0.447026475	0.67612396	Ribose import permease	NA	rbsC1	Belongs to the binding-protein-d
MNLKPGEA_	phnW	0.446479033	0.67365142	2-aminoethylphosphonat	2.6.1.37	phnW	Belongs to the class-V pyridoxal-
MNLKPGEA_	rarA	0.446037903	0.35849725	Replication-associated r	NA	rarA	ATPase related to the helicase s
MNLKPGEA_	MNLKPGEA	0.445960566	0.57971516	hypothetical protein	NA	0	Domain of unknown function (DU
MNLKPGEA_	MNLKPGEA	0.445782677	0.62792975	hypothetical protein	NA	YPO1991	isomerase
MNLKPGEA_	MNLKPGEA	0.445502552	0.48394449	hypothetical protein	NA	0	AAA ATPase domain

MNLKPGEA_	MNLKPGEA	0.442837684	0.49630565	hypothetical protein	NA	0	Tail length tape measure protei
MNLKPGEA_	lrp_1	0.442300196	0.59113864	Leucine-responsive regul	NA	0	transcriptional regulator
MNLKPGEA_	mtnK	0.4407911	0.74042734	Methylthioribose kinase	2.7.1.100	mtnK	Catalyzes the phosphorylation of
MNLKPGEA_	yajL	0.440709396	0.66998353	Protein/nucleic acid degl	3.1.2.-	thiJ	TIGRFAM DJ-1 family protein
MNLKPGEA_	MNLKPGEA	0.440652064	0.59986331	hypothetical protein	NA	ydfU	Protein of unknown function (DU
MNLKPGEA_	mhpB	0.440131481	NA	2,3-dihydroxyphenylprop	1.13.11.16	mhpB	Catalyzes the non-heme iron(II)-
MNLKPGEA_	MNLKPGEA	0.440131481	NA	hypothetical protein	NA	0	0
MNLKPGEA_	epsE_2	0.439615897	NA	Type II secretion system	NA	hofB	Type II secretory pathway, ATPa
MNLKPGEA_	gsiC_2	0.439615897	NA	Glutathione transport sy	NA	0	PFAM binding-protein-dependen
MNLKPGEA_	MNLKPGEA	0.439615897	NA	hypothetical protein	NA	#N/A	#N/A
MNLKPGEA_	MNLKPGEA	0.439615897	NA	hypothetical protein	NA	outB	Type II secretion system protein
MNLKPGEA_	phnH	0.439615897	NA	Alpha-D-ribose 1-methyl	2.7.8.37	phnH	phosphonate C-P lyase system p
MNLKPGEA_	MNLKPGEA	0.439430617	0.58094556	hypothetical protein	NA	0	Transcriptional regulator, AbiEi a
MNLKPGEA_	purR_2	0.43891909	0.39237172	HTH-type transcriptional	NA	purR	Is the main repressor of the gen
MNLKPGEA_	eutC_1	0.438838263	NA	Ethanolamine ammonia-	4.3.1.7	eutC	Belongs to the EutC family
MNLKPGEA_	MNLKPGEA	0.438838263	NA	ISNCY family transposas	NA	0	PFAM Integrase catalytic
MNLKPGEA_	MNLKPGEA	0.438838263	NA	hypothetical protein	NA	0	0
MNLKPGEA_	MNLKPGEA	0.438838263	NA	hypothetical protein	NA	0	transcriptional regulator
MNLKPGEA_	MNLKPGEA	0.438838263	NA	IS3 family transposase IS	NA	0	Transposase
MNLKPGEA_	ndmA	0.438838263	NA	Methylxanthine N1-dem	1.14.13.178	vanA	Phenylpropionate dioxygenase a
MNLKPGEA_	nimT	0.438838263	NA	2-nitroimidazole transpo	NA	yeaN	Major facilitator superfamily
MNLKPGEA_	rafB_2	0.438838263	NA	Raffinose permease	NA	0	Major facilitator superfamily
MNLKPGEA_	glnQ_6	0.438469856	0.55337223	Glutamine transport ATF	3.6.3.-	gltL	(ABC) transporter
MNLKPGEA_	otsA	0.437874737	0.28928657	Trehalose-6-phosphate s	2.4.1.15	otsA	Probably involved in the osmopr
MNLKPGEA_	MNLKPGEA	0.437786888	NA	hypothetical protein	NA	0	Type VI secretion system
MNLKPGEA_	MNLKPGEA	0.437786888	NA	hypothetical protein	NA	lysB	regulatory protein
MNLKPGEA_	xerC_6	0.437786888	NA	Tyrosine recombinase Xe	NA	0	Phage integrase, N-terminal SAI
MNLKPGEA_	derI	0.436991632	NA	D-erythrulose-4-phospha	5.3.1.34	rpiB	Ribose 5-phosphate isomerase
MNLKPGEA_	pduA_1	0.436991632	NA	Propanediol utilization p	NA	pduJ	Carbon dioxide concentrating me
MNLKPGEA_	MNLKPGEA	0.43698771	0.41920715	hypothetical protein	NA	#N/A	#N/A

MNLKPGEA_	MNLKPGEA	0.436456278	NA	hypothetical protein	NA	0	0
MNLKPGEA_	MNLKPGEA	0.436456278	NA	hypothetical protein	NA	0	mannose-6-phosphate isomeras
MNLKPGEA_	vldW_1	0.436456278	NA	Validamycin A dioxygena	1.14.11.52	efe_1	Belongs to the iron ascorbate-de
MNLKPGEA_	tatB	0.436224949	0.29125764	Sec-independent protein	NA	tatB	Part of the twin-arginine translo
MNLKPGEA_	ftsE	0.435923337	0.38646682	Cell division ATP-binding	NA	ftsE	cell division ATP-binding protein
MNLKPGEA_	rfaH	0.435282699	0.23651627	Transcription antitermin	NA	rfaH	Enhances distal genes transcript
MNLKPGEA_	MNLKPGEA	0.43262558	0.67612396	hypothetical protein	NA	0	B3 4 domain
MNLKPGEA_	MNLKPGEA	0.432476204	0.59460201	Invasin	NA	ychO	entry into host
MNLKPGEA_	MNLKPGEA	0.431831608	0.61269213	hypothetical protein	NA	0	Transcriptional regulator, LacI fa
MNLKPGEA_	rutB_2	0.431074077	0.69096001	Peroxyureidoacrylate/ure	3.5.1.110	0	Isochorismatase
MNLKPGEA_	MNLKPGEA	0.429720008	0.7032272	hypothetical protein	NA	vllY	4-hydroxyphenylpyruvate dioxyge
MNLKPGEA_	acrE	0.429686758	NA	Multidrug export protein	NA	acrE	Belongs to the membrane fusion
MNLKPGEA_	MNLKPGEA	0.429108383	0.28220528	hypothetical protein	NA	yedD	(Lipo)protein
MNLKPGEA_	sacA	0.428779459	NA	Sucrose-6-phosphate hyd	3.2.1.26	sacA	invertase
MNLKPGEA_	sppA	0.427146356	0.28205319	Protease 4	3.4.21.-	sppA	Signal peptide peptidase
MNLKPGEA_	MNLKPGEA	0.426003661	0.52978697	hypothetical protein	NA	0	Transcriptional
MNLKPGEA_	ycaC	0.425559908	0.58798723	putative hydrolase YcaC	4.-.-.-	slsA	COG1335 Amidases related to n
MNLKPGEA_	pgrR_2	0.425396455	NA	HTH-type transcriptional	NA	0	Transcriptional regulator
MNLKPGEA_	cobC_2	0.425279509	0.2313451	Adenosylcobalamin/alph	3.1.3.73	gpmB	Belongs to the phosphoglycerate
MNLKPGEA_	yijD	0.424636565	0.36677274	Inner membrane protein	NA	yijD	membrane
MNLKPGEA_	pepB	0.424210736	0.33539318	Peptidase B	3.4.11.23	pepB	Probably plays an important role
MNLKPGEA_	ftsY	0.422349798	0.26623055	Signal recognition partic	NA	ftsY	Involved in targeting and insertio
MNLKPGEA_	ilvI_2	0.422077075	0.59316594	Acetolactate synthase is	2.2.1.6	ilvI	acetolactate synthase
MNLKPGEA_	dnaT_2	0.421887314	0.55789604	Primosomal protein 1	NA	dnaT	it is also involved in inducing sta
MNLKPGEA_	ravA	0.421798441	0.38240071	ATPase RavA	3.6.3.-	ravA	Functions as an ATPase. May pla
MNLKPGEA_	araA	0.421541995	0.63221268	L-arabinose isomerase	5.3.1.4	araA	Catalyzes the conversion of L-ara
MNLKPGEA_	ycgJ	0.421264582	0.64446591	putative methyltransfera	2.1.1.-	yafE	methyltransferase
MNLKPGEA_	norR_2	0.419990939	0.53258276	Anaerobic nitric oxide re	NA	norR	transcriptional regulator
MNLKPGEA_	MNLKPGEA	0.419592869	NA	hypothetical protein	NA	#N/A	#N/A
MNLKPGEA_	lyx_1	0.419310123	NA	L-xylulose/3-keto-L-gulo	2.7.1.-	lyx	Belongs to the FGGY kinase fam

MNLKPGEA_	MNLKPGEA	0.418620938	NA	ISNCY family transposas	NA	0	Transposase
MNLKPGEA_	MNLKPGEA	0.418620938	NA	IS3 family transposase IS	NA	0	Transposase
MNLKPGEA_	MNLKPGEA	0.418620938	NA	hypothetical protein	NA	0	Protein of unknown function (DU
MNLKPGEA_	phnJ	0.418620938	NA	Alpha-D-ribose 1-methyl	4.7.1.1	phnJ	Catalyzes the breakage of the C-
MNLKPGEA_	sorB_1	0.418620938	NA	PTS system sorbose-spe	2.7.1.206	0	PTS system sorbose subfamily II
MNLKPGEA_	puuR	0.418575235	0.57652599	HTH-type transcriptional	NA	puuR	Helix-turn-helix domain
MNLKPGEA_	panD	0.418487234	0.388382	Aspartate 1-decarboxyla	4.1.1.11	panD	Catalyzes the pyruvoyl-dependen
MNLKPGEA_	arsB_2	0.418177997	0.65262788	Arsenical pump membra	NA	arsB	Involved in arsenical resistance.
MNLKPGEA_	MNLKPGEA	0.418141544	NA	hypothetical protein	NA	0	0
MNLKPGEA_	rnr	0.417603626	0.20077024	Ribonuclease R	3.1.13.1	rnr	3'-5' exoribonuclease that releas
MNLKPGEA_	MNLKPGEA	0.417565101	NA	hypothetical protein	NA	0	Glyoxalase-like domain
MNLKPGEA_	ttr	0.417565101	NA	Acetyltransferase	2.3.1.-	ttr	histone acetyltransferase HPA2 a
MNLKPGEA_	ssuB_1	0.41684318	NA	Aliphatic sulfonates imp	3.6.3.-	0	(ABC) transporter
MNLKPGEA_	MNLKPGEA	0.416316244	0.60652436	hypothetical protein	NA	yfeC	Negative Regulator
MNLKPGEA_	rbn_2	0.415694985	NA	Ribonuclease BN	3.1.26.11	0	of the beta-lactamase superfam
MNLKPGEA_	MNLKPGEA	0.415626965	NA	hypothetical protein	NA	0	Pectate lyase superfamily protei
MNLKPGEA_	lpxM	0.414665165	0.34047961	Lipid A biosynthesis myri	2.3.1.243	lpxM	Catalyzes the transfer of myrista
MNLKPGEA_	MNLKPGEA	0.414025197	0.73104251	hypothetical protein	NA	yicG	Membrane
MNLKPGEA_	rimJ	0.414012889	0.64766406	[Ribosomal protein S5]-a	2.3.1.267	rimJ	COG1670 Acetyltransferases, inc
MNLKPGEA_	scrY_3	0.413940192	NA	Sucrose porin	NA	scrY	Maltoporin (phage lambda and r
MNLKPGEA_	yafP_2	0.412862513	0.73234136	putative N-acetyltransfe	2.3.1.-	yafP	SOS response
MNLKPGEA_	dmlR_1	0.412100593	NA	HTH-type transcriptional	NA	gstR	transcriptional regulator
MNLKPGEA_	MNLKPGEA	0.411743949	0.6202708	hypothetical protein	NA	pfpI	Intracellular protease
MNLKPGEA_	hsrA_2	0.411591737	0.49630565	putative transport protei	NA	hsrA	Major facilitator superfamily
MNLKPGEA_	glmS_1	0.410874805	NA	Glutamine--fructose-6-p	2.6.1.16	0	glucosamine--fructose-6-phosph
MNLKPGEA_	ppx	0.410115701	0.13552919	Exopolyphosphatase	3.6.1.11	ppx	Catalyzes the conversion of pppG
MNLKPGEA_	mutH	0.40993744	0.68848745	DNA mismatch repair pr	NA	mutH	Sequence-specific endonuclease
MNLKPGEA_	resA	0.409634296	NA	Thiol-disulfide oxidoredu	NA	scsD	COG0526 Thiol-disulfide isomera
MNLKPGEA_	btuD_4	0.408484733	NA	Vitamin B12 import ATP	7.6.2.8	0	ABC-type nitrate sulfonate bicar
MNLKPGEA_	glpC	0.408484733	NA	Anaerobic glycerol-3-pho	NA	glpC	dehydrogenase subunit C

MNLKPGEA_ pncC_1	0.408452162	0.73611676	Nicotinamide-nucleotide	3.5.1.42	ygaD	Belongs to the CinA family
MNLKPGEA_ rseC	0.408425873	0.41977646	Protein RseC	NA	rseC	Positive regulator of
MNLKPGEA_ MNLKPGEA	0.408385877	0.51295412	hypothetical protein	NA	ydhI	Protein of unknown function (DU
MNLKPGEA_ MNLKPGEA	0.407676947	NA	hypothetical protein	NA	0	0
MNLKPGEA_ otnK_1	0.407676947	NA	3-oxo-tetronate kinase	2.7.1.217	ygbK	Putative nucleotide-binding of su
MNLKPGEA_ thiO	0.407676947	NA	Glycine oxidase	1.4.3.19	0	D-amino acid
MNLKPGEA_ yraI_1	0.407676947	NA	putative fimbrial chaper	NA	0	chaperone
MNLKPGEA_ ddpD	0.407427612	NA	putative D,D-dipeptide tr	NA	oppD	Belongs to the ABC transporter s
MNLKPGEA_ MNLKPGEA	0.407427612	NA	IS3 family transposase IS	NA	0	Transposase and inactivated der
MNLKPGEA_ rutF	0.407427612	NA	FMN reductase (NADH) I	1.5.1.42	rutF	Catalyzes the reduction of FMN
MNLKPGEA_ ddrA_1	0.406664063	NA	Diol dehydratase-reactiv	NA	0	glycerol dehydratase
MNLKPGEA_ dgoK1_2	0.405843282	NA	putative 2-dehydro-3-de	2.7.1.58	dgoK	2-keto-3-deoxy-galactonokinase
MNLKPGEA_ fabG_12	0.405843282	NA	3-oxoacyl-[acyl-carrier-p	1.1.1.100	MA20_35	Belongs to the short-chain dehyd
MNLKPGEA_ MNLKPGEA	0.405843282	NA	hypothetical protein	NA	0	COG1028 Dehydrogenases with
MNLKPGEA_ MNLKPGEA	0.405807962	0.58998059	hypothetical protein	NA	0	0
MNLKPGEA_ pgpB	0.405760916	0.44506231	Phosphatidylglycerophos	3.1.3.27	pgpB	phosphatidylglycerophosphatase
MNLKPGEA_ MNLKPGEA	0.404698592	0.38090165	hypothetical protein	NA	rnfH	Belongs to the UPF0125 (RnfH) f
MNLKPGEA_ MNLKPGEA	0.404231914	NA	hypothetical protein	NA	pduH	Dehydratase medium subunit
MNLKPGEA_ MNLKPGEA	0.404231914	NA	hypothetical protein	NA	0	Family of unknown function (DU
MNLKPGEA_ gsiD_3	0.403734413	NA	Glutathione transport sy	NA	MA20_19	N-terminal TM domain of oligop
MNLKPGEA_ MNLKPGEA	0.402848307	NA	hypothetical protein	NA	ppdC	Prepilin peptidase dependent pr
MNLKPGEA_ MNLKPGEA	0.402848307	NA	hypothetical protein	NA	MA20_36	Endoribonuclease
MNLKPGEA_ MNLKPGEA	0.402154677	NA	hypothetical protein	NA	0	Phage tail tube, TTP, lambda-lik
MNLKPGEA_ otnI	0.401102953	NA	2-oxo-tetronate isomera	5.3.1.35	ygbM	Belongs to the hyi family
MNLKPGEA_ MNLKPGEA	0.399500976	0.74283883	hypothetical protein	NA	IV02_084	Thioredoxin
MNLKPGEA_ rpoD	0.398952687	0.20689748	RNA polymerase sigma f	NA	rpoD	Sigma factors are initiation fact
MNLKPGEA_ purU	0.396659967	0.29858274	Formyltetrahydrofolate d	3.5.1.10	purU	Catalyzes the hydrolysis of 10-fo
MNLKPGEA_ codAch2	0.396618554	NA	Pterin deaminase	3.5.4.11	0	Cytosine deaminase and related
MNLKPGEA_ MNLKPGEA	0.396618554	NA	hypothetical protein	NA	0	ABC-type Fe3 transport system p
MNLKPGEA_ MNLKPGEA	0.396618554	NA	hypothetical protein	NA	0	Antioxidant protein with alkyl hy

MNLKPGEA_	rutD	0.396618554	NA	Putative aminoacrylate h	3.5.1.-	rutD	May increase the rate of sponta
MNLKPGEA_	MNLKPGEA	0.396075083	0.74621309	hypothetical protein	NA	0	metal-dependent hydrolase of tl
MNLKPGEA_	oppF_1	0.395562385	0.69286427	Oligopeptide transport A	NA	dppF	Belongs to the ABC transporter s
MNLKPGEA_	ytnP	0.395417412	0.74066537	putative quorum-quench	3.1.1.-	0	Beta-lactamase
MNLKPGEA_	MNLKPGEA	0.395284956	NA	hypothetical protein	NA	gpU	P2 GpU family protein
MNLKPGEA_	MNLKPGEA	0.395284956	NA	IS5 family transposase IS	NA	0	ISSoEn1, terminal inverted repea
MNLKPGEA_	epmA	0.39519096	0.40385959	Elongation factor P--(R)-	6.3.1.-	epmA	With EpmB is involved in the be
MNLKPGEA_	hisC_2	0.394959231	NA	Histidinol-phosphate am	2.6.1.9	MA20_08	Transcriptional regulators contai
MNLKPGEA_	yghB	0.394785232	0.44584349	Inner membrane protein	NA	yghB	Pfam SNARE associated Golgi pr
MNLKPGEA_	pdeH_1	0.394367369	0.40385959	Cyclic di-GMP phosphodi	3.1.4.52	yhjH	Diguanylate phosphodiesterase
MNLKPGEA_	dgoA_2	0.392938032	NA	2-dehydro-3-deoxy-6-pho	4.1.2.21	dgoA	KDPG and KHG aldolase
MNLKPGEA_	glpB	0.392938032	NA	Anaerobic glycerol-3-pho	1.1.5.3	glpB	Conversion of glycerol 3-phospha
MNLKPGEA_	MNLKPGEA	0.392938032	NA	hypothetical protein	NA	0	Antirestriction protein (ArdA)
MNLKPGEA_	dbpA	0.391989807	0.53240288	ATP-dependent RNA heli	3.6.4.13	dbpA	DEAD-box RNA helicase involved
MNLKPGEA_	MNLKPGEA	0.391693209	NA	hypothetical protein	NA	0	type VI secretion protein
MNLKPGEA_	qseC	0.391652712	0.74540827	Sensor protein QseC	2.7.13.3	qseC	Histidine kinase
MNLKPGEA_	clpA	0.391640085	0.08933126	ATP-dependent Clp prote	NA	clpA	Belongs to the ClpA ClpB family
MNLKPGEA_	MNLKPGEA	0.391345243	NA	hypothetical protein	NA	0	Transposase
MNLKPGEA_	MNLKPGEA	0.390477291	0.31569411	hypothetical protein	NA	0	Diguanylate cyclase
MNLKPGEA_	speE	0.390253754	0.38797742	Polyamine aminopropylt	2.5.1.-	speE	Catalyzes the irreversible transfe
MNLKPGEA_	MNLKPGEA	0.390237992	NA	hypothetical protein	NA	PP2730	Protein of unknown function (DU
MNLKPGEA_	ccmB	0.389562179	NA	Heme exporter protein B	NA	ccmB	Required for the export of heme
MNLKPGEA_	dgaE	0.389562179	NA	D-glucosaminate-6-phos	4.3.1.29	selA	PFAM aromatic amino acid beta
MNLKPGEA_	MNLKPGEA	0.389562179	NA	hypothetical protein	NA	0	Putative phage holin
MNLKPGEA_	MNLKPGEA	0.389562179	NA	hypothetical protein	NA	0	Protein of unknown function (DU
MNLKPGEA_	MNLKPGEA	0.389562179	NA	IS1 family transposase IS	NA	insB	cog cog1662
MNLKPGEA_	MNLKPGEA	0.389562179	NA	IS3 family transposase IS	NA	0	Transposase
MNLKPGEA_	MNLKPGEA	0.388653592	NA	hypothetical protein	NA	0	0
MNLKPGEA_	kefF_2	0.388612579	0.44506231	Glutathione-regulated po	1.6.5.2	kefF	Regulatory subunit of a potassiu
MNLKPGEA_	MNLKPGEA	0.388579937	NA	hypothetical protein	NA	MA20_4	Conserved protein domain typica

MNLKPGEA_	uspF	0.387874836	0.22319603	Universal stress protein	NA	uspF	Belongs to the universal stress p
MNLKPGEA_	cyaA	0.387595713	0.25398687	Adenylate cyclase	4.6.1.1	cyaA	Adenylate cyclase
MNLKPGEA_	sorC_1	0.387262772	0.2131823	Sorbitol operon regulato	NA	lsrR	Transcriptional regulator
MNLKPGEA_	mak_2	0.387108817	0.48159085	Fructokinase	2.7.1.4	mak	ROK family
MNLKPGEA_	MNLKPGEA	0.386607499	0.61862389	hypothetical protein	NA	MA20_06	transport system periplasmic co
MNLKPGEA_	MNLKPGEA	0.386518807	0.33229626	hypothetical protein	NA	0	tape measure protein
MNLKPGEA_	dmlR_18	0.385224068	0.1386739	HTH-type transcriptional	NA	yeaT	Transcriptional regulator
MNLKPGEA_	MNLKPGEA	0.384200463	NA	hypothetical protein	NA	0	Belongs to the short-chain dehyd
MNLKPGEA_	outO	0.384200463	NA	Type 4 prepilin-like prote	NA	outO	Cleaves type-4 fimbrial leader se
MNLKPGEA_	MNLKPGEA	0.381424605	0.71150775	hypothetical protein	NA	#N/A	#N/A
MNLKPGEA_	glpD	0.381273169	0.66072108	Aerobic glycerol-3-phosp	1.1.5.3	glpD	Belongs to the FAD-dependent g
MNLKPGEA_	MNLKPGEA	0.381209552	NA	hypothetical protein	NA	0	Type VI secretion
MNLKPGEA_	por_1	0.380022895	0.39318437	Polyol:NADP oxidoreduct	1.1.1.-	yeiQ	Belongs to the mannitol dehydro
MNLKPGEA_	fabB	0.379160284	0.18849089	3-oxoacyl-[acyl-carrier-p	2.3.1.41	fabB	Catalyzes the condensation reac
MNLKPGEA_	sapC	0.378823651	0.41049954	Peptide transport system	NA	sapC	peptide transport system, perme
MNLKPGEA_	allS	0.378309709	NA	HTH-type transcriptional	NA	IV02_084	transcriptional regulator
MNLKPGEA_	MNLKPGEA	0.375840687	0.5792742	hypothetical protein	NA	yphG	Domain of unknown function (DU
MNLKPGEA_	MNLKPGEA	0.374787367	NA	hypothetical protein	NA	0	PTS system, Lactose/Cellobiose
MNLKPGEA_	btuD_1	0.374535486	NA	Vitamin B12 import ATP	7.6.2.8	0	(ABC) transporter
MNLKPGEA_	tdcD	0.374269944	NA	Propionate kinase	2.7.2.15	ackA	Catalyzes the formation of acety
MNLKPGEA_	tsaD	0.374190177	0.48308641	tRNA N6-adenosine thre	2.3.1.234	tsaD	Required for the formation of a
MNLKPGEA_	mdtC	0.374000906	0.66998353	Multidrug resistance pro	NA	mdtC	Belongs to the resistance-nodula
MNLKPGEA_	dppD_2	0.373802601	NA	Dipeptide transport ATP-	NA	gsiA_3	(ABC) transporter
MNLKPGEA_	fecE	0.373785248	NA	Fe(3+) dicitrate transpor	NA	0	COG1120 ABC-type cobalamin F
MNLKPGEA_	cstA	0.373025942	0.36348171	Peptide transporter CstA	NA	cstA	Carbon starvation protein
MNLKPGEA_	livF_3	0.37268122	NA	High-affinity branched-cl	NA	urtE	ABC transporter ATP-binding pro
MNLKPGEA_	glpX	0.372275595	0.72744527	Fructose-1,6-bisphospha	3.1.3.11	glpX	Fructose-1,6-bisphosphatase
MNLKPGEA_	rcsC_3	0.371277267	0.7434175	Sensor histidine kinase R	2.7.13.3	0	PhoQ Sensor
MNLKPGEA_	pgrR_7	0.371124585	0.73314214	HTH-type transcriptional	NA	0	Transcriptional regulator
MNLKPGEA_	yigB	0.370977627	0.6293984	5-amino-6-(5-phospho-D	3.1.3.104	yigB	Hydrolase

MNLKPGEA_	ycbX	0.370663275	0.58902628	putative protein YcbX	NA	ycbX	Mosc domain protein beta barre
MNLKPGEA_	metI_2	0.370423491	0.7508301	D-methionine transport	NA	metI	ABC-type metal ion transport sy
MNLKPGEA_	MNLKPGEA	0.370227555	NA	hypothetical protein	NA	0	KilA-N
MNLKPGEA_	MNLKPGEA	0.369051037	0.7280471	hypothetical protein	NA	yqfB	Belongs to the UPF0267 family
MNLKPGEA_	rob_3	0.367582815	0.19541868	Right origin-binding prot	NA	rob	Binds to the right arm of the rep
MNLKPGEA_	lacI_1	0.366472498	0.4946049	Lactose operon represso	NA	lacI	binds specific sites in lac operon
MNLKPGEA_	lpxD_2	0.365757228	NA	UDP-3-O-(3-hydroxymyri	2.3.1.191	0	UDP-3-O-(3-hydroxymyristoyl) g
MNLKPGEA_	nagC_1	0.36542765	0.49448705	N-acetylglucosamine rep	NA	yphH	ROK family
MNLKPGEA_	emrB	0.365152157	0.44698478	Multidrug export protein	NA	emrB	Major facilitator Superfamily
MNLKPGEA_	fruB_1	0.364620924	0.65552295	Multiphosphoryl transfer	NA	fruB	Bifunctional PTS system fructos
MNLKPGEA_	MNLKPGEA	0.364402957	0.16947576	hypothetical protein	NA	0	UPF0391 membrane protein
MNLKPGEA_	slyA_1	0.362668655	0.33843932	Transcriptional regulator	NA	slyA	Transcription regulator that can
MNLKPGEA_	argP_1	0.361970559	0.53522042	HTH-type transcriptional	NA	argP	Controls the transcription of gen
MNLKPGEA_	lacF	0.36186794	0.67459775	Lactose transport system	NA	ycjO	Binding-protein-dependent trans
MNLKPGEA_	lldR_2	0.360930361	0.38322387	Putative L-lactate dehydr	NA	exuR	Transcriptional
MNLKPGEA_	ydfO	0.359022793	0.74002962	putative protein YdfO	NA	ycgX	Phage envelope protein
MNLKPGEA_	acrR_2	0.358428891	0.60180724	HTH-type transcriptional	NA	acrR	transcriptional regulator
MNLKPGEA_	hemY	0.358183043	0.39454316	Protein HemY	NA	hemY	enzyme of heme biosynthesis
MNLKPGEA_	treC	0.358137672	0.58423851	Trehalose-6-phosphate h	3.2.1.93	treC	COG0366 Glycosidases
MNLKPGEA_	sodB	0.35781786	0.40453672	Superoxide dismutase [F	1.15.1.1	sodB	Destroys radicals which are norr
MNLKPGEA_	dhaL	0.357394228	0.74588536	PEP-dependent dihydrox	2.7.1.121	dhaL	Dihydroxyacetone kinase
MNLKPGEA_	MNLKPGEA	0.357129059	0.74621309	hypothetical protein	NA	0	transposase
MNLKPGEA_	osmC	0.355738506	0.40279172	Peroxiredoxin OsmC	1.11.1.15	osmC	redox protein regulator of disulfi
MNLKPGEA_	baiA1	0.355684926	NA	3alpha-hydroxy bile acid	1.1.1.395	baiA2	KR domain
MNLKPGEA_	MNLKPGEA	0.355684926	NA	hypothetical protein	NA	tchA	LydA holin phage, holin superfar
MNLKPGEA_	ndhI	0.355684926	NA	NAD(P)H-quinone oxidor	7.1.1.-	hycF	the formate hydrogenlyase com
MNLKPGEA_	cecR	0.355203546	0.63225667	HTH-type transcriptional	NA	ybiH	Transcriptional regulator
MNLKPGEA_	serA	0.354317245	0.38777574	D-3-phosphoglycerate de	1.1.1.95	serA	Belongs to the D-isomer specific
MNLKPGEA_	MNLKPGEA	0.353714145	0.74386201	hypothetical protein	NA	ynbE	(Lipo)protein
MNLKPGEA_	MNLKPGEA	0.35292039	NA	hypothetical protein	NA	0	portal protein

MNLKPGEA_ bepE	0.352843414	0.36644798	Efflux pump membrane	NA	czcA	Belongs to the resistance-nodula
MNLKPGEA_ metI_1	0.35273907	NA	D-methionine transport	NA	0	ABC transporter (permease)
MNLKPGEA_ pduD_2	0.35273907	NA	Propanediol dehydratase	4.2.1.28	pduD	dehydratase, medium subunit
MNLKPGEA_ ybjO	0.351276361	0.42123278	Inner membrane protein	NA	ybjO	Membrane
MNLKPGEA_ MNLKPGEA	0.350991635	NA	hypothetical protein	NA	0	0
MNLKPGEA_ MNLKPGEA	0.350535359	NA	hypothetical protein	NA	#N/A	#N/A
MNLKPGEA_ purR_1	0.350497804	0.63400697	HTH-type transcriptional	NA	0	transcriptional regulator
MNLKPGEA_ MNLKPGEA	0.3501629	NA	hypothetical protein	NA	0	WxcM-like, C-terminal
MNLKPGEA_ padC	0.349920467	0.65552295	Phenolic acid decarboxyl	4.1.1.102	padC	Phenolic acid decarboxylase
MNLKPGEA_ hin_2	0.349105939	0.58027585	DNA-invertase hin	NA	0	Resolvase, N terminal domain
MNLKPGEA_ ascG_2	0.348714639	0.49397957	HTH-type transcriptional	NA	0	transcriptional regulator
MNLKPGEA_ MNLKPGEA	0.34869295	NA	hypothetical protein	NA	#N/A	#N/A
MNLKPGEA_ stp	0.34869295	NA	Multidrug resistance pro	NA	0	Permeases of the major facilitat
MNLKPGEA_ MNLKPGEA	0.347125404	NA	hypothetical protein	NA	0	phage Terminase large subunit
MNLKPGEA_ dan	0.346768774	NA	D-aminoacylase	3.5.1.81	dan	N-acyl-D-aspartate D-glutamate
MNLKPGEA_ cmk	0.346326759	0.60050698	Cytidylate kinase	2.7.4.25	cmk	Belongs to the cytidylate kinase
MNLKPGEA_ queE	0.346040183	0.31016248	7-carboxy-7-deazaguanii	4.3.99.3	queE	Catalyzes the complex heterocyc
MNLKPGEA_ yicI	0.345339769	NA	Alpha-xylosidase	3.2.1.177	yicI	Belongs to the glycosyl hydrolas
MNLKPGEA_ entS	0.343984132	0.64766406	Enterobactin exporter En	NA	entS	Exports the siderophore enterob
MNLKPGEA_ yecN	0.343539524	0.46034377	Inner membrane protein	NA	yecN	relative of glutathione S-transfe
MNLKPGEA_ ybhK	0.343493273	0.66055687	Putative gluconeogenesi	NA	ybhK	Required for morphogenesis und
MNLKPGEA_ MNLKPGEA	0.34293624	NA	IS3 family transposase IS	NA	0	Transposase and inactivated der
MNLKPGEA_ MNLKPGEA	0.34293624	NA	hypothetical protein	NA	0	phage terminase small subunit
MNLKPGEA_ sfmC	0.34293624	NA	putative fimbrial chaper	NA	0	Long polar fimbrial chaperone Lp
MNLKPGEA_ cnrA	0.341256173	0.77556958	Nickel and cobalt resista	NA	czcA	Belongs to the resistance-nodula
MNLKPGEA_ mhpD	0.340820432	NA	2-keto-4-pentenoate hyc	4.2.1.80	mhpD	hydratase
MNLKPGEA_ htrE_2	0.339761433	0.45119185	Outer membrane usher p	NA	htrE_1	Usher protein
MNLKPGEA_ lsrK	0.339680148	0.53691325	Autoinducer-2 kinase	2.7.1.189	lsrK	Catalyzes the phosphorylation of
MNLKPGEA_ hoxN	0.338816446	NA	High-affinity nickel trans	NA	hoxN	rRNA processing
MNLKPGEA_ MNLKPGEA	0.33834451	NA	hypothetical protein	NA	0	Transposase

MNLKPGEA_ cbpA	0.337724413	0.40365039	Curved DNA-binding prot	NA	cbpA	displays overlapping activities w
MNLKPGEA_ nfdA_1	0.337710396	NA	N-substituted formamid	3.5.1.91	nfdA	metal-dependent hydrolase with
MNLKPGEA_ tatD	0.337573355	0.75513071	3'-5' ssDNA/RNA exonuc	3.1.11.-	tatD	3'-5' exonuclease that prefers si
MNLKPGEA_ gltJ_1	0.33711533	0.66653629	Glutamate/aspartate im	NA	gltJ	amino acid ABC transporter
MNLKPGEA_ frdA	0.337073318	0.68983761	Fumarate reductase flav	1.3.5.4	frdA	Belongs to the FAD-dependent c
MNLKPGEA_ phnI	0.335973199	NA	Alpha-D-ribose 1-methyl	2.7.8.37	phnI	Phosphonate
MNLKPGEA_ rcnB	0.333231856	0.72554293	Nickel/cobalt homeostas	NA	yohN	Nickel cobalt homeostasis prote
MNLKPGEA_ shlB	0.3331595	NA	Hemolysin transporter pr	NA	0	Hemolysin activation secretion p
MNLKPGEA_ epsF_2	0.332457852	NA	Type II secretion system	NA	pilC	type II secretion system
MNLKPGEA_ MNLKPGEA	0.332457852	NA	hypothetical protein	NA	0	0
MNLKPGEA_ MNLKPGEA	0.332301596	0.80041078	hypothetical protein	NA	0	0
MNLKPGEA_ MNLKPGEA	0.330515152	NA	hypothetical protein	NA	0	0
MNLKPGEA_ MNLKPGEA	0.330161688	0.50834736	hypothetical protein	NA	uspA	Universal stress protein
MNLKPGEA_ MNLKPGEA	0.330130859	0.27303097	hypothetical protein	NA	dcrB	dcrb protein
MNLKPGEA_ hemH	0.329713452	0.69326167	Ferrochelatase	4.99.1.1	hemH	Catalyzes the ferrous insertion in
MNLKPGEA_ pxpB	0.329389992	NA	5-oxoprolinase subunit B	3.5.2.9	ybgJ	Allophanate hydrolase subunit 1
MNLKPGEA_ hha	0.32871411	0.36977126	Hemolysin expression-m	NA	hha	Haemolysin expression modulati
MNLKPGEA_ gbpR	0.328667095	0.58902628	HTH-type transcriptional	NA	pcaQ	transcriptional regulator
MNLKPGEA_ pobA	0.328350315	0.70709197	p-hydroxybenzoate hydro	1.14.13.2	pobA	Catalyzes the formation of protc
MNLKPGEA_ gdx_2	0.328135278	0.5229194	Guanidinium exporter	NA	0	Small Multidrug Resistance prot
MNLKPGEA_ nqrC	0.328042605	NA	Na(+)-translocating NAD	7.2.1.1	nqrC	NQR complex catalyzes the redu
MNLKPGEA_ MNLKPGEA	0.327900625	0.51295412	Polyphosphate:ADP phos	2.7.4.1	ppk2	polyphosphate kinase
MNLKPGEA_ pgaA	0.327455821	NA	Poly-beta-1,6-N-acetyl-D	NA	pgaA	Exports the biofilm adhesin poly
MNLKPGEA_ moeB	0.327185765	0.67169289	Molybdopterin-synthase	2.7.7.80	moeB	COG0476 Dinucleotide-utilizing
MNLKPGEA_ aat	0.326060823	0.53880577	Leucyl/phenylalanyl-tRN	2.3.2.6	aat	Functions in the N-end rule path
MNLKPGEA_ blc_1	0.325905467	0.58576946	Outer membrane lipopro	NA	blc	Outer Membrane Lipoprotein
MNLKPGEA_ sacX	0.325530197	0.79331415	Negative regulator of Sa	NA	scrA	PTS system sucrose-specific
MNLKPGEA_ psiF	0.325107129	0.37716927	Phosphate starvation-inc	NA	psiF	Phosphate starvation-inducible p
MNLKPGEA_ MNLKPGEA	0.324056832	NA	hypothetical protein	NA	L	head completion
MNLKPGEA_ MNLKPGEA	0.323480904	0.49842654	hypothetical protein	NA	yobH	YobH-like protein

MNLKPGEA_	fsaB	0.322655799	0.75170049	Fructose-6-phosphate al	4.1.2.-	tal	Belongs to the transaldolase far
MNLKPGEA_	MNLKPGEA	0.322562298	NA	hypothetical protein	NA	0	ISSoEn1, terminal inverted repea
MNLKPGEA_	MNLKPGEA	0.322528652	0.76153733	hypothetical protein	NA	0	peptidase activity
MNLKPGEA_	gcvA_1	0.322515706	0.38646682	Glycine cleavage system	NA	gcvA	transcriptional regulator
MNLKPGEA_	hisQ_2	0.322118902	NA	Histidine transport syste	NA	0	(ABC) transporter
MNLKPGEA_	MNLKPGEA	0.322118902	NA	hypothetical protein	NA	0	Polyketide cyclase / dehydrase a
MNLKPGEA_	ulaB_2	0.322118902	NA	Ascorbate-specific PTS s	2.7.1.194	ulaB	The phosphoenolpyruvate-deper
MNLKPGEA_	lptB_3	0.321632883	NA	Lipopolysaccharide expo	3.6.3.-	0	Part of the ABC transporter com
MNLKPGEA_	MNLKPGEA	0.321356231	0.77855624	IS3 family transposase IS	NA	0	Helix-turn-helix domain
MNLKPGEA_	MNLKPGEA	0.320721627	NA	hypothetical protein	NA	0	Lysozyme inhibitor LprI
MNLKPGEA_	nikE	0.320612359	NA	Nickel import ATP-bindir	7.2.2.11	nikE	Part of the ABC transporter com
MNLKPGEA_	srlR_4	0.3199201	0.7315085	Glucitol operon represso	NA	fucR	transcriptional regulator
MNLKPGEA_	abgB	0.317277183	NA	p-aminobenzoyl-glutama	3.5.1.-	abgB	amidohydrolase
MNLKPGEA_	MNLKPGEA	0.315997178	0.35163912	hypothetical protein	NA	#N/A	#N/A
MNLKPGEA_	MNLKPGEA	0.314876586	NA	hypothetical protein	NA	#N/A	#N/A
MNLKPGEA_	hyuA	0.313915574	NA	Hydantoin racemase	5.1.99.5	hyuE	racemase
MNLKPGEA_	MNLKPGEA	0.313915574	NA	hypothetical protein	NA	0	0
MNLKPGEA_	bluR	0.31347712	0.35910844	HTH-type transcriptional	NA	ycgE	Transcriptional regulator
MNLKPGEA_	MNLKPGEA	0.313375239	0.58165989	hypothetical protein	NA	yeaC	protein conserved in bacteria
MNLKPGEA_	licC_3	0.312412409	0.75997564	Lichenan permease IIC c	NA	0	The phosphoenolpyruvate-deper
MNLKPGEA_	ubiI	0.311863212	0.65154194	2-octaprenylphenol hydr	1.14.13.240	visC	ubiquinone biosynthesis hydroxy
MNLKPGEA_	ulaC_1	0.310173788	0.73749661	Ascorbate-specific PTS s	NA	cmtB	Phosphotransferase System
MNLKPGEA_	dhaK_2	0.310109259	0.76355264	PEP-dependent dihydrox	2.7.1.121	dhaK	Dihydroxyacetone kinase
MNLKPGEA_	MNLKPGEA	0.309472074	0.81069729	hypothetical protein	NA	phoC	phosphoesterase, PA-phosphata
MNLKPGEA_	gpmI	0.309439057	0.76355264	2,3-bisphosphoglycerate	5.4.2.12	gpmI	Catalyzes the interconversion of
MNLKPGEA_	zupT	0.307672161	0.61624193	Zinc transporter ZupT	NA	zupT	Mediates zinc uptake. May also
MNLKPGEA_	panF	0.307286607	0.71258288	Sodium/pantothenate sy	NA	panF	Belongs to the sodium solute sy
MNLKPGEA_	oadB	0.306317231	NA	Oxaloacetate decarboxyl	7.2.4.2	oadB	Na -transporting methylmalonyl
MNLKPGEA_	MNLKPGEA	0.305570046	0.80246821	hypothetical protein	NA	0	0
MNLKPGEA_	outN	0.305523467	NA	Type II secretion system	NA	0	Type II secretion system (T2SS),

MNLKPGEA_	mfd	0.304992588	0.47088662	Transcription-repair-cou	3.6.4.-	mfd	Couples transcription and DNA r
MNLKPGEA_	MNLKPGEA	0.303407335	NA	hypothetical protein	NA	0	Helix-turn-helix domain
MNLKPGEA_	MNLKPGEA	0.302958616	NA	hypothetical protein	NA	0	0
MNLKPGEA_	MNLKPGEA	0.302833211	0.67365142	hypothetical protein	NA	abrB	Ammonia monooxygenase
MNLKPGEA_	rraB	0.301612468	0.71535303	Regulator of ribonucleas	NA	rraB	Globally modulates RNA abunda
MNLKPGEA_	dnaG	0.300333048	0.32402143	DNA primase	2.7.7.-	dnaG	RNA polymerase that catalyzes
MNLKPGEA_	MNLKPGEA	0.299508032	NA	hypothetical protein	NA	0	Tail E family protein
MNLKPGEA_	cvaA	0.298109284	0.76463939	Colicin V secretion prote	NA	0	Secretion Protein
MNLKPGEA_	MNLKPGEA	0.298034119	0.67612396	hypothetical protein	NA	0	Uncharacterized protein conserv
MNLKPGEA_	MNLKPGEA	0.296967705	0.67612396	hypothetical protein	NA	yicI	Belongs to the glycosyl hydrolas
MNLKPGEA_	oleD	0.296867472	0.56750227	2-alkyl-3-oxoalkanoate r	1.1.1.412	ybjS	3-beta hydroxysteroid dehydroge
MNLKPGEA_	mhpC	0.29677607	NA	2-hydroxy-6-oxononadier	3.7.1.14	mhpC	Alpha/beta hydrolase family
MNLKPGEA_	MNLKPGEA	0.29677607	NA	hypothetical protein	NA	0	NIPSNAP family containing prote
MNLKPGEA_	galM	0.296745506	0.74826127	Aldose 1-epimerase	5.1.3.3	galM	converts alpha-aldose to the bet
MNLKPGEA_	MNLKPGEA	0.296538905	0.79156523	hypothetical protein	NA	0	DoxX
MNLKPGEA_	hycD	0.296307329	NA	Formate hydrogenlyase	NA	hycD	HycBCDEFG is part of the forma
MNLKPGEA_	MNLKPGEA	0.296307329	NA	hypothetical protein	NA	ycgR	Acts as a flagellar brake, regulat
MNLKPGEA_	MNLKPGEA	0.296307329	NA	hypothetical protein	NA	#N/A	#N/A
MNLKPGEA_	betT	0.296010516	0.77902649	High-affinity choline trar	NA	betT	Belongs to the BCCT transporter
MNLKPGEA_	MNLKPGEA	0.294571188	NA	hypothetical protein	NA	0	0
MNLKPGEA_	MNLKPGEA	0.294571188	NA	hypothetical protein	NA	#N/A	#N/A
MNLKPGEA_	MNLKPGEA	0.293576772	0.69289391	hypothetical protein	NA	#N/A	#N/A
MNLKPGEA_	dmlR_16	0.293295109	0.72026465	HTH-type transcriptional	NA	ttdR	transcriptional regulator
MNLKPGEA_	scmP	0.292953106	NA	N-acetylcysteine deacety	3.5.1.-	yxeP	amidohydrolase
MNLKPGEA_	zipA	0.292299628	0.33088992	Cell division protein ZipA	NA	zipA	Essential cell division protein tha
MNLKPGEA_	MNLKPGEA	0.291077902	0.50741452	Beta-xylosidase	3.2.1.-	bglX	Belongs to the glycosyl hydrolas
MNLKPGEA_	yhcB	0.290153537	0.50319304	Inner membrane protein	NA	yhcB	Cytochrome D ubiquinol oxidase,
MNLKPGEA_	MNLKPGEA	0.289389703	NA	hypothetical protein	NA	0	Uncharacterized conserved prote
MNLKPGEA_	hpxO	0.289315612	NA	FAD-dependent urate hy	1.14.13.113	hpxO	COG0654 2-polyprenyl-6-metho
MNLKPGEA_	MNLKPGEA	0.289315612	NA	hypothetical protein	NA	0	0

MNLKPGEA_	MNLKPGEA	0.289315612	NA	hypothetical protein	NA	0	0
MNLKPGEA_	msiK_2	0.289315612	NA	Diacetylchitobiose uptak	7.5.2.-	0	Part of the ABC transporter com
MNLKPGEA_	ridA_2	0.288750352	0.81342194	2-iminobutanoate/2-imi	3.5.99.10	0	PFAM Endoribonuclease L-PSP
MNLKPGEA_	MNLKPGEA	0.288700544	0.65813024	6-deoxy-6-sulfogluconol	3.1.1.99	yvrE	gluconolactonase
MNLKPGEA_	MNLKPGEA	0.288553534	0.4904383	hypothetical protein	NA	0	glyoxalase bleomycin resistance
MNLKPGEA_	bglH_1	0.288093854	0.73314214	Aryl-phospho-beta-D-glu	3.2.1.86	ascB	Belongs to the glycosyl hydrolas
MNLKPGEA_	MNLKPGEA	0.287672048	NA	hypothetical protein	NA	#N/A	#N/A
MNLKPGEA_	pdeB	0.287558129	0.6202708	putative cyclic di-GMP p	3.1.4.52	ylaB	signal transduction protein conta
MNLKPGEA_	nasA	0.287492123	NA	Nitrate reductase	1.7.-.-	nasA	Catalytic subunit of the nitrate r
MNLKPGEA_	hipO_2	0.287465636	NA	Hippurate hydrolase	3.5.1.32	hipO	amidohydrolase
MNLKPGEA_	mhpT	0.287385076	NA	3-(3-hydroxy-phenyl)pro	NA	mhpT	Major facilitator Superfamily
MNLKPGEA_	ybeZ	0.287286914	0.37774536	PhoH-like protein	NA	ybeZ	phosphate starvation-inducible p
MNLKPGEA_	MNLKPGEA	0.286981234	NA	hypothetical protein	NA	0	Extracellular solute-binding prot
MNLKPGEA_	fes	0.286589775	0.5803695	Enterochelin esterase	NA	fes	esterase
MNLKPGEA_	ybaK	0.286561847	0.76224114	Cys-tRNA(Pro)/Cys-tRNA	4.2.-.-	ybaK	Belongs to the prolyl-tRNA editi
MNLKPGEA_	iaaH	0.28631604	NA	Indole-3-acetyl-aspartic	3.5.1.-	abgA	Protein involved in hydrolase act
MNLKPGEA_	yicJ_4	0.286188427	NA	Inner membrane sympor	NA	0	COG2211 Na melibiose symport
MNLKPGEA_	MNLKPGEA	0.28615407	NA	hypothetical protein	NA	0	Phytanoyl-CoA dioxygenase
MNLKPGEA_	kstD	0.286148794	NA	3-oxosteroid 1-dehydrog	1.3.99.4	0	Succinate dehydrogenase fumar
MNLKPGEA_	dmlR_4	0.283862624	NA	HTH-type transcriptional	NA	0	transcriptional regulator
MNLKPGEA_	MNLKPGEA	0.283429131	0.69074743	hypothetical protein	NA	iap	Peptidase family M28
MNLKPGEA_	rna	0.283302374	0.7315085	Ribonuclease I	4.6.1.21	rna	Belongs to the RNase T2 family
MNLKPGEA_	MNLKPGEA	0.283215235	0.76549656	hypothetical protein	NA	yhfK	integral membrane protein, Ycc
MNLKPGEA_	pdeD	0.28262295	0.56727635	putative cyclic di-GMP p	3.1.4.52	adrB	EAL domain
MNLKPGEA_	dps	0.282404979	0.35823986	DNA protection during st	1.16.-.-	dps	During stationary phase, binds t
MNLKPGEA_	ynjB	0.282296666	NA	Protein YnjB	NA	ynjB	transport system periplasmic co
MNLKPGEA_	mbeC	0.282289731	0.41505871	Mobilization protein Mb	NA	0	Bacterial mobilisation protein (M
MNLKPGEA_	efeB	0.281900112	0.81443054	Deferrochelatase/peroxi	1.11.1.-	efeB	peroxidase
MNLKPGEA_	MNLKPGEA	0.281403397	NA	hypothetical protein	NA	FII	major tail tube protein
MNLKPGEA_	ilvC	0.28052586	0.60714562	Ketol-acid reductoisome	1.1.1.86	ilvC	Involved in the biosynthesis of b

MNLKPGEA_	MNLKPGEA	0.280312988	0.79834401	hypothetical protein	NA	0	Helix-turn-helix domain
MNLKPGEA_	MNLKPGEA	0.279665495	0.82180965	hypothetical protein	NA	intE	Phage integrase, N-terminal SAI
MNLKPGEA_	MNLKPGEA	0.279093795	0.38217743	IS6 family transposase IS	NA	0	DDE domain
MNLKPGEA_	ybhR_2	0.277486923	0.7782691	putative multidrug ABC t	NA	ybhR	Transport Permease Protein
MNLKPGEA_	lsrD_3	0.277320304	NA	Autoinducer 2 import sys	NA	rhaQ	Belongs to the binding-protein-d
MNLKPGEA_	cobB	0.276670751	0.70775709	NAD-dependent protein	2.3.1.286	cobB	NAD-dependent lysine deacetyla
MNLKPGEA_	nodD2_1	0.27579977	0.82180965	Nodulation protein D 2	NA	nahR	transcriptional regulator
MNLKPGEA_	zntB_1	0.275266619	0.74320505	Zinc transport protein Zr	NA	0	transporter
MNLKPGEA_	MNLKPGEA	0.274567313	0.7782691	hypothetical protein	NA	0	bleomycin resistance protein
MNLKPGEA_	dapA_3	0.274433631	NA	4-hydroxy-tetrahydrodipi	4.3.3.7	0	Belongs to the DapA family
MNLKPGEA_	dnaC	0.274101287	0.73314214	DNA replication protein I	NA	dnaC	DNA replication protein
MNLKPGEA_	glpK	0.27403264	0.67154489	Glycerol kinase	2.7.1.30	glpK	Key enzyme in the regulation of
MNLKPGEA_	MNLKPGEA	0.273112025	0.80751624	hypothetical protein	NA	0	COG1012 NAD-dependent aldeh
MNLKPGEA_	htrE_1	0.27206487	0.80809392	Outer membrane usher p	NA	htrE	Outer membrane usher protein
MNLKPGEA_	MNLKPGEA	0.27075169	0.54610599	hypothetical protein	NA	0	COG1192 ATPases involved in ch
MNLKPGEA_	yidA	0.269823314	0.69050417	Sugar phosphatase YidA	3.1.3.23	yidA	member of the haloacid dehalog
MNLKPGEA_	rop	0.26901806	0.36473572	Regulatory protein rop	NA	0	Rop protein
MNLKPGEA_	cyaY	0.268305533	0.80725714	Iron-sulfur cluster assem	NA	cyaY	Belongs to the frataxin family
MNLKPGEA_	fur	0.268190251	0.38276043	Ferric uptake regulation	NA	fur	belongs to the Fur family
MNLKPGEA_	dedD	0.266808621	0.59071823	Cell division protein Ded	NA	dedD	Non-essential cell division prote
MNLKPGEA_	ariR	0.266103822	0.49927306	putative two-component	NA	ariR	Two-component-system connec
MNLKPGEA_	MNLKPGEA	0.26527999	0.43549583	hypothetical protein	NA	0	Serine dehydrogenase proteinas
MNLKPGEA_	MNLKPGEA	0.264861878	0.65473634	hypothetical protein	NA	ydgD	Belongs to the peptidase S1B fa
MNLKPGEA_	wecF	0.264596383	NA	TDP-N-acetylfucosamine	2.4.1.325	rffT	Catalyzes the synthesis of Und-P
MNLKPGEA_	fruK	0.262562188	0.70114072	Fructose import ATP-bin	7.5.2.-	ytfR	import. Responsible for energy c
MNLKPGEA_	MNLKPGEA	0.262327244	NA	hypothetical protein	NA	0	extracellular solute-binding prot
MNLKPGEA_	pgrR_6	0.262070699	0.83639627	HTH-type transcriptional	NA	0	Transcriptional regulator
MNLKPGEA_	MNLKPGEA	0.261630647	0.64169162	hypothetical protein	NA	0	Iron-containing redox enzyme
MNLKPGEA_	fbpC2	0.261387175	0.83132676	Fe(3+) ions import ATP-b	7.2.2.7	ynjD	ABC transporter
MNLKPGEA_	rcsD	0.260665036	0.38955838	Phosphotransferase RcsI	2.7.2.-	rcsD	Component of the Rcs signaling

MNLKPGEA_	MNLKPGEA	0.25710375	NA	hypothetical protein	NA	0	type VI secretion protein
MNLKPGEA_	MNLKPGEA	0.256411166	NA	hypothetical protein	NA	0	Protein of unknown function (DU
MNLKPGEA_	mdtM_1	0.256344155	0.81699862	Multidrug resistance pro	NA	cmr	Major facilitator Superfamily
MNLKPGEA_	sasA_3	0.255896252	0.83838768	Adaptive-response sensc	2.7.-.-	0	PhoQ Sensor
MNLKPGEA_	bcr_1	0.254778268	NA	Bicyclomycin resistance	NA	tcaB	Major facilitator Superfamily
MNLKPGEA_	ccmH	0.254778268	NA	Cytochrome c-type bioge	NA	ccmH	subunit of a heme lyase
MNLKPGEA_	hin_1	0.254778268	NA	DNA-invertase hin	NA	pinE	Site-specific recombinases, DNA
MNLKPGEA_	MNLKPGEA	0.254778268	NA	hypothetical protein	NA	urtC	Belongs to the binding-protein-d
MNLKPGEA_	MNLKPGEA	0.254778268	NA	hypothetical protein	NA	ydjX	SNARE associated Golgi protein
MNLKPGEA_	nrtD	0.254778268	NA	Nitrate import ATP-bindi	7.3.2.4	nasD	(ABC) transporter
MNLKPGEA_	phnL	0.254778268	NA	Alpha-D-ribose 1-methyl	2.7.8.37	phnL	phosphonate C-P lyase system p
MNLKPGEA_	phnM	0.254778268	NA	Alpha-D-ribose 1-methyl	3.6.1.63	phnM	phosphonate metabolism protei
MNLKPGEA_	gntU	0.254492364	0.84280933	Low-affinity gluconate tr	NA	gntU	Gluconate
MNLKPGEA_	ftsA_1	0.254392527	NA	Cell division protein FtsA	NA	eutJ	Ethanolamine utilization protein
MNLKPGEA_	MNLKPGEA	0.253849744	NA	hypothetical protein	NA	ysnE	COG0454 Histone acetyltransfer
MNLKPGEA_	MNLKPGEA	0.250954256	NA	hypothetical protein	NA	terC	COG0861 Membrane protein Ter
MNLKPGEA_	yjhB	0.250951658	0.72098473	Putative metabolite tran	NA	jen	Major facilitator Superfamily
MNLKPGEA_	glaH	0.25052449	0.64981044	Glutarate 2-hydroxylase	1.14.11.-	csiD	May be involved in the control of
MNLKPGEA_	lpxC	0.249205848	0.54332203	UDP-3-O-acyl-N-acetylgl	3.5.1.108	lpxC	Catalyzes the hydrolysis of UDP-
MNLKPGEA_	ulaB_1	0.248171106	NA	Ascorbate-specific PTS s	2.7.1.194	ulaB	Phosphotransferase System
MNLKPGEA_	benC	0.247930754	NA	Benzoate 1,2-dioxygenas	NA	benC	COG0543 2-polyprenylphenol hy
MNLKPGEA_	agaC	0.247923469	NA	N-acetylgalactosamine p	NA	agaC	PTS system
MNLKPGEA_	MNLKPGEA	0.2475282	NA	hypothetical protein	NA	0	ABC-type phosphate phosphonat
MNLKPGEA_	dcuR	0.247111854	0.69704119	Transcriptional regulator	NA	dcuR	Transcriptional Regulatory prote
MNLKPGEA_	MNLKPGEA	0.246016116	0.65547223	putative protein	NA	ydiJ	Fad linked oxidase
MNLKPGEA_	bssS	0.245789302	0.5217977	Biofilm regulator BssS	NA	bssS	disruption of this gene in Escher
MNLKPGEA_	MNLKPGEA	0.245333979	0.60070104	hypothetical protein	NA	0	Helix-turn-helix domain
MNLKPGEA_	ydcZ	0.244857414	NA	Inner membrane protein	NA	ydcZ	membrane
MNLKPGEA_	hslJ	0.244559838	NA	Heat shock protein HslJ	NA	hslJ	Heat shock protein
MNLKPGEA_	yecS_2	0.244469303	NA	L-cystine transport syste	NA	yecS_3	amino acid ABC transporter

MNLKPGEA_	MNLKPGEA	0.24408343	NA	hypothetical protein	NA	eutA	ethanolamine utilization protein
MNLKPGEA_	MNLKPGEA	0.24408343	NA	hypothetical protein	NA	#N/A	#N/A
MNLKPGEA_	rapA_1	0.243103616	0.47925718	RNA polymerase-associa	3.6.4.-	rapA	Transcription regulator that acti
MNLKPGEA_	MNLKPGEA	0.242811269	NA	hypothetical protein	NA	0	P2 phage tail completion R fami
MNLKPGEA_	hflD	0.242554596	0.70849961	High frequency lysogeniz	NA	hflD	High frequency lysogenization pr
MNLKPGEA_	MNLKPGEA	0.24181221	NA	Lactonase drp35	3.1.1.-	0	gluconolactonase activity
MNLKPGEA_	mepH	0.241465979	0.58602483	Murein DD-endopeptidas	3.4.-.-	ydhO	COG0791 Cell wall-associated h
MNLKPGEA_	MNLKPGEA	0.240946661	NA	hypothetical protein	NA	0	0
MNLKPGEA_	clpP_1	0.240388276	NA	ATP-dependent Clp prote	3.4.21.92	0	Clp protease
MNLKPGEA_	dinG	0.240191841	0.7593856	ATP-dependent DNA heli	3.6.4.12	dinG	helicase
MNLKPGEA_	mhpA	0.23916026	NA	3-(3-hydroxy-phenyl)prop	1.14.13.127	mhpA	Catalyzes the insertion of one at
MNLKPGEA_	MNLKPGEA	0.23916026	NA	hypothetical protein	NA	ytmO	Luciferase Family
MNLKPGEA_	MNLKPGEA	0.23916026	NA	hypothetical protein	NA	traH	Conjugative relaxosome accesso
MNLKPGEA_	oxlT	0.23916026	NA	Oxalate:formate antipor	NA	0	Major facilitator superfamily
MNLKPGEA_	vldW_3	0.23916026	NA	Validamycin A dioxygena	1.14.11.52	efe	Belongs to the iron ascorbate-de
MNLKPGEA_	MNLKPGEA	0.238718168	NA	hypothetical protein	NA	0	0
MNLKPGEA_	MNLKPGEA	0.238718168	NA	hypothetical protein	NA	ydeK	transporter
MNLKPGEA_	cbiE	0.237592361	NA	Cobalt-precorrin-7 C(5)-r	2.1.1.289	cbiE	Catalyzes the methylation of C-5
MNLKPGEA_	MNLKPGEA	0.237592361	NA	hypothetical protein	NA	0	Cupin 2, conserved barrel domai
MNLKPGEA_	thrC	0.237267076	0.78555119	Threonine synthase	4.2.3.1	thrC	Threonine synthase
MNLKPGEA_	MNLKPGEA	0.236796571	0.70751013	hypothetical protein	NA	0	transcriptional regulator
MNLKPGEA_	MNLKPGEA	0.235980304	0.64446591	hypothetical protein	NA	ycfL	cellular response to DNA damag
MNLKPGEA_	MNLKPGEA	0.235810699	NA	hypothetical protein	NA	ygaH	L-valine transmembrane transpo
MNLKPGEA_	MNLKPGEA	0.235810699	NA	hypothetical protein	NA	0	0
MNLKPGEA_	MNLKPGEA	0.235810699	NA	hypothetical protein	NA	0	Endoribonuclease L-PSP
MNLKPGEA_	MNLKPGEA	0.235810699	NA	hypothetical protein	NA	0	Branched-chain amino acid tran
MNLKPGEA_	MNLKPGEA	0.234388944	0.83334651	hypothetical protein	NA	0	Fad linked oxidase
MNLKPGEA_	lpdC	0.233595214	0.74283883	Gallate decarboxylase	4.1.1.59	0	3-octaprenyl-4-hydroxybenzoate
MNLKPGEA_	maa	0.233483709	0.60725948	Maltose O-acetyltransfe	2.3.1.79	maa	acetyltransferase, isoleucine pat
MNLKPGEA_	gsiD_1	0.232118304	NA	Glutathione transport sy	NA	0	ABC-type dipeptide oligopeptide

MNLKPGEA_ pduL	0.232118304	NA	Phosphate propanoyltrar	2.3.1.222	pduL	Involved in 1,2-propanediol (1,2-
MNLKPGEA_ cdsA	0.2320603	0.75123184	Phosphatidate cytidylyltr	2.7.7.41	cdsA	Belongs to the CDS family
MNLKPGEA_ potD	0.23058374	0.61222012	Spermidine/putrescine-b	NA	potD	Required for the activity of the b
MNLKPGEA_ manA	0.230573533	0.547461	Mannose-6-phosphate is	5.3.1.8	manA	Belongs to the mannose-6-phosp
MNLKPGEA_ MNLKPGEA	0.230566027	0.85600967	hypothetical protein	NA	0	Acetyltransferase (GNAT) doma
MNLKPGEA_ gstB_1	0.229955847	0.8254344	Glutathione S-transferas	2.5.1.18	gst8	Glutathione S-Transferase
MNLKPGEA_ MNLKPGEA	0.229320492	0.51774858	hypothetical protein	NA	0	MbeB-like, N-term conserved re
MNLKPGEA_ plsC	0.228794434	0.52180471	1-acyl-sn-glycerol-3-pho	2.3.1.51	plsC	Belongs to the 1-acyl-sn-glycero
MNLKPGEA_ pdxA2_2	0.228098628	0.86166868	D-erythronate 4-phospha	1.1.1.409	pdxA	Catalyzes the NAD(P)-dependent
MNLKPGEA_ oadG	0.227674655	NA	Oxaloacetate decarboxyl	7.2.4.2	oadG	oxaloacetate decarboxylase gam
MNLKPGEA_ MNLKPGEA	0.226123701	0.77134584	hypothetical protein	NA	ybjT	Epimerase dehydratase
MNLKPGEA_ narX	0.225167253	0.7283828	Nitrate/nitrite sensor pr	2.7.13.3	narX	Histidine kinase
MNLKPGEA_ mmuM	0.224998018	0.81124214	Homocysteine S-methylt	2.1.1.10	mmuM	homocysteine
MNLKPGEA_ pepT	0.224836835	0.56744044	Peptidase T	3.4.11.4	pepT	Cleaves the N-terminal amino a
MNLKPGEA_ hxpB_1	0.224409192	0.84141757	Hexitol phosphatase B	3.1.3.68	0	TIGRFAM HAD-superfamily hydr
MNLKPGEA_ yqjI	0.224358365	0.81124214	Transcriptional regulator	NA	yqjI	transcriptional regulator
MNLKPGEA_ hinT	0.224163274	0.47978352	Purine nucleoside phospl	3.9.1.-	hinT	COG0537 Diadenosine tetraphos
MNLKPGEA_ ptsI	0.223240214	0.40385959	Phosphoenolpyruvate-pr	2.7.3.9	ptsI	General (non sugar-specific) cor
MNLKPGEA_ gstA	0.222000995	0.45194315	Glutathione S-transferas	2.5.1.18	gst	Belongs to the GST superfamily
MNLKPGEA_ clpX	0.220916215	0.53185812	ATP-dependent Clp prote	NA	clpX	ATP-dependent specificity comp
MNLKPGEA_ MNLKPGEA	0.220778806	NA	hypothetical protein	NA	yhdV	Protein involved in biological_pr
MNLKPGEA_ malH	0.220637275	0.82641067	Maltose-6'-phosphate gl	3.2.1.122	0	6-phospho-alpha-glucosidase
MNLKPGEA_ deoC_2	0.21860947	0.63221268	Deoxyribose-phosphate a	4.1.2.4	deoC	Catalyzes a reversible aldol reac
MNLKPGEA_ pepE	0.218379094	0.73432123	Peptidase E	3.4.13.21	pepE	Hydrolyzes dipeptides containing
MNLKPGEA_ dtpC	0.218125885	NA	Dipeptide and tripeptide	NA	yjdL	Proton-dependent permease tha
MNLKPGEA_ MNLKPGEA	0.217643405	NA	hypothetical protein	NA	#N/A	#N/A
MNLKPGEA_ MNLKPGEA	0.215093194	0.81989975	hypothetical protein	NA	0	LuxR family transcriptional regul
MNLKPGEA_ MNLKPGEA	0.214662607	0.65489482	hypothetical protein	NA	yhdN	PFAM DnaJ homologue, subfami
MNLKPGEA_ eamB	0.212722829	0.81386801	Cysteine/O-acetylserine	NA	eamB	LysE type translocator
MNLKPGEA_ cvrA	0.2121154	0.61815327	K(+)/H(+) antiporter Nha	NA	nhaP2	K( ) H( ) antiporter that extrudes

MNLKPGEA_	rhaS_9	0.212061391	0.81562616	HTH-type transcriptional	NA	0	AraC-type transcriptional regula
MNLKPGEA_	MNLKPGEA	0.211857737	0.8687739	hypothetical protein	NA	0	transcriptional regulator
MNLKPGEA_	MNLKPGEA	0.21037226	0.78911757	hypothetical protein	NA	ybaR	COG0659 Sulfate permease and
MNLKPGEA_	MNLKPGEA	0.210325982	0.71443185	hypothetical protein	NA	0	0
MNLKPGEA_	tktA_2	0.208611126	NA	Transketolase 1	2.2.1.1	tktA	Catalyzes the transfer of a two-c
MNLKPGEA_	gstB_2	0.207447066	0.81069729	Glutathione S-transferas	2.5.1.18	yncG	Glutathione S-Transferase
MNLKPGEA_	gcvH	0.207310019	0.80246821	Glycine cleavage system	NA	gcvH	The glycine cleavage system cat
MNLKPGEA_	araF	0.206291903	0.81699862	L-arabinose-binding peri	NA	araF	l-arabinose-binding periplasmic
MNLKPGEA_	grxC	0.205821825	0.75240579	Glutaredoxin 3	NA	grxC	Has a glutathione-disulfide oxid
MNLKPGEA_	MNLKPGEA	0.204505089	0.72603251	Type IV secretion systen	NA	virB11	Type II/IV secretion system prot
MNLKPGEA_	bcp	0.204406963	0.47726558	Peroxiredoxin Bcp	1.11.1.15	bcp	PFAM alkyl hydroperoxide reduc
MNLKPGEA_	yigZ	0.203859079	0.72026465	IMPACT family member	NA	yigZ	YigZ family
MNLKPGEA_	creD	0.203598872	0.87823918	Inner membrane protein	NA	creD	Inner membrane protein involve
MNLKPGEA_	ygfF	0.20257737	0.87509031	putative oxidoreductase	1.-.-.-	ygfF	Dehydrogenases with different s
MNLKPGEA_	MNLKPGEA	0.202178384	0.75240579	hypothetical protein	NA	VY92_04	Transcriptional regulator
MNLKPGEA_	MNLKPGEA	0.20194887	0.7754674	hypothetical protein	NA	yba2	protein conserved in bacteria
MNLKPGEA_	MNLKPGEA	0.20036275	0.68640445	hypothetical protein	NA	0	protein conserved in bacteria
MNLKPGEA_	MNLKPGEA	0.200285162	0.75869083	Putative transport protei	NA	ydiK_1	permease
MNLKPGEA_	MNLKPGEA	0.199948591	0.57541498	26 kDa periplasmic imm	NA	yggE	Protein of unknown function (DU
MNLKPGEA_	walR	0.198723052	0.87967643	Transcriptional regulator	NA	walR	COG0745 Response regulators c
MNLKPGEA_	oprD	0.198373833	NA	Porin D	3.4.21.-	oprD	outer membrane porin, OprD fa
MNLKPGEA_	msrB	0.19814265	0.73554084	Peptide methionine sulf	1.8.4.12	msrB	Belongs to the MsrB Met sulfoxi
MNLKPGEA_	MNLKPGEA	0.197101045	0.82435024	hypothetical protein	NA	0	tail collar domain protein
MNLKPGEA_	ghrA_2	0.197095818	0.87967643	Glyoxylate/hydroxypyruv	1.1.1.79	ghrA	D-isomer specific 2-hydroxyacid
MNLKPGEA_	MNLKPGEA	0.196877036	NA	hypothetical protein	NA	#N/A	#N/A
MNLKPGEA_	gntR_2	0.196162573	0.69530388	HTH-type transcriptional	NA	gntR	transcriptional regulator
MNLKPGEA_	gltC_2	0.195691939	NA	HTH-type transcriptional	NA	0	Transcriptional regulator
MNLKPGEA_	yfiZ	0.195628864	NA	putative siderophore tra	NA	0	Belongs to the binding-protein-d
MNLKPGEA_	uup	0.194835592	0.66944386	ABC transporter ATP-bin	NA	uup	ABC transporter C-terminal dom
MNLKPGEA_	MNLKPGEA	0.193875335	NA	hypothetical protein	NA	0	endonuclease activity

MNLKPGEA_ dsdC_1	0.191453603	0.77723227	HTH-type transcriptional	NA	dsdC	transcriptional regulator
MNLKPGEA_ sasA_1	0.191082919	NA	Adaptive-response sensc	2.7.-.-	0	PhoQ Sensor
MNLKPGEA_ yceM	0.189696175	0.80805755	Putative oxidoreductase	1.-.-.-	mviM	oxidoreductase
MNLKPGEA_ codA_1	0.189051569	0.7661108	Cytosine deaminase	3.5.4.1	codA	cytosine deaminase
MNLKPGEA_ yicJ_2	0.18852132	0.85763471	Inner membrane sympor	NA	yicJ	COG2211 Na melibiose symport
MNLKPGEA_ gpr	0.187497262	0.77928864	L-glyceraldehyde 3-phos	1.1.1.-	yghZ	reductase
MNLKPGEA_ yehW	0.186482878	0.88626513	Glycine betaine uptake s	NA	yehW	permease
MNLKPGEA_ MNLKPGEA	0.185886385	NA	hypothetical protein	NA	#N/A	#N/A
MNLKPGEA_ yiaC	0.185387302	0.74596781	Peptidyl-lysine N-acetylt	2.3.1.-	yiaC	acetyltransferase
MNLKPGEA_ nagE	0.184942894	0.78244186	PTS system N-acetylgluc	NA	nagE	Phosphotransferase System
MNLKPGEA_ pxpA_2	0.184700825	0.87509031	5-oxoprolinase subunit A	3.5.2.9	ybgL	Belongs to the UPF0271 (lamB)
MNLKPGEA_ argD	0.183910682	0.84844917	Acetylornithine/succinyl	2.6.1.11	argD	aminotransferase
MNLKPGEA_ MNLKPGEA	0.183305334	NA	hypothetical protein	NA	0	Phage small terminase subunit
MNLKPGEA_ fliY_1	0.182622009	NA	L-cystine-binding protein	NA	0	Amino acid ABC transporter sub
MNLKPGEA_ gudX	0.181809279	NA	Glucarate dehydratase-r	4.2.1.-	gudX	Belongs to the mandelate racem
MNLKPGEA_ MNLKPGEA	0.180789828	0.64704435	hypothetical protein	NA	yciU	Belongs to the UPF0263 family
MNLKPGEA_ ycbV	0.18033037	NA	putative fimbrial-like pro	NA	0	Fimbrial protein
MNLKPGEA_ manX	0.180257281	0.76153733	PTS system mannose-sp	2.7.1.191	manX	pts system
MNLKPGEA_ mrkD	0.180126396	NA	Fimbria adhesin protein	NA	mrkD	Fimbrial protein
MNLKPGEA_ hcnB	0.179724702	NA	Hydrogen cyanide syntha	1.4.99.5	ooxA	HI0933-like protein
MNLKPGEA_ kdpB	0.179724702	NA	Potassium-transporting A	7.2.2.6	kdpB	Part of the high-affinity ATP-driv
MNLKPGEA_ MNLKPGEA	0.179724702	NA	hypothetical protein	NA	0	Rhodanese
MNLKPGEA_ MNLKPGEA	0.179724702	NA	hypothetical protein	NA	mdcE	malonate decarboxylase gamma
MNLKPGEA_ MNLKPGEA	0.179724702	NA	2-haloacrylate reductase	1.3.1.103	0	COG0604 NADPH quinone reduct
MNLKPGEA_ MNLKPGEA	0.179724702	NA	hypothetical protein	NA	0	Fimbrial protein
MNLKPGEA_ pepQ	0.179304899	0.65637345	Xaa-Pro dipeptidase	3.4.13.9	pepQ	Splits dipeptides with a prolyl re
MNLKPGEA_ fucU	0.17927125	NA	L-fucose mutarotase	5.1.3.29	fucU	Involved in the anomeric convers
MNLKPGEA_ cusR	0.178166971	NA	Transcriptional regulator	NA	cusR	Transcriptional regulatory protei
MNLKPGEA_ livH_2	0.177988585	NA	High-affinity branched-cl	NA	livH	Belongs to the binding-protein-d
MNLKPGEA_ MNLKPGEA	0.177988585	NA	hypothetical protein	NA	pecM	of the drug metabolite transport

MNLKPGEA_ MNLKPGEA	0.177870162	NA	hypothetical protein	NA	yobD	UPF0266 membrane protein
MNLKPGEA_ chiP	0.177423566	0.8080127	Chitoporin	NA	chiP	Outer membrane porin
MNLKPGEA_ MNLKPGEA	0.177085554	NA	hypothetical protein	NA	0	Bacteriophage holin family HP1
MNLKPGEA_ oppF_3	0.177085554	NA	Oligopeptide transport A	NA	0	Belongs to the ABC transporter s
MNLKPGEA_ ureE	0.176145328	NA	Urease accessory protei	NA	ureE	Involved in urease metallocente
MNLKPGEA_ frmR	0.175631212	NA	Transcriptional represso	NA	frmR	protein conserved in bacteria
MNLKPGEA_ MNLKPGEA	0.175003766	NA	hypothetical protein	NA	0	Protein of unknown function (DU
MNLKPGEA_ MNLKPGEA	0.175003766	NA	hypothetical protein	NA	0	ABC-type nitrate sulfonate bicar
MNLKPGEA_ hcpA_2	0.174557437	NA	Major exported protein	NA	hcp3	Type VI secretion system effecto
MNLKPGEA_ oppD_3	0.174557437	NA	Oligopeptide transport A	NA	dppD	Belongs to the ABC transporter s
MNLKPGEA_ pobB	0.174557437	NA	Phenoxybenzoate dioxyg	1.-.-.-	vanB	Flavodoxin reductases (Ferredox
MNLKPGEA_ dedA	0.174318298	0.86203017	Protein DedA	NA	dedA	Pfam SNARE associated Golgi pr
MNLKPGEA_ glnK	0.174209735	NA	Nitrogen regulatory prot	NA	glnK	Belongs to the P(II) protein fami
MNLKPGEA_ phnX	0.174209735	NA	Phosphonoacetaldehyde	3.11.1.1	phnX	Belongs to the HAD-like hydrolas
MNLKPGEA_ dpaL	0.174152997	NA	Diaminopropionate amn	4.3.1.15	ygeX	Diaminopropionate ammonia-ly
MNLKPGEA_ mhpE	0.174152997	NA	4-hydroxy-2-oxovalerate	4.1.3.39	mhpE	Catalyzes the retro-aldol cleavag
MNLKPGEA_ lsrF	0.174097179	0.8964368	3-hydroxy-5-phosphonoo	2.3.1.245	lsrF	Involved in the degradation of pl
MNLKPGEA_ eutB_1	0.173276898	NA	Ethanolamine ammonia·	4.3.1.7	eutB	With EutC catalyzes the formati
MNLKPGEA_ ycdX	0.173158467	0.71990392	putative phosphatase Yc	3.1.3.-	ycdX	Belongs to the PHP family
MNLKPGEA_ exuT_2	0.173059178	0.84207485	Hexuronate transporter	NA	exuT	Major facilitator superfamily
MNLKPGEA_ ydjM	0.172233381	0.85017541	Inner membrane protein	NA	ydjM	membrane-bound metal-depend
MNLKPGEA_ MNLKPGEA	0.171525365	0.86013665	hypothetical protein	NA	0	TrbL/VirB6 plasmid conjugal tra
MNLKPGEA_ glnQ_4	0.171283398	NA	Glutamine transport ATF	NA	glnQ_2	amino acid ABC transporter, ATF
MNLKPGEA_ astC_2	0.170542635	0.80558918	Succinylornithine transa	2.6.1.81	argD	aminotransferase
MNLKPGEA_ rlmL	0.169606337	0.73369756	Ribosomal RNA large su	NA	rlmL	Specifically methylates the guar
MNLKPGEA_ panE	0.169147302	0.80963388	2-dehydropantoate 2-rec	1.1.1.169	panE	Catalyzes the NADPH-dependent
MNLKPGEA_ araG	0.168964496	NA	Arabinose import ATP-bi	7.5.2.12	araG	Part of the ABC transporter com
MNLKPGEA_ MNLKPGEA	0.168410289	NA	hypothetical protein	NA	pduO	adenosyltransferase
MNLKPGEA_ MNLKPGEA	0.168410289	NA	hypothetical protein	NA	0	integral membrane protein
MNLKPGEA_ MNLKPGEA	0.168259008	NA	hypothetical protein	NA	#N/A	#N/A

MNLKPGEA_	mtrA	0.168259008	NA	HTH-type transcriptional	NA	ykgD	Transcriptional
MNLKPGEA_	iprA_2	0.168252879	0.82846121	Inhibitor of hydrogen per	NA	0	Winged helix-turn-helix DNA bin
MNLKPGEA_	MNLKPGEA	0.167722463	0.85547437	hypothetical protein	NA	0	Putative glutamine amidotransf
MNLKPGEA_	MNLKPGEA	0.167654737	0.84711625	Beta-xylosidase	3.2.1.-	0	Belongs to the glycosyl hydrolas
MNLKPGEA_	MNLKPGEA	0.167199041	NA	hypothetical protein	NA	0	HNH nucleases
MNLKPGEA_	MNLKPGEA	0.167040407	0.81989975	hypothetical protein	NA	phnB	PFAM Glyoxalase bleomycin resi
MNLKPGEA_	astA_1	0.166799539	NA	Arginine N-succinyltrans	2.3.1.109	astA	arginine N-succinyltransferase
MNLKPGEA_	yicJ_1	0.166339363	NA	Inner membrane sympor	NA	yicJ	COG2211 Na melibiose symport
MNLKPGEA_	sutR_1	0.165735308	0.87609473	HTH-type transcriptional	NA	ydcN	transcriptional regulator
MNLKPGEA_	pnoA	0.165313517	0.88956097	Nitronate monooxygena	1.13.12.-	0	2-nitropropane dioxygenase
MNLKPGEA_	rbsA_3	0.164202765	0.88873326	Ribose import ATP-bindi	7.5.2.7	rbsA	import. Responsible for energy c
MNLKPGEA_	fimD_4	0.163760977	0.87476992	Outer membrane usher	NA	fimD	Fimbrial biogenesis outer memb
MNLKPGEA_	ubiC	0.163265899	0.83503937	Chorismate pyruvate-lya	4.1.3.40	ubiC	Removes the pyruvyl group from
MNLKPGEA_	MNLKPGEA	0.163174444	0.68926534	hypothetical protein	NA	cigR	response to cobalt ion
MNLKPGEA_	xanP_2	0.162921351	NA	Xanthine permease XanP	NA	xanQ	xanthine
MNLKPGEA_	MNLKPGEA	0.162889031	0.8756443	hypothetical protein	NA	yjeT	protein conserved in bacteria
MNLKPGEA_	MNLKPGEA	0.162238695	NA	IS3 family transposase IS	NA	0	Transposase and inactivated der
MNLKPGEA_	ydjH	0.162238695	NA	putative sugar kinase Yd	2.7.1.-	ydjH	belongs to the carbohydrate kina
MNLKPGEA_	carA_1	0.161898922	NA	Caffeate CoA-transferas	2.8.3.23	ydiF	CoA transferase having broad su
MNLKPGEA_	dtpB	0.161677825	0.82641067	Dipeptide and tripeptide	NA	dtpB	Proton-dependent permease tha
MNLKPGEA_	hcp	0.16086295	0.75997564	Hydroxylamine reductase	1.7.99.1	hcp	Catalyzes the reduction of hydro
MNLKPGEA_	kdgR_2	0.160480036	0.76121957	Transcriptional regulator	NA	kdgR	transcriptional regulator
MNLKPGEA_	dhaR	0.159682979	0.89087324	PTS-dependent dihydrox	NA	dhaR	Positively regulates the dhaKLM
MNLKPGEA_	ssuA_1	0.157113088	NA	Putative aliphatic sulfon	NA	0	ABC-type nitrate sulfonate bicar
MNLKPGEA_	ulaC_2	0.157113088	NA	Ascorbate-specific PTS s	NA	ulaC	Phosphotransferase System
MNLKPGEA_	emrA_1	0.156819337	0.71990392	Multidrug export protein	NA	emrA	multidrug resistance efflux pum
MNLKPGEA_	MNLKPGEA	0.156471935	0.70413166	ISNCY family transposas	NA	yadD	Putative transposase, YhgA-like
MNLKPGEA_	lysC	0.154581754	0.76965018	Lysine-sensitive aspartol	2.7.2.4	lysC	Belongs to the aspartokinase fa
MNLKPGEA_	apbC	0.153918192	0.69867968	Iron-sulfur cluster carrier	NA	mrp	Binds and transfers iron-sulfur (
MNLKPGEA_	trkH	0.153198831	0.78907004	Trk system potassium up	NA	trkH	Low-affinity potassium transpor

MNLKPGEA_	MNLKPGEA	0.153115147	0.86132613	hypothetical protein	NA	0	Acetyltransferases including N-a
MNLKPGEA_	rhaR_1	0.151891038	0.87031512	HTH-type transcriptional	NA	tetD	AraC family transcriptional regul
MNLKPGEA_	yaiA	0.151844301	0.70049435	putative protein YaiA	NA	yaiA	YaiA protein
MNLKPGEA_	dgcM	0.15159163	0.73369756	Diguanylate cyclase DgcI	2.7.7.65	ydaM	Diguanylate cyclase
MNLKPGEA_	rspR	0.15094345	0.76883828	HTH-type transcriptional	NA	ydfH	transcriptional regulator
MNLKPGEA_	sfmD	0.14943045	0.88032863	Outer membrane usher	NA	0	Fimbrial
MNLKPGEA_	loiP	0.148595304	0.76124986	Metalloprotease LoiP	3.4.24.-	yggG	metalloprotease
MNLKPGEA_	ubiF	0.147904569	0.81069729	3-demethoxyubiquinol 3-	1.14.99.60	ubiF	ubiquinone biosynthesis hydroxy
MNLKPGEA_	tus	0.146939744	NA	DNA replication terminu	NA	tus	Trans-acting protein required fo
MNLKPGEA_	ribD	0.146351974	0.83933879	Riboflavin biosynthesis p	NA	ribD	Converts 2,5-diamino-6-(ribosyla
MNLKPGEA_	MNLKPGEA	0.145939166	0.76782279	3'3'-cGAMP-specific pho	3.1.4.-	0	metal-dependent phosphohydrol
MNLKPGEA_	cynR_2	0.144746176	0.91120361	HTH-type transcriptional	NA	cynR	transcriptional regulator
MNLKPGEA_	MNLKPGEA	0.1447391	NA	hypothetical protein	NA	0	Acyltransferase
MNLKPGEA_	gpsA	0.144144699	0.75997564	Glycerol-3-phosphate de	1.1.1.94	gpsA	Glycerol-3-phosphate dehydroge
MNLKPGEA_	crcB_2	0.144107223	0.89745381	Putative fluoride ion trar	NA	crcB	Important for reducing fluoride c
MNLKPGEA_	MNLKPGEA	0.143942149	0.88112252	hypothetical protein	NA	ycbC	Gram-negative-bacterium-type c
MNLKPGEA_	metN_2	0.143855131	0.90817374	Methionine import ATP-I	3.6.3.-	metN	Part of the ABC transporter com
MNLKPGEA_	mipA	0.143794348	0.80789105	MltA-interacting protein	NA	mipA	MltA-interacting protein
MNLKPGEA_	uxaB_2	0.142163529	0.78841281	Altronate oxidoreductase	1.1.1.58	uxaB	Belongs to the mannitol dehydro
MNLKPGEA_	acpS	0.141971394	NA	Holo-[acyl-carrier-protei	2.7.8.7	acpS	Transfers the 4'-phosphopanteth
MNLKPGEA_	MNLKPGEA	0.141745131	NA	hypothetical protein	NA	0	0
MNLKPGEA_	bla_1	0.141477504	0.90124813	Beta-lactamase SHV-1	3.5.2.6	penP	Beta-lactamase
MNLKPGEA_	hemD	0.141125927	0.81699862	Uroporphyrinogen-III syn	4.2.1.75	hemD	Uroporphyrinogen-III synthase
MNLKPGEA_	MNLKPGEA	0.140698397	NA	4-hydroxyproline 2-epim	5.1.1.8	0	Belongs to the proline racemase
MNLKPGEA_	hdeD	0.139620551	NA	Protein HdeD	NA	hdeD	Acid-resistance membrane prote
MNLKPGEA_	bglY	0.139513458	0.9062942	Beta-galactosidase BglY	3.2.1.23	ganA	beta-galactosidase
MNLKPGEA_	MNLKPGEA	0.139102641	0.75997564	ISNCY family transposas	NA	yfaD	Transposase
MNLKPGEA_	MNLKPGEA	0.138838668	NA	hypothetical protein	NA	yxjC	COG2610 H gluconate symporter
MNLKPGEA_	nikA	0.138405127	NA	Nickel-binding periplasm	NA	nikA	nickel ABC transporter
MNLKPGEA_	nudL	0.137732984	0.90817374	putative Nudix hydrolase	3.6.1.-	nudL	NUDIX hydrolase

MNLKPGEA_	MNLKPGEA	0.137559324	0.73392864	hypothetical protein	NA	yiaG	transcriptional regulator
MNLKPGEA_	MNLKPGEA	0.133977756	0.82482407	hypothetical protein	NA	#N/A	#N/A
MNLKPGEA_	cfa	0.133650759	0.67798479	Cyclopropane-fatty-acyl-	2.1.1.79	cfa	synthase
MNLKPGEA_	MNLKPGEA	0.133299167	0.89261305	hypothetical protein	NA	yecH	Protein of unknown function (DU
MNLKPGEA_	menF	0.132884975	0.86154831	Isochorismate synthase I	5.4.4.2	menF	Catalyzes the conversion of chor
MNLKPGEA_	glpR_4	0.13270664	0.92034265	Glycerol-3-phosphate re	NA	0	transcriptional regulator
MNLKPGEA_	betA	0.130277058	0.89745381	Oxygen-dependent choli	1.1.99.1	betA	Involved in the biosynthesis of th
MNLKPGEA_	gabP	0.130188485	0.81108858	GABA permease	NA	gabP	Gamma-aminobutyrate
MNLKPGEA_	MNLKPGEA	0.129858971	NA	IS5 family transposase IS	NA	0	ISSoEn1, terminal inverted repea
MNLKPGEA_	MNLKPGEA	0.129499129	NA	hypothetical protein	NA	0	fatty acid desaturase
MNLKPGEA_	MNLKPGEA	0.12933905	NA	hypothetical protein	NA	0	0
MNLKPGEA_	intA_1	0.129036695	0.82482407	Prophage integrase IntA	NA	0	Belongs to the 'phage' integrase
MNLKPGEA_	glpA	0.128975213	NA	Anaerobic glycerol-3-pho	1.1.5.3	glpA	Belongs to the FAD-dependent g
MNLKPGEA_	clpP_2	0.126746216	0.66055687	ATP-dependent Clp prote	3.4.21.92	clpP	Cleaves peptides in various prote
MNLKPGEA_	yddE	0.124197431	0.86210093	putative isomerase YddE	5.1.-.-	yddE	phenazine biosynthesis protein P
MNLKPGEA_	MNLKPGEA	0.123643073	0.87967643	hypothetical protein	NA	yjbQ	Secondary thiamine-phosphate s
MNLKPGEA_	lhgD	0.121584847	0.77413656	L-2-hydroxyglutarate deh	1.1.5.-	lhgO	L-2-hydroxyglutarate oxidase Lhg
MNLKPGEA_	MNLKPGEA	0.12079416	0.90509444	hypothetical protein	NA	0	YfaZ precursor
MNLKPGEA_	MNLKPGEA	0.120033968	0.8808318	hypothetical protein	NA	carAa	Rieske [2Fe-2S] domain
MNLKPGEA_	dsdX_2	0.119905312	NA	D-serine transporter Dsd	NA	dsdX	Gluconate
MNLKPGEA_	yciE_2	0.118500922	0.90056563	Protein YciE	NA	yciE	protein conserved in bacteria
MNLKPGEA_	rhaS_6	0.111503979	0.89674235	HTH-type transcriptional	NA	0	transcriptional regulator
MNLKPGEA_	srlA	0.1113922	NA	PTS system glucitol/sorb	NA	srlA	PTS system glucitol sorbitol-spe
MNLKPGEA_	narL	0.111228644	0.90103869	Nitrate/nitrite response	NA	narL	response regulator
MNLKPGEA_	recN	0.111003993	0.86974706	DNA repair protein RecN	NA	recN	May be involved in recombinatic
MNLKPGEA_	chiA1	0.110582961	0.89674235	Chitinase A1	3.2.1.14	chiA1	chitinase
MNLKPGEA_	hdfR_5	0.109343859	0.93707738	HTH-type transcriptional	NA	yvbU	transcriptional regulator
MNLKPGEA_	ybiU	0.108337197	0.9337214	putative protein YbiU	NA	ybiU	Protein of unknown function (DU
MNLKPGEA_	cdhR	0.107242015	0.93883346	HTH-type transcriptional	NA	adpA	Transcriptional regulator contair
MNLKPGEA_	MNLKPGEA	0.106922949	NA	hypothetical protein	NA	0	head-tail adaptor

MNLKPGEA_	nirD	0.106922949	NA	Nitrite reductase (NADH	1.7.1.15	nirD	Nitrite reductase
MNLKPGEA_	pucM	0.10686966	NA	5-hydroxyisourate hydrol	3.5.2.17	uraH	Belongs to the transthyretin fam
MNLKPGEA_	fepD	0.106421157	0.88673236	Ferric enterobactin trans	NA	fepD	Belongs to the binding-protein-d
MNLKPGEA_	glpF_2	0.106241972	NA	Glycerol uptake facilitat	NA	glpF	Belongs to the MIP aquaporin (T
MNLKPGEA_	ghrA_1	0.105299542	NA	Glyoxylate/hydroxypyruv	1.1.1.79	ghrA	D-isomer specific 2-hydroxyacid
MNLKPGEA_	carA_2	0.104841495	0.88401284	Carbamoyl-phosphate sy	6.3.5.5	carA	Belongs to the CarA family
MNLKPGEA_	nhaK	0.104745565	0.8698482	Sodium, potassium, lithi	NA	yjcE	NhaP-type Na H and K H antipor
MNLKPGEA_	arnF	0.104215181	NA	putative 4-amino-4-deox	NA	arnF	Translocates 4-amino-4-deoxy-L
MNLKPGEA_	nfi	0.104066893	0.91377552	Endonuclease V	3.1.21.7	nfi	DNA repair enzyme involved in t
MNLKPGEA_	tuf1_1	0.103908193	0.76782279	Elongation factor Tu 1	NA	tuf	This protein promotes the GTP-d
MNLKPGEA_	mdtH_1	0.103769826	NA	Multidrug resistance pro	NA	0	Major facilitator superfamily
MNLKPGEA_	madC	0.103692117	NA	Malonyl-S-ACP:biotin-pr	2.1.3.10	mdcD	Beta subunit
MNLKPGEA_	mdh_2	0.103692117	NA	NAD-dependent methan	1.1.1.244	eutG	alcohol dehydrogenase
MNLKPGEA_	rhtC_2	0.102984374	NA	Threonine efflux protein	NA	rhtC	PFAM Lysine exporter protein (L
MNLKPGEA_	ydhP_2	0.102621329	NA	Inner membrane transpo	NA	ydhP	Major facilitator Superfamily
MNLKPGEA_	hisJ_2	0.102556925	NA	Histidine-binding peripla	NA	argT	Belongs to the bacterial solute-b
MNLKPGEA_	cbiT	0.1018245	NA	Cobalt-precorrin-6B C(15	2.1.1.196	cobL	precorrin-6y C5,15-methyltransf
MNLKPGEA_	MNLKPGEA	0.1018245	NA	hypothetical protein	NA	hofN	carbon utilization
MNLKPGEA_	MNLKPGEA	0.1018245	NA	hypothetical protein	NA	0	ImpA domain protein
MNLKPGEA_	thlA_2	0.1018245	NA	Acetyl-CoA acetyltransfe	2.3.1.9	phbA	Catalyzes the final step of fatty a
MNLKPGEA_	malP_3	0.101769437	0.73674612	Maltodextrin phosphoryl	2.4.1.1	glgP	Phosphorylase is an important a
MNLKPGEA_	dsbE	0.101414741	NA	Thiol:disulfide interchan	NA	dsbE	Thiol disulfide interchange prote
MNLKPGEA_	MNLKPGEA	0.10140703	NA	hypothetical protein	NA	0	amino acid ABC transporter
MNLKPGEA_	oprM_1	0.100762811	0.94219443	Outer membrane protei	NA	eefC	RND efflux system, outer memb
MNLKPGEA_	priC	0.100677401	0.93568072	Primosomal replication p	NA	priC	primosomal replication protein
MNLKPGEA_	MNLKPGEA	0.09996579	NA	hypothetical protein	NA	0	Fimbrial protein
MNLKPGEA_	MNLKPGEA	0.098648776	NA	hypothetical protein	NA	0	0
MNLKPGEA_	ulaE_1	0.098467722	NA	L-ribulose-5-phosphate 3	5.1.3.22	sgbU	3-epimerase
MNLKPGEA_	mrcA	0.098418864	0.87970233	Penicillin-binding protei	NA	mrcA	penicillin-binding protein 1A
MNLKPGEA_	lexA_2	0.098120503	NA	LexA repressor	3.4.21.88	0	LexA DNA binding domain

MNLKPGEA_	MNLKPGEA	0.097029954	NA	hypothetical protein	NA	0	0
MNLKPGEA_	MNLKPGEA	0.096197157	NA	PKHD-type hydroxylase	1.14.11.-	ybiX	PkhD-type hydroxylase
MNLKPGEA_	cynR_3	0.094789206	0.94488713	HTH-type transcriptional	NA	ybhD	transcriptional regulator
MNLKPGEA_	eutQ	0.093528132	NA	Ethanolamine utilization	NA	eutQ	Ethanolamine utilization protein
MNLKPGEA_	klcA_1	0.093528132	NA	Antirestriction protein Kl	NA	0	Antirestriction protein
MNLKPGEA_	MNLKPGEA	0.092301198	0.71443185	hypothetical protein	NA	0	Bacterial mobilisation protein (M
MNLKPGEA_	fdx	0.092097547	0.86203017	2Fe-2S ferredoxin	NA	fdx	Ferredoxin, 2Fe-2S type, ISC syst
MNLKPGEA_	MNLKPGEA	0.092034435	NA	hypothetical protein	NA	0	ABC-type nitrate sulfonate bicar
MNLKPGEA_	cbdA	0.090534064	NA	2-halobenzoate 1,2-diox	1.14.12.13	benA	COG4638 Phenylpropionate diox
MNLKPGEA_	MNLKPGEA	0.090186521	0.90497565	hypothetical protein	NA	yqhA	UPF0114 protein
MNLKPGEA_	moaC	0.088494991	0.94864146	Cyclic pyranopterin mon	4.6.1.17	moaC	Catalyzes the conversion of (8S)-
MNLKPGEA_	cpo	0.088342264	0.88056947	Non-heme chloroperoxic	1.11.1.10	cpo	Alpha beta hydrolase
MNLKPGEA_	hycA	0.086269246	NA	Formate hydrogenlyase	NA	hycA	seems to prevent binding of FhlA
MNLKPGEA_	menB	0.085399718	0.92675094	1,4-dihydroxy-2-naphtho	4.1.3.36	menB	Converts o-succinylbenzoyl-CoA (
MNLKPGEA_	MNLKPGEA	0.085150773	0.9307201	hypothetical protein	NA	yjgM	Acetyltransferase
MNLKPGEA_	feaR	0.085090634	0.9337214	Transcriptional activator	NA	feaR	transcriptional regulator
MNLKPGEA_	MNLKPGEA	0.084111015	0.92584368	ISNCY family transposas	NA	0	Transposase
MNLKPGEA_	lcfB	0.083766924	NA	Long-chain-fatty-acid--C	6.2.1.3	0	AMP-binding enzyme C-terminal
MNLKPGEA_	yofA_2	0.082983923	NA	HTH-type transcriptional	NA	dgdR	transcriptional regulator
MNLKPGEA_	MNLKPGEA	0.082222049	0.95322656	putative protein	NA	MA20_32	Circularly permuted ATP-grasp ty
MNLKPGEA_	MNLKPGEA	0.081882961	0.9421681	hypothetical protein	NA	malM	maltose operon periplasmic
MNLKPGEA_	dctA_1	0.080790263	0.90996526	Aerobic C4-dicarboxylate	NA	dctA	Belongs to the dicarboxylate am
MNLKPGEA_	ada_1	0.08022497	0.95322656	Bifunctional transcriptio	NA	ogt	Involved in the cellular defense a
MNLKPGEA_	dcm_2	0.080016143	0.83933879	DNA-cytosine methyltra	2.1.1.37	dcm	Belongs to the class I-like SAM-b
MNLKPGEA_	puuC	0.076248812	0.96036225	NADP/NAD-dependent a	1.2.1.5	puuC	belongs to the aldehyde dehydrc
MNLKPGEA_	dmdB	0.074616314	0.94488713	3-methylmercaptopropic	6.2.1.44	0	COG0318 Acyl-CoA synthetases (
MNLKPGEA_	melB	0.074165668	0.93041122	Melibiose carrier protein	NA	melB	MFS/sugar transport protein
MNLKPGEA_	tpiA	0.0720261	0.86203017	Triosephosphate isomera	5.3.1.1	tpiA	Involved in the gluconeogenesis.
MNLKPGEA_	scoB	0.071300959	NA	putative succinyl-CoA:3-k	2.8.3.5	scoB	COG2057 Acyl CoA acetate 3-ket
MNLKPGEA_	MNLKPGEA	0.071258809	NA	hypothetical protein	NA	0	0

MNLKPGEA_	dgoD	0.070787568	NA	D-galactonate dehydrata	4.2.1.6	dgoD	Catalyzes the dehydration of D-g
MNLKPGEA_	lsrA	0.068764398	0.95495528	Autoinducer 2 import AT	3.6.3.-	lsrA	Part of the ABC transporter com
MNLKPGEA_	MNLKPGEA	0.068394743	0.93851396	hypothetical protein	NA	0	O-Antigen ligase
MNLKPGEA_	nudB	0.068180175	0.92687989	Dihydroneopterin triphos	3.6.1.67	nudB	dihydroneopterin triphosphate
MNLKPGEA_	iprA_1	0.0679338	0.95339478	Inhibitor of hydrogen per	NA	0	Winged helix-turn-helix DNA bin
MNLKPGEA_	rsxD	0.06567308	NA	Ion-translocating oxidore	7.-.-.-	rnfD	Part of a membrane complex inv
MNLKPGEA_	yaeQ	0.065597632	0.87509031	putative protein YaeQ	NA	yaeQ	protein conserved in bacteria
MNLKPGEA_	MNLKPGEA	0.065567223	0.96036225	hypothetical protein	NA	pecS	transcriptional regulator
MNLKPGEA_	MNLKPGEA	0.065462201	0.94474664	hypothetical protein	NA	0	helix_turn_helix, Lux Regulon
MNLKPGEA_	clcB_1	0.065442055	0.95876371	Voltage-gated ClC-type c	NA	clcA_2	Chloride channel
MNLKPGEA_	MNLKPGEA	0.065216367	0.92034265	hypothetical protein	NA	0	Universal stress protein
MNLKPGEA_	dmsC_2	0.064542945	NA	Anaerobic dimethyl sulfo	NA	dmsC	Dimethyl sulfoxide reductase
MNLKPGEA_	tdcF	0.064532767	0.94684841	Putative reactive interm	3.5.4.-	yjgF	Endoribonuclease L-PSP
MNLKPGEA_	lptE	0.064382537	0.89331274	LPS-assembly lipoprotein	NA	lptE	Together with LptD, is involved i
MNLKPGEA_	MNLKPGEA	0.063786167	0.90497565	hypothetical protein	NA	waaE	Glycosyl transferase
MNLKPGEA_	citB_1	0.063750508	NA	Transcriptional regulator	NA	dpiA	transcriptional regulatory protei
MNLKPGEA_	yaaA	0.061791741	0.91610292	Peroxide stress resistanc	NA	yaaA	Belongs to the UPF0246 family
MNLKPGEA_	dgoT_2	0.061170833	NA	D-galactonate transporte	NA	0	COG0477 Permeases of the maj
MNLKPGEA_	ybhN	0.060854577	0.93688219	Inner membrane protein	NA	ybhN	Membrane
MNLKPGEA_	pykF	0.060829921	0.88829344	Pyruvate kinase I	2.7.1.40	pykF	Belongs to the pyruvate kinase f
MNLKPGEA_	garP	0.060505431	0.95736807	putative galactarate trar	NA	garP	transporter
MNLKPGEA_	chbB	0.058630817	0.94488713	PTS system N,N'-diacety	2.7.1.196	chbB	protein IIA transfers a phosphory
MNLKPGEA_	MNLKPGEA	0.058038041	0.95317706	hypothetical protein	NA	#N/A	#N/A
MNLKPGEA_	budA	0.054222114	NA	Alpha-acetolactate deca	4.1.1.5	budA	Alpha-acetolactate decarboxylas
MNLKPGEA_	mnmC	0.053880306	0.95686273	tRNA 5-methylaminome	NA	mnmC	Catalyzes the last two steps in t
MNLKPGEA_	acrB_1	0.053718549	0.92675094	Multidrug efflux pump su	NA	acrD	Belongs to the resistance-nodula
MNLKPGEA_	mdtM_2	0.053564295	0.95734095	Multidrug resistance pro	NA	cmr	Major facilitator Superfamily
MNLKPGEA_	por_2	0.052497244	0.95686273	Polyol:NADP oxidoreduct	1.1.1.-	ydfI	Belongs to the mannitol dehydro
MNLKPGEA_	MNLKPGEA	0.051355164	0.96015283	hypothetical protein	NA	0	lipolytic protein G-D-S-L family
MNLKPGEA_	MNLKPGEA	0.050738535	0.90144805	hypothetical protein	NA	0	Chlorite dismutase

MNLKPGEA_	MNLKPGEA	0.050640327	0.92208141	hypothetical protein	NA	#N/A	#N/A
MNLKPGEA_	ackA	0.050520732	0.88626513	Acetate kinase	2.7.2.1	ackA	Catalyzes the formation of acety
MNLKPGEA_	ompN_2	0.050151394	0.96033077	Outer membrane porin I	NA	ompN	Belongs to the Gram-negative p
MNLKPGEA_	rhaS_5	0.050139023	0.96401338	HTH-type transcriptional	NA	0	transcriptional regulator
MNLKPGEA_	pgrR_5	0.049870496	0.94219443	HTH-type transcriptional	NA	0	LysR substrate binding domain
MNLKPGEA_	lldR_3	0.049704461	0.9583707	Putative L-lactate dehydı	NA	uxuR	Transcriptional
MNLKPGEA_	dmlA	0.048945743	0.96741745	D-malate dehydrogenase	1.1.1.83	dmlA	Isocitrate/isopropylmalate dehy
MNLKPGEA_	ttuB_2	0.048198688	0.95322656	Putative tartrate transpc	NA	0	Major facilitator superfamily
MNLKPGEA_	mobB	0.048164065	0.95472331	Molybdopterin-guanine (	NA	mobB	molybdopterin-guanine dinucleo
MNLKPGEA_	MNLKPGEA	0.047947616	0.92208141	hypothetical protein	NA	0	0
MNLKPGEA_	ivy	0.047715465	0.88626513	Inhibitor of vertebrate ly	NA	0	Inhibitor of vertebrate lysozyme
MNLKPGEA_	mltF_2	0.046977639	0.96033077	Membrane-bound lytic n	4.2.2.-	mltF	Murein-degrading enzyme that (
MNLKPGEA_	iaaA	0.046841263	0.96280851	Isoaspartyl peptidase	3.4.19.5	iaaA	asparaginase
MNLKPGEA_	MNLKPGEA	0.045681849	0.9583707	putative protein	NA	yhiN	HI0933 family
MNLKPGEA_	MNLKPGEA	0.045480731	0.9480187	Tagatose kinase	2.7.1.101	0	2-dehydro-3-deoxygluconokinase
MNLKPGEA_	pcaJ	0.044944595	NA	3-oxoadipate CoA-transf	2.8.3.6	pcaJ	COG2057 Acyl CoA acetate 3-ket
MNLKPGEA_	ybhA	0.044572595	0.97206174	Pyridoxal phosphate pho	3.1.3.74	ybhA	hydrolases of the HAD superfam
MNLKPGEA_	vdh	0.044560645	0.95543531	Vanillin dehydrogenase	1.2.1.67	0	belongs to the aldehyde dehydrc
MNLKPGEA_	hipO_1	0.044345456	0.95269506	Hippurate hydrolase	3.5.1.32	hipO	amidohydrolase
MNLKPGEA_	MNLKPGEA	0.043143117	0.95430207	hypothetical protein	NA	yacH	Protein of unknown function (DU
MNLKPGEA_	MNLKPGEA	0.043030851	NA	hypothetical protein	NA	yceK	(Lipo)protein
MNLKPGEA_	ilvB_2	0.04288131	NA	Acetolactate synthase is	2.2.1.6	0	Thiamine pyrophosphate enzym
MNLKPGEA_	MNLKPGEA	0.042537489	0.96417071	hypothetical protein	NA	0	CBS-domain-containing membra
MNLKPGEA_	adeQ	0.041888603	NA	Adenine permease AdeC	NA	yicO	permease
MNLKPGEA_	truB	0.041841618	0.95322656	tRNA pseudouridine synt	5.4.99.25	truB	Responsible for synthesis of pse
MNLKPGEA_	MNLKPGEA	0.041586085	0.93688219	hypothetical protein	NA	0	Domain of unknown function (DU
MNLKPGEA_	ccmA	0.040255921	NA	Cytochrome c biogenesis	7.6.2.5	ccmA	once thought to export heme, th
MNLKPGEA_	MNLKPGEA	0.039319679	0.93967983	hypothetical protein	NA	yaeP	Belongs to the UPF0253 family
MNLKPGEA_	aaeB_1	0.038921695	0.94864146	p-hydroxybenzoic acid ef	NA	aaeB	Forms an efflux pump with AaeA
MNLKPGEA_	MNLKPGEA	0.038845459	NA	hypothetical protein	NA	0	Fimbrial protein

MNLKPGEA_	cusS	0.038790017	0.97206174	Sensor histidine kinase C	2.7.13.3	cusS	member of a two-component re
MNLKPGEA_	metI_3	0.03784221	NA	D-methionine transport s	NA	metI	ABC transporter (permease)
MNLKPGEA_	cobC_1	0.037678689	NA	Adenosylcobalamin/alph	3.1.3.73	cobC	Belongs to the phosphoglycerate
MNLKPGEA_	dipZ	0.037678689	NA	Protein DipZ	NA	dipZ	cytochrome c biogenesis protein
MNLKPGEA_	yhcH_2	0.037678689	NA	putative protein YhcH	NA	yjgK	Domain of unknown function (DU
MNLKPGEA_	trxA	0.037501308	0.92723147	Thioredoxin 1	NA	trxA	Belongs to the thioredoxin famil
MNLKPGEA_	MNLKPGEA	0.036864283	0.96477398	hypothetical protein	NA	sseB	enhanced serine sensitivity prote
MNLKPGEA_	galB	0.036317395	NA	4-oxalmesaconate hydra	4.2.1.83	MA20_26	PFAM LmbE family protein
MNLKPGEA_	asd_2	0.036243932	0.9745689	Aspartate-semialdehyde	1.2.1.11	0	Semialdehyde dehydrogenase, N
MNLKPGEA_	iolU_2	0.036101079	NA	scyllo-inositol 2-dehydro	1.1.1.371	dhdh	oxidoreductase
MNLKPGEA_	MNLKPGEA	0.036101079	NA	hypothetical protein	NA	0	Aldo/keto reductase family
MNLKPGEA_	nudK_2	0.035466874	NA	GDP-mannose pyrophosp	3.6.1.-	nudK_2	Nudix-type nucleoside diphospha
MNLKPGEA_	recQ	0.034565222	0.96033077	ATP-dependent DNA heli	3.6.4.12	recQ	DNA helicase
MNLKPGEA_	MNLKPGEA	0.034271734	NA	IS3 family transposase IS	NA	0	Transposase and inactivated der
MNLKPGEA_	dsbD_1	0.034230231	NA	Thiol:disulfide interchan	1.8.1.8	dsbD	Disulphide bond corrector protei
MNLKPGEA_	tdcB	0.034230231	NA	L-threonine dehydratase	4.3.1.19	tdcB	Catalyzes the anaerobic formati
MNLKPGEA_	MNLKPGEA	0.03412965	NA	hypothetical protein	NA	0	NMT1-like family
MNLKPGEA_	rutR	0.033963704	0.96477398	HTH-type transcriptional	NA	rutR	transcriptional regulator
MNLKPGEA_	dppA_3	0.033433819	NA	Periplasmic dipeptide tra	NA	MA20_19	Bacterial extracellular solute-bir
MNLKPGEA_	MNLKPGEA	0.033433819	NA	hypothetical protein	NA	phnE	Phosphonate ABC transporter
MNLKPGEA_	MNLKPGEA	0.032959493	0.96836263	hypothetical protein	NA	ycaI	DNA internalization-related com
MNLKPGEA_	ada_2	0.032594334	0.96272321	Bifunctional transcriptio	NA	ada	Involved in the cellular defense a
MNLKPGEA_	MNLKPGEA	0.031695728	NA	hypothetical protein	NA	0	Baseplate J-like protein
MNLKPGEA_	fabG_6	0.031678276	NA	3-oxoacyl-[acyl-carrier-p	1.1.1.100	0	KR domain
MNLKPGEA_	betB_1	0.031438042	NA	NAD/NADP-dependent b	1.2.1.8	aldA	Aldehyde dehydrogenase family
MNLKPGEA_	atl	0.031050781	0.97206174	DNA base-flipping protei	NA	ybaZ	methylated DNA-protein cystein
MNLKPGEA_	MNLKPGEA	0.030865361	NA	hypothetical protein	NA	#N/A	#N/A
MNLKPGEA_	MNLKPGEA	0.030865361	NA	hypothetical protein	NA	0	0
MNLKPGEA_	artM_1	0.03082844	0.97451894	Arginine transport ATP-b	NA	yecC	(ABC) transporter
MNLKPGEA_	galC	0.030758112	NA	4-carboxy-4-hydroxy-2-o	4.1.3.17	ligK	methyltransferase

MNLKPGEA_	fusA_1	0.030680932	0.91744976	Elongation factor G	NA	fusA	Catalyzes the GTP-dependent rib
MNLKPGEA_	MNLKPGEA	0.030423786	0.97925677	Gluconate 2-dehydrogen	1.1.99.3	adhB	Cytochrome c
MNLKPGEA_	ureF	0.030251713	NA	Urease accessory protei	NA	ureF	Required for maturation of urea
MNLKPGEA_	ugpB_1	0.030174463	0.95472331	sn-glycerol-3-phosphate	NA	ugpB	ABC transporter substrate-bindi
MNLKPGEA_	dsdA	0.029823015	0.97472332	D-serine dehydratase	4.3.1.18	dsdA	Belongs to the serine threonine
MNLKPGEA_	phnS	0.028758922	NA	Putative 2-aminoethylph	NA	phnS	Bacterial extracellular solute-bir
MNLKPGEA_	lgoT_2	0.028315409	0.98047677	putative L-galactonate t	NA	yjjL	Major facilitator superfamily
MNLKPGEA_	MNLKPGEA	0.028043036	NA	hypothetical protein	NA	eutP	ethanolamine utilization protein
MNLKPGEA_	ssuA_2	0.028043036	NA	Putative aliphatic sulfon	NA	0	(ABC) transporter
MNLKPGEA_	ygdR_4	0.027642469	0.97207598	putative lipoprotein YgdI	NA	ygdi3	(LipO)protein
MNLKPGEA_	cobD_2	0.027274498	NA	Cobalamin biosynthesis	NA	cobD	Converts cobyric acid to cobinam
MNLKPGEA_	qmcA	0.026626541	0.96417071	Protein QmcA	NA	qmcA	COG0330 Membrane protease s
MNLKPGEA_	asnC	0.0263516	0.97371012	Regulatory protein AsnC	NA	asnC	transcriptional
MNLKPGEA_	ydeP	0.026299681	0.97206174	Protein YdeP	NA	ydeP	Belongs to the prokaryotic molyl
MNLKPGEA_	mltG	0.025476474	0.97452056	Endolytic murein transgl	4.2.2.-	mltG	Functions as a peptidoglycan ter
MNLKPGEA_	ilvM	0.025410202	NA	Acetolactate synthase is	2.2.1.6	ilvM	acetolactate synthase
MNLKPGEA_	yehZ	0.024474895	0.9611315	Glycine betaine-binding	NA	yehZ	Periplasmic glycine betaine chol
MNLKPGEA_	mdtK	0.024129373	0.95653073	Multidrug resistance pro	NA	mdtK	Multidrug efflux pump
MNLKPGEA_	MNLKPGEA	0.02391598	NA	hypothetical protein	NA	0	YebO-like protein
MNLKPGEA_	MNLKPGEA	0.021911032	0.95453549	hypothetical protein	NA	csiE	Stationary phase inducible prote
MNLKPGEA_	ptsO	0.021879609	0.98136093	Phosphocarrier protein N	NA	ptsH	PTS HPr component phosphoryla
MNLKPGEA_	bcsQ_2	0.021487838	0.98047677	Cellulose biosynthesis pr	NA	yhjQ	Cellulose synthase
MNLKPGEA_	dkgA	0.02084947	0.97206174	2,5-diketo-D-gluconic aci	1.1.1.274	dkgA	reductase
MNLKPGEA_	pxpC	0.020655019	0.98564497	5-oxoprolinase subunit C	3.5.2.9	ybgK	Allophanate hydrolase subunit 2
MNLKPGEA_	pqiB	0.020575711	0.97294274	Intermembrane transpor	NA	pqiB	paraquat-inducible protein b
MNLKPGEA_	lepB	0.020387238	0.97206174	Signal peptidase I	3.4.21.89	lepB	Belongs to the peptidase S26 fa
MNLKPGEA_	hpt	0.019197392	0.97855651	Hypoxanthine phosphorib	2.4.2.8	hpt	Belongs to the purine pyrimidine
MNLKPGEA_	MNLKPGEA	0.01901443	NA	hypothetical protein	NA	0	Putative bacterial toxin ydaT
MNLKPGEA_	rpoE	0.018701393	0.95495528	ECF RNA polymerase sig	NA	rpoE	Belongs to the sigma-70 factor f
MNLKPGEA_	hcpA_1	0.018653329	NA	Major exported protein	NA	0	Type VI secretion system effecto

MNLKPGEA_	livF_6	0.017985362	NA	High-affinity branched-c	NA	livF	Branched-chain amino acid tran
MNLKPGEA_	ppsC	0.017137509	0.98136093	Phthiocerol synthesis pol	2.3.1.41	qor	COG0604 NADPH quinone reduc
MNLKPGEA_	MNLKPGEA	0.016759811	0.97358494	hypothetical protein	NA	yifE	protein conserved in bacteria
MNLKPGEA_	MNLKPGEA	0.016083834	0.98490336	hypothetical protein	NA	0	Glycosyl transferase, family 2
MNLKPGEA_	tolC	0.015134271	0.96272321	Outer membrane protei	NA	tolC	type I secretion outer membran
MNLKPGEA_	MNLKPGEA	0.01394493	NA	hypothetical protein	NA	0	Phage head-tail joining protein
MNLKPGEA_	prc	0.012335942	0.9745689	Tail-specific protease	3.4.21.102	prc	Belongs to the peptidase S41A f
MNLKPGEA_	ybfF	0.011921662	0.99065556	Esterase YbfF	3.1.-.-	ybfF	Alpha beta hydrolase
MNLKPGEA_	MNLKPGEA	0.010866032	0.98136093	hypothetical protein	NA	0	Belongs to the small heat shock
MNLKPGEA_	MNLKPGEA	0.010199661	0.99317259	hypothetical protein	NA	yedE	transporter component
MNLKPGEA_	dsbG	0.009276092	0.99274264	Thiol:disulfide interchan	NA	dsbG	Required for disulfide bond form
MNLKPGEA_	yebS	0.008571827	0.99029563	Intermembrane transpor	NA	yebS	paraquat-inducible protein A
MNLKPGEA_	MNLKPGEA	0.007917729	0.98196186	hypothetical protein	NA	0	Diguanylate cyclase
MNLKPGEA_	pstC	0.007762243	0.9950576	Phosphate transport syst	NA	pstC	probably responsible for the trar
MNLKPGEA_	lutR	0.007757853	0.99274264	HTH-type transcriptional	NA	dgoR	FCD domain
MNLKPGEA_	cynR_4	0.007240939	0.994788	HTH-type transcriptional	NA	0	transcriptional regulator
MNLKPGEA_	MNLKPGEA	0.007226203	NA	hypothetical protein	NA	ycgG	Diguanylate phosphodiesterase
MNLKPGEA_	MNLKPGEA	0.006723125	NA	hypothetical protein	NA	yjiX	Selenoprotein, putative
MNLKPGEA_	yybH	0.006056628	0.99274264	putative protein YybH	NA	yybH	SnoaL-like domain
MNLKPGEA_	aaeX	0.005645325	0.99323195	Protein AaeX	NA	aaeX	Protein of unknown function (DU
MNLKPGEA_	MNLKPGEA	0.005076101	NA	hypothetical protein	NA	0	0
MNLKPGEA_	cspE	0.003197605	0.989625	Cold shock-like protein C	NA	cspE	SMART Cold shock protein
MNLKPGEA_	MNLKPGEA	0.002929872	0.99511075	hypothetical protein	NA	0	0
MNLKPGEA_	oxyR_3	0.00272814	0.99518439	Hydrogen peroxide-induc	NA	ywbI	transcriptional regulator
MNLKPGEA_	MNLKPGEA	0.001878876	NA	hypothetical protein	NA	0	domain, Protein
MNLKPGEA_	intS_2	0.001131876	0.9981889	Prophage integrase IntS	NA	int	Belongs to the 'phage' integrase
MNLKPGEA_	MNLKPGEA	-0.000393525	0.99938447	hypothetical protein	NA	yecE	Protein of unknown function DUI
MNLKPGEA_	gyrB	-0.00090166	0.99770831	DNA gyrase subunit B	5.6.2.2	gyrB	A type II topoisomerase that neg
MNLKPGEA_	upp	-0.001389926	0.99743242	Uracil phosphoribosyltra	2.4.2.9	upp	Catalyzes the conversion of urac
MNLKPGEA_	pdxA	-0.001951766	0.99713464	4-hydroxythreonine-4-ph	1.1.1.262	pdxA	Catalyzes the NAD(P)-dependent

MNLKPGEA_	MNLKPGEA	-0.005449362	0.994788	hypothetical protein	NA	0	transcriptional regulator
MNLKPGEA_	yhaJ_3	-0.005483773	0.99599339	HTH-type transcriptional	NA	0	transcriptional regulator
MNLKPGEA_	dgoK1_1	-0.005636027	0.99480218	putative 2-dehydro-3-de	2.7.1.58	dgoK	2-keto-3-deoxy-galactonokinase
MNLKPGEA_	hemF	-0.006013335	0.99511075	Oxygen-dependent coprc	1.3.3.3	hemF	Involved in the heme biosynthes
MNLKPGEA_	ccpA_2	-0.006164205	0.99459703	Catabolite control protei	NA	0	transcriptional regulator
MNLKPGEA_	MNLKPGEA	-0.00694458	0.99439772	hypothetical protein	NA	yhbP	Belongs to the UPF0306 family
MNLKPGEA_	glvR	-0.007376683	0.99439772	HTH-type transcriptional	NA	ybbH_1	transcriptional regulator
MNLKPGEA_	MNLKPGEA	-0.007728628	0.9950576	hypothetical protein	NA	0	ankyrin repeat
MNLKPGEA_	MNLKPGEA	-0.008136267	NA	hypothetical protein	NA	yaaW	protein conserved in bacteria
MNLKPGEA_	MNLKPGEA	-0.010102252	0.99274264	hypothetical protein	NA	0	Nucleoside recognition family pr
MNLKPGEA_	yibN	-0.010248891	0.98603684	putative protein YibN	NA	yibN	rhodanese-related sulfurtransfe
MNLKPGEA_	clcB_2	-0.010748248	0.99421027	Voltage-gated ClC-type c	NA	clcB	Probably acts as an electrical sh
MNLKPGEA_	puuB_2	-0.01233627	NA	Gamma-glutamylputres	1.4.3.-	ordL	oxidoreductase
MNLKPGEA_	yecS_1	-0.012708402	0.99317259	L-cystine transport syste	NA	yecS	amino acid ABC transporter
MNLKPGEA_	MNLKPGEA	-0.015143325	0.97175381	hypothetical protein	NA	ygiB	Belongs to the UPF0441 family
MNLKPGEA_	pdeK	-0.017445932	0.97206174	putative cyclic di-GMP pl	3.1.4.52	yhjK	the EAL-domain portion of HmsF
MNLKPGEA_	xylB_3	-0.018921829	0.98394462	Aryl-alcohol dehydrogen	1.1.1.90	0	COG1062 Zn-dependent alcohol
MNLKPGEA_	yraI_2	-0.019240374	NA	putative fimbrial chaper	NA	0	pilus organization
MNLKPGEA_	elfC	-0.021555376	0.98394462	putative outer membran	NA	0	Usher protein
MNLKPGEA_	metI_4	-0.021641923	0.98594211	D-methionine transport	NA	metI	ABC-type metal ion transport sy
MNLKPGEA_	mlaE	-0.021695005	NA	Intermembrane phosphc	NA	mlaE	COG0767 ABC-type transport sy
MNLKPGEA_	wzzE	-0.022888241	0.97175381	ECA polysaccharide chai	NA	wzzE	Modulates the polysaccharide ch
MNLKPGEA_	narZ	-0.022992181	0.96967178	Respiratory nitrate reduc	1.7.5.1	narZ	Belongs to the prokaryotic molyl
MNLKPGEA_	potA_3	-0.023022091	0.97404786	Spermidine/putrescine i	7.6.2.11	potA	Part of the ABC transporter com
MNLKPGEA_	soxS_3	-0.023187529	NA	Regulatory protein SoxS	NA	0	Transcriptional regulator
MNLKPGEA_	ybhF_1	-0.023241833	NA	putative multidrug ABC t	NA	ybhF	(ABC) transporter
MNLKPGEA_	pdxI	-0.023664679	0.98394462	Pyridoxine 4-dehydrogen	1.1.1.65	ydbC	oxidoreductase
MNLKPGEA_	MNLKPGEA	-0.024103847	NA	hypothetical protein	NA	0	Uncharacterized protein conserv
MNLKPGEA_	norB_2	-0.02476205	NA	Quinolone resistance pro	NA	norB	Quinolone resistance protein
MNLKPGEA_	mprA	-0.025637044	0.95117791	Transcriptional represso	NA	mprA	Transcriptional

MNLKPGEA_ symE	-0.025753598	0.97684517	Endoribonuclease SymE	3.1.-.-	0	Toxin SymE, type I toxin-antitoxi
MNLKPGEA_ gor	-0.026337192	0.97206174	Glutathione reductase	1.8.1.7	gor	Belongs to the class-I pyridine n
MNLKPGEA_ xerC_4	-0.02733637	0.97206174	Tyrosine recombinase Xe	NA	0	Phage integrase family
MNLKPGEA_ adhE_2	-0.027381692	0.9337214	Aldehyde-alcohol dehydr	NA	adhE	belongs to the iron- containing a
MNLKPGEA_ MNLKPGEA	-0.027552295	0.97472332	hypothetical protein	NA	#N/A	#N/A
MNLKPGEA_ iclR	-0.028333002	0.97150244	Transcriptional represso	NA	iclR	transcriptional regulator
MNLKPGEA_ yiaW_2	-0.028539002	NA	Inner membrane protein	NA	yiaW	Protein of unknown function (DU
MNLKPGEA_ tdcC	-0.028719974	NA	Threonine/serine transp	NA	tdcC	Involved in the import of threoni
MNLKPGEA_ MNLKPGEA	-0.028928574	NA	hypothetical protein	NA	0	cytochrome complex assembly
MNLKPGEA_ rluE	-0.02928937	0.96033077	Ribosomal large subunit	5.4.99.20	rluE	Belongs to the pseudouridine sy
MNLKPGEA_ MNLKPGEA	-0.029300034	NA	hypothetical protein	NA	0	0
MNLKPGEA_ lvr	-0.030400487	NA	Levodione reductase	1.1.1.-	benD	Belongs to the short-chain dehy
MNLKPGEA_ rbsC_8	-0.030555434	NA	Ribose import permease	NA	rhaP	Belongs to the binding-protein-d
MNLKPGEA_ yhhT_2	-0.030678153	0.97206174	Putative transport protei	NA	perM	permease
MNLKPGEA_ ppnP	-0.030860087	0.95359644	Pyrimidine/purine nucle	2.4.2.1	ppnP	Catalyzes the phosphorolysis of
MNLKPGEA_ MNLKPGEA	-0.031052645	NA	putative protein	NA	comEA	Competence protein ComEA
MNLKPGEA_ MNLKPGEA	-0.031076225	NA	IS110 family transposase	NA	0	Transposase
MNLKPGEA_ MNLKPGEA	-0.031076225	NA	hypothetical protein	NA	0	0
MNLKPGEA_ MNLKPGEA	-0.031319882	NA	hypothetical protein	NA	#N/A	#N/A
MNLKPGEA_ msuD_1	-0.031319882	NA	Methanesulfonate monc	1.14.14.5	ssuD	Catalyzes the desulfonation of a
MNLKPGEA_ MNLKPGEA	-0.031330819	NA	hypothetical protein	NA	#N/A	#N/A
MNLKPGEA_ MNLKPGEA	-0.031908378	0.95057673	hypothetical protein	NA	0	0
MNLKPGEA_ cbiF	-0.032090479	NA	Cobalt-precorrin-4 C(11)	2.1.1.271	cobM	Precorrin-4 C(11)-methyltransfe
MNLKPGEA_ MNLKPGEA	-0.032090479	NA	IS3 family transposase IS	NA	0	Transposase and inactivated der
MNLKPGEA_ MNLKPGEA	-0.032498419	0.97294274	hypothetical protein	NA	yjcO	Sel1 repeat
MNLKPGEA_ MNLKPGEA	-0.033037237	NA	IS3 family transposase IS	NA	0	Transposase
MNLKPGEA_ ompA_1	-0.033037237	NA	Outer membrane protei	NA	0	Belongs to the ompA family
MNLKPGEA_ MNLKPGEA	-0.03323058	NA	hypothetical protein	NA	0	amino acid ABC transporter
MNLKPGEA_ rbsK_1	-0.03323058	NA	Ribokinase	2.7.1.15	0	Catalyzes the phosphorylation of
MNLKPGEA_ ccmE	-0.033439298	NA	Cytochrome c-type bioge	NA	ccmE	Heme chaperone required for th

MNLKPGEA_	hisS	-0.033547582	0.94551917	Histidine--tRNA ligase	6.1.1.21	hisS	histidyl-tRNA synthetase
MNLKPGEA_	mexB	-0.03445127	NA	Multidrug resistance pro	NA	mexB	Belongs to the resistance-nodula
MNLKPGEA_	betI_3	-0.035067719	NA	HTH-type transcriptional	NA	betI	Repressor involved in choline reg
MNLKPGEA_	MNLKPGEA	-0.035237164	NA	hypothetical protein	NA	0	protein conserved in bacteria
MNLKPGEA_	xylG_2	-0.035237164	NA	Xylose import ATP-bindi	7.5.2.10	rbsA	(ABC) transporter
MNLKPGEA_	gnd	-0.035318939	0.94219443	6-phosphogluconate deh	1.1.1.44	gnd	Catalyzes the oxidative decarbox
MNLKPGEA_	xylF_1	-0.035644462	0.96477398	D-xylose-binding peripla	NA	xylF	D-xylose ABC transporter peripla
MNLKPGEA_	mdoB	-0.035831711	0.93068042	Phosphoglycerol transfe	2.7.8.20	mdoB	Phosphoglycerol transferase anc
MNLKPGEA_	amn	-0.036319792	0.94864146	AMP nucleosidase	3.2.2.4	amn	Catalyzes the hydrolysis of the N
MNLKPGEA_	fucA	-0.036357545	NA	L-fuculose phosphate alc	4.1.2.17	fucA	Catalyzes the cleavage of L-fucu
MNLKPGEA_	MNLKPGEA	-0.036357545	NA	hypothetical protein	NA	0	COG0491 Zn-dependent hydrola
MNLKPGEA_	crnA	-0.036938764	NA	Creatinine amidohydrola	3.5.2.10	0	Creatininase
MNLKPGEA_	glpE_2	-0.036938764	NA	Thiosulfate sulfurtransfe	2.8.1.1	MA20_21	sulfurtransferase
MNLKPGEA_	MNLKPGEA	-0.036980497	0.96120574	hypothetical protein	NA	ygiQ	UPF0313 protein
MNLKPGEA_	adh1	-0.037688329	NA	Long-chain-alcohol dehy	1.1.1.192	dhaT	alcohol dehydrogenase
MNLKPGEA_	gntK	-0.038701208	0.97206174	Thermoresistant gluconc	2.7.1.12	gntK	Gluconokinase
MNLKPGEA_	clpV1	-0.039144611	0.96694497	Protein ClpV1	NA	tssH	Belongs to the ClpA ClpB family
MNLKPGEA_	MNLKPGEA	-0.039773025	NA	hypothetical protein	NA	#N/A	#N/A
MNLKPGEA_	pdeN	-0.039872616	0.95495528	putative cyclic di-GMP pl	3.1.4.52	rtn	Involved in resistance to the pha
MNLKPGEA_	MNLKPGEA	-0.043477027	0.95495528	IS3 family transposase IS	NA	0	Transposase
MNLKPGEA_	speG	-0.044556746	0.96477398	Spermidine N(1)-acetylt	2.3.1.57	speG	Catalyzes the formation of N(1)-
MNLKPGEA_	yigL	-0.046053139	0.92208141	Pyridoxal phosphate pho	3.1.3.74	yigL	Hydrolase
MNLKPGEA_	ulaF	-0.046456058	0.97206174	L-ribulose-5-phosphate 4	5.1.3.4	ulaF	Catalyzes the isomerization of L-
MNLKPGEA_	MNLKPGEA	-0.046779454	NA	hypothetical protein	NA	0	ABC transporter substrate-bindi
MNLKPGEA_	speB	-0.047303557	0.95734095	Agmatinase	3.5.3.11	speB	Belongs to the arginase family
MNLKPGEA_	selD	-0.048181612	0.96015283	Selenide, water dikinase	2.7.9.3	selD	Synthesizes selenophosphate fro
MNLKPGEA_	gabR_3	-0.04819789	0.96015283	HTH-type transcriptional	NA	gabR_4	Transcriptional regulators contai
MNLKPGEA_	gldA	-0.05060953	0.94579406	Glycerol dehydrogenase	1.1.1.6	gldA	glycerol dehydrogenase
MNLKPGEA_	MNLKPGEA	-0.050751001	0.95495528	hypothetical protein	NA	0	Bacterial regulatory proteins, te
MNLKPGEA_	aroE_1	-0.051090084	0.93709977	Shikimate dehydrogenas	1.1.1.25	aroE	Involved in the biosynthesis of th

MNLKPGEA_ ulaA_3	-0.053379318	NA	Ascorbate-specific PTS s	NA	ulaA	pts system
MNLKPGEA_ rhaS_1	-0.053564106	0.9583707	HTH-type transcriptional	NA	0	transcriptional regulator
MNLKPGEA_ sopB	-0.054088961	0.9337214	Protein SopB	NA	sopB	Belongs to the ParB family
MNLKPGEA_ leuA_1	-0.054112764	NA	2-isopropylmalate synth	2.3.3.13	leuA	Catalyzes the condensation of th
MNLKPGEA_ rhaR_5	-0.054199512	0.96764521	HTH-type transcriptional	NA	rhaR	Activates expression of the rhaS
MNLKPGEA_ bdcA_1	-0.054292888	NA	Cyclic-di-GMP-binding bi	NA	yjgI	COG1028 Dehydrogenases with
MNLKPGEA_ ybcJ	-0.05432541	0.95317706	putative protein YbcJ	NA	ybcJ	Ribosome-associated protein
MNLKPGEA_ fkpA	-0.055124125	0.88873326	FKBP-type peptidyl-proly	5.2.1.8	fkpA	Peptidyl-prolyl cis-trans
MNLKPGEA_ malG_2	-0.055355953	0.95495528	Maltose/maltodextrin tr	NA	malG	transport
MNLKPGEA_ yhhX	-0.055778986	0.92034265	putative oxidoreductase	1.-.-.-	yhhX	oxidoreductase
MNLKPGEA_ MNLKPGEA	-0.055984758	NA	hypothetical protein	NA	0	Protein of unknown function (DU
MNLKPGEA_ hemX	-0.056565372	0.93735527	Protein HemX	NA	hemX	enzyme of heme biosynthesis
MNLKPGEA_ nusB	-0.057628151	0.88873326	Transcription antitermin	NA	nusB	Involved in transcription antiterr
MNLKPGEA_ ompR_2	-0.060251878	0.94551917	Transcriptional regulator	NA	ompR	Response regulators consisting c
MNLKPGEA_ fldA	-0.060303241	0.89674235	Flavodoxin	NA	fldA	Low-potential electron donor to
MNLKPGEA_ traD	-0.060504497	0.89773926	Coupling protein TraD	NA	0	Type IV secretory system Conjug
MNLKPGEA_ focA	-0.060714352	0.85546024	putative formate transpo	NA	focA	Formate nitrite
MNLKPGEA_ MNLKPGEA	-0.060751195	0.86802214	hypothetical protein	NA	gmr_2	CHASE4 domain
MNLKPGEA_ MNLKPGEA	-0.060954804	0.94219443	hypothetical protein	NA	stbD	Fimbrial protein
MNLKPGEA_ MNLKPGEA	-0.061002976	0.89674235	hypothetical protein	NA	yfcZ	protein conserved in bacteria
MNLKPGEA_ garK_1	-0.062858568	0.95495528	Glycerate 2-kinase	2.7.1.165	glxK	Belongs to the glycerate kinase f
MNLKPGEA_ MNLKPGEA	-0.063211896	NA	hypothetical protein	NA	yfeD	Putative transcription regulator (
MNLKPGEA_ yiaB	-0.064385122	NA	Inner membrane protein	NA	yiaB	Membrane
MNLKPGEA_ fadB	-0.066816281	0.89757088	Fatty acid oxidation com	NA	fadB	Involved in the aerobic and anae
MNLKPGEA_ tatC	-0.067417308	0.92208141	Sec-independent protein	NA	tatC	Part of the twin-arginine translo
MNLKPGEA_ dmlR_9	-0.069072516	NA	HTH-type transcriptional	NA	0	transcriptional regulator
MNLKPGEA_ vldW_2	-0.069081506	0.96033077	Validamycin A dioxygena	1.14.11.52	0	Belongs to the iron ascorbate-de
MNLKPGEA_ MNLKPGEA	-0.069668553	0.92168668	putative protein	NA	ydcJ	protein conserved in bacteria
MNLKPGEA_ lamB_2	-0.07092748	0.93559169	Maltoporin	NA	lamB	involved in the transport of malt
MNLKPGEA_ tamA	-0.071478699	0.87816646	Translocation and assem	NA	ytfM	COG0729 Outer membrane prot

MNLKPGEA_	MNLKPGEA	-0.074458714	0.92584368	hypothetical protein	NA	0	0
MNLKPGEA_	metQ_4	-0.074532873	0.87826065	D-methionine-binding lip	NA	metQ	Belongs to the NlpA lipoprotein
MNLKPGEA_	amyA	-0.075133392	0.89745381	Cytoplasmic alpha-amyla	3.2.1.1	amyA	Cytoplasmic alpha-amylase
MNLKPGEA_	yagG_1	-0.075243669	0.93521774	Putative glycoside/catio	NA	0	Major Facilitator
MNLKPGEA_	sohB	-0.075500097	0.95277249	putative protease SohB	3.4.21.-	sohB	peptidase
MNLKPGEA_	pspF	-0.075655635	0.93967983	Psp operon transcription	NA	pspF	transcriptional activator
MNLKPGEA_	ansB	-0.075943078	0.95141938	L-asparaginase	3.5.1.1	0	Belongs to the asparaginase 1 fa
MNLKPGEA_	phoP_1	-0.076422949	NA	Virulence transcriptional	NA	phoP_1	COG0745 Response regulators c
MNLKPGEA_	MNLKPGEA	-0.076899798	0.89674235	hypothetical protein	NA	kch	COG1226 Kef-type K transport sy
MNLKPGEA_	mntA	-0.077150862	0.92245175	Manganese-binding lipo	NA	znuA	Belongs to the bacterial solute-b
MNLKPGEA_	MNLKPGEA	-0.077601425	0.93688219	hypothetical protein	NA	0	0
MNLKPGEA_	MNLKPGEA	-0.0777039	NA	hypothetical protein	NA	yddR	Zn-dependent hydrolases of the
MNLKPGEA_	MNLKPGEA	-0.080202491	0.92687989	hypothetical protein	NA	ydeE	Major facilitator Superfamily
MNLKPGEA_	MNLKPGEA	-0.080892221	NA	hypothetical protein	NA	yaiZ	Protein of unknown function (DU
MNLKPGEA_	dcuA	-0.081421828	0.89261305	Anaerobic C4-dicarboxyla	NA	dcuA	Responsible for the transport of
MNLKPGEA_	dppA_2	-0.081518845	0.85675236	Periplasmic dipeptide tra	NA	sapA	ABC-Type Dipeptide Transport Sy
MNLKPGEA_	recD2	-0.081569064	0.77004092	ATP-dependent RecD-lik	3.6.4.12	trwC	TrwC relaxase
MNLKPGEA_	gmhA	-0.081575273	0.89385826	Phosphoheptose isomera	5.3.1.28	gmhA	Catalyzes the isomerization of s
MNLKPGEA_	phnO	-0.081840818	NA	Aminoalkylphosphonate	2.3.1.280	0	Acetyltransferase (GNAT) doma
MNLKPGEA_	MNLKPGEA	-0.082404614	0.92602642	hypothetical protein	NA	yiiD	histone acetyltransferase HPA2 a
MNLKPGEA_	MNLKPGEA	-0.082933767	NA	hypothetical protein	NA	0	0
MNLKPGEA_	dmsD	-0.08302488	0.94684841	Tat proofreading chaper	NA	dmsD	Required for biogenesis assemb
MNLKPGEA_	ypdB	-0.083307796	0.93735527	Transcriptional regulator	NA	ypdB	response regulator
MNLKPGEA_	MNLKPGEA	-0.083329977	0.81443054	hypothetical protein	NA	yidQ	(Lipo)protein
MNLKPGEA_	leuC	-0.083995423	NA	3-isopropylmalate dehyc	4.2.1.33	leuC	Catalyzes the isomerization betv
MNLKPGEA_	MNLKPGEA	-0.085164954	0.80963388	hypothetical protein	NA	#N/A	#N/A
MNLKPGEA_	MNLKPGEA	-0.086358961	NA	hypothetical protein	NA	0	0
MNLKPGEA_	fimA	-0.086863473	NA	Type-1 fimbrial protein,	NA	0	cell adhesion
MNLKPGEA_	frdB	-0.087047253	0.9407749	Fumarate reductase iror	1.3.5.1	frdB	Belongs to the succinate dehydr
MNLKPGEA_	yicJ_3	-0.087581505	0.93446457	Inner membrane sympor	NA	yicJ	COG2211 Na melibiose symport

MNLKPGEA_ glnD	-0.087965775	0.86974706	Bifunctional uridylyltrans	NA	glnD	Modifies, by uridylylation and de
MNLKPGEA_ rng	-0.090037525	0.89807315	Ribonuclease G	3.1.26.-	rng	Involved in the processing of the
MNLKPGEA_ MNLKPGEA	-0.090043356	NA	hypothetical protein	NA	0	0
MNLKPGEA_ narK	-0.090640021	NA	Nitrate/nitrite transport	NA	narK	nitrate nitrite transporter
MNLKPGEA_ degQ	-0.090944637	0.82744743	Periplasmic pH-depende	3.4.21.107	degQ	Belongs to the peptidase S1C fa
MNLKPGEA_ MNLKPGEA	-0.090971675	NA	hypothetical protein	NA	0	0
MNLKPGEA_ MNLKPGEA	-0.091087025	0.94684841	hypothetical protein	NA	0	Nad-dependent epimerase dehy
MNLKPGEA_ feuC	-0.092100208	NA	Iron-uptake system perm	NA	feuC	Belongs to the binding-protein-d
MNLKPGEA_ ulaE_2	-0.093181883	NA	L-ribulose-5-phosphate 3	5.1.3.22	ulaE	3-epimerase
MNLKPGEA_ rpoH	-0.093906268	0.84711625	RNA polymerase sigma f	NA	rpoH	Sigma factors are initiation fact
MNLKPGEA_ alsE_2	-0.094392527	NA	D-allulose-6-phosphate 3	5.1.3.-	alsE	3-epimerase
MNLKPGEA_ oppD_1	-0.094743574	NA	Oligopeptide transport A	NA	0	(ABC) transporter
MNLKPGEA_ ureA	-0.095131806	NA	Urease subunit gamma	3.5.1.5	ureA	Belongs to the urease gamma su
MNLKPGEA_ MNLKPGEA	-0.095472166	0.95323895	hypothetical protein	NA	0	0
MNLKPGEA_ hflX	-0.095894593	0.83817963	GTPase HflX	NA	hflX	GTPase that associates with the
MNLKPGEA_ MNLKPGEA	-0.096378189	0.89757088	Mono(2-hydroxyethyl) te	3.1.1.102	0	Tannase and feruloyl esterase
MNLKPGEA_ MNLKPGEA	-0.096439658	NA	IS6 family transposase IS	NA	0	Transposase IS66 family
MNLKPGEA_ MNLKPGEA	-0.096616149	NA	hypothetical protein	NA	ygbA	Nitrous oxide-stimulated promo
MNLKPGEA_ MNLKPGEA	-0.096686115	0.93735527	hypothetical protein	NA	0	Anti-sigma regulatory factor (Se
MNLKPGEA_ MNLKPGEA	-0.097217416	NA	hypothetical protein	NA	yhhW_1	Belongs to the pirin family
MNLKPGEA_ MNLKPGEA	-0.097307136	NA	hypothetical protein	NA	0	Protein involved in biological_pr
MNLKPGEA_ yeaR_1	-0.097307136	NA	putative protein YeaR	NA	yeaR	Domain of unknown function (DU
MNLKPGEA_ cmoA	-0.09753467	0.89674235	Carboxy-S-adenosyl-L-m	2.1.3.-	cmoA	Catalyzes the conversion of S-ad
MNLKPGEA_ fbaA_1	-0.097802782	0.77084159	Fructose-bisphosphate a	4.1.2.13	fbaA	Fructose-bisphosphate aldolase,
MNLKPGEA_ MNLKPGEA	-0.098251677	NA	IS3 family transposase IS	NA	0	Transposase and inactivated der
MNLKPGEA_ MNLKPGEA	-0.098251677	NA	Acetyltransferase	2.3.1.-	0	histone acetyltransferase HPA2 a
MNLKPGEA_ ygdR_1	-0.09830965	0.86210093	putative lipoprotein YgdI	NA	ygdR	(Lipo)protein
MNLKPGEA_ lamB_1	-0.098692937	NA	Maltoporin	NA	lamB	Maltoporin (phage lambda and r
MNLKPGEA_ bepG	-0.098779243	0.93110428	Efflux pump membrane	NA	bepG	Belongs to the resistance-nodula
MNLKPGEA_ MNLKPGEA	-0.09886293	NA	hypothetical protein	NA	ybgA	Conserved Protein

MNLKPGEA_	rutA	-0.099111312	NA	Pyrimidine monooxygena	1.14.99.46	rutA	Catalyzes the pyrimidine ring op
MNLKPGEA_	rnhA	-0.099294681	0.87476992	Ribonuclease HI	3.1.26.4	rnhA	Endonuclease that specifically d
MNLKPGEA_	xylF_2	-0.100264865	0.88112252	D-xylose-binding peripla	NA	0	PFAM Periplasmic binding prote
MNLKPGEA_	xecA1	-0.10134146	0.89674235	2-hydroxypropyl-CoM lya	4.4.1.23	metE	Catalyzes the transfer of a meth
MNLKPGEA_	dacD	-0.101683733	0.92201895	D-alanyl-D-alanine carbc	3.4.16.4	dacC	Belongs to the peptidase S11 fa
MNLKPGEA_	pyrD	-0.102357433	0.8964368	Dihydroorotate dehydrog	1.3.5.2	pyrD	Catalyzes the conversion of dihy
MNLKPGEA_	rlmB	-0.102876288	0.88476456	23S rRNA (guanosine-2'-	2.1.1.185	rlmB	Specifically methylates the ribos
MNLKPGEA_	rbsB_4	-0.103715124	0.66011131	Ribose import binding pr	NA	rbsB	Periplasmic
MNLKPGEA_	MNLKPGEA	-0.106300224	NA	NADH:quinone reductase	1.6.5.11	0	COG2070 Dioxygenases related
MNLKPGEA_	dmlR_20	-0.106741557	NA	HTH-type transcriptional	NA	0	transcriptional regulator
MNLKPGEA_	oppA_1	-0.108433757	0.78875085	Periplasmic oligopeptide	NA	oppA	ABC transporter substrate-bindi
MNLKPGEA_	kdpE	-0.109989711	0.92915338	KDP operon transcriptior	NA	kdpE	response regulator
MNLKPGEA_	kdsB	-0.110181344	0.82763446	3-deoxy-manno-octulosc	2.7.7.38	kdsB	Activates KDO (a required 8-carb
MNLKPGEA_	fabG_11	-0.110447617	NA	3-oxoacyl-[acyl-carrier-p	1.1.1.100	0	KR domain
MNLKPGEA_	nikB	-0.111515094	NA	Nickel transport system	NA	nikB	transport
MNLKPGEA_	yebT	-0.111622977	0.78555119	Intermembrane transpor	NA	yebT	paraquat-inducible protein b
MNLKPGEA_	yeiG	-0.111764495	0.89822118	S-formylglutathione hydı	3.1.2.12	yeiG	Serine hydrolase involved in the
MNLKPGEA_	cadC	-0.111915159	0.89188242	Transcriptional activator	NA	cadC	transcriptional
MNLKPGEA_	MNLKPGEA	-0.111986597	NA	hypothetical protein	NA	0	type VI secretion protein
MNLKPGEA_	nuoE	-0.112343678	0.89674235	NADH-quinone oxidoredu	7.1.1.-	nuoE	NADH dehydrogenase
MNLKPGEA_	thiQ	-0.112361288	NA	Thiamine import ATP-bir	3.6.3.-	thiQ	Part of the ABC transporter com
MNLKPGEA_	trmL_2	-0.112404991	0.91035418	tRNA (cytidine(34)-2'-O)	2.1.1.207	lasT	Catalyzes the formation of 2'O-r
MNLKPGEA_	amiC_2	-0.114912762	NA	Aliphatic amidase expres	NA	urtA	COG0683 ABC-type branched-ch
MNLKPGEA_	dasC	-0.115399714	0.9321652	Diacetylchitobiose uptak	NA	togN	PFAM binding-protein-depender
MNLKPGEA_	yajO_3	-0.116479603	0.91356647	1-deoxyxylulose-5-phosp	1.1.-.-	0	oxidoreductases (related to aryl-
MNLKPGEA_	fabG_8	-0.11877854	NA	3-oxoacyl-[acyl-carrier-p	1.1.1.100	IV02_097	COG1028 Dehydrogenases with
MNLKPGEA_	efp	-0.119287863	0.69165233	Elongation factor P	NA	efp	Involved in peptide bond synthes
MNLKPGEA_	clcA	-0.12029674	0.85577729	H(+)/Cl(-) exchange tran	NA	clcA	Probably acts as an electrical sh
MNLKPGEA_	nudK_1	-0.120328458	NA	GDP-mannose pyrophosp	3.6.1.-	nudK	GDP-mannose pyrophosphatase
MNLKPGEA_	fabI	-0.122085482	0.74588536	Enoyl-[acyl-carrier-prote	1.3.1.9	fabI	Enoyl- acyl-carrier-protein reduc

MNLKPGEA_	MNLKPGEA	-0.122984168	0.91985562	hypothetical protein	NA	#N/A	#N/A
MNLKPGEA_	MNLKPGEA	-0.123065952	0.90639206	hypothetical protein	NA	0	DinB family
MNLKPGEA_	mntB_5	-0.123102424	0.8808318	Manganese transport sy	NA	mntC	ABC-type Mn2 Zn2 transport sys
MNLKPGEA_	hcxB	-0.124161084	0.89261305	Hydroxycarboxylate dehy	1.1.1.-	ybiC	Belongs to the LDH2 MDH2 oxid
MNLKPGEA_	amaB_2	-0.124631631	NA	N-carbamoyl-L-amino ac	3.5.1.87	0	the allantoate amidohydrolase f
MNLKPGEA_	yceB	-0.125195252	0.78601971	putative lipoprotein YceE	NA	yceB	Lipoprotein
MNLKPGEA_	holB	-0.127510611	0.8871129	DNA polymerase III subu	2.7.7.7	holB	dna polymerase iii
MNLKPGEA_	rcdA	-0.127689336	0.8964368	HTH-type transcriptional	NA	ybjK	transcriptional regulator
MNLKPGEA_	dmlR_3	-0.127998125	0.88626513	HTH-type transcriptional	NA	aaeR	Transcriptional regulator
MNLKPGEA_	yedJ	-0.12827319	0.84547676	putative protein YedJ	NA	yedJ	Metal-dependent phosphohydrol
MNLKPGEA_	tusA	-0.12831425	NA	Sulfur carrier protein Tus	NA	tusA	Sulfur carrier protein involved in
MNLKPGEA_	fimD_6	-0.130543839	0.9205127	Outer membrane usher p	NA	stbC	PapC C-terminal domain
MNLKPGEA_	fimC_2	-0.132341204	NA	Chaperone protein FimC	NA	0	Pili assembly chaperone PapD, C
MNLKPGEA_	MNLKPGEA	-0.133653703	0.9205127	hypothetical protein	NA	0	0
MNLKPGEA_	mscS	-0.13396597	0.71443185	Small-conductance mecl	NA	mscS	Mechanosensitive Ion channel
MNLKPGEA_	norR_1	-0.134166587	NA	Anaerobic nitric oxide re	NA	atoC	COG2204 Response regulator co
MNLKPGEA_	fimD_5	-0.13498461	NA	Outer membrane usher p	NA	fimD_3	Usher protein
MNLKPGEA_	queC	-0.135761058	0.88491035	7-cyano-7-deazaguanine	6.3.4.20	queC	Catalyzes the ATP-dependent co
MNLKPGEA_	pheP	-0.138473756	NA	Phenylalanine-specific p	NA	pheP	PFAM amino acid permease-ass
MNLKPGEA_	pcp	-0.138824911	0.89808336	Pyrrolidone-carboxylate p	3.4.19.3	pcp	Removes 5-oxoproline from vari
MNLKPGEA_	coaD	-0.138944615	0.86285128	Phosphopantetheine ade	2.7.7.3	coaD	Reversibly transfers an adenylyl
MNLKPGEA_	mamB	-0.14085379	NA	Magnetosome protein M	NA	fieF	Belongs to the cation diffusion f
MNLKPGEA_	ynfE_2	-0.141313372	NA	Putative dimethyl sulfoxi	1.8.99.-	ynfE	Belongs to the prokaryotic molyl
MNLKPGEA_	MNLKPGEA	-0.141368694	0.6965422	hypothetical protein	NA	ycfP	Belongs to the UPF0227 family
MNLKPGEA_	yhgF	-0.141527222	0.79610635	Protein YhgF	NA	tex	accessory protein
MNLKPGEA_	ppc	-0.141551311	0.76463939	Phosphoenolpyruvate ca	4.1.1.31	ppc	Forms oxaloacetate, a four-carb
MNLKPGEA_	ribX_1	-0.14157567	NA	Riboflavin transport syst	NA	0	ABC-type nitrate sulfonate bicar
MNLKPGEA_	rhaS_2	-0.143072783	0.89261305	HTH-type transcriptional	NA	yqhC	transcriptional regulator
MNLKPGEA_	MNLKPGEA	-0.143679529	NA	hypothetical protein	NA	0	Bacterial regulatory proteins, lu
MNLKPGEA_	tsaE	-0.144008994	0.89674235	tRNA threonylcarbamoyl	NA	yjeE	ATPase or kinase

MNLKPGEA_ glnQ_7	-0.145271978	NA	Glutamine transport ATI	3.6.3.-	gltL	(ABC) transporter
MNLKPGEA_ rnhB	-0.145728464	0.8687739	Ribonuclease HII	3.1.26.4	rnhB	Endonuclease that specifically d
MNLKPGEA_ rpoC	-0.145791153	0.61430358	DNA-directed RNA polyn	2.7.7.6	rpoC	DNA-dependent RNA polymeras
MNLKPGEA_ metH	-0.146055969	0.79585332	Methionine synthase	2.1.1.13	metH	methionine synthase
MNLKPGEA_ rof	-0.146965904	0.74596781	Protein rof	NA	rof	Suppresses temperature-sensiti
MNLKPGEA_ ychF	-0.147971034	0.65582113	Ribosome-binding ATPas	NA	ychF	ATPase that binds to both the 7(
MNLKPGEA_ MNLKPGEA	-0.149820439	0.83132676	hypothetical protein	NA	yddW	Lipoprotein
MNLKPGEA_ MNLKPGEA	-0.150323225	NA	hypothetical protein	NA	MA20_18	Belongs to the UPF0311 family
MNLKPGEA_ acrB_2	-0.150467455	0.74540954	Multidrug efflux pump s	NA	acrB	Belongs to the resistance-nodula
MNLKPGEA_ MNLKPGEA	-0.150644554	0.77928864	hypothetical protein	NA	VPA0243	protein conserved in bacteria
MNLKPGEA_ sgrR_1	-0.151149842	0.85600967	HTH-type transcriptional	NA	ybaE	ABC transporter substrate-bindi
MNLKPGEA_ jefA_2	-0.151557338	NA	Drug efflux pump JefA	NA	0	Major facilitator superfamily
MNLKPGEA_ metC_1	-0.151842504	0.81989975	Cystathionine beta-lyase	4.4.1.13	metC	cystathionine beta-lyase
MNLKPGEA_ cidA	-0.153892087	NA	Holin-like protein CidA	NA	cidA	LrgA family
MNLKPGEA_ mgtA	-0.154332336	0.90437935	Magnesium-transporting	7.2.2.14	mgtA	ATPase, P-type (transporting), H
MNLKPGEA_ opgE	-0.154414875	0.8428563	Phosphoethanolamine tr	2.7.-.-	ybiP	membrane-associated metal-de
MNLKPGEA_ MNLKPGEA	-0.154718125	NA	hypothetical protein	NA	0	Domain of unknown function (DU
MNLKPGEA_ yedR	-0.154718125	NA	Inner membrane protein	NA	yedR	0
MNLKPGEA_ csdE	-0.155138165	NA	Sulfur acceptor protein C	NA	csdE	cysteine desulfurase, sulfur acce
MNLKPGEA_ hutI	-0.155587578	0.87332138	Imidazolonepropionase	3.5.2.7	hutI	Imidazolone-5-propionate hydro
MNLKPGEA_ rhaB	-0.155875794	NA	L-Rhamnulokinase	2.7.1.5	rhaB	Involved in the catabolism of L-r
MNLKPGEA_ mexA	-0.156706468	NA	Multidrug resistance pro	NA	mexA	Belongs to the membrane fusion
MNLKPGEA_ MNLKPGEA	-0.156858054	NA	IS3 family transposase IS	NA	0	Transposase and inactivated der
MNLKPGEA_ gntT	-0.156909427	0.81699862	High-affinity gluconate t	NA	gntT	Gluconate
MNLKPGEA_ otnK_3	-0.157600906	NA	3-oxo-tetronate kinase	2.7.1.217	ygbK	Putative nucleotide-binding of su
MNLKPGEA_ MNLKPGEA	-0.157716384	NA	hypothetical protein	NA	ybcL	PFAM PEBP family protein
MNLKPGEA_ proY_2	-0.157798625	0.82482407	Proline-specific permeas	NA	proY	Cryptic permease that may be ir
MNLKPGEA_ MNLKPGEA	-0.157858482	0.88476456	hypothetical protein	NA	0	Nucleotidyl transferase AbiEii to
MNLKPGEA_ MNLKPGEA	-0.158457529	0.70709197	hypothetical protein	NA	#N/A	#N/A
MNLKPGEA_ xylA_2	-0.15874826	NA	Xylose isomerase	5.3.1.5	xylA	Belongs to the xylose isomerase

MNLKPGEA_	phnC	-0.158771107	NA	Phosphate-import ATP-b	7.3.2.1	phnC	Part of the ABC transporter com
MNLKPGEA_	MNLKPGEA	-0.15944249	NA	hypothetical protein	NA	0	cell adhesion
MNLKPGEA_	talB_1	-0.159735306	NA	Transaldolase B	2.2.1.2	tal	Transaldolase is important for tl
MNLKPGEA_	galD	-0.159749231	NA	4-oxalomesaconate taut	5.3.2.8	fldA	protein conserved in bacteria
MNLKPGEA_	MNLKPGEA	-0.159915514	NA	hypothetical protein	NA	cydA	oxidase, subunit
MNLKPGEA_	MNLKPGEA	-0.159967515	NA	IS6 family transposase IS	NA	0	Transposase IS66 family
MNLKPGEA_	MNLKPGEA	-0.160263958	NA	hypothetical protein	NA	yaaI	Belongs to the UPF0412 family
MNLKPGEA_	uidB	-0.16046177	NA	Glucuronide carrier prote	NA	0	transporter
MNLKPGEA_	MNLKPGEA	-0.160559363	0.86064897	hypothetical protein	NA	ycbJ	Phosphotransferase enzyme fam
MNLKPGEA_	MNLKPGEA	-0.160912934	NA	putative protein	NA	MA20_32	protein conserved in bacteria
MNLKPGEA_	uhpB	-0.160912934	NA	Signal transduction histi	2.7.13.3	uhpB	Histidine kinase
MNLKPGEA_	nth	-0.162491551	0.89745381	Endonuclease III	4.2.99.18	nth	DNA repair enzyme that has bot
MNLKPGEA_	iolD	-0.162559866	NA	3D-(3,5/4)-trihydroxycycl	3.7.1.22	iolD	Belongs to the TPP enzyme fami
MNLKPGEA_	amiD	-0.162568627	0.88956097	N-acetylmuramoyl-L-ala	3.5.1.28	amiD	N-acetylmuramoyl-L-alanine am
MNLKPGEA_	MNLKPGEA	-0.16372009	0.87509031	hypothetical protein	NA	0	Acetyltransferase (GNAT) doma
MNLKPGEA_	aqpZ	-0.164156871	0.83132676	Aquaporin Z	NA	aqpZ	Channel that permits osmoticall
MNLKPGEA_	MNLKPGEA	-0.164231205	0.65489482	hypothetical protein	NA	0	sequence-specific DNA binding
MNLKPGEA_	malS	-0.164514401	NA	Periplasmic alpha-amyla	3.2.1.1	malS	alpha-amylase
MNLKPGEA_	MNLKPGEA	-0.164716927	0.83888998	hypothetical protein	NA	0	0
MNLKPGEA_	pnbA	-0.166703586	0.84901515	Para-nitrobenzyl esteras	3.1.1.-	pnbA	Belongs to the type-B carboxyles
MNLKPGEA_	ydiB_2	-0.168316966	NA	Quinate/shikimate dehy	1.1.1.282	0	shikimate dehydrogenase
MNLKPGEA_	iolT	-0.168772915	0.88433626	Major myo-inositol trans	NA	csbC	Major facilitator Superfamily
MNLKPGEA_	fetB	-0.169070075	0.89261305	putative iron export perr	NA	ybbM	transport system permease com
MNLKPGEA_	MNLKPGEA	-0.170398424	NA	hypothetical protein	NA	0	DNA primase
MNLKPGEA_	MNLKPGEA	-0.170649747	0.79834401	hypothetical protein	NA	0	cellulase activity
MNLKPGEA_	virB9	-0.171497142	0.86101188	Type IV secretion system	NA	virB9	Conjugal transfer protein
MNLKPGEA_	MNLKPGEA	-0.174033703	0.75344428	hypothetical protein	NA	0	COG0463 Glycosyltransferases i
MNLKPGEA_	scrK_2	-0.174393731	0.85832974	Fructokinase	2.7.1.4	frk	COG0524 Sugar kinases, ribokina
MNLKPGEA_	citD	-0.174990173	NA	Citrate lyase acyl carrier	NA	0	Covalent carrier of the coenzyme
MNLKPGEA_	hexR_1	-0.17501387	0.70849961	HTH-type transcriptional	NA	hexR	transcriptional regulator

MNLKPGEA_	MNLKPGEA	-0.175179827	0.73392864	hypothetical protein	NA	hrpA	ATP-dependent helicase hrpA
MNLKPGEA_	yfdX	-0.17580525	NA	Protein YfdX	NA	yfdX	YfdX protein
MNLKPGEA_	yibF	-0.176076206	0.80809392	putative GST-like protein	NA	yibF	Glutathione S-Transferase
MNLKPGEA_	MNLKPGEA	-0.178016977	0.81069729	hypothetical protein	NA	yaiL	protein conserved in bacteria
MNLKPGEA_	sspB	-0.178408354	0.70572181	Stringent starvation prot	NA	sspB	stringent starvation protein b
MNLKPGEA_	proC	-0.178873036	0.71508473	Pyrroline-5-carboxylate r	1.5.1.2	proC	Catalyzes the reduction of 1-pyr
MNLKPGEA_	yafQ	-0.181272461	0.7782691	mRNA interferase toxin	3.1.-.-	0	TIGRFAM addiction module toxi
MNLKPGEA_	alaC	-0.181969604	0.66161587	Glutamate-pyruvate ami	2.6.1.2	yfdZ	aminotransferase
MNLKPGEA_	MNLKPGEA	-0.182100852	0.66072108	hypothetical protein	NA	#N/A	#N/A
MNLKPGEA_	ilvN	-0.182177105	0.88873326	Acetolactate synthase is	2.2.1.6	ilvN	acetolactate synthase
MNLKPGEA_	gudP_1	-0.182252352	0.87509031	putative glucarate transp	NA	gudP	transporter
MNLKPGEA_	MNLKPGEA	-0.184521879	0.82435024	IS3 family transposase IS	NA	0	Transposase and inactivated der
MNLKPGEA_	gpFI	-0.185236223	NA	Putative prophage major	NA	0	Tail sheath protein
MNLKPGEA_	MNLKPGEA	-0.186415375	0.81069729	hypothetical protein	NA	ychE	UPF0056 membrane protein
MNLKPGEA_	hcaB	-0.186686189	0.89773926	3-phenylpropionate-dihy	1.3.1.87	yxnA	Belongs to the short-chain dehy
MNLKPGEA_	MNLKPGEA	-0.186747607	0.87079687	hypothetical protein	NA	0	alcohol dehydrogenase
MNLKPGEA_	nrdH	-0.187888916	0.82435024	Glutaredoxin-like protein	NA	nrdH	Glutaredoxin-like protein NrdH
MNLKPGEA_	csbX_2	-0.190349004	0.89745381	Alpha-ketoglutarate perr	NA	csbX	Major facilitator Superfamily
MNLKPGEA_	MNLKPGEA	-0.191665501	NA	hypothetical protein	NA	0	Protein of unknown function (DU
MNLKPGEA_	sdhE	-0.191668492	0.63400697	FAD assembly factor SdH	NA	ygfY	An FAD assembly protein, which
MNLKPGEA_	oadA	-0.192296943	NA	Oxaloacetate decarboxyl	7.2.4.2	oadA	Oxaloacetate
MNLKPGEA_	namA_2	-0.192587855	0.81538732	NADPH dehydrogenase	1.6.99.1	fccA	NADH flavin oxidoreductase
MNLKPGEA_	exuT_4	-0.193434485	0.79334163	Hexuronate transporter	NA	exuT_1	Major facilitator superfamily
MNLKPGEA_	mdcG	-0.194310537	NA	Phosphoribosyl-dephospl	2.7.7.66	mdcG	Phosphoribosyl-dephospho-CoA
MNLKPGEA_	MNLKPGEA	-0.194310537	NA	hypothetical protein	NA	0	Structural component (Phage or
MNLKPGEA_	MNLKPGEA	-0.195374697	NA	hypothetical protein	NA	0	0
MNLKPGEA_	MNLKPGEA	-0.195434479	0.87823918	hypothetical protein	NA	ybhG	Secretion protein
MNLKPGEA_	chbA_4	-0.195511959	NA	PTS system N,N'-diacety	NA	chbA	Phosphotransferase System
MNLKPGEA_	yqjF	-0.1955521	NA	Inner membrane protein	NA	yqjF	membrane
MNLKPGEA_	aspT_2	-0.196473185	0.58496739	Aspartate/alanine antipo	NA	ybjL	transport protein

MNLKPGEA_	nhoA	-0.196648554	0.87978491	Arylamine N-acetyltrans	2.3.1.5	nhoA	Belongs to the arylamine N-acet
MNLKPGEA_	sucD	-0.197383415	0.5758626	Succinate--CoA ligase [A	6.2.1.5	sucD	Succinyl-CoA synthetase functio
MNLKPGEA_	nhaR	-0.197573784	0.80234212	Transcriptional activator	NA	nhaR	transcriptional regulator
MNLKPGEA_	MNLKPGEA	-0.19763057	0.77051933	hypothetical protein	NA	yfjD	Mg2 and Co2 transporter CorB
MNLKPGEA_	wbgU_2	-0.197916401	0.64766406	UDP-N-acetylglucosamir	5.1.3.7	wbnF	epimerase dehydratase
MNLKPGEA_	MNLKPGEA	-0.198022453	NA	hypothetical protein	NA	0	0
MNLKPGEA_	MNLKPGEA	-0.199815325	NA	hypothetical protein	NA	0	Chitinase class I
MNLKPGEA_	nfuA	-0.201721657	0.63191089	Fe/S biogenesis protein	NA	nfuA	Involved in iron-sulfur cluster bic
MNLKPGEA_	ybgI	-0.202031789	0.8428563	GTP cyclohydrolase 1 typ	NA	ybgI	metal-binding protein
MNLKPGEA_	MNLKPGEA	-0.202656426	NA	hypothetical protein	NA	0	LysM domain
MNLKPGEA_	yycB	-0.203482941	NA	putative transporter YycI	NA	cynX	transporter
MNLKPGEA_	infB	-0.203882993	0.65920359	Translation initiation fac	NA	infB	One of the essential component
MNLKPGEA_	MNLKPGEA	-0.204193639	NA	hypothetical protein	NA	0	Sugar ABC Transporter
MNLKPGEA_	MNLKPGEA	-0.204279435	0.58943817	hypothetical protein	NA	0	BRO family, N-terminal domain
MNLKPGEA_	fdhF_3	-0.204505086	0.64990422	Formate dehydrogenase	1.17.1.9	fdhF	Belongs to the prokaryotic molyl
MNLKPGEA_	MNLKPGEA	-0.205684344	0.76883828	hypothetical protein	NA	yeiB	Membrane
MNLKPGEA_	cedA	-0.20584814	0.62755586	Cell division activator Ce	NA	cedA	Cell division activator CedA
MNLKPGEA_	ybdG_1	-0.207943896	0.854663	Miniconductance mecha	NA	ybdG	Mechanosensitive Ion channel
MNLKPGEA_	MNLKPGEA	-0.209053729	NA	IS5 family transposase IS	NA	0	ISSoEn1, terminal inverted repea
MNLKPGEA_	MNLKPGEA	-0.209635464	NA	hypothetical protein	NA	0	ABC transporter substrate-bindi
MNLKPGEA_	MNLKPGEA	-0.210436875	NA	hypothetical protein	NA	flaR	adenylate kinase
MNLKPGEA_	ubiD	-0.210841612	0.63221268	3-octaprenyl-4-hydroxyb	4.1.1.98	ubiD	Catalyzes the decarboxylation of
MNLKPGEA_	MNLKPGEA	-0.210982668	0.87031512	hypothetical protein	NA	0	Citrate transporter
MNLKPGEA_	MNLKPGEA	-0.211305206	NA	hypothetical protein	NA	0	TolA C-terminal
MNLKPGEA_	btuD_7	-0.211518415	NA	Vitamin B12 import ATP	7.6.2.8	0	Belongs to the ABC transporter s
MNLKPGEA_	MNLKPGEA	-0.211599046	0.73392864	hypothetical protein	NA	ynaA	Prophage tail length tape measu
MNLKPGEA_	ushA	-0.212110616	0.73310772	Protein UshA	NA	ushA	Belongs to the 5'-nucleotidase f
MNLKPGEA_	MNLKPGEA	-0.212800942	0.76599254	hypothetical protein	NA	#N/A	#N/A
MNLKPGEA_	sdiA	-0.213296418	0.70193448	Regulatory protein SdiA	NA	expR	Transcriptional
MNLKPGEA_	galF	-0.213501026	0.58602483	UTP--glucose-1-phospha	2.7.7.9	galU	UTP-glucose-1-phosphate uridyl

MNLKPGEA_	MNLKPGEA	-0.213617227	0.76312636	hypothetical protein	NA	ybdD	Pfam:DUF466
MNLKPGEA_	sbcC	-0.215228894	0.83019951	Nuclease SbcCD subunit	NA	sbcC	SbcCD cleaves DNA hairpin struc
MNLKPGEA_	yccS	-0.215571625	0.8055428	Inner membrane protein	NA	yccS	Membrane
MNLKPGEA_	MNLKPGEA	-0.215830226	NA	hypothetical protein	NA	0	Plasmid partition ParA protein
MNLKPGEA_	yadV_4	-0.216014651	NA	putative fimbrial chaper	NA	stbB	Pili assembly chaperone PapD, C
MNLKPGEA_	MNLKPGEA	-0.2163873	NA	hypothetical protein	NA	htxA	Protein involved in biosynthesis
MNLKPGEA_	MNLKPGEA	-0.216672078	0.75997564	hypothetical protein	NA	yejA	ABC-type oligopeptide transport
MNLKPGEA_	MNLKPGEA	-0.21668074	0.74168363	hypothetical protein	NA	fxsA	protein affecting phage T7 exclu
MNLKPGEA_	MNLKPGEA	-0.216924515	NA	hypothetical protein	NA	0	Protein of unknown function (DU
MNLKPGEA_	MNLKPGEA	-0.217029202	0.86699166	hypothetical protein	NA	ymjA	Protein of unknown function (DU
MNLKPGEA_	folD	-0.217317032	0.74002962	Bifunctional protein FolD	NA	folD	Catalyzes the oxidation of 5,10-
MNLKPGEA_	yiaA	-0.217437493	NA	Inner membrane protein	NA	yiaA	Membrane
MNLKPGEA_	metE	-0.217442169	0.64105383	5-methyltetrahydropterc	2.1.1.14	metE	Catalyzes the transfer of a meth
MNLKPGEA_	gsiC_3	-0.21753989	NA	Glutathione transport sy	NA	gsiC	ABC-type dipeptide oligopeptide
MNLKPGEA_	MNLKPGEA	-0.218071839	NA	hypothetical protein	NA	yoaG	Domain of unknown function (DU
MNLKPGEA_	MNLKPGEA	-0.218435666	NA	hypothetical protein	NA	#N/A	#N/A
MNLKPGEA_	xseA	-0.21884742	0.69471585	Exodeoxyribonuclease 7	3.1.11.6	xseA	Bidirectionally degrades single-s
MNLKPGEA_	glpE_1	-0.218881072	0.75670534	Thiosulfate sulfurtransfe	2.8.1.1	glpE	Catalyzes, although with low eff
MNLKPGEA_	MNLKPGEA	-0.219242568	NA	hypothetical protein	NA	0	PAAR motif
MNLKPGEA_	proA_1	-0.21977926	NA	Gamma-glutamyl phosp	1.2.1.41	eutE	Aldehyde dehydrogenase
MNLKPGEA_	kduD_1	-0.221443284	NA	2-dehydro-3-deoxy-D-glu	1.1.1.127	kduD	COG1028 Dehydrogenases with
MNLKPGEA_	viaA	-0.222359149	0.7782691	Protein ViaA	NA	viaA	VWA domain protein interacting
MNLKPGEA_	tdcE	-0.222620172	0.87816646	PFL-like enzyme TdcE	2.3.1.-	tdcE	formate acetyltransferase
MNLKPGEA_	hsrA_1	-0.224068305	0.84329656	putative transport protei	NA	hsrA_1	Major facilitator Superfamily
MNLKPGEA_	envC	-0.224369067	0.68451399	Murein hydrolase activat	NA	envC	peptidase
MNLKPGEA_	bepA_2	-0.225814116	0.56750227	Beta-barrel assembly-er	3.4.-.-	bepA	Functions as both a chaperone a
MNLKPGEA_	nuoF	-0.226360125	0.79175638	NADH-quinone oxidored	7.1.1.-	nuoF	NDH-1 shuttles electrons from N
MNLKPGEA_	ygiC	-0.226604838	0.55230946	Putative acid--amine lig	6.3.1.-	ygiC	Glutathionylspermidine synthase
MNLKPGEA_	MNLKPGEA	-0.227321932	0.87509031	hypothetical protein	NA	0	0
MNLKPGEA_	cpdA_1	-0.22792561	0.59877874	3',5'-cyclic adenosine m	3.1.4.53	cpdA	Hydrolyzes cAMP to 5'-AMP. Play

MNLKPGEA_	tuf1_2	-0.228250422	0.5217977	Elongation factor Tu 1	NA	tuf	This protein promotes the GTP-d
MNLKPGEA_	MNLKPGEA	-0.229776667	0.87509031	hypothetical protein	NA	yceH	Belongs to the UPF0502 family
MNLKPGEA_	ftnA_1	-0.229790723	0.77084159	Bacterial non-heme ferri	1.16.3.2	ftnA	Iron-storage protein
MNLKPGEA_	ftsX	-0.229842733	0.71698735	Cell division protein FtsX	NA	ftsX	Part of the ABC transporter FtsE
MNLKPGEA_	crl	-0.230238251	0.58464337	Sigma factor-binding pro	NA	crl	Binds to the sigma-S subunit of
MNLKPGEA_	MNLKPGEA	-0.23066825	0.79570801	hypothetical protein	NA	mmrA	Major facilitator Superfamily
MNLKPGEA_	envZ	-0.232372428	0.75203667	Osmolarity sensor protei	2.7.13.3	envZ	PhoQ Sensor
MNLKPGEA_	rlmN	-0.232546069	0.64090979	Dual-specificity RNA me	2.1.1.192	rlmN	Specifically methylates position
MNLKPGEA_	fucP_1	-0.2346897	0.85017541	L-fucose-proton symport	NA	fucP	transporter
MNLKPGEA_	cnoX	-0.235148763	0.7434175	Chaperedoxin	NA	ybbN	Thioredoxin
MNLKPGEA_	yhaJ_1	-0.236025624	0.85546024	HTH-type transcriptional	NA	yhaJ	transcriptional regulator
MNLKPGEA_	macB	-0.236283503	0.78185124	Macrolide export ATP-bi	3.6.3.-	macB	Part of the tripartite efflux syste
MNLKPGEA_	fdhE	-0.236372771	0.65364199	Protein FdhE	NA	fdhE	Necessary for formate dehydrog
MNLKPGEA_	yajO_1	-0.236789208	NA	1-deoxyxylulose-5-phosp	1.1.-.-	0	Aldo keto reductase
MNLKPGEA_	syrM1	-0.237006244	0.84795051	HTH-type transcriptional	NA	syrM1	transcriptional regulator
MNLKPGEA_	MNLKPGEA	-0.239661986	NA	hypothetical protein	NA	0	Sulfatase-modifying factor enzy
MNLKPGEA_	entC	-0.239997251	0.67679115	Isochorismate synthase	5.4.4.2	entC	Isochorismate synthase
MNLKPGEA_	btuD_8	-0.240501173	NA	Vitamin B12 import ATP	7.6.2.8	0	Part of the ABC transporter com
MNLKPGEA_	ydfG	-0.241390978	0.65364199	NADP-dependent 3-hydr	1.1.1.381	ydfG	Belongs to the short-chain dehy
MNLKPGEA_	uspC	-0.241500341	0.52088277	Universal stress protein	NA	uspC	Required for resistance to DNA-
MNLKPGEA_	MNLKPGEA	-0.24187491	NA	hypothetical protein	NA	0	0
MNLKPGEA_	MNLKPGEA	-0.244036233	0.57600144	hypothetical protein	NA	#N/A	#N/A
MNLKPGEA_	leuD1	-0.245635668	NA	3-isopropylmalate dehyc	4.2.1.33	leuD	Catalyzes the isomerization betv
MNLKPGEA_	gmk	-0.246419011	0.54332203	Guanylate kinase	2.7.4.8	gmk	Essential for recycling GMP and
MNLKPGEA_	MNLKPGEA	-0.246583836	NA	hypothetical protein	NA	0	type VI secretion protein
MNLKPGEA_	pglJ_1	-0.247335394	0.82338875	N-acetylgalactosamine-I	2.4.1.291	rfaB	glycosyl transferase group 1
MNLKPGEA_	phoP_3	-0.248618905	0.71875824	Virulence transcriptional	NA	phoP	Response regulators consisting
MNLKPGEA_	ascG_1	-0.249101845	0.65637345	HTH-type transcriptional	NA	ascG	Transcriptional regulator
MNLKPGEA_	dadA_1	-0.250003987	0.55126817	D-amino acid dehydroge	1.4.99.-	dadA	Oxidative deamination of D-ami
MNLKPGEA_	MNLKPGEA	-0.250556048	0.71443185	hypothetical protein	NA	0	0

MNLKPGEA_ iolE_4	-0.250586353	0.69813127	Inososе dehydratase	4.2.1.44	iolE	Catalyzes the dehydration of ino
MNLKPGEA_ parM_1	-0.251162294	0.61222012	Plasmid segregation pro	NA	0	PFAM StbA family protein
MNLKPGEA_ hin_4	-0.251863212	0.67365142	DNA-invertase hin	NA	tnpR	Resolvase
MNLKPGEA_ arcB	-0.251902892	0.58464337	Aerobic respiration contı	2.7.13.3	arcB	PhoQ Sensor
MNLKPGEA_ MNLKPGEA	-0.252015228	0.86132613	hypothetical protein	NA	0	Catalyzes the reversible phospha
MNLKPGEA_ gpx1	-0.253761955	NA	Hydroperoxy fatty acid re	1.11.1.22	gpo	Belongs to the glutathione perox
MNLKPGEA_ artP	-0.254719645	0.61013332	Arginine transport ATP-b	3.6.3.-	artP	Arginine ABC transporter, ATP-b
MNLKPGEA_ iolG_6	-0.255309995	NA	Inositol 2-dehydrogenase	1.1.1.18	iolG	Involved in the oxidation of myo-
MNLKPGEA_ MNLKPGEA	-0.25554895	0.34872647	hypothetical protein	NA	slyD	Peptidyl-prolyl cis-trans
MNLKPGEA_ recF	-0.255843953	0.82190155	DNA replication and repa	NA	recF	it is required for DNA replicatior
MNLKPGEA_ nimR_5	-0.255870425	0.77948178	HTH-type transcriptional	NA	yeaM	Transcriptional regulator
MNLKPGEA_ fdnG_2	-0.256392246	0.85652652	Formate dehydrogenase	1.17.5.3	fdnG	Belongs to the prokaryotic molyb
MNLKPGEA_ kup	-0.259914333	0.42073657	Low affinity potassium t	NA	kup	transport of potassium into the (
MNLKPGEA_ ogt	-0.260930656	0.77334927	Methylated-DNA--protei	2.1.1.63	ogt	Involved in the cellular defense a
MNLKPGEA_ tal	-0.261262562	0.53984835	Transaldolase	2.2.1.2	tal	Transaldolase is important for th
MNLKPGEA_ rafB_1	-0.261651277	0.82718237	Raffinose permease	NA	0	Major facilitator superfamily
MNLKPGEA_ MNLKPGEA	-0.262114092	NA	hypothetical protein	NA	0	Antibiotic biosynthesis monooxy
MNLKPGEA_ MNLKPGEA	-0.263114727	NA	hypothetical protein	NA	0	0
MNLKPGEA_ MNLKPGEA	-0.263114727	NA	hypothetical protein	NA	gpI	tail protein
MNLKPGEA_ nimR_1	-0.263362581	0.85763471	HTH-type transcriptional	NA	0	AraC family transcriptional regul
MNLKPGEA_ MNLKPGEA	-0.263668	0.64265709	hypothetical protein	NA	ygfB	Belongs to the UPF0149 family
MNLKPGEA_ MNLKPGEA	-0.2636812	NA	hypothetical protein	NA	0	Pectate lyase superfamily protei
MNLKPGEA_ atsA	-0.263845781	NA	Arylsulfatase	3.1.6.1	atsA	COG3119 Arylsulfatase A and re
MNLKPGEA_ qorB	-0.264619119	0.82522451	Quinone oxidoreductase	1.6.5.2	ytfG	NmrA family
MNLKPGEA_ virB	-0.264696385	0.69396074	Virulence regulon transc	NA	parB	Belongs to the ParB family
MNLKPGEA_ ddpC_1	-0.264901689	NA	putative D,D-dipeptide tı	NA	0	Binding-protein-dependent trans
MNLKPGEA_ MNLKPGEA	-0.265090423	0.48097034	hypothetical protein	NA	ytfB	Opacity-associated protein A
MNLKPGEA_ MNLKPGEA	-0.265201434	NA	hypothetical protein	NA	miaE	Hydroxylase for synthesis of 2-m
MNLKPGEA_ azoR_1	-0.265497932	NA	FMN-dependent NADH-a	1.7.1.17	azoR	Catalyzes the reductive cleavage
MNLKPGEA_ intA_5	-0.265692055	0.45756975	Prophage integrase IntA	NA	intB	Belongs to the 'phage' integrase

MNLKPGEA_	acs	-0.2686404	0.6735575	Acetyl-coenzyme A synth	6.2.1.1	acsA	Catalyzes the conversion of acet
MNLKPGEA_	MNLKPGEA	-0.268730784	NA	hypothetical protein	NA	0	Protein of unknown function (DU
MNLKPGEA_	msrQ	-0.269378256	0.44698478	Protein-methionine-sulfo	NA	msrQ	Part of the MsrPQ system that r
MNLKPGEA_	mog	-0.269429494	0.50106436	Molybdopterin adenylylt	2.7.7.75	mog	Molybdenum cofactor
MNLKPGEA_	recX	-0.27026842	0.71421646	Regulatory protein RecX	NA	recX	Regulatory protein recX
MNLKPGEA_	MNLKPGEA	-0.271139712	NA	hypothetical protein	NA	bcsF	Cellulose biosynthesis protein Bc
MNLKPGEA_	MNLKPGEA	-0.271953104	NA	hypothetical protein	NA	0	Baseplate assembly protein
MNLKPGEA_	ccmC	-0.272213324	NA	Heme exporter protein C	NA	ccmC	Required for the export of heme
MNLKPGEA_	glpQ	-0.272593387	0.80067413	Glycerophosphodiester p	3.1.4.46	glpQ	glycerophosphoryl diester phosp
MNLKPGEA_	fosA	-0.27264521	NA	Glutathione transferase	2.5.1.18	fosA	Glutathione transferase
MNLKPGEA_	MNLKPGEA	-0.27264521	NA	hypothetical protein	NA	0	0
MNLKPGEA_	ssuD	-0.27264521	NA	Alkanesulfonate monoox	1.14.14.5	ssuD	Catalyzes the desulfonation of a
MNLKPGEA_	MNLKPGEA	-0.272832986	0.55109734	putative acyl-CoA thioes	3.1.2.-	yciA	acyl-CoA thioester hydrolase
MNLKPGEA_	ybiI_1	-0.273167744	NA	putative protein YbiI	NA	0	Prokaryotic dksA/traR C4-type zi
MNLKPGEA_	ybiB	-0.273348512	0.75240579	putative protein YbiB	NA	ybiB	Glycosyl transferase
MNLKPGEA_	ortT	-0.273660118	0.81069729	Orphan toxin OrtT	NA	ydcX	Toxin GhoT_OrtT
MNLKPGEA_	pstS	-0.27369039	0.72554293	Phosphate-binding prote	NA	pstS	Part of the ABC transporter com
MNLKPGEA_	ribC	-0.273703442	0.66031116	Riboflavin synthase	2.5.1.9	ribE	Riboflavin synthase
MNLKPGEA_	MNLKPGEA	-0.274685937	NA	hypothetical protein	NA	ycaR	Belongs to the UPF0434 family
MNLKPGEA_	kefC_2	-0.275279443	0.71411533	Glutathione-regulated p	NA	kefC	Belongs to the monovalent catic
MNLKPGEA_	chuR	-0.276321764	0.84329656	Anaerobic sulfatase-mat	1.1.99.-	0	Iron-sulfur cluster-binding doma
MNLKPGEA_	cpdB	-0.277848188	0.77771109	2',3'-cyclic-nucleotide 2'	3.1.3.6	cpdB	Belongs to the 5'-nucleotidase f
MNLKPGEA_	MNLKPGEA	-0.278294628	0.77835211	hypothetical protein	NA	#N/A	#N/A
MNLKPGEA_	MNLKPGEA	-0.278875583	NA	hypothetical protein	NA	0	0
MNLKPGEA_	tsgA	-0.279379639	0.82178072	Protein TsgA	NA	tsgA	Protein tsgA homolog
MNLKPGEA_	asnB	-0.279600666	0.59998888	Asparagine synthetase B	6.3.5.4	asnB	asparagine synthase, glutamine-
MNLKPGEA_	MNLKPGEA	-0.281589452	0.7910367	hypothetical protein	NA	yibQ	protein conserved in bacteria
MNLKPGEA_	rbfA	-0.282425767	0.6404632	30S ribosome-binding fa	NA	rbfA	One of several proteins that assi
MNLKPGEA_	MNLKPGEA	-0.282745097	0.35910844	hypothetical protein	NA	0	Protein of unknown function (DU
MNLKPGEA_	cysW	-0.283054482	NA	Sulfate transport system	NA	cysW	(ABC) transporter

MNLKPGEA_ MNLKPGEA	-0.2845884	NA	hypothetical protein	NA	0	Ead/Ea22-like protein
MNLKPGEA_ yceI	-0.284765811	0.58602483	Protein YceI	NA	yceI	Belongs to the UPF0312 family
MNLKPGEA_ purC	-0.28500049	0.74972576	Phosphoribosylaminoimi	6.3.2.6	purC	Belongs to the SAICAR synthetas
MNLKPGEA_ MNLKPGEA	-0.285921138	0.55426849	hypothetical protein	NA	0	Protein involved in biological_pr
MNLKPGEA_ pcpR_2	-0.286318866	NA	PCP degradation transcri	NA	0	Transcriptional regulator
MNLKPGEA_ ptsJ	-0.286979325	0.81761699	Vitamin B6 salvage path	NA	ptsJ	Transcriptional regulators contai
MNLKPGEA_ yadV_5	-0.287306358	NA	putative fimbrial chaper	NA	fimB	Pili assembly chaperone PapD, C
MNLKPGEA_ dnaE	-0.287980359	0.4451557	DNA polymerase III subu	2.7.7.7	dnaE	DNA polymerase
MNLKPGEA_ cysN	-0.289410787	0.72147481	Sulfate adenylyltransfera	2.7.7.4	cysN	Belongs to the TRAFAC class tra
MNLKPGEA_ pepA	-0.289542893	0.50919854	Cytosol aminopeptidase	3.4.11.1	pepA	Presumably involved in the proce
MNLKPGEA_ MNLKPGEA	-0.290526522	0.64446591	hypothetical protein	NA	#N/A	#N/A
MNLKPGEA_ grcA	-0.290781037	0.68054746	Autonomous glycyl radic	NA	grcA	Acts as a radical domain for dan
MNLKPGEA_ fadR	-0.29144731	0.50650437	Fatty acid metabolism re	NA	fadR	Multifunctional regulator of fatt
MNLKPGEA_ MNLKPGEA	-0.292369749	NA	putative phosphatase	3.1.3.-	0	phosphoserine phosphatase
MNLKPGEA_ murR	-0.293597359	0.7315085	HTH-type transcriptional	NA	yfhH	Transcriptional regulator
MNLKPGEA_ ppiD	-0.293765239	0.58094556	Peptidyl-prolyl cis-trans i	5.2.1.8	ppiD	peptidylprolyl isomerase
MNLKPGEA_ pldA	-0.294040977	0.69156088	Phospholipase A1	3.1.1.32	pldA	Phospholipase
MNLKPGEA_ fabG_9	-0.29435032	NA	3-oxoacyl-[acyl-carrier-p	1.1.1.100	0	COG1028 Dehydrogenases with
MNLKPGEA_ frdC	-0.29448208	NA	Fumarate reductase sub	NA	frdC	Seems to be involved in the ancl
MNLKPGEA_ MNLKPGEA	-0.294862376	0.58421133	hypothetical protein	NA	yjbB	Na Pi-Cotransporter
MNLKPGEA_ wecE	-0.295571791	0.76782279	dTDP-4-amino-4,6-dideo	2.6.1.59	wecE	Catalyzes the synthesis of dTDP-
MNLKPGEA_ MNLKPGEA	-0.295664441	NA	hypothetical protein	NA	0	protein conserved in bacteria
MNLKPGEA_ srlB_1	-0.295664441	NA	PTS system glucitol/sorb	NA	srlB	PTS system glucitol sorbitol-spe
MNLKPGEA_ gltA_1	-0.29626208	0.21491423	Citrate synthase	2.3.3.16	gltA	Belongs to the citrate synthase f
MNLKPGEA_ MNLKPGEA	-0.296812877	0.66072108	hypothetical protein	NA	ybfA	Membrane
MNLKPGEA_ oppA_2	-0.297655833	0.45937711	Periplasmic oligopeptide	NA	oppA3	ABC transporter substrate-bindi
MNLKPGEA_ dhmA	-0.298932121	NA	Haloalkane dehalogenas	3.8.1.5	0	Alpha beta hydrolase
MNLKPGEA_ umuC_6	-0.299185983	0.55946751	Protein UmuC	NA	umuC	DNA polymerase
MNLKPGEA_ MNLKPGEA	-0.300985712	0.82522709	hypothetical protein	NA	0	Sulfatase-modifying factor enzy
MNLKPGEA_ MNLKPGEA	-0.302880039	NA	hypothetical protein	NA	0	Protein of unknown function (DU

MNLKPGEA_ iprA_3	-0.303515003	0.55785367	Inhibitor of hydrogen per	NA	0	Winged helix-turn-helix DNA bin
MNLKPGEA_ bglB	-0.303873266	0.83633878	6-phospho-beta-glucosic	3.2.1.86	bglB	Belongs to the glycosyl hydrolas
MNLKPGEA_ ypdA	-0.304984188	0.73693028	Sensor histidine kinase Y	2.7.13.3	ypdA	Histidine kinase
MNLKPGEA_ eda	-0.305527427	0.74002962	KHG/KDPG aldolase	NA	eda	Aldolase
MNLKPGEA_ oprB	-0.309088728	0.73234136	Porin B	NA	oprB	COG3659 Carbohydrate-selective
MNLKPGEA_ proP_1	-0.31041031	0.60481527	Proline/betaine transpor	NA	proP_4	Major facilitator superfamily
MNLKPGEA_ dmlR_6	-0.311029805	NA	HTH-type transcriptional	NA	0	transcriptional regulator
MNLKPGEA_ MNLKPGEA	-0.312117624	NA	hypothetical protein	NA	#N/A	#N/A
MNLKPGEA_ apbE_2	-0.313295672	0.80304823	FAD:protein FMN transfe	2.7.1.180	nosX	Flavin transferase that catalyzes
MNLKPGEA_ ydiB_1	-0.313776682	NA	Quinate/shikimate dehy	1.1.1.282	0	shikimate
MNLKPGEA_ nqrB	-0.314049538	NA	Na(+)-translocating NAD	7.2.1.1	nqrB	NQR complex catalyzes the redu
MNLKPGEA_ pqqE	-0.315221051	NA	PqqA peptide cyclase	1.21.98.4	pqqE	Pyrroloquinoline quinone biosynt
MNLKPGEA_ MNLKPGEA	-0.315534226	0.49842654	hypothetical protein	NA	0	Capsule assembly protein Wzi
MNLKPGEA_ MNLKPGEA	-0.315569773	NA	IS6 family transposase IS	NA	0	Transposase IS66 family
MNLKPGEA_ gltX	-0.316055527	0.39934656	Glutamate--tRNA ligase	6.1.1.17	gltX	Catalyzes the attachment of glut
MNLKPGEA_ ccpA_1	-0.316301337	NA	Catabolite control protei	NA	0	transcriptional regulator
MNLKPGEA_ MNLKPGEA	-0.316301337	NA	hypothetical protein	NA	0	Branched-chain amino acid trans
MNLKPGEA_ gmuR	-0.317283221	NA	HTH-type transcriptional	NA	gmuR	GntR family
MNLKPGEA_ artI	-0.317509159	0.64458716	Putative ABC transporter	NA	artI	belongs to the bacterial solute-b
MNLKPGEA_ rbsD	-0.31857084	0.42944752	D-ribose pyranase	5.4.99.62	rbsD	Catalyzes the interconversion of
MNLKPGEA_ MNLKPGEA	-0.318645778	NA	IS1595 family transposas	NA	0	EamA-like transporter family
MNLKPGEA_ MNLKPGEA	-0.319849679	NA	hypothetical protein	NA	0	0
MNLKPGEA_ MNLKPGEA	-0.320942889	0.81699862	hypothetical protein	NA	0	Outer membrane protein protec
MNLKPGEA_ cysB	-0.321174826	0.61794949	HTH-type transcriptional	NA	cysB	transcriptional regulator
MNLKPGEA_ MNLKPGEA	-0.321995447	NA	hypothetical protein	NA	0	0
MNLKPGEA_ MNLKPGEA	-0.322549017	0.38605951	hypothetical protein	NA	ytfL	Hemolysins and related proteins
MNLKPGEA_ ygjV	-0.324447612	0.75997564	Inner membrane protein	NA	ygjV	Membrane
MNLKPGEA_ gltP	-0.324960714	0.73783408	Proton/glutamate-aspar	NA	gltP	Belongs to the dicarboxylate am
MNLKPGEA_ MNLKPGEA	-0.327960817	NA	hypothetical protein	NA	0	Domain of unknown function (DU
MNLKPGEA_ dppB_2	-0.328184092	NA	Dipeptide transport syste	NA	ddpB	Binding-protein-dependent trans

MNLKPGEA_ ubiJ_1	-0.328602999	0.75997564	Ubiquinone biosynthesis	NA	yhbT	lipid carrier protein
MNLKPGEA_ gsiC_4	-0.328861597	NA	Glutathione transport sy	NA	MA20_19	Binding-protein-dependent trans
MNLKPGEA_ hipA	-0.328957758	NA	Serine/threonine-protein	2.7.11.1	hipA	protein related to capsule biosyr
MNLKPGEA_ tyrB_1	-0.331714344	NA	Aromatic-amino-acid am	2.6.1.57	tyrB	aminotransferase
MNLKPGEA_ potH	-0.331854679	NA	Putrescine transport syst	NA	potH	ABC-type spermidine putrescine
MNLKPGEA_ yiiM	-0.332876744	0.75344428	Protein YiiM	NA	yiiM	protein conserved in bacteria
MNLKPGEA_ uvrY	-0.333022509	0.44322011	Response regulator UvrY	NA	uvrY	response regulator
MNLKPGEA_ ptrB	-0.335417651	0.40790876	Protease 2	3.4.21.83	ptrB	Protease II
MNLKPGEA_ MNLKPGEA	-0.33564201	0.63590099	hypothetical protein	NA	0	0
MNLKPGEA_ nrdI	-0.335699664	0.67210255	Protein NrdI	NA	nrdI	Probably involved in ribonucleoti
MNLKPGEA_ yajI	-0.336142012	0.80725714	putative lipoprotein YajI	NA	yajI	Lipoprotein
MNLKPGEA_ rnk	-0.337084077	0.47443455	Regulator of nucleoside	NA	rnk	regulator of nucleoside diphosph
MNLKPGEA_ surA	-0.337307483	0.45252514	Chaperone SurA	5.2.1.8	surA	Chaperone involved in the correc
MNLKPGEA_ mtlD	-0.337401277	0.51748126	Mannitol-1-phosphate 5-	1.1.1.17	mtlD	Mannitol-1-Phosphate 5-Dehydr
MNLKPGEA_ MNLKPGEA	-0.337874467	0.78557967	hypothetical protein	NA	0	Alanyl-tRNA synthetase
MNLKPGEA_ licC_4	-0.337966445	0.52182605	Lichenan permease IIC c	NA	0	The phosphoenolpyruvate-deper
MNLKPGEA_ MNLKPGEA	-0.339103915	0.77135454	putative protein	NA	0	Zn-dependent hydrolases of the
MNLKPGEA_ pulA	-0.340196153	0.78147541	Pullulanase	3.2.1.41	pulA	Belongs to the glycosyl hydrolas
MNLKPGEA_ farR	-0.340922739	0.73234136	HTH-type transcriptional	NA	hpaR	helix_turn_helix multiple antibic
MNLKPGEA_ MNLKPGEA	-0.340924404	0.77902649	hypothetical protein	NA	0	50S ribosomal protein L21
MNLKPGEA_ scrY_1	-0.341078436	NA	Sucrose porin	NA	0	maltoporin
MNLKPGEA_ dcuB	-0.34216548	0.76463939	Anaerobic C4-dicarboxyla	NA	dcuB	Responsible for the transport of
MNLKPGEA_ gutQ	-0.342740772	0.73234136	Arabinose 5-phosphate i	5.3.1.13	kdsD	Arabinose 5-phosphate isomeras
MNLKPGEA_ miaA	-0.344042667	0.09982332	tRNA dimethylallyltransf	2.5.1.75	miaA	Catalyzes the transfer of a dime
MNLKPGEA_ leuO	-0.34409005	0.69458226	HTH-type transcriptional	NA	leuO	transcriptional regulator
MNLKPGEA_ tsaR_2	-0.345402909	0.81538732	HTH-type transcriptional	NA	tdcA	Transcriptional regulator
MNLKPGEA_ MNLKPGEA	-0.345418555	0.72656212	hypothetical protein	NA	0	COG0834 ABC-type amino acid t
MNLKPGEA_ MNLKPGEA	-0.34624301	0.77148285	hypothetical protein	NA	0	Plasmid stability protein
MNLKPGEA_ MNLKPGEA	-0.348466243	0.59747454	hypothetical protein	NA	#N/A	#N/A
MNLKPGEA_ ctpF_1	-0.348592799	0.36677274	putative cation-transport	3.6.3.-	0	ATPase, P-type (transporting), H

MNLKPGEA_	MNLKPGEA	-0.348727732	0.71990392	hypothetical protein	NA	0	transporter
MNLKPGEA_	lgoD	-0.349087701	NA	L-galactonate-5-dehydro	1.1.1.414	yjjN	Alcohol dehydrogenase GroES dc
MNLKPGEA_	prr	-0.349127147	0.51501638	Gamma-aminobutyralde	1.2.1.19	prr	belongs to the aldehyde dehydrc
MNLKPGEA_	marR	-0.349398876	0.77148285	Multiple antibiotic resist	NA	marR	transcriptional regulator
MNLKPGEA_	MNLKPGEA	-0.350030805	0.71535303	hypothetical protein	NA	yohO	UPF0387 membrane protein Yol
MNLKPGEA_	rplL	-0.350532769	0.15476105	50S ribosomal protein L7	NA	rplL	Forms part of the ribosomal stal
MNLKPGEA_	MNLKPGEA	-0.350623441	0.33229626	hypothetical protein	NA	#N/A	#N/A
MNLKPGEA_	sulA	-0.351280752	0.42944752	Cell division inhibitor Sul	NA	sulA	Component of the SOS system a
MNLKPGEA_	greB	-0.352762988	0.71990392	Transcription elongation	NA	greB	Necessary for efficient RNA poly
MNLKPGEA_	parA	-0.352890683	0.37371869	Plasmid partition proteir	NA	parA	AAA domain
MNLKPGEA_	MNLKPGEA	-0.353064419	0.7947996	hypothetical protein	NA	yeaO	MarR family transcriptional regu
MNLKPGEA_	pdeA	-0.353627979	0.70484608	putative cyclic di-GMP pl	3.1.4.52	0	MASE1
MNLKPGEA_	MNLKPGEA	-0.355153193	0.40385959	hypothetical protein	NA	#N/A	#N/A
MNLKPGEA_	ychQ	-0.35674001	0.69165233	Protein YchQ	NA	sirB2	Invasion gene expression up-reg
MNLKPGEA_	macA	-0.357118669	0.67169289	Macrolide export proteir	NA	macA	Belongs to the membrane fusion
MNLKPGEA_	metR	-0.359631128	NA	HTH-type transcriptional	NA	metR	transcriptional regulator
MNLKPGEA_	MNLKPGEA	-0.361426417	0.38276043	hypothetical protein	NA	yejL	Belongs to the UPF0352 family
MNLKPGEA_	yebZ	-0.362601766	0.73392864	Inner membrane protein	NA	yebZ	copper resistance protein
MNLKPGEA_	MNLKPGEA	-0.36329964	NA	IS3 family transposase IS	NA	0	Integrase core domain
MNLKPGEA_	cbiO	-0.364094641	NA	Cobalt import ATP-bindir	7.-.-.-	cbiO	Responsible for energy coupling
MNLKPGEA_	mntP	-0.364246274	NA	putative manganese effl	NA	mntP	Probably functions as a mangan
MNLKPGEA_	cusA	-0.364476021	NA	Cation efflux system pro	NA	cusA	Belongs to the resistance-nodula
MNLKPGEA_	purT	-0.364521707	NA	Formate-dependent pho	2.1.2.-	purT	Involved in the de novo purine bi
MNLKPGEA_	folX	-0.364924056	0.43106948	Dihydroneopterin triphos	5.1.99.7	folX	Catalyzes the formation of dihyc
MNLKPGEA_	gabD_2	-0.366418655	0.43406811	Succinate-semialdehyde	1.2.1.79	gabD	belongs to the aldehyde dehydrc
MNLKPGEA_	sdhC	-0.366545402	0.14784042	Succinate dehydrogenas	NA	sdhC	succinate dehydrogenase
MNLKPGEA_	MNLKPGEA	-0.366554723	NA	hypothetical protein	NA	0	Phage gp6-like head-tail connec
MNLKPGEA_	MNLKPGEA	-0.366723865	NA	hypothetical protein	NA	0	Major facilitator superfamily
MNLKPGEA_	MNLKPGEA	-0.366829463	0.73749661	hypothetical protein	NA	0	COG1664 Integral membrane pr
MNLKPGEA_	MNLKPGEA	-0.366930177	0.68054746	IS5 family transposase IS	NA	insH5	COG3039 Transposase and inact

MNLKPGEA_ umuD_1	-0.367771379	0.54438098	Protein UmuD	3.4.21.-	umuD	Belongs to the peptidase S24 fa
MNLKPGEA_ yojI	-0.368603664	0.75170049	ABC transporter ATP-bin	NA	yojI	Cyclic peptide transporter
MNLKPGEA_ rluD	-0.369126152	0.44923842	Ribosomal large subunit	5.4.99.23	rluD	Responsible for synthesis of pse
MNLKPGEA_ gdhA_1	-0.371434173	0.16885502	Glutamate dehydrogena	1.4.1.3	gdhA	Belongs to the Glu Leu Phe Val d
MNLKPGEA_ MNLKPGEA	-0.37187299	0.21488712	hypothetical protein	NA	wza	polysaccharide export
MNLKPGEA_ MNLKPGEA	-0.372103571	0.18488282	hypothetical protein	NA	ybeD	Belongs to the UPF0250 family
MNLKPGEA_ MNLKPGEA	-0.372140536	0.63950728	hypothetical protein	NA	nuc	PLD-like domain
MNLKPGEA_ yiaD	-0.372464858	NA	putative lipoprotein YiaD	NA	yiaD	Belongs to the ompA family
MNLKPGEA_ astB_1	-0.372825978	0.80067413	N-succinylarginine dihyd	3.5.3.23	astB	Catalyzes the hydrolysis of N(2)-
MNLKPGEA_ nupC_1	-0.37292283	0.29378784	Nucleoside permease Nu	NA	nupC	Belongs to the concentrative nuc
MNLKPGEA_ lyx_2	-0.372923297	NA	L-xylulose/3-keto-L-gulo	2.7.1.-	eryA	Belongs to the FGGY kinase fam
MNLKPGEA_ ligB	-0.373108565	NA	DNA ligase B	6.5.1.2	ligB	Catalyzes the formation of phos
MNLKPGEA_ MNLKPGEA	-0.373135102	NA	Alpha-ketoglutaric semia	1.2.1.26	aldH	Aldehyde dehydrogenase family
MNLKPGEA_ nikC	-0.373135102	NA	Nickel transport system	NA	nikC	transport
MNLKPGEA_ narU	-0.373682169	0.59429066	Nitrate/nitrite transport	NA	narU	nitrate nitrite transporter
MNLKPGEA_ gpt	-0.374234313	0.57273586	Xanthine phosphoribosyl	2.4.2.22	gpt	Acts on guanine, xanthine and to
MNLKPGEA_ MNLKPGEA	-0.374234683	0.75240579	hypothetical protein	NA	eutG	alcohol dehydrogenase
MNLKPGEA_ MNLKPGEA	-0.375682251	NA	hypothetical protein	NA	0	phage terminase small subunit
MNLKPGEA_ MNLKPGEA	-0.376755862	0.78058271	hypothetical protein	NA	MA20_32	PFAM 20S proteasome, A and B
MNLKPGEA_ MNLKPGEA	-0.377854066	NA	IS3 family transposase IS	NA	0	Transposase and inactivated der
MNLKPGEA_ ggt	-0.377941948	0.49683805	Glutathione hydrolase pr	3.4.19.13	ggt	Gamma-glutamyltransferase
MNLKPGEA_ MNLKPGEA	-0.377964099	NA	hypothetical protein	NA	0	0
MNLKPGEA_ MNLKPGEA	-0.37826773	NA	Magnesium transporter	NA	mgtE-1	Acts as a magnesium transporte
MNLKPGEA_ MNLKPGEA	-0.37826773	NA	hypothetical protein	NA	0	transcriptional regulator
MNLKPGEA_ yheS_3	-0.378427117	0.75154365	putative ABC transporter	NA	0	ABC transporter
MNLKPGEA_ ydcS	-0.378736162	0.31322447	Bifunctional polyhydroxy	2.3.1.-	ydcS	Spermidine putrescine ABC trans
MNLKPGEA_ MNLKPGEA	-0.378760593	NA	hypothetical protein	NA	0	0
MNLKPGEA_ yehY	-0.378823228	0.41540058	Glycine betaine uptake s	NA	yehY	permease
MNLKPGEA_ MNLKPGEA	-0.379623999	NA	hypothetical protein	NA	sgcQ	BtpA family membrane complex
MNLKPGEA_ pdeC	-0.379758178	0.59707861	putative cyclic di-GMP p	3.1.4.52	yjcC	signal transduction protein conta

MNLKPGEA_ MNLKPGEA	-0.380594922	NA	hypothetical protein	NA	0	Glyoxalase/Bleomycin resistanc
MNLKPGEA_ pgsA	-0.380858045	0.71282742	CDP-diacylglycerol--glyce	2.7.8.5	pgsA	Belongs to the CDP-alcohol phos
MNLKPGEA_ sstT	-0.381475659	0.35421172	Serine/threonine transpo	NA	sstT	Involved in the import of serine
MNLKPGEA_ MNLKPGEA	-0.382484119	NA	hypothetical protein	NA	0	Lipoate-protein ligase
MNLKPGEA_ MNLKPGEA	-0.382493864	0.67234607	hypothetical protein	NA	yigA	protein conserved in bacteria
MNLKPGEA_ aer	-0.383036659	0.32439135	Aerotaxis receptor	NA	aer	chemotaxis, protein
MNLKPGEA_ folM	-0.383263962	0.6293984	Dihydromonapterin redu	1.5.1.50	folM	reductase
MNLKPGEA_ prlC	-0.384476375	0.38150079	Oligopeptidase A	3.4.24.70	prlC	oligopeptidase
MNLKPGEA_ hslR	-0.384927102	0.69230701	Heat shock protein 15	NA	hslR	Belongs to the HSP15 family
MNLKPGEA_ ybiR	-0.385167342	0.33138136	Inner membrane protein	NA	ybiR	Citrate transporter
MNLKPGEA_ MNLKPGEA	-0.38551191	0.59176485	hypothetical protein	NA	0	Major facilitator Superfamily
MNLKPGEA_ rpsA	-0.385964665	0.4212445	30S ribosomal protein S1	NA	rpsA	thus facilitating recognition of tl
MNLKPGEA_ corA	-0.388962928	0.38276043	Magnesium transport pr	NA	corA	Mediates influx of magnesium i
MNLKPGEA_ cueR	-0.389406467	0.52356144	HTH-type transcriptional	NA	cueR	Transcriptional regulator
MNLKPGEA_ yobA	-0.389723194	0.48558167	Protein YobA	NA	yobA	Resistance protein
MNLKPGEA_ pntB	-0.395943461	0.58878635	NAD(P) transhydrogenas	7.1.1.1	pntB	The transhydrogenation betwee
MNLKPGEA_ yqjC	-0.396182879	0.08796934	Protein YqjC	NA	yqjC	Protein of unknown function (DU
MNLKPGEA_ xynB	-0.39829877	0.73369756	Beta-xylosidase	3.2.1.37	0	Belongs to the glycosyl hydrolas
MNLKPGEA_ nepI_3	-0.398859012	0.76394415	Purine ribonucleoside ef	NA	opdE	Major facilitator Superfamily
MNLKPGEA_ dcm_1	-0.399121349	0.42306103	DNA-cytosine methyltra	2.1.1.37	dcm	Methyl-transferase
MNLKPGEA_ aspA	-0.399558046	0.17317803	Aspartate ammonia-lyas	4.3.1.1	aspA	Aspartate ammonia-lyase
MNLKPGEA_ acuI	-0.400268514	0.67827125	putative acrylyl-CoA redu	1.3.1.84	yhdH	COG0604 NADPH quinone reduc
MNLKPGEA_ dauA_2	-0.400490159	NA	C4-dicarboxylic acid tran	NA	ychM	transporter
MNLKPGEA_ pldB	-0.401193572	0.25186479	Lysophospholipase L2	3.1.1.5	pldB	Lysophospholipase
MNLKPGEA_ yifK	-0.401822628	0.76394415	putative transport protei	NA	yifK	'involved in the transport across
MNLKPGEA_ MNLKPGEA	-0.401920235	0.30418788	hypothetical protein	NA	0	0
MNLKPGEA_ MNLKPGEA	-0.403722834	0.70114072	hypothetical protein	NA	yjcB	membrane
MNLKPGEA_ MNLKPGEA	-0.40451338	0.44878116	hypothetical protein	NA	0	0
MNLKPGEA_ MNLKPGEA	-0.4050859	NA	hypothetical protein	NA	0	0
MNLKPGEA_ thrS	-0.405129994	0.15657111	Threonine--tRNA ligase	6.1.1.3	thrS	Catalyzes the attachment of thre

MNLKPGEA_	hutG	-0.405169633	0.72893371	Formimidoylglutamase	3.5.3.8	hutG	Catalyzes the conversion of N-fo
MNLKPGEA_	fetA	-0.405973572	0.64446591	putative iron export ATP-	3.6.3.-	ybbL	abc transporter atp-binding prot
MNLKPGEA_	MNLKPGEA	-0.406886766	NA	hypothetical protein	NA	gutM	Glucitol operon activator
MNLKPGEA_	MNLKPGEA	-0.407261054	0.27779421	hypothetical protein	NA	marB	Multiple antibiotic resistance
MNLKPGEA_	tktA_1	-0.408334406	0.44383467	Transketolase 1	2.2.1.1	tktA	Catalyzes the transfer of a two-(
MNLKPGEA_	ftsQ	-0.408942559	0.68983761	Cell division protein FtsC	NA	ftsQ	Essential cell division protein. M
MNLKPGEA_	MNLKPGEA	-0.409090084	0.73687157	hypothetical protein	NA	0	Type IV secretory pathway, VirB3
MNLKPGEA_	rbsB_3	-0.410999336	0.7738162	Ribose import binding pr	NA	rbsB	PFAM Periplasmic binding prote
MNLKPGEA_	MNLKPGEA	-0.412471889	0.68054746	hypothetical protein	NA	#N/A	#N/A
MNLKPGEA_	nrdR	-0.41252861	0.7315085	Transcriptional represso	NA	nrdR	Negatively regulates transcriptic
MNLKPGEA_	katE	-0.413874254	0.32762237	Catalase HPII	1.11.1.6	katE	serves to protect cells from the t
MNLKPGEA_	ppk	-0.413941759	0.23926454	Polyphosphate kinase	2.7.4.1	ppk	Catalyzes the reversible transfer
MNLKPGEA_	yafJ	-0.415331028	0.52045701	Putative glutamine amic	2.4.2.-	yafJ	glutamine amidotransferase
MNLKPGEA_	MNLKPGEA	-0.416069201	0.13079323	hypothetical protein	NA	yeeX	Belongs to the UPF0265 family
MNLKPGEA_	arfB	-0.416161809	0.58609916	Peptidyl-tRNA hydrolase	3.1.1.29	yaeJ	chain release factor
MNLKPGEA_	wzyE	-0.416628844	0.67169289	putative ECA polymerase	NA	wzyE	Probably involved in the polymer
MNLKPGEA_	pfeA	-0.418301449	0.70709197	Ferric enterobactin recep	NA	fepA	Receptor
MNLKPGEA_	dtpA	-0.41909193	0.21850144	Dipeptide and tripeptide	NA	dtpA	Proton-dependent permease tha
MNLKPGEA_	MNLKPGEA	-0.419513964	NA	hypothetical protein	NA	0	adenylate kinase activity
MNLKPGEA_	MNLKPGEA	-0.420141243	0.2235144	putative NTE family prot	NA	rssA	esterase of the alpha-beta hydro
MNLKPGEA_	fmt	-0.420423261	0.31025248	Methionyl-tRNA formylt	2.1.2.9	fmt	Attaches a formyl group to the f
MNLKPGEA_	MNLKPGEA	-0.420763387	NA	hypothetical protein	NA	tssB	type VI secretion protein
MNLKPGEA_	MNLKPGEA	-0.421187325	NA	hypothetical protein	NA	0	of the drug metabolite transport
MNLKPGEA_	rlhA_2	-0.421494935	0.58114513	23S rRNA 5-hydroxycytid	NA	ydcP	peptidase U32
MNLKPGEA_	MNLKPGEA	-0.421586357	0.32731043	hypothetical protein	NA	yqiB	protein conserved in bacteria
MNLKPGEA_	phnR	-0.421599752	0.75668924	Putative transcriptional r	NA	phnR	UTRA
MNLKPGEA_	MNLKPGEA	-0.422044464	0.71535303	hypothetical protein	NA	0	membrane transporter protein
MNLKPGEA_	phoU	-0.422859485	0.68451399	Phosphate-specific trans	NA	phoU	Part of the phosphate (Pho) regu
MNLKPGEA_	mtnA	-0.423583447	NA	Methylthioribose-1-phos	5.3.1.23	mtnA	Catalyzes the interconversion of
MNLKPGEA_	MNLKPGEA	-0.423648359	0.74980197	hypothetical protein	NA	cysW_1	ABC-type Fe3 transport system p

MNLKPGEA_	ldhA	-0.423675161	0.43331934	D-lactate dehydrogenase	1.1.1.28	ldhA	Belongs to the D-isomer specific
MNLKPGEA_	MNLKPGEA	-0.424025306	NA	hypothetical protein	NA	todE	Glyoxalase/Bleomycin resistance
MNLKPGEA_	catD	-0.424051279	0.75344428	3-oxoadipate enol-lactor	3.1.1.24	pcaD	3-oxoadipate enol-lactonase
MNLKPGEA_	MNLKPGEA	-0.424078559	NA	hypothetical protein	NA	0	Domain of unknown function (DU
MNLKPGEA_	yagG_2	-0.424332353	NA	Putative glycoside/catior	NA	0	Major Facilitator
MNLKPGEA_	MNLKPGEA	-0.424714511	0.58261398	hypothetical protein	NA	0	Glycosyltransferase family 9 (he
MNLKPGEA_	bglF_2	-0.424945107	NA	PTS system beta-glucosi	NA	bglF	Phosphotransferase System
MNLKPGEA_	proX	-0.425045021	0.72797769	Glycine betaine/proline I	NA	proX	glycine, betaine
MNLKPGEA_	citC	-0.425524018	NA	[Citrate [pro-3S]-lyase] l	6.2.1.22	citC	Acetylation of prosthetic group (
MNLKPGEA_	pgrR_1	-0.425630378	0.61013332	HTH-type transcriptional	NA	Z012_074	Transcriptional regulator
MNLKPGEA_	MNLKPGEA	-0.426336147	NA	hypothetical protein	NA	0	transcriptional regulator
MNLKPGEA_	nsrR	-0.427507077	0.28764822	HTH-type transcriptional	NA	nsrR	Nitric oxide-sensitive repressor c
MNLKPGEA_	MNLKPGEA	-0.42795632	0.57971516	hypothetical protein	NA	yjbJ	Belongs to the UPF0337 (CsbD) f
MNLKPGEA_	yceO	-0.428084645	NA	putative protein YceO	NA	0	Protein of unknown function (DU
MNLKPGEA_	moaD	-0.42819619	NA	Molybdopterin synthase	NA	moaD	Involved in sulfur transfer in the
MNLKPGEA_	hadI	-0.428289499	NA	2-hydroxyisocaproyl-CoA	3.-.-.-	yjiL	4 iron, 4 sulfur cluster binding
MNLKPGEA_	yeiP	-0.428519952	0.55219725	Elongation factor P-like p	NA	yeiP	Elongation factor P
MNLKPGEA_	yciN	-0.428959222	0.24451732	Protein YciN	NA	yciN	Protein of unknown function (DU
MNLKPGEA_	yffB	-0.42896003	0.59484343	Protein YffB	NA	yffB	Belongs to the ArsC family
MNLKPGEA_	bcsA	-0.42963181	0.58142153	Cellulose synthase catal	2.4.1.12	bcsA	Cellulose synthase
MNLKPGEA_	MNLKPGEA	-0.430726826	0.74650575	hypothetical protein	NA	0	Protein of unknown function (DU
MNLKPGEA_	mutM	-0.430934122	0.75240579	Formamidopyrimidine-D	3.2.2.23	fpg	Involved in base excision repair c
MNLKPGEA_	secB	-0.431117868	0.24461686	Protein-export protein Se	NA	secB	One of the proteins required for
MNLKPGEA_	MNLKPGEA	-0.431139547	NA	hypothetical protein	NA	0	Membrane
MNLKPGEA_	solA	-0.431534096	0.59113864	N-methyl-L-tryptophan c	1.5.3.-	solA	Belongs to the MSOX MTOX fam
MNLKPGEA_	galP	-0.432058944	0.58576946	Galactose-proton sympo	NA	galP	Major facilitator Superfamily
MNLKPGEA_	rfaQ	-0.432305519	0.58458328	Lipopolysaccharide core	2.-.-.-	rfaQ	heptosyltransferase
MNLKPGEA_	artJ_1	-0.43240299	0.67639216	ABC transporter arginine	NA	artJ	belongs to the bacterial solute-b
MNLKPGEA_	MNLKPGEA	-0.433119088	0.19128331	hypothetical protein	NA	ftsK	COG1674 DNA segregation ATPa
MNLKPGEA_	MNLKPGEA	-0.434202245	0.46975324	hypothetical protein	NA	ybgS	YbgS-like protein

MNLKPGEA_ ygdG	-0.434294488	0.71990392	Flap endonuclease Xni	3.1.-.-	xni	Has flap endonuclease activity. I
MNLKPGEA_ mscK	-0.434993896	0.48414101	Mechanosensitive chann	NA	kefA	mechanosensitive ion channel
MNLKPGEA_ dnaK_2	-0.435140757	0.50834736	Chaperone protein DnaK	NA	dnaK	Heat shock 70 kDa protein
MNLKPGEA_ umuD_2	-0.436318493	0.67169289	Protein UmuD	3.4.21.-	umuD	Belongs to the peptidase S24 fa
MNLKPGEA_ sgbE	-0.437288184	NA	L-ribulose-5-phosphate 4	5.1.3.4	sgbE	Catalyzes the isomerization of L-
MNLKPGEA_ MNLKPGEA	-0.437928295	0.74168272	hypothetical protein	NA	0	Pkd domain containing protein
MNLKPGEA_ metN_3	-0.438830924	0.65087561	Methionine import ATP-I	3.6.3.-	metN	Part of the ABC transporter com
MNLKPGEA_ MNLKPGEA	-0.438957976	0.67612396	hypothetical protein	NA	yqkA	GrpB protein
MNLKPGEA_ emrA_2	-0.439604153	0.66998353	Colistin resistance protei	NA	hlyD	Secretion protein
MNLKPGEA_ lsrB_3	-0.441417607	NA	Autoinducer 2-binding pı	NA	rhaS	(ABC) transporter
MNLKPGEA_ dhaD	-0.441475777	0.5227595	Glycerol dehydrogenase	1.1.1.6	gldA	glycerol dehydrogenase
MNLKPGEA_ rlmA	-0.442064364	NA	23S rRNA (guanine(745)	2.1.1.187	rrmA	Methyl-transferase
MNLKPGEA_ yfcE	-0.44284902	0.556445	Phosphodiesterase YfcE	3.1.4.-	yfcE	Phosphoesterase
MNLKPGEA_ MNLKPGEA	-0.443267498	0.70114072	hypothetical protein	NA	Z012_10	tape measure protein
MNLKPGEA_ MNLKPGEA	-0.443454455	NA	hypothetical protein	NA	ynfA	UPF0060 membrane protein
MNLKPGEA_ MNLKPGEA	-0.443581972	NA	hypothetical protein	NA	0	0
MNLKPGEA_ iscA	-0.445137511	0.2189482	Iron-binding protein IscA	NA	iscA	Is able to transfer iron-sulfur clu
MNLKPGEA_ dnaA	-0.445636535	0.41857147	Chromosomal replicatior	NA	dnaA	it binds specifically double-stran
MNLKPGEA_ rpsL	-0.447412471	0.21491423	30S ribosomal protein S1	NA	rpsL	Interacts with and stabilizes bas
MNLKPGEA_ hemC	-0.451591809	0.55824265	Porphobilinogen deamin	2.5.1.61	hemC	Tetrapolymerization of the mon
MNLKPGEA_ radD	-0.451679142	0.58165989	Putative DNA repair heli	3.6.4.12	yejH	Type III restriction protein res su
MNLKPGEA_ MNLKPGEA	-0.451826271	0.77134584	hypothetical protein	NA	0	0
MNLKPGEA_ MNLKPGEA	-0.45220651	0.73351604	hypothetical protein	NA	comF	Competence protein
MNLKPGEA_ epmB	-0.452458179	0.50595233	L-lysine 2,3-aminomutas	5.4.3.-	epmB	lysine 2,3-aminomutase
MNLKPGEA_ xthA	-0.452483857	0.53929426	Exodeoxyribonuclease III	3.1.11.2	xthA	Exodeoxyribonuclease III
MNLKPGEA_ argG	-0.452683196	0.18085212	Argininosuccinate synthe	6.3.4.5	argG	Belongs to the argininosuccinate
MNLKPGEA_ spy	-0.45326106	0.33536817	Periplasmic chaperone S	NA	spy	P pilus assembly Cpx signaling p
MNLKPGEA_ hexR_3	-0.455318638	0.49709515	HTH-type transcriptional	NA	Z012_10	transcriptional regulator
MNLKPGEA_ lnt	-0.456237655	0.54464975	Apolipoprotein N-acyltra	2.3.1.269	lnt	Transfers the fatty acyl group or
MNLKPGEA_ guaD_1	-0.457958134	NA	Guanine deaminase	3.5.4.3	guaD	deaminase

MNLKPGEA_	MNLKPGEA	-0.457958134	NA	hypothetical protein	NA	0	periplasmic binding protein
MNLKPGEA_	livF_2	-0.458062398	NA	High-affinity branched-c	NA	livF	Branched-chain amino acid tran
MNLKPGEA_	agp_2	-0.458099011	NA	Glucose-1-phosphatase	3.1.3.10	appA	Acid phosphatase
MNLKPGEA_	MNLKPGEA	-0.458193806	NA	hypothetical protein	NA	0	0
MNLKPGEA_	phoC	-0.458221266	0.29343396	Major phosphate-irrepre	3.1.3.2	phoC	Acid phosphatase
MNLKPGEA_	plsY	-0.458229022	0.48189507	putative glycerol-3-phos	2.3.1.15	plsY	Catalyzes the transfer of an acyl
MNLKPGEA_	era	-0.458377488	0.48957215	GTPase Era	NA	era	An essential GTPase that binds k
MNLKPGEA_	gabR_1	-0.458737796	0.47395288	HTH-type transcriptional	NA	gabR_1	Transcriptional regulators contai
MNLKPGEA_	MNLKPGEA	-0.458911568	0.68983761	hypothetical protein	NA	ybdJ	membrane
MNLKPGEA_	bfd	-0.459472627	0.25530329	Bacterioferritin-associat	NA	bfd	Bacterioferritin-associated ferre
MNLKPGEA_	MNLKPGEA	-0.459479289	0.58998059	hypothetical protein	NA	#N/A	#N/A
MNLKPGEA_	MNLKPGEA	-0.460103465	0.55092912	hypothetical protein	NA	yheU	Belongs to the UPF0270 family
MNLKPGEA_	MNLKPGEA	-0.461140568	0.4746141	hypothetical protein	NA	#N/A	#N/A
MNLKPGEA_	norW_2	-0.462320543	NA	Nitric oxide reductase Fl	1.18.1.-	nirB	Belongs to the nitrite and sulfite
MNLKPGEA_	mngR_2	-0.463234144	0.4830638	Mannosyl-D-glycerate tr	NA	0	UTRA
MNLKPGEA_	MNLKPGEA	-0.463325305	0.68926534	hypothetical protein	NA	0	heme binding
MNLKPGEA_	ptsN	-0.4643575	0.34085921	Nitrogen regulatory prot	NA	ptsN	PTS IIA-like nitrogen-regulatory
MNLKPGEA_	MNLKPGEA	-0.465243622	NA	hypothetical protein	NA	0	ABC transporter substrate-bindi
MNLKPGEA_	agp_1	-0.465338505	0.33355756	Glucose-1-phosphatase	3.1.3.10	agp	Acid phosphatase
MNLKPGEA_	uxaA	-0.466291312	0.57645033	Altronate dehydratase	4.2.1.7	uxaA	Catalyzes the dehydration of gal
MNLKPGEA_	lexA_1	-0.467110692	0.58584665	LexA repressor	3.4.21.88	prpA	Repressor
MNLKPGEA_	MNLKPGEA	-0.467254822	NA	hypothetical protein	NA	0	COG2197 Response regulator co
MNLKPGEA_	dtpD	-0.469217175	0.58114513	Dipeptide permease D	NA	dtpD	Proton-dependent permease tha
MNLKPGEA_	purD	-0.469576288	0.56204901	Phosphoribosylamine--gl	6.3.4.13	purD	Belongs to the GARS family
MNLKPGEA_	recR	-0.469672449	0.54021318	Recombination protein F	NA	recR	May play a role in DNA repair. It
MNLKPGEA_	MNLKPGEA	-0.470165072	NA	hypothetical protein	NA	hycH	Formate hydrogen-lyase
MNLKPGEA_	MNLKPGEA	-0.470239273	NA	IS3 family transposase IS	NA	0	Transposase and inactivated der
MNLKPGEA_	ubiG	-0.470522159	0.48523815	Ubiquinone biosynthesis	2.1.1.222	ubiG	O-methyltransferase that cataly
MNLKPGEA_	ygiW_2	-0.470863467	0.46464601	Protein YgiW	NA	0	PFAM Bacterial OB fold (BOF) p
MNLKPGEA_	pstB	-0.470907214	0.53067843	Phosphate import ATP-b	7.3.2.1	pstB	Part of the ABC transporter com

MNLKPGEA_	rsxE	-0.471906787	0.65332954	Ion-translocating oxidore	7.-.-.-	rnfE	Part of a membrane complex inv
MNLKPGEA_	glgC	-0.471921695	0.30935092	Glucose-1-phosphate ad	2.7.7.27	glgC	Catalyzes the synthesis of ADP-g
MNLKPGEA_	serC	-0.472755462	0.23245251	Phosphoserine aminotra	2.6.1.52	serC	Catalyzes the reversible conversi
MNLKPGEA_	hypD	-0.473486804	NA	Hydrogenase maturatior	NA	hypD	Belongs to the HypD family
MNLKPGEA_	aroE_2	-0.473888339	NA	Shikimate dehydrogenas	1.1.1.25	ydiB	The actual biological function of
MNLKPGEA_	MNLKPGEA	-0.475109653	NA	hypothetical protein	NA	0	0
MNLKPGEA_	typA	-0.475306769	0.15657111	GTP-binding protein Typ	NA	typA	GTP-binding protein TypA
MNLKPGEA_	MNLKPGEA	-0.478074853	0.68054746	hypothetical protein	NA	0	Plasmid stability protein
MNLKPGEA_	MNLKPGEA	-0.47815925	NA	hypothetical protein	NA	0	0
MNLKPGEA_	MNLKPGEA	-0.478238621	NA	hypothetical protein	NA	0	0
MNLKPGEA_	hlyB	-0.478607506	0.59060145	Alpha-hemolysin translo	NA	0	COG2274 ABC-type bacteriocin l
MNLKPGEA_	carB_2	-0.47958656	0.60696406	Carbamoyl-phosphate sy	NA	bccA	carboxylase
MNLKPGEA_	bamE	-0.479861525	0.07980343	Outer membrane protei	NA	bamE	Part of the outer membrane pro
MNLKPGEA_	cmtAa	-0.480512863	NA	p-cumate 2,3-dioxygena	1.18.1.3	andAa	Pyridine nucleotide-disulphide o
MNLKPGEA_	MNLKPGEA	-0.480512863	NA	hypothetical protein	NA	0	Protein of unknown function (DU
MNLKPGEA_	tsaR_3	-0.480521647	NA	HTH-type transcriptional	NA	abgR	transcriptional regulator
MNLKPGEA_	yfeZ	-0.480701714	NA	Inner membrane protein	NA	yfeZ	Protein of unknown function (DU
MNLKPGEA_	melA	-0.480876464	0.72037257	Alpha-galactosidase	3.2.1.22	melA	Catalyses the hydrolysis of termi
MNLKPGEA_	mngA	-0.480926662	NA	PTS system 2-O-alpha-m	NA	frvA	PTS IIA-like nitrogen-regulatory
MNLKPGEA_	satP	-0.482571064	0.69369016	Succinate-acetate/proto	NA	yaaH	GPR1 FUN34 yaaH family protei
MNLKPGEA_	rhaS_13	-0.483036432	0.36963366	HTH-type transcriptional	NA	yijO	transcriptional regulator
MNLKPGEA_	pat_2	-0.483202063	0.56150775	Phosphinothricin N-acety	2.3.1.183	pat	N-acetyltransferase
MNLKPGEA_	trkA	-0.484293336	0.27585863	Trk system potassium up	NA	trkA	found to be peripherally associat
MNLKPGEA_	nimR_4	-0.485467427	0.51774858	HTH-type transcriptional	NA	0	transcriptional regulator
MNLKPGEA_	cybB	-0.485887573	0.24418833	Cytochrome b561	NA	cybB	Cytochrome B561
MNLKPGEA_	mrcB	-0.486376709	0.23245251	Penicillin-binding protein	NA	mrcB	Cell wall formation. Synthesis of
MNLKPGEA_	MNLKPGEA	-0.486591591	NA	hypothetical protein	NA	yxjG	methionine synthase
MNLKPGEA_	MNLKPGEA	-0.487695614	0.67298775	2-dehydropantoate 2-rec	1.1.1.169	0	Catalyzes the NADPH-dependent
MNLKPGEA_	fadI	-0.488487676	0.47266922	3-ketoacyl-CoA thiolase	2.3.1.16	fadI	Catalyzes the final step of fatty a
MNLKPGEA_	glaR	-0.489619357	0.39318437	HTH-type transcriptional	NA	csiR	Transcriptional

MNLKPGEA_	MNLKPGEA	-0.489774428	0.20804054	hypothetical protein	NA	0	TrfB plasmid transcriptional repr
MNLKPGEA_	MNLKPGEA	-0.491346592	NA	hypothetical protein	NA	ynjA	Antioxidant protein with alkyl hy
MNLKPGEA_	eutS	-0.493909834	NA	Ethanolamine utilization	NA	eutS	ethanolamine utilization protein
MNLKPGEA_	MNLKPGEA	-0.494445831	NA	hypothetical protein	NA	0	Family of unknown function (DU
MNLKPGEA_	MNLKPGEA	-0.495226546	0.44818779	hypothetical protein	NA	ppdB	prepilin peptidase dependent pr
MNLKPGEA_	eryD	-0.496370102	0.66393108	Erythritol catabolism reg	NA	smoC	transcriptional regulator
MNLKPGEA_	rluF	-0.496496433	0.33138136	Dual-specificity RNA pse	5.4.99.-	rluF	Belongs to the pseudouridine sy
MNLKPGEA_	MNLKPGEA	-0.496688524	0.63349188	hypothetical protein	NA	yfbS	COG0471 Di- and tricarboxylate
MNLKPGEA_	MNLKPGEA	-0.496825074	0.46962222	hypothetical protein	NA	0	Hydrolase
MNLKPGEA_	arnB	-0.498562451	0.70709197	UDP-4-amino-4-deoxy-L-	2.6.1.87	arnB	Belongs to the DegT DnrJ EryC1
MNLKPGEA_	sbmC	-0.499053504	0.30355302	DNA gyrase inhibitor	NA	sbmC	Inhibits the supercoiling activity
MNLKPGEA_	aroL	-0.499123476	0.646813	Shikimate kinase 2	2.7.1.71	aroL	Catalyzes the specific phosphory
MNLKPGEA_	gap_2	-0.499529656	0.39705713	Glyceraldehyde-3-phospl	1.2.1.12	gap	Belongs to the glyceraldehyde-3
MNLKPGEA_	nqrE	-0.500966064	NA	Na(+)-translocating NAD	7.2.1.1	nqrE	NQR complex catalyzes the redu
MNLKPGEA_	lapB	-0.502209332	0.51599454	Lipopolysaccharide asser	NA	lapB	Modulates cellular lipopolysacch
MNLKPGEA_	creB	-0.50284051	0.71011991	Transcriptional regulator	NA	creB	Response regulators consisting c
MNLKPGEA_	MNLKPGEA	-0.503742927	0.53805099	hypothetical protein	NA	ybbP	ABC-type transport system invol
MNLKPGEA_	yqhD	-0.504763974	0.49709515	Alcohol dehydrogenase \	1.1.1.-	yqhD	alcohol dehydrogenase
MNLKPGEA_	kdsD	-0.507420002	0.52983596	Arabinose 5-phosphate i	5.3.1.13	kdsD	Arabinose 5-phosphate isomera
MNLKPGEA_	nuoB	-0.509101398	0.21656529	NADH-quinone oxidoredu	7.1.1.-	nuoB	NDH-1 shuttles electrons from N
MNLKPGEA_	xseB	-0.509733817	0.32220531	Exodeoxyribonuclease 7	3.1.11.6	xseB	Bidirectionally degrades single-s
MNLKPGEA_	MNLKPGEA	-0.509734105	NA	hypothetical protein	NA	0	0
MNLKPGEA_	MNLKPGEA	-0.509968727	NA	hypothetical protein	NA	0	Protein of unknown function (DU
MNLKPGEA_	qseF	-0.510167171	0.42034146	Transcriptional regulator	NA	yfhA	COG2204 Response regulator co
MNLKPGEA_	mlaF	-0.510792136	0.55126817	Intermembrane phosphc	3.6.3.-	mlaF	(ABC) transporter
MNLKPGEA_	hisC_1	-0.51100405	0.72797769	Histidinol-phosphate am	2.6.1.9	hisC	Belongs to the class-II pyridoxal-
MNLKPGEA_	relA	-0.511025613	0.24981206	GTP pyrophosphokinase	2.7.6.5	relA	In eubacteria ppGpp (guanosine
MNLKPGEA_	ruvC	-0.511521319	0.73310772	Crossover junction endoc	3.1.22.4	ruvC	Nuclease that resolves Holliday j
MNLKPGEA_	rstA	-0.511909272	0.45937711	Transcriptional regulator	NA	rstA	Response regulators consisting c
MNLKPGEA_	aaaT	-0.512397295	0.47443455	L-amino acid N-acetyltra	2.3.1.-	yhhY	acetyltransferase

MNLKPGEA_	ycdY	-0.513080043	0.43914872	Chaperone protein YcdY	NA	ycdY	chaperone
MNLKPGEA_	pgrR_8	-0.513497728	0.50449411	HTH-type transcriptional	NA	0	transcriptional regulator
MNLKPGEA_	rseA	-0.514090205	0.12941273	Anti-sigma-E factor Rse/	NA	rseA	An anti-sigma factor for extracy
MNLKPGEA_	MNLKPGEA	-0.51455251	NA	hypothetical protein	NA	#N/A	#N/A
MNLKPGEA_	ynjC	-0.51455251	NA	Inner membrane ABC tra	NA	ynjC	transport system permease com
MNLKPGEA_	ykfA	-0.516402227	NA	putative murein peptide	3.4.16.-	0	proteins, homologs of microcin (
MNLKPGEA_	MNLKPGEA	-0.516762051	0.53832633	hypothetical protein	NA	#N/A	#N/A
MNLKPGEA_	dtnK	-0.516863613	NA	D-threonate kinase	2.7.1.219	ygbK	type III effector
MNLKPGEA_	licC_5	-0.517759875	0.57645033	Lichenan permease IIC c	NA	bglF	The phosphoenolpyruvate-deper
MNLKPGEA_	glrK	-0.518336753	0.3824258	Sensor histidine kinase (	2.7.13.3	yfhK	PhoQ Sensor
MNLKPGEA_	flk	-0.518441369	0.60845498	Flagellar regulator flk	NA	flk	Acts as a regulator of flagellar g
MNLKPGEA_	rbn_1	-0.52001626	0.51786586	Ribonuclease BN	3.1.-.-	rnz	Zinc phosphodiesterase, which c
MNLKPGEA_	tabA	-0.520655782	NA	Toxin-antitoxin biofilm p	NA	tabA	Toxin-antitoxin biofilm protein T
MNLKPGEA_	yhhW	-0.521531301	0.58602483	Quercetin 2,3-dioxygena	1.13.11.24	yhhW	Belongs to the pirin family
MNLKPGEA_	MNLKPGEA	-0.521615008	0.64689754	hypothetical protein	NA	yncJ	Protein of unknown function (DU
MNLKPGEA_	cbiQ	-0.522632062	NA	Cobalt transport protein	NA	cbiQ	cobalt transport protein
MNLKPGEA_	folC	-0.522831359	0.61339925	Dihydrofolate synthase/f	6.3.2.12	folC	Functions in two distinct reactio
MNLKPGEA_	alkB	-0.523606689	NA	Alpha-ketoglutarate-dep	1.14.11.33	alkB	Alkylated DNA repair protein
MNLKPGEA_	MNLKPGEA	-0.52491474	NA	hypothetical protein	NA	0	Flavin Reductase
MNLKPGEA_	yiaX1	-0.52491474	NA	putative protein YiaX1	NA	0	Domain of unknown function (DU
MNLKPGEA_	MNLKPGEA	-0.525446728	NA	IS3 family transposase IS	NA	0	Transposase
MNLKPGEA_	yqcC	-0.526190656	NA	putative protein YqcC	NA	yqcC	protein conserved in bacteria
MNLKPGEA_	pldh-t	-0.526292239	0.69156088	Pyridoxal 4-dehydrogena	1.1.1.107	pldh-t	KR domain
MNLKPGEA_	MNLKPGEA	-0.527054301	NA	IS3 family transposase IS	NA	0	Transposase and inactivated der
MNLKPGEA_	rlmG	-0.527640227	0.57297537	Ribosomal RNA large su	2.1.1.174	rlmG	Specifically methylates the guar
MNLKPGEA_	fabR	-0.528304021	0.29348995	HTH-type transcriptional	NA	fabR	Represses the transcription of fa
MNLKPGEA_	pgtC	-0.528606516	0.5217977	Phosphoglycerate transp	NA	pgtC	ABC-type Fe3 transport system,
MNLKPGEA_	MNLKPGEA	-0.530492145	0.71443185	hypothetical protein	NA	0	0
MNLKPGEA_	namA_1	-0.531928108	0.45555157	NADPH dehydrogenase	1.6.99.1	namA	COG1902 NADH flavin oxidoredu
MNLKPGEA_	maeB	-0.532460752	0.18534662	NADP-dependent malic e	1.1.1.40	maeB	Malic enzyme

MNLKPGEA_ yedK_3	-0.532469845	0.28895959	SOS response-associate	3.4.-.-	0	peptidase activity
MNLKPGEA_ fucK	-0.533017138	NA	L-fuculokinase	2.7.1.51	fucK	Belongs to the FGGY kinase fam
MNLKPGEA_ MNLKPGEA	-0.536199427	0.11129398	hypothetical protein	NA	0	0
MNLKPGEA_ csbX_1	-0.537009831	0.63832874	Alpha-ketoglutarate per	NA	csbX	Major facilitator superfamily
MNLKPGEA_ pgl_1	-0.537768091	0.13853164	6-phosphogluconolacton	3.1.1.31	pgl	Catalyzes the hydrolysis of 6-phc
MNLKPGEA_ kduD_2	-0.538704854	0.69286427	2-dehydro-3-deoxy-D-glu	1.1.1.127	kduD	COG1028 Dehydrogenases with
MNLKPGEA_ acsAB	-0.538881129	0.68054746	Cellulose synthase 1	NA	bcsA	Cellulose synthase
MNLKPGEA_ can_1	-0.539174905	0.39816003	Carbonic anhydrase 2	4.2.1.1	can	Reversible hydration of carbon d
MNLKPGEA_ fruB_2	-0.542114688	0.29272892	Multiphosphoryl transfer	NA	fruB_2	phosphotransferase system, IIa
MNLKPGEA_ pqiA	-0.542207677	0.34221152	Intermembrane transpor	NA	pqiA	paraquat-inducible protein A
MNLKPGEA_ catA	-0.542884338	0.68848745	Catechol 1,2-dioxygenas	1.13.11.1	catA	catechol 1,2-dioxygenase
MNLKPGEA_ ytfP	-0.54299912	0.08502679	Gamma-glutamylcyclotr	NA	ytfP	AIG2 family
MNLKPGEA_ pcaF	-0.543867882	0.63400697	Beta-ketoadipyl-CoA thic	2.3.1.174	pcaF	Catalyzes the final step of fatty a
MNLKPGEA_ glpR_5	-0.544682831	NA	Glycerol-3-phosphate re	NA	ygbI	DeoR C terminal sensor domain
MNLKPGEA_ smrA	-0.545358231	0.45937711	putative DNA endonucle	3.1.-.-	ydaL	protein conserved in bacteria
MNLKPGEA_ ydcF	-0.545399072	0.63392429	Protein YdcF	NA	ydcF	DUF218 domain
MNLKPGEA_ tpx	-0.545764196	0.12903044	Thiol peroxidase	1.11.1.15	tpx	Thiol-specific peroxidase that ca
MNLKPGEA_ fhuA_1	-0.546124584	0.36544986	Ferrichrome outer mem	NA	foxA	Receptor
MNLKPGEA_ msiK_1	-0.547340042	NA	Diacetylchitobiose uptak	7.5.2.-	ugpC_2	Belongs to the ABC transporter s
MNLKPGEA_ hisA	-0.548189195	0.68761805	1-(5-phosphoribosyl)-5-[	5.3.1.16	hisA	1-(5-phosphoribosyl)-5- (5-phosp
MNLKPGEA_ hisP	-0.548348042	0.45659186	Histidine transport ATP-b	NA	hisP	abc transporter atp-binding prot
MNLKPGEA_ ybiV	-0.54847669	0.25530329	Sugar phosphatase YbiV	3.1.3.23	supH	Hydrolase
MNLKPGEA_ nepI_1	-0.549192119	NA	Purine ribonucleoside ef	NA	nepI	Major facilitator Superfamily
MNLKPGEA_ nusA	-0.549244676	0.12423929	Transcription terminatio	NA	nusA	Participates in both transcriptior
MNLKPGEA_ ycfS	-0.549486943	0.37450058	putative L,D-transpeptid	2.-.-.-	ycfS	ErfK YbiS YcfS YnhG family prote
MNLKPGEA_ MNLKPGEA	-0.549688885	NA	hypothetical protein	NA	0	Binding-protein-dependent trans
MNLKPGEA_ MNLKPGEA	-0.549979072	NA	IS6 family transposase IS	NA	0	Transposase IS66 family
MNLKPGEA_ MNLKPGEA	-0.550108481	0.67827125	hypothetical protein	NA	yadS	membrane
MNLKPGEA_ hslO	-0.551703349	0.32889779	33 kDa chaperonin	NA	hslO	Redox regulated molecular chap
MNLKPGEA_ pnp	-0.552920295	0.04543969	Polyribonucleotide nucle	2.7.7.8	pnp	Involved in mRNA degradation. C

MNLKPGEA_	dnaK_1	-0.553727734	NA	Chaperone protein DnaK	NA	yegD	Belongs to the heat shock protei
MNLKPGEA_	argT	-0.553833013	0.27465309	Lysine/arginine/ornithin	NA	argT	belongs to the bacterial solute-b
MNLKPGEA_	lpxP	-0.55541509	0.25356654	Lipid A biosynthesis paln	2.3.1.242	lpxL	Catalyzes the transfer of laurate
MNLKPGEA_	menC	-0.555487181	NA	o-succinylbenzoate synth	4.2.1.113	menC	Converts 2-succinyl-6-hydroxy-2,
MNLKPGEA_	ybhF_2	-0.556315696	0.67154489	putative multidrug ABC t	NA	ybhF	(ABC) transporter
MNLKPGEA_	MNLKPGEA	-0.558409138	NA	hypothetical protein	NA	0	0
MNLKPGEA_	MNLKPGEA	-0.558464692	0.38445118	hypothetical protein	NA	yhdP	Membrane
MNLKPGEA_	nagZ	-0.560250764	0.15516903	Beta-hexosaminidase	3.2.1.52	nagZ	Plays a role in peptidoglycan rec
MNLKPGEA_	mglA_3	-0.560335411	0.67154489	Galactose/methyl galact	7.5.2.11	mglA_1	import. Responsible for energy c
MNLKPGEA_	ompN_1	-0.560612488	0.38376686	Outer membrane porin N	NA	ompS1	Belongs to the Gram-negative p
MNLKPGEA_	yecM	-0.562470672	0.59252861	Protein YecM	NA	yecM	protein conserved in bacteria
MNLKPGEA_	MNLKPGEA	-0.564481429	NA	hypothetical protein	NA	0	DNA-binding transcription factor
MNLKPGEA_	selB	-0.564538187	0.66924036	Selenocysteine-specific e	NA	selB	Translation elongation factor
MNLKPGEA_	puuB_1	-0.56722892	0.70049435	Gamma-glutamylputres	1.4.3.-	puuB	oxidoreductase
MNLKPGEA_	leuA_2	-0.567367403	0.53752148	2-isopropylmalate synth	2.3.3.13	leuA	Catalyzes the condensation of th
MNLKPGEA_	tenA_2	-0.567396345	0.61862389	Aminopyrimidine aminol	3.5.99.2	0	Catalyzes an amino-pyrimidine h
MNLKPGEA_	eutK	-0.56769765	NA	Ethanolamine utilization	NA	eutK	ethanolamine utilization protein
MNLKPGEA_	MNLKPGEA	-0.56862736	0.6658464	hypothetical protein	NA	hetM	Male sterility protein
MNLKPGEA_	cvpA	-0.569462789	0.50671429	Colicin V production prot	NA	cvpA	Colicin v production
MNLKPGEA_	fcuA	-0.569780308	0.58998059	Ferrichrome receptor Fcu	NA	fcuA	receptor
MNLKPGEA_	MNLKPGEA	-0.570207413	NA	hypothetical protein	NA	0	type VI secretion protein
MNLKPGEA_	MNLKPGEA	-0.57095994	NA	hypothetical protein	NA	0	Type VI secretion
MNLKPGEA_	MNLKPGEA	-0.571050078	0.19896159	hypothetical protein	NA	#N/A	#N/A
MNLKPGEA_	MNLKPGEA	-0.571402175	NA	IS3 family transposase IS	NA	0	Integrase core domain
MNLKPGEA_	aroD	-0.571995167	0.39275465	3-dehydroquinate dehydr	4.2.1.10	aroD	Involved in the third step of the c
MNLKPGEA_	citF	-0.572121208	0.67051502	Citrate lyase alpha chain	4.1.3.6	citF	Citrate lyase alpha subunit
MNLKPGEA_	rfaG	-0.572800222	0.5792742	Lipopolysaccharide core	2.4.-.-	rfaG	Catalyzes the addition of the firs
MNLKPGEA_	dmlR_15	-0.573516483	0.58161507	HTH-type transcriptional	NA	0	transcriptional regulator
MNLKPGEA_	ubiH	-0.577713225	0.5350342	2-octaprenyl-6-methoxyp	1.14.13.-	ubiH	hydroxylase
MNLKPGEA_	artM_2	-0.577772409	0.03603361	Arginine ABC transporter	NA	artM	(ABC) transporter

MNLKPGEA_ yedS	-0.577914828	0.15108173	Outer membrane protei	NA	ompF	Belongs to the Gram-negative p
MNLKPGEA_ glnA	-0.578582227	0.34500222	Glutamine synthetase	6.3.1.2	glnA	glutamine synthetase
MNLKPGEA_ MNLKPGEA	-0.580013232	0.71535303	hypothetical protein	NA	0	0
MNLKPGEA_ hflK	-0.582371857	0.29393812	Modulator of FtsH prote	NA	hflK	HflC and HflK could encode or re
MNLKPGEA_ MNLKPGEA	-0.58332949	0.61862389	hypothetical protein	NA	0	Type VI secretion, EvfE, EvfF, Im
MNLKPGEA_ yesR	-0.584776145	NA	Unsaturated rhamnogal	3.2.1.172	rhiN	Glycosyl Hydrolase Family 88
MNLKPGEA_ MNLKPGEA	-0.58554194	NA	hypothetical protein	NA	#N/A	#N/A
MNLKPGEA_ mgtC	-0.585741311	NA	Protein MgtC	NA	mgtC	MgtC SapB transporter
MNLKPGEA_ kdsC	-0.586427884	0.24260693	3-deoxy-D-manno-octulc	3.1.3.45	kdsC	Involved in the biosynthesis of li
MNLKPGEA_ thiI	-0.587251449	0.25398687	tRNA sulfurtransferase	2.8.1.4	thiI	Catalyzes the ATP-dependent tra
MNLKPGEA_ rhmR	-0.587605505	NA	putative HTH-type transc	NA	rhmR	Transcriptional regulator
MNLKPGEA_ dapF	-0.59175629	0.24036624	Diaminopimelate epime	5.1.1.7	dapF	Catalyzes the stereoinversion of
MNLKPGEA_ kbl	-0.594417708	0.30418788	2-amino-3-ketobutyrate	2.3.1.29	kbl	Catalyzes the decarboxylative co
MNLKPGEA_ MNLKPGEA	-0.595062382	0.27970156	hypothetical protein	NA	ydiZ	endoribonuclease activity
MNLKPGEA_ MNLKPGEA	-0.595846702	0.52238936	hypothetical protein	NA	lpxO	Aspartyl Asparaginyl beta-hydro
MNLKPGEA_ rhtC_3	-0.595855143	NA	Threonine efflux protein	NA	rhtC	threonine efflux protein
MNLKPGEA_ yjiE	-0.595985756	0.14665213	HTH-type transcriptional	NA	yjiE	transcriptional regulator
MNLKPGEA_ cysE	-0.596489317	0.25739233	Serine acetyltransferase	2.3.1.30	cysE	serine acetyltransferase
MNLKPGEA_ feaB_1	-0.596514386	0.37704134	Phenylacetaldehyde deh	1.2.1.39	feaB	belongs to the aldehyde dehydrc
MNLKPGEA_ uvrC	-0.597596029	0.09043554	UvrABC system protein C	NA	uvrC	The UvrABC repair system catal
MNLKPGEA_ cyoE	-0.597896374	0.18273785	Protoheme IX farnesyltra	2.5.1.141	cyoE	Converts heme B (protoheme IX)
MNLKPGEA_ MNLKPGEA	-0.59905839	NA	hypothetical protein	NA	#N/A	#N/A
MNLKPGEA_ cynT	-0.600410308	0.3029838	Carbonic anhydrase 1	4.2.1.1	cynT	Reversible hydration of carbon d
MNLKPGEA_ yhbO	-0.601653097	0.38675135	Protein/nucleic acid deg	3.1.2.-	yhbO	intracellular protease
MNLKPGEA_ yheS_2	-0.602814911	0.50039822	putative ABC transporter	NA	yheS	ABC transporter
MNLKPGEA_ acuR	-0.603279759	0.56553909	Transcriptional regulator	NA	nemR	transcriptional regulator
MNLKPGEA_ cscB	-0.603599471	NA	Sucrose permease	NA	lacY_2	Major facilitator superfamily
MNLKPGEA_ yhfA	-0.604786501	0.43546434	Protein YhfA	NA	yhfA	Redox protein regulator of disulf
MNLKPGEA_ MNLKPGEA	-0.605000615	0.51866758	hypothetical protein	NA	0	Part of the outer membrane pro
MNLKPGEA_ MNLKPGEA	-0.605034172	0.1148752	hypothetical protein	NA	yajG	Lipoprotein

MNLKPGEA_	pykA	-0.605305515	0.16885502	Pyruvate kinase II	2.7.1.40	pykA	Belongs to the pyruvate kinase f
MNLKPGEA_	speC	-0.606924909	0.58602483	Constitutive ornithine de	4.1.1.17	speC	decarboxylase
MNLKPGEA_	MNLKPGEA	-0.607553107	0.15538795	hypothetical protein	NA	yoaE	membrane protein, terc
MNLKPGEA_	ddpB	-0.607624768	NA	putative D,D-dipeptide tı	NA	dppB_1	Binding-protein-dependent trans
MNLKPGEA_	basR	-0.608870035	0.64943631	Transcriptional regulator	NA	basR	Response regulators consisting c
MNLKPGEA_	tdk	-0.61068477	0.27774351	Thymidine kinase	2.7.1.21	tdk	thymidine kinase
MNLKPGEA_	pepP	-0.611183148	0.16231334	Xaa-Pro aminopeptidase	3.4.11.9	pepP	aminopeptidase
MNLKPGEA_	MNLKPGEA	-0.611905675	NA	hypothetical protein	NA	yncC	transcriptional regulator
MNLKPGEA_	MNLKPGEA	-0.613330167	0.53575164	hypothetical protein	NA	0	0
MNLKPGEA_	MNLKPGEA	-0.614589188	NA	hypothetical protein	NA	0	0
MNLKPGEA_	cysM	-0.615044668	0.58908758	Cysteine synthase B	2.5.1.47	cysM	Belongs to the cysteine synthase
MNLKPGEA_	rafR	-0.615248743	0.57971516	HTH-type transcriptional	NA	rafR	PFAM Periplasmic binding prote
MNLKPGEA_	MNLKPGEA	-0.615334622	0.18130387	hypothetical protein	NA	0	Nacht domain
MNLKPGEA_	MNLKPGEA	-0.615589701	NA	IS3 family transposase IS	NA	0	Integrase core domain
MNLKPGEA_	MNLKPGEA	-0.615857787	0.64577905	hypothetical protein	NA	0	cellulase activity
MNLKPGEA_	ubiJ_2	-0.616044777	0.40623766	Ubiquinone biosynthesis	NA	yigP	protein conserved in bacteria
MNLKPGEA_	MNLKPGEA	-0.617395577	0.6333067	hypothetical protein	NA	yhiI	Secretion protein
MNLKPGEA_	pptA	-0.617457716	0.49842654	Tautomerase PptA	5.3.2.-	pptA	Belongs to the 4-oxalocrotonate
MNLKPGEA_	puuP	-0.618322411	0.34224963	Putrescine importer Puul	NA	puuP	Amino Acid
MNLKPGEA_	MNLKPGEA	-0.618719961	NA	hypothetical protein	NA	#N/A	#N/A
MNLKPGEA_	baeR	-0.620670402	0.37569641	Transcriptional regulator	NA	baeR	response regulator
MNLKPGEA_	mliC	-0.62072196	NA	Membrane-bound lysozy	NA	mliC	membrane-bound lysozyme inhi
MNLKPGEA_	pbpC	-0.621315021	0.63877491	Penicillin-binding proteir	NA	pbpC	penicillin-binding protein 1C
MNLKPGEA_	rlmJ	-0.62168171	0.37494632	Ribosomal RNA large su	2.1.1.266	rlmJ	Specifically methylates the ader
MNLKPGEA_	MNLKPGEA	-0.62199124	0.70007931	hypothetical protein	NA	0	0
MNLKPGEA_	tsx	-0.622283026	0.20445969	Nucleoside-specific char	NA	tsx	nucleoside-specific channel-forn
MNLKPGEA_	mdtN	-0.622349302	NA	Multidrug resistance pro	NA	0	multidrug resistance
MNLKPGEA_	MNLKPGEA	-0.623909423	NA	hypothetical protein	NA	0	Acetyltransferase GNAT Family
MNLKPGEA_	ybdL	-0.624904975	NA	Methionine aminotransf	2.6.1.88	ybdL	aminotransferase
MNLKPGEA_	chrR	-0.625350475	0.42306103	Quinone reductase	1.6.5.2	yieF	NAD(P)H-dependent FMN reduct

MNLKPGEA_ yfgG	-0.626052148	0.16397629	Protein YfgG	NA	yfgG	Protein of unknown function (DU
MNLKPGEA_ ftsP	-0.626279097	0.51748126	Cell division protein FtsP	NA	ftsP	Cell division protein that is requi
MNLKPGEA_ ygfZ	-0.626504339	0.45353975	tRNA-modifying protein	NA	ygfZ	Folate-binding protein involved i
MNLKPGEA_ MNLKPGEA	-0.627484283	NA	hypothetical protein	NA	0	0
MNLKPGEA_ rhmD	-0.627737478	0.53905972	L-rhamnonate dehydrata	4.2.1.90	rhmD	Catalyzes the dehydration of L-rl
MNLKPGEA_ nupC_2	-0.627761769	0.49842654	Nucleoside permease Nu	NA	nupC	Belongs to the concentrative nuc
MNLKPGEA_ MNLKPGEA	-0.628636567	0.25398687	hypothetical protein	NA	0	nuclear chromosome segregatio
MNLKPGEA_ rbsA_5	-0.629031678	0.25498175	Ribose import ATP-bindi	7.5.2.7	rbsA	import. Responsible for energy c
MNLKPGEA_ MNLKPGEA	-0.629628472	NA	hypothetical protein	NA	0	0
MNLKPGEA_ pfp	-0.629639754	0.57541498	Pyrophosphate--fructose	2.7.1.90	0	Catalyzes the phosphorylation of
MNLKPGEA_ lgoR	-0.629827352	0.38557126	putative HTH-type transc	NA	yjjM	Transcriptional regulator
MNLKPGEA_ rapA_2	-0.630018352	0.24555956	RNA polymerase-associa	3.6.4.-	0	DNA RNA helicase, superfamily
MNLKPGEA_ yhbU	-0.630501841	NA	putative protease YhbU	3.4.-.-	yhbU	Peptidase U32
MNLKPGEA_ MNLKPGEA	-0.630934233	0.04157434	hypothetical protein	NA	osmY_1	Periplasmic or secreted lipoprot
MNLKPGEA_ ndh	-0.631210052	0.38646682	NADH dehydrogenase	1.6.99.3	ndh	NADH dehydrogenase
MNLKPGEA_ MNLKPGEA	-0.632612668	NA	hypothetical protein	NA	0	0
MNLKPGEA_ MNLKPGEA	-0.634750112	0.41009022	hypothetical protein	NA	yigI	protein possibly involved in arom
MNLKPGEA_ leuE	-0.635072676	0.4650368	Leucine efflux protein	NA	leuE	Efflux Protein
MNLKPGEA_ caiT	-0.636133486	0.37181399	L-carnitine/gamma-buty	NA	yeaV	Belongs to the BCCT transporter
MNLKPGEA_ pdxA2_1	-0.637524941	NA	D-threonate 4-phosphate	1.1.1.408	pdxA2	Catalyzes the NAD(P)-dependent
MNLKPGEA_ MNLKPGEA	-0.637663428	NA	hypothetical protein	NA	0	0
MNLKPGEA_ oppF_2	-0.640955005	0.52940997	Oligopeptide transport A	NA	0	(ABC) transporter
MNLKPGEA_ MNLKPGEA	-0.642007175	0.59747454	hypothetical protein	NA	0	flavin-nucleotide-binding protein
MNLKPGEA_ ycfH	-0.642023657	0.04047699	putative metal-depende	3.1.-.-	ycfH	TatD family
MNLKPGEA_ yebC	-0.642157537	0.33474413	putative transcriptional r	NA	yebC	transcriptional regulatory protei
MNLKPGEA_ ppa_1	-0.642376602	NA	Inorganic pyrophosphata	3.6.1.1	0	Catalyzes the hydrolysis of inorg
MNLKPGEA_ MNLKPGEA	-0.644562986	0.21925521	hypothetical protein	NA	#N/A	#N/A
MNLKPGEA_ uppP	-0.644865103	0.5182666	Undecaprenyl-diphospha	3.6.1.27	uppP	Catalyzes the dephosphorylation
MNLKPGEA_ cysG_1	-0.644939101	0.42306103	Siroheme synthase	NA	cysG	Multifunctional enzyme that cat
MNLKPGEA_ ribE	-0.645291015	0.23139842	6,7-dimethyl-8-ribityllum	2.5.1.78	ribH	Catalyzes the formation of 6,7-d

MNLKPGEA_ fabH	-0.6454698	0.3029838	3-oxoacyl-[acyl-carrier-p	2.3.1.180	fabH	Catalyzes the condensation reac
MNLKPGEA_ endA	-0.645536814	NA	Endonuclease-1	3.1.21.1	endA	endonuclease I
MNLKPGEA_ rsd	-0.646079798	0.06131121	Regulator of sigma D	NA	rsd	Binds RpoD and negatively regul
MNLKPGEA_ nadK	-0.646705768	0.1604727	NAD kinase	2.7.1.23	nadK	Involved in the regulation of the
MNLKPGEA_ putA	-0.647204503	0.42393944	Bifunctional protein PutA	NA	putA	Oxidizes proline to glutamate fo
MNLKPGEA_ deoA	-0.647774259	0.23025218	Thymidine phosphorylas	2.4.2.4	deoA	The enzymes which catalyze the
MNLKPGEA_ MNLKPGEA	-0.647922523	NA	hypothetical protein	NA	yciZ	Belongs to the UPF0509 family
MNLKPGEA_ MNLKPGEA	-0.648149937	0.57840246	hypothetical protein	NA	yfaZ	YfaZ precursor
MNLKPGEA_ eryH	-0.648307493	NA	L-erythrulose-1-phospha	5.3.1.33	tpiA2	triose-phosphate isomerase
MNLKPGEA_ rppH_2	-0.649175107	0.10677728	RNA pyrophosphohydrol	3.6.1.-	nudH	Accelerates the degradation of t
MNLKPGEA_ ychN	-0.650142395	0.28232673	Protein YchN	NA	ychN	conserved protein involved in int
MNLKPGEA_ folB	-0.65019685	NA	Dihydroneopterin aldolas	4.1.2.25	folB	Catalyzes the conversion of 7,8-d
MNLKPGEA_ kdsA	-0.650210239	0.08824074	2-dehydro-3-deoxyphosp	2.5.1.55	kdsA	Belongs to the KdsA family
MNLKPGEA_ MNLKPGEA	-0.650587052	NA	hypothetical protein	NA	0	Gamma-glutamyl cyclotransfera
MNLKPGEA_ MNLKPGEA	-0.651228709	0.61036897	hypothetical protein	NA	#N/A	#N/A
MNLKPGEA_ manC1	-0.651287653	0.22455143	Mannose-1-phosphate g	2.7.7.13	cpsB	Belongs to the mannose-6-phosp
MNLKPGEA_ purA	-0.65173978	0.15988976	Adenylosuccinate synthe	6.3.4.4	purA	Plays an important role in the de
MNLKPGEA_ ygiW_1	-0.652461604	0.51231936	Protein YgiW	NA	ygiW	Bacterial OB fold (BOF) protein
MNLKPGEA_ virB5	-0.65308067	0.27292797	Type IV secretion system	NA	0	Type IV secretion system protein
MNLKPGEA_ gcvR	-0.653431251	0.10358632	Glycine cleavage system	NA	gcvR	glycine cleavage system
MNLKPGEA_ wecB	-0.653584211	0.35134134	UDP-N-acetylglucosamin	5.1.3.14	wecB	Catalyzes the reversible epimeri
MNLKPGEA_ dinI_2	-0.653670215	0.29684083	DNA damage-inducible p	NA	dinI	SOS response
MNLKPGEA_ hypF	-0.654698355	NA	Carbamoyltransferase Hy	6.2.-.-	hypF	Along with HypE, it catalyzes the
MNLKPGEA_ plsB	-0.654742883	0.10186838	Glycerol-3-phosphate ac	2.3.1.15	plsB	Belongs to the GPAT DAPAT fam
MNLKPGEA_ tadA	-0.6549022	NA	tRNA-specific adenosine	3.5.4.33	tadA	Catalyzes the deamination of ad
MNLKPGEA_ cdaR_1	-0.65499411	0.50429531	Carbohydrate diacid regu	NA	0	Putative sugar diacid recognition
MNLKPGEA_ MNLKPGEA	-0.656454855	NA	hypothetical protein	NA	yaeF	cysteine-type peptidase activity
MNLKPGEA_ MNLKPGEA	-0.658199154	0.60725948	hypothetical protein	NA	0	Membrane
MNLKPGEA_ nagAb	-0.662341877	0.51645397	Naphthalene 1,2-dioxyge	NA	ndoA	Rieske [2Fe-2S] domain
MNLKPGEA_ MNLKPGEA	-0.662414359	NA	hypothetical protein	NA	0	Diguanylate cyclase

MNLKPGEA_ yiaJ	-0.663561376	0.60481527	DNA-binding transcriptic	NA	yiaJ	transcriptional regulator
MNLKPGEA_ MNLKPGEA	-0.663928021	0.54625339	hypothetical protein	NA	ybaP	protein conserved in bacteria
MNLKPGEA_ MNLKPGEA	-0.664491849	0.10056822	hypothetical protein	NA	0	DNA methylAse
MNLKPGEA_ cydX	-0.665007008	0.43055413	Cytochrome bd-I ubiquin	7.1.1.7	ybgT	Cyd operon protein YbgT
MNLKPGEA_ xanP_1	-0.665479355	NA	Xanthine permease XanP	NA	xanP	xanthine
MNLKPGEA_ pflB	-0.665659493	0.00943105	Formate acetyltransfera	2.3.1.54	pflB	formate C-acetyltransferase glyc
MNLKPGEA_ fabA	-0.668950448	0.09528753	3-hydroxydecanoyl-[acyl-	4.2.1.59	fabA	Necessary for the introduction o
MNLKPGEA_ lpxH	-0.669550044	NA	UDP-2,3-diacylglucosam	3.6.1.54	lpxH	Hydrolyzes the pyrophosphate bo
MNLKPGEA_ ytjB	-0.670236065	0.45706472	putative inner membran	NA	smp	membrane protein affecting her
MNLKPGEA_ aroP_1	-0.671860349	NA	Aromatic amino acid tra	NA	aroP	amino acid
MNLKPGEA_ lacG_1	-0.672184892	NA	Lactose transport systen	NA	ugpE	probably responsible for the trar
MNLKPGEA_ lepA	-0.673070765	0.22151059	Elongation factor 4	3.6.5.-	lepA	Required for accurate and efficie
MNLKPGEA_ bamB	-0.673545118	0.10868914	Outer membrane protein	NA	bamB	Part of the outer membrane pro
MNLKPGEA_ MNLKPGEA	-0.673676172	NA	hypothetical protein	NA	0	0
MNLKPGEA_ plsX	-0.673883626	0.05884007	Phosphate acyltransfera	2.3.1.274	plsX	Catalyzes the reversible formati
MNLKPGEA_ scrB	-0.675073388	0.59282661	Sucrose-6-phosphate hyc	3.2.1.26	scrB	invertase
MNLKPGEA_ MNLKPGEA	-0.675202855	NA	hypothetical protein	NA	yfiP	DTW domain containing protein
MNLKPGEA_ pyrC	-0.676680157	NA	Dihydroorotase	3.5.2.3	pyrC	Catalyzes the reversible cyclizati
MNLKPGEA_ pcaK_3	-0.676717698	NA	4-hydroxybenzoate trans	NA	0	Major facilitator Superfamily
MNLKPGEA_ rpoN	-0.676720494	0.01444891	RNA polymerase sigma-	NA	rpoN	Sigma factors are initiation fact
MNLKPGEA_ acrF	-0.676942068	0.24529738	Multidrug export protein	NA	acrF	Belongs to the resistance-nodula
MNLKPGEA_ gltD	-0.677220483	0.38890617	Glutamate synthase [NA	1.4.1.13	gltD	Glutamate synthase
MNLKPGEA_ MNLKPGEA	-0.677345498	NA	hypothetical protein	NA	0	Pectate lyase superfamily protei
MNLKPGEA_ lptB_2	-0.677603942	0.13191339	Lipopolysaccharide expo	3.6.3.-	lptB	abc transporter atp-binding prot
MNLKPGEA_ MNLKPGEA	-0.678043811	0.44383467	hypothetical protein	NA	0	Domain of unknown function (DU
MNLKPGEA_ mdoC	-0.679381245	0.1830403	Glucans biosynthesis prc	2.1.-.-	mdoC	Necessary for the succinyl substi
MNLKPGEA_ mltC	-0.682584328	0.44982631	Membrane-bound lytic n	4.2.2.-	mltC	Murein-degrading enzyme. May
MNLKPGEA_ yidG	-0.683774288	NA	Inner membrane protein	NA	yidG	Membrane
MNLKPGEA_ rpe	-0.683853019	0.4451029	Ribulose-phosphate 3-ep	5.1.3.1	rpe	Belongs to the ribulose-phospha
MNLKPGEA_ MNLKPGEA	-0.684228261	0.41920715	hypothetical protein	NA	BP3797	of the drug metabolite transport

MNLKPGEA_ rbsA_6	-0.685717129	0.3906211	Ribose import ATP-bindi	7.5.2.7	0	import. Responsible for energy c
MNLKPGEA_ elaA	-0.686514463	0.40385959	Protein ElaA	NA	elaA	Acyltransferase
MNLKPGEA_ MNLKPGEA	-0.686673526	0.52955853	hypothetical protein	NA	yehS	protein conserved in bacteria
MNLKPGEA_ rbsA_1	-0.686771829	0.56033052	Ribose import ATP-bindi	7.5.2.7	rbsA_4	import. Responsible for energy c
MNLKPGEA_ cobT_2	-0.688751522	NA	Nicotinate-nucleotide--d	2.4.2.21	cobT	Catalyzes the synthesis of alpha-
MNLKPGEA_ rocC	-0.689070633	NA	Amino-acid permease R	NA	mmuP	amino acid
MNLKPGEA_ ugpC_1	-0.690578671	NA	sn-glycerol-3-phosphate	7.6.2.10	ugpC	Belongs to the ABC transporter s
MNLKPGEA_ ribY	-0.690963475	NA	Riboflavin-binding protei	NA	0	COG0715 ABC-type nitrate sulfo
MNLKPGEA_ nadD	-0.692165229	NA	Nicotinate-nucleotide ac	2.7.7.18	nadD	Catalyzes the reversible adenyla
MNLKPGEA_ crp	-0.692238393	0.00283063	cAMP-activated global tr	NA	crp	COG0664 cAMP-binding proteins
MNLKPGEA_ ydcV_2	-0.692524745	0.43331934	Inner membrane ABC tra	NA	potC	ABC-type spermidine putrescine
MNLKPGEA_ yihD	-0.6926357	0.18498116	Protein YihD	NA	yihD	protein conserved in bacteria
MNLKPGEA_ uxaC	-0.693311647	0.33867897	Uronate isomerase	5.3.1.12	uxaC	glucuronate isomerase
MNLKPGEA_ galA	-0.693345104	NA	Gallate dioxygenase	1.13.11.57	ligB	Extradiol catechol dioxygenase t
MNLKPGEA_ dinI_1	-0.693587287	0.08768152	DNA damage-inducible p	NA	0	DinI-like family
MNLKPGEA_ MNLKPGEA	-0.694310514	0.35307997	hypothetical protein	NA	rfbP	COG2148 Sugar transferases inv
MNLKPGEA_ MNLKPGEA	-0.695478682	NA	IS256 family transposase	NA	0	transposase
MNLKPGEA_ kefF_1	-0.695994662	NA	Glutathione-regulated p	1.6.5.2	0	Flavodoxin-like fold
MNLKPGEA_ djlA	-0.69696011	0.58201649	Co-chaperone protein Djl	NA	djlA	Regulatory DnaK co-chaperone.
MNLKPGEA_ ccmF	-0.697242477	NA	Cytochrome c-type bioge	NA	ccmF	Cytochrome c-type biogenesis pr
MNLKPGEA_ codB	-0.697242477	NA	Cytosine permease	NA	codB	permease
MNLKPGEA_ ygfX	-0.697643022	0.31787929	Inner membrane protein	NA	ygfX	Membrane
MNLKPGEA_ ycaO	-0.697824472	0.43554412	Ribosomal protein S12 n	NA	ycaO	redox protein regulator of disulfi
MNLKPGEA_ tag	-0.699323901	0.30984725	DNA-3-methyladenine gl	3.2.2.20	tag	glycosylase
MNLKPGEA_ yqjE	-0.701776854	0.029935	Inner membrane protein	NA	yqjE	Membrane
MNLKPGEA_ holC	-0.701925661	0.46949719	DNA polymerase III subu	2.7.7.7	holC	DNA polymerase III chi subunit
MNLKPGEA_ feoC	-0.702909506	0.5168348	putative [Fe-S]-depende	NA	feoC	metal cluster binding
MNLKPGEA_ trmL_1	-0.703025593	NA	tRNA (cytidine(34)-2'-O)	2.1.1.207	trmL	Methylates the ribose at the nuc
MNLKPGEA_ znuA	-0.703961939	0.00768892	High-affinity zinc uptake	NA	znuA	ABC-type Zn2 transport system,
MNLKPGEA_ hflC	-0.704039498	0.06312947	Modulator of FtsH prote	NA	hflC	HflC and HflK could regulate a pr

MNLKPGEA_	yoaA	-0.704360023	0.35943877	putative ATP-dependent	3.6.4.12	yoaA	helicase
MNLKPGEA_	MNLKPGEA	-0.704794797	NA	ISNCY family transposas	NA	0	PFAM Integrase catalytic
MNLKPGEA_	rsxC_2	-0.705001512	0.5803695	Ion-translocating oxidore	7.-.-.-	rnfC	Part of a membrane complex inv
MNLKPGEA_	MNLKPGEA	-0.705156867	0.47149227	hypothetical protein	NA	0	terminase
MNLKPGEA_	MNLKPGEA	-0.705445588	NA	hypothetical protein	NA	0	Transcriptional regulator
MNLKPGEA_	eptA	-0.70573738	0.39158086	Phosphoethanolamine tr	2.7.-.-	eptA	membrane-associated metal-de
MNLKPGEA_	MNLKPGEA	-0.706254702	0.59103585	hypothetical protein	NA	N	Major capsid protein
MNLKPGEA_	pucI	-0.70685652	NA	putative allantoin perme	NA	pucI	uracil, thiamine, allantoin
MNLKPGEA_	MNLKPGEA	-0.70693314	NA	hypothetical protein	NA	puuE	deacetylase
MNLKPGEA_	nlpD_1	-0.707368639	0.57652599	Murein hydrolase activat	NA	nlpD	COG0739 Membrane proteins re
MNLKPGEA_	fbp	-0.708982132	0.01682596	Fructose-1,6-bisphospha	3.1.3.11	fbp	D-fructose-1,6-bisphosphate 1-p
MNLKPGEA_	MNLKPGEA	-0.710719937	NA	hypothetical protein	NA	0	type VI secretion system effecto
MNLKPGEA_	iscR	-0.710817576	0.12367207	HTH-type transcriptional	NA	iscR	Regulates the transcription of se
MNLKPGEA_	accD	-0.711182637	0.03551327	Acetyl-coenzyme A carbo	2.1.3.15	accD	Component of the acetyl coenzy
MNLKPGEA_	ispG	-0.712211959	0.09551865	4-hydroxy-3-methylbut-2	1.17.7.3	ispG	Converts 2C-methyl-D-erythritol
MNLKPGEA_	secM	-0.712278419	0.26274649	Secretion monitor	NA	secM	Regulates secA expression by tra
MNLKPGEA_	atpG	-0.712515499	0.22455143	ATP synthase gamma ch	NA	atpG	Produces ATP from ADP in the pr
MNLKPGEA_	ttuC'	-0.712717406	0.52038345	putative tartrate dehydro	1.1.1.93	ttuC	Tartrate dehydrogenase
MNLKPGEA_	nfsB	-0.71296299	0.2155121	Oxygen-insensitive NAD(	1.-.-.-	nfnB	Nitroreductase
MNLKPGEA_	citE	-0.714549154	NA	Citrate lyase subunit bet	4.1.3.6	mclA	Belongs to the HpcH HpaI aldola
MNLKPGEA_	murJ	-0.714885872	0.42944752	putative lipid II flippase	NA	murJ	Involved in peptidoglycan biosyn
MNLKPGEA_	sthA	-0.715184858	0.14665213	Soluble pyridine nucleoti	1.6.1.1	sthA	Conversion of NADPH, generated
MNLKPGEA_	gsiB	-0.716020755	0.31108572	Glutathione-binding prot	NA	gsiB	Extracellular solute-binding prot
MNLKPGEA_	MNLKPGEA	-0.716675934	0.00215608	hypothetical protein	NA	yaeH	Belongs to the UPF0325 family
MNLKPGEA_	nadE	-0.718086732	0.05273234	NH(3)-dependent NAD(+	6.3.1.5	nadE	Catalyzes the ATP-dependent an
MNLKPGEA_	MNLKPGEA	-0.718270954	NA	hypothetical protein	NA	ppdA	prepilin peptidase dependent pr
MNLKPGEA_	pssA	-0.718416779	0.01901546	CDP-diacylglycerol--serir	2.7.8.8	pssA	Catalyzes de novo synthesis of p
MNLKPGEA_	gpmA	-0.718488971	0.00193616	2,3-bisphosphoglycerate	5.4.2.11	gpmA	Belongs to the phosphoglycerate
MNLKPGEA_	MNLKPGEA	-0.718538252	NA	hypothetical protein	NA	#N/A	#N/A
MNLKPGEA_	folE	-0.718965687	0.03055713	GTP cyclohydrolase 1	3.5.4.16	folE	GTP cyclohydrolase

MNLKPGEA_	ygiN	-0.719401571	0.08144923	putative quinol monooxy	1.-.-.-	ygiN	monooxygenase
MNLKPGEA_	MNLKPGEA	-0.720168394	0.58007505	hypothetical protein	NA	mta_1	transcriptional regulator
MNLKPGEA_	pitA	-0.720782816	0.00996401	Low-affinity inorganic ph	NA	pitA	phosphate transporter
MNLKPGEA_	ibpA	-0.721366885	0.24867404	Small heat shock proteir	NA	ibpA	Associates with aggregated prot
MNLKPGEA_	iolE_1	-0.722130574	NA	Inosose dehydratase	4.2.1.44	iolE	Xylose isomerase domain protei
MNLKPGEA_	MNLKPGEA	-0.722851857	0.34815856	hypothetical protein	NA	yfbU	Belongs to the UPF0304 family
MNLKPGEA_	MNLKPGEA	-0.723036044	0.51038167	hypothetical protein	NA	#N/A	#N/A
MNLKPGEA_	gmhB	-0.723180186	0.34989565	D-glycero-beta-D-mannc	3.1.3.82	gmhB	D,D-heptose 1,7-bisphosphate ph
MNLKPGEA_	mdoH	-0.724227281	0.04807207	Glucans biosynthesis glu	2.4.1.-	mdoH	Involved in the biosynthesis of os
MNLKPGEA_	panB	-0.724946176	0.47318408	3-methyl-2-oxobutanoat	2.1.2.11	panB	Catalyzes the reversible reactior
MNLKPGEA_	ptsH	-0.725724641	0.03339656	Phosphocarrier protein H	NA	ptsH	Phosphocarrier protein Hpr
MNLKPGEA_	nrdD	-0.725834288	0.33872512	Anaerobic ribonucleoside	1.1.98.6	nrdD	Ribonucleoside-triphosphate rec
MNLKPGEA_	MNLKPGEA	-0.726347701	NA	hypothetical protein	NA	#N/A	#N/A
MNLKPGEA_	aroA	-0.727733849	0.43709995	3-phosphoshikimate 1-ca	2.5.1.19	aroA	Catalyzes the transfer of the enc
MNLKPGEA_	thpR	-0.728719532	NA	RNA 2',3'-cyclic phospho	3.1.4.58	ligT	Hydrolyzes RNA 2',3'-cyclic phos
MNLKPGEA_	phoR	-0.729207604	0.41145316	Phosphate regulon sensc	2.7.13.3	phoR	Histidine kinase
MNLKPGEA_	rutG	-0.729514007	NA	Putative pyrimidine pern	NA	rutG	Xanthine uracil
MNLKPGEA_	tcyP	-0.730114368	0.23738091	L-cystine uptake protein	NA	ydjN	Belongs to the dicarboxylate am
MNLKPGEA_	MNLKPGEA	-0.731357761	0.34500222	hypothetical protein	NA	0	TIR domain
MNLKPGEA_	MNLKPGEA	-0.731510973	0.12239864	hypothetical protein	NA	yciY	0
MNLKPGEA_	uvrB	-0.731911669	0.05038845	UvrABC system protein B	NA	uvrB	damaged site, the DNA wraps ar
MNLKPGEA_	damX	-0.732015848	0.21575157	Cell division protein Dam	NA	damX	Cell division protein DamX
MNLKPGEA_	MNLKPGEA	-0.73229982	0.40385959	hypothetical protein	NA	0	Protein of unknown function (DU
MNLKPGEA_	MNLKPGEA	-0.732421153	NA	hypothetical protein	NA	0	BNR repeat-like domain
MNLKPGEA_	dmlR_14	-0.732522957	0.23651627	HTH-type transcriptional	NA	0	LysR substrate binding domain
MNLKPGEA_	rseP	-0.73259948	0.1807672	Regulator of sigma-E pro	3.4.24.-	rseP	zinc metalloprotease
MNLKPGEA_	ibpB_1	-0.73297282	0.17173679	Small heat shock proteir	NA	ibpB	Associates with aggregated prot
MNLKPGEA_	bcsE	-0.733692604	0.42973011	Cyclic di-GMP binding pr	NA	bcsE	cellulose biosynthesis protein Bc
MNLKPGEA_	rsmF	-0.734178632	NA	Ribosomal RNA small su	2.1.1.178	rsmF	Specifically methylates the cytos
MNLKPGEA_	hisQ_1	-0.734790611	0.51242518	Histidine transport syste	NA	hisQ	(ABC) transporter

MNLKPGEA_ srkA	-0.735328988	0.10192039	Stress response kinase A	2.7.11.1	srkA	A protein kinase that phosphoryl
MNLKPGEA_ guaB	-0.735368996	0.09770416	Inosine-5'-monophospha	1.1.1.205	guaB	Catalyzes the conversion of inosi
MNLKPGEA_ algC	-0.735690018	0.2982651	Phosphomannomutase/p	5.4.2.2	manB	phosphomannomutase
MNLKPGEA_ citA_2	-0.735734806	0.57840246	Sensor histidine kinase C	2.7.13.3	citA	Signal transduction histidine kin
MNLKPGEA_ mshA_1	-0.735778185	0.2810573	D-inositol-3-phosphate g	2.4.1.250	rfbU	glycosyl transferase group 1
MNLKPGEA_ gsiC_1	-0.736028161	NA	Glutathione transport sy	NA	0	ABC-type dipeptide oligopeptide
MNLKPGEA_ MNLKPGEA	-0.736028161	NA	hypothetical protein	NA	0	0
MNLKPGEA_ trmA	-0.736177912	0.42073657	tRNA/tmRNA (uracil-C(5	2.1.1.-	trmA	Dual-specificity methyltransfera
MNLKPGEA_ ribB	-0.737117534	0.10384526	3,4-dihydroxy-2-butanon	4.1.99.12	ribB	Catalyzes the conversion of D-rib
MNLKPGEA_ btsS	-0.737419798	0.04724426	Sensor histidine kinase B	2.7.13.3	yehU	Histidine kinase
MNLKPGEA_ MNLKPGEA	-0.737811595	NA	hypothetical protein	NA	0	cell adhesion
MNLKPGEA_ umuC_3	-0.738170272	0.56730683	Protein UmuC	NA	umuC	DNA polymerase
MNLKPGEA_ malP_1	-0.738318812	NA	PTS system maltose-spe	NA	ptsG_1	PTS system
MNLKPGEA_ betB_2	-0.738418851	NA	NAD/NADP-dependent b	1.2.1.8	betB	belongs to the aldehyde dehydrc
MNLKPGEA_ MNLKPGEA	-0.739626282	0.55816722	hypothetical protein	NA	0	Sugar isomerase
MNLKPGEA_ hokE	-0.740817116	0.04861015	Toxic protein HokE	NA	hokE	Hok/gef family
MNLKPGEA_ MNLKPGEA	-0.741296922	NA	hypothetical protein	NA	0	Capsid scaffolding
MNLKPGEA_ wbgU_1	-0.742070399	0.07664422	UDP-N-acetylglucosamir	5.1.3.7	wbnF	epimerase dehydratase
MNLKPGEA_ MNLKPGEA	-0.743722332	NA	putative zinc-binding alc	1.1.1.1	ybdR	COG1063 Threonine dehydrogen
MNLKPGEA_ MNLKPGEA	-0.74572198	0.2285534	hypothetical protein	NA	0	Cleaves both 3' and 5' ssDNA ex
MNLKPGEA_ MNLKPGEA	-0.746825539	0.45301608	hypothetical protein	NA	Z012_02(	0
MNLKPGEA_ lpxL_1	-0.746864138	0.25498175	Lipid A biosynthesis laur	2.3.1.241	lpxL	Catalyzes the transfer of laurate
MNLKPGEA_ glgA	-0.748138392	0.05210417	Glycogen synthase	2.4.1.21	glgA	Synthesizes alpha-1,4-glucan ch
MNLKPGEA_ ygdR_3	-0.750249821	0.16578199	putative lipoprotein YgdI	NA	ygdR	(Lipo)protein
MNLKPGEA_ MNLKPGEA	-0.751196739	0.22236257	hypothetical protein	NA	hpuB	Receptor
MNLKPGEA_ amiA	-0.751464395	0.15826306	N-acetylmuramoyl-L-ala	3.5.1.28	amiA	N-acetylmuramoyl-L-alanine am
MNLKPGEA_ recC	-0.754547761	0.25810827	RecBCD enzyme subunit	3.1.11.5	recC	A helicase nuclease that prepare
MNLKPGEA_ guaD_2	-0.754616076	NA	Guanine deaminase	3.5.4.3	guaD	Guanine deaminase
MNLKPGEA_ MNLKPGEA	-0.75619433	0.09188184	hypothetical protein	NA	0	PFAM Integrase catalytic
MNLKPGEA_ MNLKPGEA	-0.757701456	0.41019829	IS1 family transposase IS	NA	0	IS1 transposase

MNLKPGEA_	MNLKPGEA	-0.758323743	0.42944752	hypothetical protein	NA	rmuC	DNA Recombination protein Rm
MNLKPGEA_	ispU	-0.759014398	0.19193357	Ditrans,polycis-undecapr	2.5.1.31	uppS	Catalyzes the sequential conden
MNLKPGEA_	mepM	-0.759292777	0.01683751	Murein DD-endopeptidas	3.4.24.-	yebA	COG0739 Membrane proteins re
MNLKPGEA_	MNLKPGEA	-0.759600757	0.35128813	hypothetical protein	NA	0	0
MNLKPGEA_	rpsG	-0.760069574	0.00341398	30S ribosomal protein S7	NA	rpsG	One of the primary rRNA binding
MNLKPGEA_	MNLKPGEA	-0.760796479	0.54820051	hypothetical protein	NA	yfiM	Required for high salt suppressio
MNLKPGEA_	citG_2	-0.762676155	NA	2-(5''-triphosphoribosyl)-	2.4.2.52	citG	2-(5''-triphosphoribosyl)-3'-deph
MNLKPGEA_	elbB	-0.764204354	0.36237473	Glyoxalase ElbB	4.2.1.-	elbB	Displays glyoxalase activity, cata
MNLKPGEA_	rbsC_4	-0.764570733	NA	Ribose import permease	NA	0	Belongs to the binding-protein-d
MNLKPGEA_	accC	-0.765646759	0.08806507	Biotin carboxylase	6.3.4.14	accC	An AccC homodimer forms the b
MNLKPGEA_	MNLKPGEA	-0.765839455	0.54438098	hypothetical protein	NA	0	Protein of unknown function (DU
MNLKPGEA_	prfB	-0.766022658	0.14411081	Peptide chain release fa	NA	prfB	Peptide chain release factor 2 di
MNLKPGEA_	rimO	-0.766632149	0.36473572	Ribosomal protein S12 n	2.8.4.4	rimO	Catalyzes the methylthiolation o
MNLKPGEA_	dapD	-0.767439211	0.0503274	2,3,4,5-tetrahydropyridir	2.3.1.117	dapD	Belongs to the transferase hexa
MNLKPGEA_	nudJ	-0.767676567	0.42073657	Phosphatase NudJ	3.6.1.-	nudJ	Belongs to the Nudix hydrolase f
MNLKPGEA_	mtlK	-0.76818634	NA	Mannitol 2-dehydrogena	1.1.1.67	dalD	Belongs to the mannitol dehydro
MNLKPGEA_	nadC	-0.768213644	0.31487868	Nicotinate-nucleotide py	2.4.2.19	nadC	Belongs to the NadC ModD fami
MNLKPGEA_	recO	-0.768756316	0.43444089	DNA repair protein RecC	NA	recO	Involved in DNA repair and RecF
MNLKPGEA_	bluF_1	-0.769653543	0.32131698	Blue light- and temperat	NA	0	EAL domain
MNLKPGEA_	yveA	-0.769841509	NA	Aspartate-proton sympo	NA	yveA	Amino Acid
MNLKPGEA_	MNLKPGEA	-0.770128539	NA	hypothetical protein	NA	pqqF	Belongs to the peptidase M16 fa
MNLKPGEA_	galK	-0.771153177	0.38835747	Galactokinase	2.7.1.6	galK	Catalyzes the transfer of the gar
MNLKPGEA_	pduW	-0.77186225	NA	putative propionate kina	2.7.2.15	pduW	Catalyzes the formation of acety
MNLKPGEA_	ecpC	-0.772228745	NA	putative outer membran	NA	ecpC	Part of the ecpRABCDE operon, v
MNLKPGEA_	malY	-0.773238141	NA	Protein MalY	NA	malY	Bifunctional PLP-dependent enzy
MNLKPGEA_	rseB	-0.776810874	0.09364898	Sigma-E factor regulator	NA	rseB	Negative regulator of sigma E a
MNLKPGEA_	MNLKPGEA	-0.778897048	0.53516914	hypothetical protein	NA	yddH	Flavin reductase
MNLKPGEA_	MNLKPGEA	-0.77912373	NA	hypothetical protein	NA	0	DNA N-6-adenine-methyltransfe
MNLKPGEA_	mak_1	-0.779159235	NA	Fructokinase	2.7.1.4	mak	ROK family
MNLKPGEA_	nagR	-0.77985703	0.31559248	HTH-type transcriptional	NA	hutC	histidine utilization repressor

MNLKPGEA_	glcR_2	-0.779927455	0.41530145	HTH-type transcriptional	NA	0	transcriptional regulator
MNLKPGEA_	msbA_2	-0.780066811	0.45955472	Lipid A export ATP-bindi	7.5.2.6	cydC	(ABC) transporter
MNLKPGEA_	MNLKPGEA	-0.781071404	0.02933111	hypothetical protein	NA	0	0
MNLKPGEA_	MNLKPGEA	-0.782568071	0.54645246	hypothetical protein	NA	#N/A	#N/A
MNLKPGEA_	MNLKPGEA	-0.782606477	0.05356814	ISNCY family transposas	NA	0	Transposase
MNLKPGEA_	MNLKPGEA	-0.782614892	0.03448946	hypothetical protein	NA	0	0
MNLKPGEA_	MNLKPGEA	-0.783027905	0.47149227	hypothetical protein	NA	0	protein conserved in bacteria
MNLKPGEA_	ompC	-0.783342971	0.01347212	Outer membrane porin (	NA	ompC	Belongs to the Gram-negative p
MNLKPGEA_	MNLKPGEA	-0.783602446	NA	IS6 family transposase IS	NA	0	Transposase IS66 family
MNLKPGEA_	parM_2	-0.783721395	0.17211676	Plasmid segregation pro	NA	stbA	PFAM StbA family protein
MNLKPGEA_	fadJ	-0.785359883	0.13707291	Fatty acid oxidation com	NA	fadJ	Involved in the aerobic and anae
MNLKPGEA_	lldD_2	-0.786208443	0.35700519	L-lactate dehydrogenase	1.1.-.-	lldD	Catalyzes the conversion of L-lac
MNLKPGEA_	glmU	-0.786745052	0.01787743	Bifunctional protein Glm	NA	glmU	Catalyzes the last two sequentia
MNLKPGEA_	ndhC	-0.787875803	0.03881302	NAD(P)H-quinone oxidor	7.1.1.-	nuoA	NDH-1 shuttles electrons from N
MNLKPGEA_	ydcV_3	-0.788021163	0.37371869	Inner membrane ABC tra	NA	potI	ABC-type spermidine putrescine
MNLKPGEA_	MNLKPGEA	-0.78813099	NA	hypothetical protein	NA	0	Amino acid permease
MNLKPGEA_	rbsR_4	-0.788386271	0.22215982	Ribose operon repressor	NA	rbsR	Is the main repressor of the gen
MNLKPGEA_	yfeX	-0.789145934	0.16361833	Dye-decolorizing peroxid	1.11.1.-	yfeX	peroxidase
MNLKPGEA_	yhjJ	-0.789888349	0.118512	Protein YhjJ	NA	yhjJ	Peptidase, M16
MNLKPGEA_	ahr	-0.789984861	0.26004561	Aldehyde reductase Ahr	1.1.1.2	yjgB	alcohol dehydrogenase
MNLKPGEA_	aglB	-0.791107981	NA	6-phospho-alpha-glucosi	3.2.1.122	aglB	6-phospho-alpha-glucosidase
MNLKPGEA_	hldE	-0.792468707	0.45937711	Bifunctional protein HldE	NA	hldE	Catalyzes the ADP transfer from
MNLKPGEA_	arnT	-0.792583757	0.3532429	Undecaprenyl phosphate	2.4.2.43	arnT	Catalyzes the transfer of the L-A
MNLKPGEA_	cbiJ	-0.793471764	NA	Cobalt-precorrin-6A redu	1.3.1.106	cobK	reductase
MNLKPGEA_	MNLKPGEA	-0.794701564	NA	hypothetical protein	NA	yhbS	acetyltransferase
MNLKPGEA_	aroF	-0.794843573	0.10955768	Phospho-2-dehydro-3-de	2.5.1.54	aroF	Stereospecific condensation of p
MNLKPGEA_	hmp	-0.795017479	0.51712856	Flavohemoprotein	1.14.12.17	hmp	Is involved in NO detoxification i
MNLKPGEA_	artQ_2	-0.795628874	0.24172376	Arginine ABC transporte	NA	artQ	arginine transporter permease s
MNLKPGEA_	fucO	-0.795657733	NA	Lactaldehyde reductase	1.1.1.77	fucO	alcohol dehydrogenase
MNLKPGEA_	barA	-0.796952645	0.34001821	Signal transduction histi	2.7.13.3	barA	PhoQ Sensor

MNLKPGEA_	MNLKPGEA	-0.797452318	NA	Ferredoxin--NADP reduct	1.18.1.2	gltD	Glutamate synthase
MNLKPGEA_	lpfB	-0.79836047	NA	putative fimbrial chaper	NA	sthB	chaperone
MNLKPGEA_	MNLKPGEA	-0.798449599	0.23828672	hypothetical protein	NA	0	Acetyltransferase (GNAT) doma
MNLKPGEA_	exbB	-0.799644228	0.03392502	Biopolymer transport pr	NA	exbB	tonB-system energizer ExbB
MNLKPGEA_	MNLKPGEA	-0.80187294	0.37371869	ISNCY family transposas	NA	0	PFAM Integrase catalytic
MNLKPGEA_	yibH_3	-0.802515852	NA	Inner membrane protein	NA	yiaV	Secretion Protein
MNLKPGEA_	MNLKPGEA	-0.803349925	0.05544247	hypothetical protein	NA	0	0
MNLKPGEA_	clcD	-0.804046006	0.01685151	Carboxymethylenebuten	3.1.1.45	ysgA	Dienelactone hydrolase
MNLKPGEA_	apbE_1	-0.804843482	NA	FAD:protein FMN transfe	2.7.1.180	apbE	Flavin transferase that catalyzes
MNLKPGEA_	yhcH_1	-0.805829084	NA	putative protein YhcH	NA	yiaL	Domain of unknown function (DU
MNLKPGEA_	ssuC_1	-0.806212853	NA	Putative aliphatic sulfon	NA	ssuC	ABC-type nitrate sulfonate bicar
MNLKPGEA_	zraS	-0.808053652	NA	Sensor protein ZraS	2.7.13.3	zraS	Member of the two-component
MNLKPGEA_	cobU	-0.808416394	NA	Bifunctional adenosylcob	2.7.1.156	cobU	Catalyzes ATP-dependent phospl
MNLKPGEA_	iolE_3	-0.808648464	NA	Inosose dehydratase	4.2.1.44	iolE	Catalyzes the dehydration of ino
MNLKPGEA_	lolB	-0.80866982	0.32614754	Outer-membrane lipopro	NA	lolB	Plays a critical role in the incorp
MNLKPGEA_	metC_2	-0.809836105	NA	Cystathionine beta-lyase	4.4.1.13	metC	Catalyzes the formation of L-hor
MNLKPGEA_	parE	-0.809946049	0.23828672	DNA topoisomerase 4 su	5.6.2.2	parE	Topoisomerase IV is essential fo
MNLKPGEA_	yceF	-0.810355291	0.19193357	7-methyl-GTP pyrophosp	3.6.1.-	yceF	Maf-like protein
MNLKPGEA_	valS	-0.811912297	0.00048361	Valine--tRNA ligase	6.1.1.9	valS	amino acids such as threonine, t
MNLKPGEA_	MNLKPGEA	-0.812545231	NA	hypothetical protein	NA	ymfL	0
MNLKPGEA_	truC	-0.812545231	NA	tRNA pseudouridine synt	5.4.99.26	truC	Pseudouridine synthase
MNLKPGEA_	exuT_3	-0.812590276	NA	Hexuronate transporter	NA	0	Sugar (and other) transporter
MNLKPGEA_	dmlR_2	-0.814154407	0.51295412	HTH-type transcriptional	NA	yhjC	transcriptional regulator
MNLKPGEA_	btuR	-0.815270463	NA	Corrinoid adenosyltransf	2.5.1.17	cobO	Required for both de novo synth
MNLKPGEA_	MNLKPGEA	-0.816520403	0.5182666	hypothetical protein	NA	0	Antibiotic biosynthesis monooxy
MNLKPGEA_	MNLKPGEA	-0.818963103	0.52118975	hypothetical protein	NA	0	capsid protein
MNLKPGEA_	MNLKPGEA	-0.818975039	0.51378411	hypothetical protein	NA	yadE	Polysaccharide deacetylase
MNLKPGEA_	rpmD	-0.819844937	0.12638468	50S ribosomal protein L3	NA	rpmD	Ribosomal protein L30
MNLKPGEA_	yedA	-0.820649706	NA	putative inner membran	NA	yedA	of the drug metabolite transport
MNLKPGEA_	suhB_1	-0.8207396	0.061337	Inositol-1-monophospha	3.1.3.25	suhB	Inositol monophosphatase

MNLKPGEA_ zntA	-0.821052926	NA	Zinc/cadmium/lead-trar	3.6.3.3	zntA	P-type atpase
MNLKPGEA_ czcO	-0.821893078	NA	putative oxidoreductase	1.-.-.-	0	oxidoreductase
MNLKPGEA_ MNLKPGEA	-0.82190855	NA	hypothetical protein	NA	0	Protein of unknown function (DU
MNLKPGEA_ MNLKPGEA	-0.822357301	NA	hypothetical protein	NA	yfdN	PerC transcriptional activator
MNLKPGEA_ MNLKPGEA	-0.822357301	NA	D-threonine aldolase	4.1.2.42	dsd	Putative serine dehydratase dom
MNLKPGEA_ mnmG	-0.82385263	0.11026034	tRNA uridine 5-carboxyn	NA	gidA	NAD-binding protein involved in
MNLKPGEA_ xerC_1	-0.825144802	0.3906211	Tyrosine recombinase Xe	NA	int	Phage integrase family
MNLKPGEA_ igaA	-0.826522017	0.17789062	Intracellular growth atte	NA	yrfF	Intracellular growth attenuator
MNLKPGEA_ yeiR	-0.82709639	0.19538088	Zinc-binding GTPase Yei	3.6.-.-	yeiR	cobalamin synthesis protein, P47
MNLKPGEA_ MNLKPGEA	-0.827432091	0.43777833	hypothetical protein	NA	0	0
MNLKPGEA_ frr	-0.828794844	0.02256656	Ribosome-recycling fact	NA	frr	Responsible for the release of ri
MNLKPGEA_ pgi	-0.829532222	0.00554227	Glucose-6-phosphate isc	5.3.1.9	pgi	Belongs to the GPI family
MNLKPGEA_ hycI	-0.833180691	NA	Hydrogenase 3 maturati	3.4.23.51	hycI	hydrogenase 3 maturation prote
MNLKPGEA_ accA	-0.835001234	0.01335391	Acetyl-coenzyme A carb	2.1.3.15	accA	Component of the acetyl coenzy
MNLKPGEA_ ruvA	-0.835861747	0.33705293	Holliday junction ATP-de	3.6.4.12	ruvA	The RuvA-RuvB complex in the p
MNLKPGEA_ MNLKPGEA	-0.835881993	0.06445579	hypothetical protein	NA	0	SIR2-like domain
MNLKPGEA_ MNLKPGEA	-0.836561712	NA	hypothetical protein	NA	#N/A	#N/A
MNLKPGEA_ rhaS_4	-0.836620055	NA	HTH-type transcriptional	NA	0	Transcriptional regulator
MNLKPGEA_ MNLKPGEA	-0.838259132	NA	hypothetical protein	NA	0	Prohead protease
MNLKPGEA_ ybjN	-0.838282798	0.24166756	putative protein YbjN	NA	ybjN	sensory transduction regulator
MNLKPGEA_ ipuF	-0.838601965	NA	Gamma-glutamyl-L-1-hy	3.4.-.-	guaA2	glutamine amidotransferase
MNLKPGEA_ MNLKPGEA	-0.839081399	0.18085212	hypothetical protein	NA	0	0
MNLKPGEA_ lldR_1	-0.840503305	NA	Putative L-lactate dehyd	NA	lldR	Represses the lctPRD operon
MNLKPGEA_ MNLKPGEA	-0.841372263	0.43462739	hypothetical protein	NA	0	portal protein
MNLKPGEA_ fabG_7	-0.841893331	0.02161945	3-oxoacyl-[acyl-carrier-p	1.1.1.100	fabG	reductase
MNLKPGEA_ icd	-0.842434988	0.00263918	Isocitrate dehydrogenase	1.1.1.42	icd	TIGRFAM isocitrate dehydrogen
MNLKPGEA_ MNLKPGEA	-0.842561884	0.17211676	hypothetical protein	NA	virB1	Transglycosylase SLT domain
MNLKPGEA_ cysH_2	-0.842606736	NA	Phosphoadenosine phosp	1.8.4.8	ybdN	phosphoadenosine phosphosulfa
MNLKPGEA_ corC	-0.84262238	0.00777149	Magnesium and cobalt e	NA	corC	Mg2 and Co2 transporter CorC
MNLKPGEA_ MNLKPGEA	-0.842811094	0.33950012	hypothetical protein	NA	rbn	UPF0761 membrane protein

MNLKPGEA_	lgoT_3	-0.843373983	NA	putative L-galactonate tr	NA	yjjL	Major facilitator superfamily
MNLKPGEA_	oxyR_5	-0.843412382	0.16578199	Hydrogen peroxide-induc	NA	oxyR	Transcriptional regulator
MNLKPGEA_	ddlB	-0.843566157	0.27098387	D-alanine--D-alanine ligz	6.3.2.4	ddl	Belongs to the D-alanine--D-alar
MNLKPGEA_	malK_2	-0.843953125	NA	Maltose/maltodextrin in	7.5.2.1	malK	Part of the ABC transporter com
MNLKPGEA_	thiM	-0.845394047	0.20235647	Hydroxyethylthiazole kin	2.7.1.50	thiM	Catalyzes the phosphorylation of
MNLKPGEA_	pspA_1	-0.846011839	0.15308374	Phosphoserine phosphat	3.1.3.3	0	Phosphoglycerate mutase family
MNLKPGEA_	tas	-0.847847004	0.43985138	Protein tas	NA	tas	Aldo keto reductase
MNLKPGEA_	mdoG	-0.848219525	0.00911553	Glucans biosynthesis prc	NA	mdoG	Involved in the biosynthesis of os
MNLKPGEA_	rep_1	-0.848595898	0.49525682	ATP-dependent DNA heli	3.6.4.12	0	DNA helicase
MNLKPGEA_	queF	-0.849002088	0.19267323	NADPH-dependent 7-cya	1.7.1.13	queF	Catalyzes the NADPH-dependent
MNLKPGEA_	secF	-0.851664958	0.01564395	Protein translocase subu	NA	secF	Part of the Sec protein transloca
MNLKPGEA_	MNLKPGEA	-0.852013337	0.22322617	hypothetical protein	NA	0	0
MNLKPGEA_	btuC	-0.854254825	0.50210987	Vitamin B12 import syst	NA	btuC	Part of the ABC transporter com
MNLKPGEA_	MNLKPGEA	-0.855156619	NA	hypothetical protein	NA	#N/A	#N/A
MNLKPGEA_	zraP	-0.856838389	NA	Zinc resistance-associate	NA	zraP	Binds zinc. Could be an importar
MNLKPGEA_	cntO	-0.857751296	0.39663794	Metal-pseudopaline rece	NA	0	Receptor
MNLKPGEA_	pgaB	-0.857949356	0.49837349	Poly-beta-1,6-N-acetyl-D	3.5.1.-	pgaB	Polysaccharide deacetylase
MNLKPGEA_	MNLKPGEA	-0.858320354	0.42307838	hypothetical protein	NA	yjfP	esterase activity towards palmit
MNLKPGEA_	MNLKPGEA	-0.858635084	0.33340067	hypothetical protein	NA	0	response regulator
MNLKPGEA_	MNLKPGEA	-0.858740959	0.38276043	putative ABC transporter	NA	0	Belongs to the binding-protein-d
MNLKPGEA_	MNLKPGEA	-0.859319945	0.36963366	hypothetical protein	NA	ydbJ	Lipoprotein
MNLKPGEA_	MNLKPGEA	-0.860691737	NA	hypothetical protein	NA	0	0
MNLKPGEA_	gatB	-0.861735094	NA	PTS system galactitol-sp	2.7.1.200	gatB	The phosphoenolpyruvate-deper
MNLKPGEA_	MNLKPGEA	-0.862069976	NA	IS3 family transposase IS	NA	0	Transposase and inactivated der
MNLKPGEA_	atpC	-0.863266837	0.01188692	ATP synthase epsilon cha	NA	atpC	Produces ATP from ADP in the pr
MNLKPGEA_	MNLKPGEA	-0.863293371	0.51599454	hypothetical protein	NA	0	Protein of unknown function (DU
MNLKPGEA_	sbcD	-0.864625107	0.48741852	Nuclease SbcCD subunit	NA	sbcD	SbcCD cleaves DNA hairpin struc
MNLKPGEA_	MNLKPGEA	-0.866103708	NA	hypothetical protein	NA	0	PFAM transmembrane pair dom
MNLKPGEA_	aroH	-0.867448101	0.2827359	Phospho-2-dehydro-3-de	2.5.1.54	aroH	Stereospecific condensation of p
MNLKPGEA_	MNLKPGEA	-0.867508133	NA	hypothetical protein	NA	yggU	Belongs to the UPF0235 family

MNLKPGEA_ fsr	-0.867670738	0.2810573	Fosmidomycin resistanc	NA	fsr	fosmidomycin resistance protein
MNLKPGEA_ cpxR	-0.867731184	0.07223555	Transcriptional regulator	NA	cpxR	Response regulators consisting c
MNLKPGEA_ ydgH	-0.867828711	0.03435714	Protein YdgH	NA	ydgH	Protein of unknown function (DU
MNLKPGEA_ ispA	-0.868259388	0.08647519	Farnesyl diphosphate syr	2.5.1.10	ispA	Belongs to the FPP GGPP syntha
MNLKPGEA_ roxA_2	-0.869481398	NA	50S ribosomal protein L1	1.14.11.47	ycfD	Cupin 4 family protein
MNLKPGEA_ mtnN	-0.869969193	0.04670317	5'-methylthioadenosine/	3.2.2.9	mtnN	Catalyzes the irreversible cleava
MNLKPGEA_ MNLKPGEA	-0.87008599	0.06741541	hypothetical protein	NA	yqjK	Membrane
MNLKPGEA_ rhaS_11	-0.871090896	NA	HTH-type transcriptional	NA	0	transcriptional regulator
MNLKPGEA_ cbiL	-0.872419959	NA	Cobalt-precorrin-2 C(20)-	2.1.1.151	cobI	Belongs to the precorrin methylt
MNLKPGEA_ oppD_2	-0.872710868	0.42944752	Oligopeptide transport A	NA	oppD	Belongs to the ABC transporter s
MNLKPGEA_ acnB	-0.8734039	0.00608838	Aconitate hydratase B	4.2.1.3	acnB	Belongs to the aconitase IPM isc
MNLKPGEA_ priA	-0.874155751	0.47722411	Primosomal protein N'	3.6.4.-	priA	Involved in the restart of stalled
MNLKPGEA_ mscM	-0.874737704	0.17879808	Miniconductance mecha	NA	yjeP	mechanosensitive ion channel
MNLKPGEA_ pyrB	-0.876347615	NA	Aspartate carbamoyltrar	2.1.3.2	pyrB	Belongs to the ATCase OTCase f
MNLKPGEA_ glk	-0.877296653	0.20461722	Glucokinase	2.7.1.2	glk	Belongs to the bacterial glucokir
MNLKPGEA_ cytR_2	-0.877300463	0.23379939	HTH-type transcriptional	NA	cytR	transcriptional
MNLKPGEA_ MNLKPGEA	-0.877906263	0.01400683	hypothetical protein	NA	yafD	UPF0294 protein
MNLKPGEA_ ulaC_3	-0.877906614	NA	Ascorbate-specific PTS s	NA	ulaC	PTS IIA-like nitrogen-regulatory p
MNLKPGEA_ repB	-0.878377898	0.00261202	RepFIB replication prote	NA	repA	RePlication protein
MNLKPGEA_ lptC	-0.879177098	0.06094438	Lipopolysaccharide expor	NA	lptC	Involved in the assembly of lipop
MNLKPGEA_ MNLKPGEA	-0.879974285	NA	hypothetical protein	NA	0	Fimbrial protein
MNLKPGEA_ ygiF	-0.880996235	0.36677274	Inorganic triphosphatase	3.6.1.25	ygiF	Adenylate cyclase
MNLKPGEA_ glpT_1	-0.881117302	0.48554216	Glycerol-3-phosphate tra	NA	glpT	transporter
MNLKPGEA_ benM_1	-0.881225375	0.47230945	HTH-type transcriptional	NA	budR	transcriptional regulator
MNLKPGEA_ citA_1	-0.88143835	0.35828896	Sensor histidine kinase C	2.7.13.3	citA	signal transduction histidine kina
MNLKPGEA_ isfD	-0.881812714	NA	Sulfoacetaldehyde reduc	1.1.1.313	ydfG	Belongs to the short-chain dehyc
MNLKPGEA_ cdh	-0.884168777	0.47669278	CDP-diacylglycerol pyrop	3.6.1.26	cdh	CDP-diacylglycerol
MNLKPGEA_ tyrR	-0.884384452	0.19128331	Transcriptional regulator	NA	tyrR	Transcriptional regulator of aror
MNLKPGEA_ MNLKPGEA	-0.885361597	0.48006215	putative protein	NA	virK	protein conserved in bacteria
MNLKPGEA_ hipB	-0.885438925	NA	Antitoxin HipB	NA	hipB	Antitoxin component of a type II

MNLKPGEA_	rfaF	-0.886676501	0.10358632	ADP-heptose--LPS hepto	2.-.-.-	rfaF	heptosyltransferase
MNLKPGEA_	MNLKPGEA	-0.886840878	NA	hypothetical protein	NA	0	0
MNLKPGEA_	nuoI	-0.887583983	0.44923842	NADH-quinone oxidoredu	7.1.1.-	nuoI	NDH-1 shuttles electrons from N
MNLKPGEA_	ispF	-0.888698883	NA	2-C-methyl-D-erythritol 2	4.6.1.12	ispF	Involved in the biosynthesis of is
MNLKPGEA_	panC	-0.888717731	0.22811917	Pantothenate synthetase	6.3.2.1	panC	Catalyzes the condensation of pa
MNLKPGEA_	cmoB	-0.889732243	0.20738031	tRNA U34 carboxymethy	2.5.1.-	cmoB	Catalyzes carboxymethyl transfe
MNLKPGEA_	MNLKPGEA	-0.891173506	0.20461722	hypothetical protein	NA	afuA	ABC transporter substrate-bindi
MNLKPGEA_	MNLKPGEA	-0.891600732	NA	hypothetical protein	NA	csgA	short-chain dehydrogenase
MNLKPGEA_	purF	-0.892032708	0.00158088	Amidophosphoribosyltra	2.4.2.14	purF	Catalyzes the formation of phosp
MNLKPGEA_	yahK	-0.892111225	0.20650549	Aldehyde reductase YahI	1.1.1.2	yahK	alcohol dehydrogenase
MNLKPGEA_	yrdA_1	-0.892217032	0.23469379	Protein YrdA	NA	yrdA	COG0663 Carbonic anhydrases a
MNLKPGEA_	znuC	-0.892366453	0.03627959	Zinc import ATP-binding	7.2.2.-	znuC	Part of the ABC transporter com
MNLKPGEA_	cloR	-0.894393064	NA	4-hydroxy-3-prenylpheny	1.13.11.83	fucA_2	COG0235 Ribulose-5-phosphate
MNLKPGEA_	lysN_2	-0.894482728	0.46677238	2-aminoadipate transam	2.6.1.39	ydcR	Transcriptional regulators contai
MNLKPGEA_	xerD_1	-0.895277262	0.34224963	Tyrosine recombinase Xe	NA	xerD	recombinase XerD
MNLKPGEA_	argE_3	-0.89631119	0.25134856	Acetylornithine deacetyla	3.5.1.16	argE	Belongs to the peptidase M20A
MNLKPGEA_	cobT_1	-0.897576433	NA	Nicotinate-nucleotide--d	2.4.2.21	cobT	Catalyzes the synthesis of alpha-
MNLKPGEA_	lysP	-0.897943672	0.00544188	Lysine-specific permease	NA	lysP	amino acid
MNLKPGEA_	MNLKPGEA	-0.8994079	0.42124028	hypothetical protein	NA	0	Multi-copper polyphenol oxidore
MNLKPGEA_	metK	-0.899744663	0.06508168	S-adenosylmethionine sy	2.5.1.6	metK	Catalyzes the formation of S-ade
MNLKPGEA_	aplK	-0.901282333	0.47088662	Apulose kinase	2.7.1.-	glpK2	Belongs to the FGGY kinase fam
MNLKPGEA_	mutY	-0.901668564	0.35163912	Adenine DNA glycosylase	3.2.2.31	mutY	a g-specific adenine glycosylase
MNLKPGEA_	rcsC_4	-0.90286578	0.46133732	Sensor histidine kinase R	2.7.13.3	virA	Histidine kinase
MNLKPGEA_	iolG_3	-0.904537358	NA	Myo-inositol 2-dehydrog	1.1.1.18	0	2-dehydrogenase
MNLKPGEA_	ppiA	-0.904683467	0.16361833	Peptidyl-prolyl cis-trans i	5.2.1.8	ppiA	PPIases accelerate the folding o
MNLKPGEA_	menH_4	-0.905434547	NA	2-succinyl-6-hydroxy-2,4	4.2.99.20	0	Alpha beta hydrolase
MNLKPGEA_	hupB	-0.906270259	0.22272994	DNA-binding protein HU	NA	hupB	Histone-like DNA-binding protei
MNLKPGEA_	MNLKPGEA	-0.906746216	NA	hypothetical protein	NA	0	PTS system glucitol sorbitol-spe
MNLKPGEA_	hycE	-0.906957562	NA	Formate hydrogenlyase s	NA	hycE	HycBCDEFG is part of the forma
MNLKPGEA_	csrD	-0.907049652	0.03915233	RNase E specificity factc	NA	csrD	GGDEF domain

MNLKPGEA_	MNLKPGEA	-0.908187784	NA	hypothetical protein	NA	0	COG0454 Histone acetyltransfer
MNLKPGEA_	hokA	-0.908830098	0.0567873	Protein HokA	NA	hokA	PFAM Hok gef
MNLKPGEA_	ulaA_2	-0.909100704	NA	Ascorbate-specific PTS s	NA	0	protein conserved in bacteria
MNLKPGEA_	araB_2	-0.909181617	NA	Ribulokinase	2.7.1.16	araB	Belongs to the ribulokinase fami
MNLKPGEA_	MNLKPGEA	-0.909181617	NA	hypothetical protein	NA	0	Membrane
MNLKPGEA_	eptB	-0.909954858	0.0936547	Kdo(2)-lipid A phosphoet	2.7.8.42	eptB	membrane-associated metal-de
MNLKPGEA_	MNLKPGEA	-0.91140818	0.0513922	hypothetical protein	NA	ydiH	Domain of unknown function
MNLKPGEA_	ugpB_2	-0.911926622	NA	sn-glycerol-3-phosphate-	NA	MA20_28	Extracellular solute-binding prot
MNLKPGEA_	can_2	-0.911997447	NA	Carbonic anhydrase 2	4.2.1.1	0	Reversible hydration of carbon d
MNLKPGEA_	MNLKPGEA	-0.912569402	0.02645885	hypothetical protein	NA	#N/A	#N/A
MNLKPGEA_	hldD	-0.912618392	0.0088826	ADP-L-glycero-D-manno-	5.1.3.20	hldD	Catalyzes the interconversion be
MNLKPGEA_	MNLKPGEA	-0.914455103	0.35170351	hypothetical protein	NA	0	Required for disulfide bond form
MNLKPGEA_	MNLKPGEA	-0.916851421	0.10186838	hypothetical protein	NA	0	0
MNLKPGEA_	ydgC	-0.919494969	NA	Inner membrane protein	NA	ydgC	membrane protein required for
MNLKPGEA_	rpsI	-0.9198829	0.02656026	30S ribosomal protein S9	NA	rpsI	Belongs to the universal ribosom
MNLKPGEA_	MNLKPGEA	-0.921923199	0.04500584	hypothetical protein	NA	yneF	Diguanylate cyclase
MNLKPGEA_	fabF_1	-0.922124197	NA	3-oxoacyl-[acyl-carrier-p	2.3.1.179	fabF2	Catalyzes the condensation reac
MNLKPGEA_	MNLKPGEA	-0.922317632	0.04371936	hypothetical protein	NA	#N/A	#N/A
MNLKPGEA_	MNLKPGEA	-0.922514375	0.38322387	IS3 family transposase IS	NA	0	Transposase and inactivated der
MNLKPGEA_	idi	-0.924682039	0.187641	Isopentenyl-diphosphate	5.3.3.2	idi	Catalyzes the 1,3-allylic rearrang
MNLKPGEA_	argO	-0.925483191	NA	Arginine exporter protei	NA	argO	Involved in the export of arginine
MNLKPGEA_	sspA	-0.925517012	0.00443755	Stringent starvation prot	NA	sspA	stringent starvation protein A
MNLKPGEA_	MNLKPGEA	-0.925615765	0.33412798	hypothetical protein	NA	gloA	glyoxalase bleomycin resistance
MNLKPGEA_	tagG	-0.926243651	0.02365066	Teichoic acid translocati	NA	kpsM	Transport permease protein
MNLKPGEA_	topA_2	-0.927008125	0.00034205	DNA topoisomerase 1	5.6.2.1	topA	Releases the supercoiling and to
MNLKPGEA_	yecD	-0.928197775	0.33996064	Isochorismatase family p	3.-.-.-	yecD	Hydrolase
MNLKPGEA_	yahB	-0.928541238	0.44929187	putative HTH-type transc	NA	ydhB	Transcriptional regulator
MNLKPGEA_	fhuC_2	-0.928755609	0.46085684	Iron(3+)-hydroxamate im	7.2.2.16	fhuC	ABC-type cobalamin Fe3 -sidero
MNLKPGEA_	pcaR_3	-0.93063412	0.24099062	Pca regulon regulatory p	NA	0	Transcriptional regulator
MNLKPGEA_	MNLKPGEA	-0.93071114	0.06485075	hypothetical protein	NA	yifL	Prokaryotic lipoprotein-attachme

MNLKPGEA_ fadH	-0.934832316	0.29759123	2,4-dienoyl-CoA reductas	1.3.1.34	fadH	COG1902 NADH flavin oxidoredu
MNLKPGEA_ purR_3	-0.935350901	0.39454316	HTH-type transcriptional	NA	cytR_1	Periplasmic binding protein LacI
MNLKPGEA_ oxyR_4	-0.935617988	NA	Hydrogen peroxide-induc	NA	ilvY	transcriptional regulator
MNLKPGEA_ ispD	-0.938931659	NA	2-C-methyl-D-erythritol 4	2.7.7.60	ispD	Catalyzes the formation of 4-dip
MNLKPGEA_ deoB	-0.941818042	0.01655903	Phosphopentomutase	5.4.2.7	deoB	Phosphotransfer between the C1
MNLKPGEA_ udp	-0.941842197	0.16414214	Uridine phosphorylase	2.4.2.3	udp	Catalyzes the reversible phospho
MNLKPGEA_ gcvA_5	-0.941949994	NA	Glycine cleavage system	NA	0	LysR substrate binding domain
MNLKPGEA_ MNLKPGEA	-0.944395362	NA	hypothetical protein	NA	eutR	transcriptional regulator
MNLKPGEA_ btsT	-0.944977987	0.3992003	Pyruvate/proton sympor	NA	cstA	Carbon starvation protein
MNLKPGEA_ MNLKPGEA	-0.94512096	0.44131635	hypothetical protein	NA	#N/A	#N/A
MNLKPGEA_ selU	-0.945259591	NA	tRNA 2-selenouridine sy	2.5.1.-	selU	Catalyzes the transfer of seleniu
MNLKPGEA_ yjeM	-0.945802381	NA	Inner membrane transpo	NA	yjeM	amino acid
MNLKPGEA_ trmD	-0.947099683	0.02681604	tRNA (guanine-N(1)-)-m	2.1.1.228	trmD	Belongs to the RNA methyltrans
MNLKPGEA_ MNLKPGEA	-0.947465148	0.43857911	hypothetical protein	NA	0	COG0451 Nucleoside-diphospha
MNLKPGEA_ phoP_2	-0.947978415	0.18032408	Alkaline phosphatase syı	NA	adeR	response regulator
MNLKPGEA_ srlE	-0.948677541	NA	PTS system glucitol/sorb	2.7.1.198	srlE	PTS system glucitol sorbitol-spe
MNLKPGEA_ gshB	-0.948745001	0.17630054	Glutathione synthetase	6.3.2.3	gshB	Belongs to the prokaryotic GSH s
MNLKPGEA_ MNLKPGEA	-0.948885088	0.09951933	hypothetical protein	NA	#N/A	#N/A
MNLKPGEA_ phoQ	-0.950597567	0.37371869	Sensor protein PhoQ	2.7.13.3	phoQ	PhoQ Sensor
MNLKPGEA_ bcsZ	-0.951732961	NA	Endoglucanase	3.2.1.4	bcsZ	Belongs to the glycosyl hydrolas
MNLKPGEA_ ampH	-0.951960451	0.38276043	D-alanyl-D-alanine-carbo	3.4.-.-	ampH	This protein has no known enzyr
MNLKPGEA_ MNLKPGEA	-0.952974695	0.16136412	hypothetical protein	NA	frsA	Belongs to the UPF0255 family
MNLKPGEA_ MNLKPGEA	-0.953752523	0.23339116	hypothetical protein	NA	ydbH	Dicarboxylate transport
MNLKPGEA_ ftsB	-0.955492523	0.0898616	Cell division protein FtsB	NA	ftsB	Essential cell division protein. M
MNLKPGEA_ glnE	-0.956345964	0.2556722	Bifunctional glutamine s	NA	glnE	Involved in the regulation of glut
MNLKPGEA_ MNLKPGEA	-0.956513408	0.43755908	Putative hydro-lyase	4.2.1.-	0	Belongs to the D-glutamate cycl
MNLKPGEA_ ybhQ	-0.956530502	0.00030311	Inner membrane protein	NA	ybhQ	inner membrane protein YbhQ
MNLKPGEA_ yhhS_2	-0.957096745	NA	putative MFS-type transp	NA	0	MFS-type transporter
MNLKPGEA_ MNLKPGEA	-0.957397126	0.25530329	hypothetical protein	NA	ybgE	cyd operon protein YbgE
MNLKPGEA_ MNLKPGEA	-0.959547506	NA	hypothetical protein	NA	0	Phosphoadenosine phosphosulfa

MNLKPGEA_	occR	-0.960903939	NA	Octopine catabolism/upt	NA	lysR	transcriptional regulator
MNLKPGEA_	dgaF	-0.961517441	NA	2-dehydro-3-deoxy-phos	4.1.2.14	0	2-dehydro-3-deoxyphosphooctor
MNLKPGEA_	minE	-0.963363242	0.1231709	Cell division topological	NA	minE	Prevents the cell division inhibiti
MNLKPGEA_	MNLKPGEA	-0.963940592	0.16181879	hypothetical protein	NA	0	Bacteriophage CI repressor C-ter
MNLKPGEA_	fdhF_2	-0.965135465	NA	Formate dehydrogenase	1.17.1.9	fdhF_2	Spermidine putrescine ABC trans
MNLKPGEA_	glmS_2	-0.96563783	0.00178031	Glutamine--fructose-6-p	2.6.1.16	glmS	Catalyzes the first step in hexosa
MNLKPGEA_	thyA	-0.966197888	0.14633813	Thymidylate synthase	2.1.1.45	thyA	Catalyzes the reductive methylat
MNLKPGEA_	pdxH	-0.966643511	0.14470861	Pyridoxine/pyridoxamine	1.4.3.5	pdxH	Catalyzes the oxidation of either
MNLKPGEA_	gdhA_2	-0.966683056	0.03204074	NADP-specific glutamate	1.4.1.4	gdhA	Belongs to the Glu Leu Phe Val d
MNLKPGEA_	MNLKPGEA	-0.967065799	0.05660169	hypothetical protein	NA	0	regulation of DNA-templated tra
MNLKPGEA_	entD	-0.967763304	NA	Enterobactin synthase co	2.7.8.-	entD	Belongs to the P-Pant transferas
MNLKPGEA_	slt	-0.969182915	0.01319422	Soluble lytic murein tran	4.2.2.-	slt	Soluble lytic murein transglycosy
MNLKPGEA_	gph	-0.97078453	0.29877571	Phosphoglycolate phospl	3.1.3.18	gph	Phosphoglycolate phosphatase
MNLKPGEA_	bepF	-0.971830089	NA	Efflux pump periplasmic	NA	mexE	Belongs to the membrane fusion
MNLKPGEA_	panS	-0.971858211	NA	Pantothenate precursors	NA	yocS	Bile acid sodium symporter
MNLKPGEA_	intA_3	-0.972079542	NA	Prophage integrase IntA	NA	int	Belongs to the 'phage' integrase
MNLKPGEA_	nagK	-0.972949396	NA	N-acetyl-D-glucosamine	2.7.1.59	nagK	Catalyzes the phosphorylation of
MNLKPGEA_	MNLKPGEA	-0.972967268	NA	hypothetical protein	NA	0	Protein conserved in bacteria
MNLKPGEA_	chbA_1	-0.973392793	NA	PTS system N,N'-diacety	NA	chbA	PTS system, cellobiose-specific I
MNLKPGEA_	pcm	-0.973512419	0.30775501	Protein-L-isoaspartate O	2.1.1.77	pcm	Catalyzes the methyl esterificati
MNLKPGEA_	yhhQ	-0.974046445	0.35849725	Queuosine precursor tra	NA	yhhQ	Involved in the import of queuos
MNLKPGEA_	holE	-0.975156296	0.35379911	DNA polymerase III subu	2.7.7.7	holE	DNA polymerase III
MNLKPGEA_	rlmD	-0.975832851	0.02965223	23S rRNA (uracil(1939)-(	2.1.1.190	rlmD	Catalyzes the formation of 5-me
MNLKPGEA_	umuD_3	-0.976044243	NA	Protein UmuD	3.4.21.-	umuD	Belongs to the peptidase S24 fa
MNLKPGEA_	yihX	-0.976098659	0.22802842	Alpha-D-glucose 1-phosp	3.1.3.10	yihX	hydrolase
MNLKPGEA_	cbiH	-0.977146406	NA	putative cobalt-factor III	2.1.1.-	cbiH	precorrin-3B C17-methyltransfer
MNLKPGEA_	MNLKPGEA	-0.977701362	NA	IS5 family transposase IS	NA	insH5	COG3039 Transposase and inact
MNLKPGEA_	ybaL	-0.977958911	0.02936018	Putative cation/proton a	NA	ybaL	Belongs to the monovalent catic
MNLKPGEA_	oprM_2	-0.978054142	0.43176987	Outer membrane protein	NA	mdtQ	RND efflux system, outer memb
MNLKPGEA_	aceF	-0.979900312	0.000492	Dihydrolipoyllysine-resid	2.3.1.12	aceF	The pyruvate dehydrogenase cor

MNLKPGEA_ yddG	-0.980007892	NA	Aromatic amino acid exp	NA	yddG	of the drug metabolite transport
MNLKPGEA_ clsB	-0.981640574	0.14211512	Cardiolipin synthase B	2.7.8.-	clsB	Catalyzes the phosphatidyl group
MNLKPGEA_ gatA	-0.981810711	NA	PTS system galactitol-sp	NA	gatA	Phosphoenolpyruvate-dependent
MNLKPGEA_ yoaD	-0.982832886	NA	Putative 2-hydroxyacid d	1.1.1.-	0	Belongs to the D-isomer specific
MNLKPGEA_ MNLKPGEA	-0.985360183	NA	hypothetical protein	NA	0	Protein of unknown function (DU
MNLKPGEA_ iolB	-0.985952753	0.35379911	5-deoxy-glucuronate isor	5.3.1.30	iolB	5-deoxyglucuronate isomerase
MNLKPGEA_ xynR_1	-0.987128553	0.42199979	HTH-type transcriptional	NA	pcaR	helix_turn_helix isocitrate lyase
MNLKPGEA_ MNLKPGEA	-0.987581711	NA	hypothetical protein	NA	0	exonuclease activity
MNLKPGEA_ cycB	-0.990879918	NA	Cyclodextrin-binding prot	NA	cycB	Functions in the MalKFGE ABC tr
MNLKPGEA_ ybhS	-0.990989365	NA	putative multidrug ABC t	NA	ybhS	ABC-type multidrug transport sy
MNLKPGEA_ gltC_4	-0.991809994	NA	HTH-type transcriptional	NA	0	Transcriptional regulator
MNLKPGEA_ MNLKPGEA	-0.992157657	NA	hypothetical protein	NA	0	0
MNLKPGEA_ wecH	-0.993280244	0.22191083	O-acetyltransferase Wec	2.3.1.-	wecH	Responsible for the incorporatio
MNLKPGEA_ ydhP_1	-0.993486671	0.1386739	Inner membrane transpo	NA	ydhP	Major facilitator Superfamily
MNLKPGEA_ MNLKPGEA	-0.995773931	NA	IS5 family transposase IS	NA	0	ISSoEn1, terminal inverted repea
MNLKPGEA_ ygfA	-0.996043542	0.34521963	5-formyltetrahydrofolate	6.3.3.2	ygfA	Belongs to the 5-formyltetrahyd
MNLKPGEA_ btuE	-0.996265344	0.03691402	Thioredoxin/glutathione	1.11.1.15	btuE	Belongs to the glutathione perox
MNLKPGEA_ MNLKPGEA	-0.996949924	NA	hypothetical protein	NA	0	Transcriptional regulator
MNLKPGEA_ moeA	-0.997658169	0.29348143	Molybdopterin molybder	2.10.1.1	moeA	molybdopterin
MNLKPGEA_ iscU	-0.997691591	0.03774785	Iron-sulfur cluster assem	NA	iscU	A scaffold on which IscS assemb
MNLKPGEA_ MNLKPGEA	-0.998619034	NA	hypothetical protein	NA	#N/A	#N/A
MNLKPGEA_ ftsL	-0.999980259	0.0369587	Cell division protein FtsL	NA	ftsL	Essential cell division protein. M
MNLKPGEA_ brnQ	-1.001258906	0.01788841	Branched-chain amino a	NA	brnQ	Component of the transport syst
MNLKPGEA_ sprT	-1.001677442	NA	Protein SprT	NA	sprT	Belongs to the SprT family
MNLKPGEA_ malK_1	-1.002062107	0.30004022	Maltose/maltodextrin in	7.5.2.1	ganK	Belongs to the ABC transporter s
MNLKPGEA_ tolQ	-1.002681255	0.21882786	Tol-Pal system protein T	NA	tolQ	MotA/TolQ/ExbB proton channe
MNLKPGEA_ nrdA	-1.002847224	0.0244967	Ribonucleoside-diphosph	1.17.4.1	nrdA	Provides the precursors necessar
MNLKPGEA_ yciB	-1.002901849	0.09043554	putative intracellular sep	NA	ispZ	probably involved in intracellular
MNLKPGEA_ greA	-1.003973025	0.01417391	Transcription elongation	NA	greA	Necessary for efficient RNA poly
MNLKPGEA_ rep_2	-1.004861578	0.2835106	ATP-dependent DNA heli	3.6.4.12	rep	it can initiate unwinding at a nic

MNLKPGEA_	vdcD	-1.005364743	NA	Protein VdcD	NA	bsdD	4-hydroxybenzoate decarboxylas
MNLKPGEA_	arsB_1	-1.005448083	NA	Arsenical pump membra	NA	arsB	Involved in arsenical resistance.
MNLKPGEA_	wecC	-1.00593972	0.15602268	UDP-N-acetyl-D-mannos	1.1.1.336	wecC	Belongs to the UDP-glucose GDF
MNLKPGEA_	MNLKPGEA	-1.006327717	0.40648457	hypothetical protein	NA	0	Protein of unknown function (DU
MNLKPGEA_	MNLKPGEA	-1.007394202	NA	hypothetical protein	NA	0	integral membrane protein
MNLKPGEA_	smpB	-1.007526019	0.05106827	SsrA-binding protein	NA	smpB	Required for rescue of stalled ril
MNLKPGEA_	rclR	-1.007617463	NA	RCS-specific HTH-type tr	NA	alkR	Transcriptional regulator
MNLKPGEA_	thrB	-1.009012404	NA	Homoserine kinase	2.7.1.39	thrB	Catalyzes the ATP-dependent ph
MNLKPGEA_	glnB	-1.009650462	0.058033	Nitrogen regulatory prot	NA	glnB	Belongs to the P(II) protein fami
MNLKPGEA_	MNLKPGEA	-1.010006815	NA	hypothetical protein	NA	0	Transcriptional
MNLKPGEA_	tgt	-1.0112509	0.12065656	Queuine tRNA-ribosyltra	2.4.2.29	tgt	Catalyzes the base-exchange of
MNLKPGEA_	minC	-1.011488041	0.02571074	Septum site-determining	NA	minC	Cell division inhibitor that blocks
MNLKPGEA_	malX	-1.011973556	0.34500222	PTS system maltose-spe	NA	malX	PTS system
MNLKPGEA_	ugpA_1	-1.013342955	NA	sn-glycerol-3-phosphate	NA	ugpA	With UgpEC is involved in the up
MNLKPGEA_	ppiC_2	-1.013550446	0.33715728	Peptidyl-prolyl cis-trans i	5.2.1.8	ppiC	peptidylprolyl isomerase
MNLKPGEA_	aaeA_2	-1.014335691	NA	p-hydroxybenzoic acid ef	NA	ydhJ	Belongs to the membrane fusion
MNLKPGEA_	MNLKPGEA	-1.0146265	NA	hypothetical protein	NA	ydbL	protein conserved in bacteria
MNLKPGEA_	pgm	-1.014665338	0.01565035	Phosphoglucomutase	5.4.2.2	pgm	Phosphoglucomutase
MNLKPGEA_	lysU	-1.015235102	0.30984725	Lysine--tRNA ligase, hea	6.1.1.6	lysS	Belongs to the class-II aminoacy
MNLKPGEA_	MNLKPGEA	-1.015812281	0.20399103	hypothetical protein	NA	yecF	Protein of unknown function (DU
MNLKPGEA_	dcd	-1.016326989	0.21597641	dCTP deaminase	3.5.4.13	dcd	Belongs to the dCTP deaminase
MNLKPGEA_	MNLKPGEA	-1.016443802	0.4697791	hypothetical protein	NA	0	0
MNLKPGEA_	aroP_2	-1.017204855	0.02681604	Aromatic amino acid tra	NA	aroP	amino acid
MNLKPGEA_	dtd	-1.017297376	NA	D-aminoacyl-tRNA deacy	3.1.1.96	dtd	rejects L-amino acids rather tha
MNLKPGEA_	MNLKPGEA	-1.017306989	0.408996	hypothetical protein	NA	#N/A	#N/A
MNLKPGEA_	nnr	-1.017778063	0.13410684	Bifunctional NAD(P)H-hy	NA	nnrD	Bifunctional enzyme that catalyz
MNLKPGEA_	nuoC	-1.018533995	0.03037562	NADH-quinone oxidored	7.1.1.-	nuoC	NDH-1 shuttles electrons from N
MNLKPGEA_	prmC	-1.019980203	NA	Release factor glutamin	2.1.1.297	prmC	Methylates the class 1 translatic
MNLKPGEA_	ptsP	-1.020171963	0.15829238	Phosphoenolpyruvate-de	2.7.3.9	ptsP	Belongs to the PEP-utilizing enzy
MNLKPGEA_	dusC	-1.021571529	NA	tRNA-dihydrouridine(16)	1.3.1.-	dusC	Catalyzes the synthesis of 5,6-di

MNLKPGEA_ ssuB_3	-1.021571529	NA	Aliphatic sulfonates imp	3.6.3.-	ssuB	Part of the ABC transporter com
MNLKPGEA_ rhaS_14	-1.022179867	0.39939642	HTH-type transcriptional	NA	rhaS	Activates expression of the rhaB
MNLKPGEA_ alr	-1.022365319	NA	Alanine racemase, biosy	5.1.1.1	alr	Catalyzes the interconversion of
MNLKPGEA_ hslV	-1.022388382	0.01213962	ATP-dependent protease	3.4.25.2	hslV	Protease subunit of a proteasom
MNLKPGEA_ rsmJ	-1.023961407	NA	Ribosomal RNA small su	2.1.1.242	rsmJ	Specifically methylates the guar
MNLKPGEA_ mglB	-1.024150841	0.01396671	D-galactose-binding peri	NA	mglB	Wtih MglAC is involved in the tra
MNLKPGEA_ MNLKPGEA	-1.027357044	NA	putative protein	NA	MA20_32	Transglutaminase
MNLKPGEA_ MNLKPGEA	-1.028083558	NA	hypothetical protein	NA	0	0
MNLKPGEA_ trmB	-1.030792556	0.05089738	tRNA (guanine-N(7)-)-m	2.1.1.33	trmB	catalyzes the formation of N(7)-
MNLKPGEA_ ylaC	-1.031377547	0.05891989	Inner membrane protein	NA	ylaC	Membrane
MNLKPGEA_ bgaA	-1.031712425	NA	Beta-galactosidase BgaA	3.2.1.23	bgaA	beta-galactosidase
MNLKPGEA_ mgsA	-1.031796579	0.20308941	Methylglyoxal synthase	4.2.3.3	mgsA	Methylglyoxal synthase
MNLKPGEA_ araC_2	-1.031954275	0.22852447	Arabinose operon regula	NA	mmsR	regulates the araBAD and araFG
MNLKPGEA_ serS	-1.03289069	0.00451644	Serine--tRNA ligase	6.1.1.11	serS	Catalyzes the attachment of seri
MNLKPGEA_ fepG	-1.032937167	NA	Ferric enterobactin trans	NA	fepG	Belongs to the binding-protein-d
MNLKPGEA_ ybfE	-1.034196564	0.39607251	putative protein YbfE	NA	ybfE	CopG domain protein DNA-bindi
MNLKPGEA_ tsf	-1.035799496	0.0127868	Elongation factor Ts	NA	tsf	Associates with the EF-Tu.GDP c
MNLKPGEA_ potA_1	-1.036533214	NA	Spermidine/putrescine i	7.6.2.11	potA_1	Belongs to the ABC transporter s
MNLKPGEA_ prfC	-1.036577318	0.03501207	Peptide chain release fa	NA	prfC	Increases the formation of ribos
MNLKPGEA_ pgrR_9	-1.037120839	NA	HTH-type transcriptional	NA	0	Transcriptional regulator
MNLKPGEA_ MNLKPGEA	-1.038117831	0.26400288	hypothetical protein	NA	ameR	transcriptional regulator
MNLKPGEA_ sapF	-1.038498503	0.23469379	Peptide transport system	NA	sapF	ATPase activity
MNLKPGEA_ rpsB	-1.038873426	8.26E-07	30S ribosomal protein S2	NA	rpsB	ribosomal protein
MNLKPGEA_ MNLKPGEA	-1.039727232	NA	hypothetical protein	NA	com1	DSBA-like thioredoxin domain
MNLKPGEA_ artJ_2	-1.040062923	0.32681298	ABC transporter arginine	NA	artJ_3	belongs to the bacterial solute-b
MNLKPGEA_ cmpR_1	-1.041375736	0.07615414	HTH-type transcriptional	NA	lrhA	Transcriptional regulator
MNLKPGEA_ dadX	-1.041514671	0.02235414	Alanine racemase, catab	5.1.1.1	alr	Catalyzes the interconversion of
MNLKPGEA_ entH	-1.042852136	0.39318437	Proofreading thioesteras	3.1.2.-	entH	Required for optimal enterobact
MNLKPGEA_ rph	-1.043139747	0.12006999	Ribonuclease PH	2.7.7.56	rph	Phosphorolytic exoribonuclease
MNLKPGEA_ MNLKPGEA	-1.044931562	0.27932312	putative ABC transporter	NA	ybbA	(ABC) transporter

MNLKPGEA_ glpR_1	-1.045135401	0.27098387	Glycerol-3-phosphate re	NA	glpR	transcriptional regulator
MNLKPGEA_ bcsQ_1	-1.045948241	0.39318437	Cellulose biosynthesis pr	NA	yhjQ	cellulose synthase operon protei
MNLKPGEA_ norG_2	-1.046023647	NA	HTH-type transcriptional	NA	yjiR	Transcriptional regulators contai
MNLKPGEA_ yheS_1	-1.046788474	0.09528753	putative ABC transporter	NA	ydiF	ATPase components of ABC tran
MNLKPGEA_ MNLKPGEA	-1.04832127	NA	hypothetical protein	NA	0	Major facilitator Superfamily
MNLKPGEA_ intA_2	-1.048613578	0.00179611	Prophage integrase IntA	NA	intA	Arm DNA-binding domain
MNLKPGEA_ rdgB	-1.049308266	NA	dITP/XTP pyrophosphata	3.6.1.66	rdgB	Pyrophosphatase that catalyzes
MNLKPGEA_ MNLKPGEA	-1.049467787	0.38972954	Carnitine monooxygenas	1.14.13.239	yfaE	Ferredoxin
MNLKPGEA_ hiuH	-1.050183429	NA	5-hydroxyisourate hydrol	3.5.2.17	uraH	Belongs to the transthyretin fam
MNLKPGEA_ rbsR_1	-1.051256056	0.38910762	Ribose operon repressor	NA	0	Transcriptional
MNLKPGEA_ iolG_1	-1.051425822	NA	Inositol 2-dehydrogenase	1.1.1.369	0	oxidoreductase
MNLKPGEA_ wecD	-1.052662731	NA	dTDP-fucosamine acetyl	2.3.1.210	wecD	Catalyzes the acetylation of dTD
MNLKPGEA_ pilQ	-1.054857293	NA	Type IV pilus biogenesis	NA	pilQ	(Type IV) pilus
MNLKPGEA_ ybaN	-1.055846442	0.04757845	Inner membrane protein	NA	ybaN	Membrane
MNLKPGEA_ lrp_2	-1.056859606	NA	Leucine-responsive regul	NA	0	Transcriptional
MNLKPGEA_ MNLKPGEA	-1.057163048	NA	hypothetical protein	NA	0	0
MNLKPGEA_ sasA_2	-1.058736548	0.17173679	Adaptive-response sensc	2.7.-.-	chvG	Histidine kinase-like ATPases
MNLKPGEA_ fliY_4	-1.05908011	NA	L-cystine-binding protein	NA	0	Belongs to the bacterial solute-b
MNLKPGEA_ MNLKPGEA	-1.059238967	NA	hypothetical protein	NA	0	Pectate lyase superfamily protei
MNLKPGEA_ cadA	-1.059576306	0.31787929	Inducible lysine decarbo	4.1.1.18	cadA	decarboxylase
MNLKPGEA_ MNLKPGEA	-1.060083279	0.27296096	hypothetical protein	NA	0	Molybdenum ABC transporter, p
MNLKPGEA_ MNLKPGEA	-1.061796714	0.08301768	hypothetical protein	NA	0	Domain of unknown function DU
MNLKPGEA_ hdeB_1	-1.061987106	NA	Acid stress chaperone H	NA	hdeB	Required for optimal acid stress
MNLKPGEA_ MNLKPGEA	-1.062328439	0.00403251	hypothetical protein	NA	0	acetyltransferase
MNLKPGEA_ gluQ	-1.062619741	0.39275465	Glutamyl-Q tRNA(Asp) s	6.1.1.-	gluQ	Catalyzes the tRNA-independent
MNLKPGEA_ MNLKPGEA	-1.062895714	0.13179585	putative protein	NA	yqcA	flavodoxin binds one FMN molec
MNLKPGEA_ MNLKPGEA	-1.062943162	0.42347445	hypothetical protein	NA	#N/A	#N/A
MNLKPGEA_ aroB	-1.063192579	0.09285572	3-dehydroquinate syntha	4.2.3.4	aroB	Catalyzes the conversion of 3-de
MNLKPGEA_ cutA	-1.063267474	0.31616812	Divalent-cation tolerance	NA	cutA	Involved in resistance toward he
MNLKPGEA_ rodZ	-1.063686687	0.0163256	Cytoskeleton protein Roc	NA	rodZ	Cytoskeletal protein that is invol

MNLKPGEA_	MNLKPGEA	-1.06565093	NA	hypothetical protein	NA	0	Bacteriophage replication gene
MNLKPGEA_	dapAL	-1.066131671	NA	putative DapA-like lyase	4.-.-.-	dapA2	Dihydrodipicolinate synthetase f
MNLKPGEA_	vsr	-1.066753751	0.30512024	Very short patch repair p	3.1.-.-	vsr	May nick specific sequences tha
MNLKPGEA_	MNLKPGEA	-1.06683737	0.38176531	hypothetical protein	NA	0	protein conserved in bacteria
MNLKPGEA_	cadB	-1.068021385	NA	putative cadaverine/lysi	NA	cadB	antiporter
MNLKPGEA_	gabD_1	-1.068622844	NA	Succinate-semialdehyde	1.2.1.79	gabD	belongs to the aldehyde dehydrc
MNLKPGEA_	dmlR_19	-1.068909042	0.16997474	HTH-type transcriptional	NA	yafC	Transcriptional regulator
MNLKPGEA_	MNLKPGEA	-1.069782206	0.37564912	hypothetical protein	NA	yhbQ	endonuclease containing a URI d
MNLKPGEA_	lplA	-1.070516352	0.37622912	Lipoate-protein ligase A	6.3.1.20	lplA	Catalyzes both the ATP-depende
MNLKPGEA_	rhmT	-1.070525033	NA	Inner membrane transpo	NA	rhmT	Major facilitator superfamily
MNLKPGEA_	glmM	-1.070933823	0.21597328	Phosphoglucosamine mu	5.4.2.10	glmM	Catalyzes the conversion of gluc
MNLKPGEA_	hycG	-1.071647755	NA	Formate hydrogenlyase s	NA	hycG	NADH ubiquinone oxidoreductas
MNLKPGEA_	yeaX_2	-1.0717297	NA	Carnitine monooxygenas	1.14.13.239	yeaX	Flavodoxin reductases (Ferredox
MNLKPGEA_	yfhL	-1.072286258	0.37764481	Ferredoxin YfhL	NA	yfhL	Ferredoxin
MNLKPGEA_	rsmH	-1.074357744	0.0103901	Ribosomal RNA small su	2.1.1.199	rsmH	Specifically methylates the N4 p
MNLKPGEA_	bioF	-1.076350201	0.48393238	8-amino-7-oxononanoat	2.3.1.47	bioF	Catalyzes the decarboxylative co
MNLKPGEA_	MNLKPGEA	-1.07721183	0.13459464	hypothetical protein	NA	wbbN	Glycosyl Transferase
MNLKPGEA_	talB_2	-1.077217426	0.00801507	Transaldolase B	2.2.1.2	tal	Transaldolase is important for th
MNLKPGEA_	treA	-1.077648163	0.04820067	Periplasmic trehalase	3.2.1.28	treA	Provides the cells with the abilit
MNLKPGEA_	lptA	-1.078973031	0.01157709	Lipopolysaccharide expo	NA	lptA	Involved in the assembly of lipop
MNLKPGEA_	yghA	-1.082116063	0.17317803	putative oxidoreductase	1.-.-.-	yhxD	Dehydrogenases with different s
MNLKPGEA_	MNLKPGEA	-1.084466749	0.05411929	hypothetical protein	NA	cytR_1	Periplasmic binding protein LacI
MNLKPGEA_	attM	-1.084470765	0.37919809	N-acyl homoserine lacto	3.1.1.81	attM	Metallo-beta-lactamase superfa
MNLKPGEA_	MNLKPGEA	-1.085354444	0.23897602	hypothetical protein	NA	scsA	resistance, protein
MNLKPGEA_	anmK	-1.085542657	0.17934987	Anhydro-N-acetylmuram	2.7.1.170	anmK	Catalyzes the specific phosphory
MNLKPGEA_	cbiM	-1.085915272	NA	Cobalt transport protein	NA	cbiM	Part of the energy-coupling facto
MNLKPGEA_	nlpE	-1.086980221	0.19319877	Lipoprotein NlpE	NA	cutF	Copper homeostasis
MNLKPGEA_	srlR_3	-1.088419841	0.19464266	Glucitol operon represso	NA	srlR	Transcriptional
MNLKPGEA_	dmlR_13	-1.088974466	0.03864654	HTH-type transcriptional	NA	0	transcriptional regulator
MNLKPGEA_	chbR	-1.088994633	0.19430908	HTH-type transcriptional	NA	chbR	transcriptional regulator

MNLKPGEA_	MNLKPGEA	-1.091896446	0.37448553	hypothetical protein	NA	ybgK	Allophanate hydrolase subunit 2
MNLKPGEA_	nqrD	-1.091928022	NA	Na(+)-translocating NAD	7.2.1.1	nqrD	NQR complex catalyzes the redu
MNLKPGEA_	MNLKPGEA	-1.094248886	NA	putative ABC transporter	NA	0	(ABC) transporter
MNLKPGEA_	MNLKPGEA	-1.0962834	NA	IS3 family transposase IS	NA	0	Transposase
MNLKPGEA_	spoT	-1.097937672	0.00816205	Bifunctional (p)ppGpp sy	NA	spoT	In eubacteria ppGpp (guanosine
MNLKPGEA_	orn	-1.097995484	0.09206426	Oligoribonuclease	3.1.-.-	orn	3'-to-5' exoribonuclease specific
MNLKPGEA_	cytR_3	-1.098341845	0.0455575	HTH-type transcriptional	NA	0	transcriptional
MNLKPGEA_	gabR_2	-1.098917285	0.3635011	HTH-type transcriptional	NA	gabR_2	Transcriptional regulators contai
MNLKPGEA_	rhlE	-1.099103134	NA	ATP-dependent RNA heli	3.6.4.13	rhlE	DEAD-box RNA helicase involved
MNLKPGEA_	MNLKPGEA	-1.099599775	NA	hypothetical protein	NA	0	Acyltransferase
MNLKPGEA_	MNLKPGEA	-1.100660007	0.19300942	hypothetical protein	NA	0	0
MNLKPGEA_	MNLKPGEA	-1.101048804	NA	hypothetical protein	NA	0	0
MNLKPGEA_	lapA	-1.101566227	0.14470861	Lipopolysaccharide asser	NA	lapA	Involved in the assembly of lipop
MNLKPGEA_	yfeO	-1.101922855	0.07714708	Putative ion-transport pr	NA	yfeO	ion-transport protein
MNLKPGEA_	MNLKPGEA	-1.10224157	NA	hypothetical protein	NA	0	Uncharacterized protein conserv
MNLKPGEA_	rlmF	-1.102288213	0.36458407	Ribosomal RNA large su	2.1.1.181	rlmF	Specifically methylates the ader
MNLKPGEA_	ratA	-1.102328036	0.11129398	Ribosome association to	NA	ratA	oligoketide cyclase lipid transpor
MNLKPGEA_	ppsA	-1.103498723	0.0010098	Phosphoenolpyruvate syr	2.7.9.2	ppsA	Catalyzes the phosphorylation of
MNLKPGEA_	btuF_2	-1.104419056	0.35892757	Vitamin B12-binding pro	NA	0	periplasmic binding protein
MNLKPGEA_	MNLKPGEA	-1.104958593	NA	hypothetical protein	NA	msgA	Virulence protein msgA
MNLKPGEA_	deoC_1	-1.105464955	NA	Deoxyribose-phosphate a	4.1.2.4	deoC	Catalyzes a reversible aldol reac
MNLKPGEA_	plaP	-1.106409798	0.04445667	Low-affinity putrescine i	NA	yeeF	Amino Acid
MNLKPGEA_	tonB	-1.106847268	0.05014291	Protein TonB	NA	tonB	Interacts with outer membrane
MNLKPGEA_	yejB	-1.107169758	NA	Inner membrane ABC tra	NA	yejB	ABC transporter (permease)
MNLKPGEA_	yeaW	-1.108422793	0.30567257	Carnitine monooxygenas	1.14.13.239	yeaW	COG4638 Phenylpropionate diox
MNLKPGEA_	ydfK_1	-1.108461214	0.36205082	putative membrane prot	NA	yqgA	Membrane
MNLKPGEA_	fis	-1.109671177	0.06478754	DNA-binding protein Fis	NA	fis	Activates ribosomal RNA transcr
MNLKPGEA_	MNLKPGEA	-1.11087036	0.10965519	hypothetical protein	NA	0	enterobacterial common antiger
MNLKPGEA_	MNLKPGEA	-1.110927162	NA	hypothetical protein	NA	0	KTSC domain
MNLKPGEA_	nimR_3	-1.111048312	0.20065089	HTH-type transcriptional	NA	MA20_01	AraC-like ligand binding domain

MNLKPGEA_	MNLKPGEA	-1.111122174	0.17741055	hypothetical protein	NA	0	0
MNLKPGEA_	lpdA	-1.111252748	2.68E-05	Dihydrolipoyl dehydroge	1.8.1.4	lpdA	COG1249 Pyruvate 2-oxoglutara
MNLKPGEA_	bamA_2	-1.111718165	0.19842458	Outer membrane protei	NA	bamA	Part of the outer membrane pro
MNLKPGEA_	MNLKPGEA	-1.112373921	NA	hypothetical protein	NA	0	Iron-regulated membrane protei
MNLKPGEA_	rayT	-1.113910513	NA	REP-associated tyrosine	NA	yafM	Transposase and inactivated der
MNLKPGEA_	MNLKPGEA	-1.115963471	NA	hypothetical protein	NA	citA	Is involved in the uptake of citra
MNLKPGEA_	MNLKPGEA	-1.116323634	0.05891989	hypothetical protein	NA	lbgB	Glycosyltransferase family 9 (he
MNLKPGEA_	rhaM	-1.116411595	NA	L-rhamnose mutarotase	5.1.3.32	rhaM	Involved in the anomeric convers
MNLKPGEA_	MNLKPGEA	-1.118215271	0.37371869	hypothetical protein	NA	0	0
MNLKPGEA_	ydgA	-1.118471601	0.08301768	Protein YdgA	NA	ydgA	protein conserved in bacteria
MNLKPGEA_	lipA	-1.120151967	0.00320207	Lipoyl synthase	2.8.1.8	lipA	Catalyzes the radical-mediated i
MNLKPGEA_	glpG	-1.120452569	0.16539077	Rhomboid protease GlpG	3.4.21.105	glpG	Rhomboid-type serine protease
MNLKPGEA_	MNLKPGEA	-1.120682603	0.04820067	hypothetical protein	NA	ygdQ	membrane protein, terc
MNLKPGEA_	ulaG	-1.121671473	0.44852112	putative L-ascorbate-6-p	3.1.1.-	ulaG	Probably catalyzes the hydrolysis
MNLKPGEA_	hisJ_1	-1.121936188	0.06840854	Histidine-binding peripla	NA	hisJ	belongs to the bacterial solute-b
MNLKPGEA_	fimF	-1.123533082	NA	Protein FimF	NA	fimF	Fimbrial protein
MNLKPGEA_	nudE	-1.124824996	0.05557325	ADP compounds hydrola	3.6.1.-	nudE	Hydrolase
MNLKPGEA_	rcsA	-1.125742755	0.00819883	Transcriptional regulato	NA	rcsA	Component of the Rcs signaling
MNLKPGEA_	ahpC_1	-1.126551387	4.56E-05	Alkyl hydroperoxide redu	1.11.1.15	ahpC	C-terminal domain of 1-Cys perc
MNLKPGEA_	MNLKPGEA	-1.126758899	NA	hypothetical protein	NA	nylB	Beta-lactamase
MNLKPGEA_	ycjG	-1.126951603	0.35892757	L-Ala-D/L-Glu epimerase	5.1.1.20	ycjG	Belongs to the mandelate racem
MNLKPGEA_	phoA	-1.12738773	0.14869967	Alkaline phosphatase	3.1.3.1	phoA	Belongs to the alkaline phospha
MNLKPGEA_	ygbE	-1.128233891	0.44193456	Inner membrane protein	NA	ygbE	membrane
MNLKPGEA_	lolE	-1.12954777	0.14633813	Lipoprotein-releasing sys	NA	lolE	Lipoprotein releasing system tra
MNLKPGEA_	xylH_1	-1.130138273	NA	Xylose transport system	NA	xylH	Belongs to the binding-protein-d
MNLKPGEA_	mutS2	-1.130939129	0.06317249	Endonuclease MutS2	3.1.-.-	yfcN	Belongs to the UPF0115 family
MNLKPGEA_	hisI	-1.133166384	0.45252804	Histidine biosynthesis bi	3.5.4.19	hisI	Catalyzes the hydrolysis of the a
MNLKPGEA_	folK	-1.13329917	NA	2-amino-4-hydroxy-6-hy	2.7.6.3	folK	2-amino-4-hydroxy-6-hydroxyme
MNLKPGEA_	tusE	-1.135006673	0.21989024	Sulfurtransferase TusE	2.8.1.-	tusE	part of a sulfur-relay system
MNLKPGEA_	MNLKPGEA	-1.135459608	0.21852772	hypothetical protein	NA	0	0

MNLKPGEA_	MNLKPGEA	-1.136277819	NA	hypothetical protein	NA	0	Uncharacterized conserved prote
MNLKPGEA_	mglC	-1.136598801	0.2753194	Galactoside transport sy	NA	mglC	Belongs to the binding-protein-d
MNLKPGEA_	fabF_2	-1.136658839	0.11194947	3-oxoacyl-[acyl-carrier-p	2.3.1.179	fabF	Catalyzes the condensation reac
MNLKPGEA_	dnaX	-1.137744844	0.14125548	DNA polymerase III subu	2.7.7.7	dnaX	DNA polymerase III is a complex
MNLKPGEA_	gloB	-1.138415889	0.02016833	Hydroxyacylglutathione h	3.1.2.6	gloB	Thiolesterase that catalyzes the
MNLKPGEA_	rplB	-1.140845285	6.21E-05	50S ribosomal protein L2	NA	rplB	One of the primary rRNA binding
MNLKPGEA_	fadM	-1.14188971	0.2142873	Long-chain acyl-CoA thio	3.1.2.-	tesC	Thioesterase
MNLKPGEA_	MNLKPGEA	-1.142140029	0.34032494	hypothetical protein	NA	0	0
MNLKPGEA_	dlgD	-1.143585904	0.43755908	2,3-diketo-L-gulonate re	1.1.1.130	dlgD	Catalyzes the reduction of 2,3-di
MNLKPGEA_	MNLKPGEA	-1.144582781	NA	hypothetical protein	NA	#N/A	#N/A
MNLKPGEA_	rimK	-1.145434136	0.43709995	Ribosomal protein S6--L·	6.3.2.-	rimK	Belongs to the RimK family
MNLKPGEA_	cbiK	-1.146959358	NA	Sirohydrochlorin cobalto	4.99.1.3	cbiK	Catalyzes the insertion of Co(2)
MNLKPGEA_	cysG_2	-1.147048695	0.2784927	Siroheme synthase	NA	cysG	Multifunctional enzyme that cat
MNLKPGEA_	rplM	-1.14732935	0.00310713	50S ribosomal protein L1	NA	rplM	This protein is one of the early a
MNLKPGEA_	bcsB_2	-1.147842543	0.34644271	Cyclic di-GMP-binding pr	NA	bcsB	Cellulose synthase
MNLKPGEA_	nasD	-1.148025866	0.43285641	Nitrite reductase [NAD(F	1.7.1.4	nirB	Belongs to the nitrite and sulfite
MNLKPGEA_	apaH	-1.148467638	0.15308374	Bis(5'-nucleosyl)-tetraph	3.6.1.41	apaH	Hydrolyzes diadenosine 5',5'''-P1
MNLKPGEA_	MNLKPGEA	-1.148645611	0.27292797	hypothetical protein	NA	rpfI	Protein of unknown function (DU
MNLKPGEA_	ampG	-1.148833346	0.34802577	Anhydromuropeptide pe	NA	ampG	Major facilitator Superfamily
MNLKPGEA_	sdhA	-1.150126686	0.00139371	Succinate dehydrogenas	1.3.5.1	sdhA	Belongs to the FAD-dependent c
MNLKPGEA_	MNLKPGEA	-1.150275026	NA	hypothetical protein	NA	iolH	Sugar phosphate isomerases epi
MNLKPGEA_	yesO	-1.151203752	0.34032494	Putative ABC transporter	NA	yesO	ABC transporter substrate-bindi
MNLKPGEA_	ettA	-1.1512194	0.00110765	Energy-dependent transl	NA	yjjK	abc transporter atp-binding prot
MNLKPGEA_	etp	-1.151242263	0.08704866	Low molecular weight p	3.1.3.48	etp	Low molecular weight phosphat
MNLKPGEA_	dauR	-1.15128958	0.00026615	Transcriptional regulator	NA	yheO	protein conserved in bacteria
MNLKPGEA_	virB4	-1.152594424	0.01564534	Type IV secretion system	NA	trwK	CagE, TrbE, VirB family, compon
MNLKPGEA_	hipO_4	-1.152879743	0.34289921	Hippurate hydrolase	3.5.1.32	0	amidohydrolase
MNLKPGEA_	hexR_2	-1.153322412	0.34477151	HTH-type transcriptional	NA	ybbH_1	transcriptional regulator
MNLKPGEA_	ampE	-1.153758075	0.34804128	Protein AmpE	NA	ampE	regulatory protein AmpE
MNLKPGEA_	MNLKPGEA	-1.155028918	NA	hypothetical protein	NA	0	Antitermination protein

MNLKPGEA_ gatD	-1.155710057	NA	Galactitol 1-phosphate 5	1.1.1.251	gatD	5-dehydrogenase
MNLKPGEA_ MNLKPGEA	-1.15619611	0.00066261	hypothetical protein	NA	yjhX	Belongs to the UPF0386 family
MNLKPGEA_ MNLKPGEA	-1.156361465	NA	hypothetical protein	NA	mdcF	auxin efflux carrier
MNLKPGEA_ fabZ	-1.158921587	0.00246532	3-hydroxyacyl-[acyl-carri	4.2.1.59	fabZ	Involved in unsaturated fatty aci
MNLKPGEA_ bamA_1	-1.159085809	0.00010169	Outer membrane protei	NA	bamA	Part of the outer membrane pro
MNLKPGEA_ narW	-1.159654948	NA	putative nitrate reductas	NA	narJ	nitrate reductase molybdenum c
MNLKPGEA_ MNLKPGEA	-1.161931033	0.2646366	hypothetical protein	NA	yqgE	Belongs to the UPF0301 (AlgH) f
MNLKPGEA_ araD	-1.163747591	NA	L-ribulose-5-phosphate 4	5.1.3.4	araD	Catalyzes the isomerization of L-
MNLKPGEA_ grpE	-1.163878156	0.02235549	Protein GrpE	NA	grpE	Participates actively in the respc
MNLKPGEA_ infC	-1.165103682	0.00044412	Translation initiation fac	NA	infC	IF-3 binds to the 30S ribosomal s
MNLKPGEA_ MNLKPGEA	-1.167132203	0.33295463	hypothetical protein	NA	yidR	Biopolymer transporter Tol
MNLKPGEA_ higB2	-1.169142561	0.25868415	Putative toxin HigB2	NA	VY92_07	protein conserved in bacteria
MNLKPGEA_ yfcF	-1.170374427	0.25735352	Glutathione S-transferas	2.5.1.18	yfcF	Glutathione S-transferase
MNLKPGEA_ MNLKPGEA	-1.170906733	0.32889779	hypothetical protein	NA	sthE	Fimbrial protein
MNLKPGEA_ sxy	-1.170958013	0.19406993	Protein Sxy	NA	sxy	regulator of competence-specifi
MNLKPGEA_ zur	-1.171637097	0.01293658	Zinc uptake regulation p	NA	zur	belongs to the Fur family
MNLKPGEA_ MNLKPGEA	-1.173002263	0.19934341	hypothetical protein	NA	0	protein conserved in bacteria
MNLKPGEA_ dgcN	-1.173778196	0.42347445	Diguanylate cyclase DgcI	2.7.7.65	yfiN	Diguanylate cyclase
MNLKPGEA_ iraP	-1.175630134	0.02161945	Anti-adapter protein IraP	NA	iraP	Inhibits RpoS proteolysis by regu
MNLKPGEA_ malZ	-1.17862312	0.42254061	Maltodextrin glucosidase	3.2.1.20	malZ	Belongs to the glycosyl hydrolas
MNLKPGEA_ pabC	-1.178893549	0.42108893	Aminodeoxychorismate l	4.1.3.38	pabC	4-amino-4-deoxychorismate lyas
MNLKPGEA_ MNLKPGEA	-1.178921094	NA	hypothetical protein	NA	0	PFAM Transposase, IS204 IS100
MNLKPGEA_ proY_1	-1.179178709	NA	Proline-specific permeas	NA	proY	Amino acid permease-associate
MNLKPGEA_ MNLKPGEA	-1.180808011	NA	hypothetical protein	NA	ybaM	Protein of unknown function (DU
MNLKPGEA_ MNLKPGEA	-1.181454352	NA	hypothetical protein	NA	0	Protein of unknown function (DU
MNLKPGEA_ mrdA_1	-1.183071554	0.33355756	Peptidoglycan D,D-transp	3.4.16.4	mrdA	Catalyzes cross-linking of the pe
MNLKPGEA_ mppA	-1.183077383	0.01097807	Periplasmic murein pept	NA	mppA	ABC transporter substrate-bindi
MNLKPGEA_ cyoC	-1.184266261	0.0027909	Cytochrome bo(3) ubiqui	NA	cyoC	oxidase subunit
MNLKPGEA_ MNLKPGEA	-1.185071968	NA	hypothetical protein	NA	0	Fimbrial protein
MNLKPGEA_ cydD	-1.186740658	0.41900818	ATP-binding/permease p	NA	cydD	(ABC) transporter

MNLKPGEA_	garL	-1.186838413	0.42073657	5-keto-4-deoxy-D-glucar	4.1.2.20	garL	Belongs to the HpcH HpaI aldola
MNLKPGEA_	MNLKPGEA	-1.187556361	0.41871003	hypothetical protein	NA	ypeB	protein conserved in bacteria
MNLKPGEA_	metAS	-1.189186551	0.32889779	Homoserine O-succinyltr	2.3.1.46	metAS	Transfers a succinyl group from
MNLKPGEA_	dkgB	-1.190098979	0.31896731	2,5-diketo-D-gluconic aci	1.1.1.346	dkgB	reductase
MNLKPGEA_	pyrG_2	-1.190269281	NA	CTP synthase	6.3.4.2	pyrG2	CTP synthase
MNLKPGEA_	MNLKPGEA	-1.192066857	0.19627378	hypothetical protein	NA	0	Restriction endonuclease
MNLKPGEA_	grxA	-1.193437057	0.25798207	Glutaredoxin 1	NA	grxA	Glutaredoxin
MNLKPGEA_	ribZ_1	-1.193495499	NA	Riboflavin transporter Ri	NA	0	Major facilitator superfamily
MNLKPGEA_	gcvP	-1.194879217	0.09459229	Glycine dehydrogenase (	1.4.4.2	gcvP	The glycine cleavage system cat
MNLKPGEA_	ahcY	-1.195921615	0.41871003	Adenosylhomocysteinase	3.3.1.1	0	May play a key role in the regula
MNLKPGEA_	pgtB	-1.196588693	0.03138361	Phosphoglycerate transp	2.7.13.3	pgtB	His Kinase A (phosphoacceptor)
MNLKPGEA_	MNLKPGEA	-1.197909743	0.31536256	Leu/Ile/Val-binding prot	NA	livJ	With LivFGHM is involved in the
MNLKPGEA_	yncE_2	-1.198533265	0.08811404	putative protein YncE	NA	0	amine dehydrogenase activity
MNLKPGEA_	glcR_1	-1.200084971	NA	HTH-type transcriptional	NA	0	transcriptional regulator
MNLKPGEA_	ftsN	-1.200207413	0.31974518	Cell division protein FtsN	NA	ftsN	Essential cell division protein tha
MNLKPGEA_	MNLKPGEA	-1.200368377	NA	hypothetical protein	NA	0	Antioxidant protein with alkyl hy
MNLKPGEA_	galT	-1.200908643	0.31662922	Galactose-1-phosphate u	2.7.7.12	galT	galactose-1-phosphate uridylyltr
MNLKPGEA_	MNLKPGEA	-1.201081226	0.13670251	putative protein	NA	yjaG	Protein of unknown function (DU
MNLKPGEA_	cooF	-1.202187756	NA	Iron-sulfur protein	NA	ysaA	electron transport
MNLKPGEA_	secY	-1.204654419	5.70E-06	Protein translocase subu	NA	secY	The central subunit of the protei
MNLKPGEA_	truD	-1.205179391	0.07784709	tRNA pseudouridine synt	5.4.99.27	truD	Responsible for synthesis of pse
MNLKPGEA_	MNLKPGEA	-1.205191431	0.00382079	hypothetical protein	NA	0	0
MNLKPGEA_	MNLKPGEA	-1.205908844	0.41009022	IS3 family transposase IS	NA	0	HTH-like domain
MNLKPGEA_	crcB_1	-1.208160203	0.06059551	Putative fluoride ion trar	NA	crcB	Important for reducing fluoride c
MNLKPGEA_	xylG_1	-1.208954165	0.408996	Xylose import ATP-bindi	7.5.2.10	xylG	import. Responsible for energy c
MNLKPGEA_	argR	-1.210446785	0.03185464	Arginine repressor	NA	argR	Regulates arginine biosynthesis
MNLKPGEA_	MNLKPGEA	-1.212473776	NA	hypothetical protein	NA	0	AraC family transcriptional regul
MNLKPGEA_	MNLKPGEA	-1.212665037	0.00306604	hypothetical protein	NA	0	sequence-specific DNA binding
MNLKPGEA_	hda	-1.213982261	0.24099062	DnaA regulatory inactiva	NA	hda	Mediates the interaction of DNA
MNLKPGEA_	hisD	-1.214746338	0.4212445	Histidinol dehydrogenase	1.1.1.23	hisD	Catalyzes the sequential NAD-de

MNLKPGEA_	MNLKPGEA	-1.217119955	0.15992771	Thermostable carboxype	3.4.17.19	ctaQ	Broad specificity carboxypetidas
MNLKPGEA_	MNLKPGEA	-1.217613819	NA	hypothetical protein	NA	0	HNH nucleases
MNLKPGEA_	fimD_1	-1.218787083	0.21378964	Outer membrane usher	NA	fimD	Usher protein
MNLKPGEA_	hcaR_2	-1.221226341	NA	Hca operon transcription	NA	0	Transcriptional regulator
MNLKPGEA_	lgoT_1	-1.221938148	0.40300305	putative L-galactonate tı	NA	0	Major facilitator Superfamily
MNLKPGEA_	rihC	-1.222235966	0.31705872	Non-specific ribonucleos	3.2.-.-	rihC	Belongs to the IUNH family
MNLKPGEA_	ddc	-1.22224338	0.13003502	L-2,4-diaminobutyrate d	4.1.1.86	ddc	decarboxylase
MNLKPGEA_	MNLKPGEA	-1.222358295	0.32402143	hypothetical protein	NA	0	0
MNLKPGEA_	nudF	-1.222758201	0.15750694	ADP-ribose pyrophospha	3.6.1.13	nudF	COG0494 NTP pyrophosphohydr
MNLKPGEA_	MNLKPGEA	-1.222915133	NA	hypothetical protein	NA	0	Major facilitator Superfamily
MNLKPGEA_	cynR_5	-1.223160911	0.402058	HTH-type transcriptional	NA	MA20_0(	transcriptional regulator
MNLKPGEA_	yeeO	-1.223882728	0.23291554	putative FMN/FAD expo	NA	yeeO	Mate efflux family protein
MNLKPGEA_	purK	-1.224184575	0.41920715	N5-carboxyaminoimidaz	6.3.4.18	purK	Catalyzes the ATP-dependent co
MNLKPGEA_	MNLKPGEA	-1.225047309	0.41387641	hypothetical protein	NA	0	Protein involved in biological_pr
MNLKPGEA_	MNLKPGEA	-1.225748282	NA	hypothetical protein	NA	yhcC	radical SAM protein
MNLKPGEA_	eco	-1.227621056	0.02900971	Ecotin	NA	eco	General inhibitor of pancreatic s
MNLKPGEA_	MNLKPGEA	-1.229099213	NA	hypothetical protein	NA	#N/A	#N/A
MNLKPGEA_	glnQ_2	-1.229397294	0.40663472	Glutamine transport ATF	NA	artM_2	(ABC) transporter
MNLKPGEA_	MNLKPGEA	-1.230569407	0.03706438	hypothetical protein	NA	yecJ	Protein of unknown function (DU
MNLKPGEA_	dnaN	-1.232402329	0.03910289	Beta sliding clamp	NA	dnaN	Confers DNA tethering and proce
MNLKPGEA_	pheA	-1.23245159	0.06223013	Bifunctional chorismate	NA	pheA	chorismate mutase
MNLKPGEA_	cysA	-1.233066048	0.2982651	Sulfate/thiosulfate impc	7.3.2.3	cysA	Part of the ABC transporter com
MNLKPGEA_	MNLKPGEA	-1.234608624	0.00479358	hypothetical protein	NA	#N/A	#N/A
MNLKPGEA_	lpfA_2	-1.235850306	NA	putative major fimbrial s	NA	yraH	Part of the yraHIJK fimbrial oper
MNLKPGEA_	murP	-1.239452853	NA	PTS system N-acetylmur	NA	murP	The phosphoenolpyruvate-deper
MNLKPGEA_	yheI	-1.239562659	0.106317	putative multidrug resist	3.6.3.-	mdlA	Involved in lipid A export and po
MNLKPGEA_	MNLKPGEA	-1.239753937	0.24710759	hypothetical protein	NA	ychJ	Belongs to the UPF0225 family
MNLKPGEA_	bamD	-1.241378034	4.04E-05	Outer membrane protei	NA	bamD	Part of the outer membrane pro
MNLKPGEA_	MNLKPGEA	-1.241862536	0.3976771	hypothetical protein	NA	0	Glyoxalase/Bleomycin resistanc
MNLKPGEA_	rbsB_1	-1.241895702	0.17349053	Ribose import binding pı	NA	0	ABC transporter substrate-bindi

MNLKPGEA_	MNLKPGEA	-1.243608392	0.03514029	hypothetical protein	NA	0	0
MNLKPGEA_	srlR_2	-1.244179967	0.06675065	Glucitol operon represso	NA	0	Transcriptional
MNLKPGEA_	ydfK_2	-1.244427468	NA	putative membrane prot	NA	0	Protein of unknown function (DU
MNLKPGEA_	MNLKPGEA	-1.246891745	0.39540461	hypothetical protein	NA	0	Cupin 2, conserved barrel domai
MNLKPGEA_	argH	-1.247067569	0.08021684	Argininosuccinate lyase	4.3.2.1	argH	argininosuccinate lyase
MNLKPGEA_	xylB_1	-1.24893755	0.29485607	Xylulose kinase	2.7.1.17	xylB	xylulose kinase
MNLKPGEA_	treR	-1.250510338	0.30371681	HTH-type transcriptional	NA	treR	trehalose
MNLKPGEA_	MNLKPGEA	-1.251963551	NA	hypothetical protein	NA	0	protein conserved in bacteria
MNLKPGEA_	mtnC	-1.252078353	0.3906211	Enolase-phosphatase E1	3.1.3.77	mtnC	Bifunctional enzyme that catalyz
MNLKPGEA_	MNLKPGEA	-1.25251463	1.17E-05	hypothetical protein	NA	0	TrbM
MNLKPGEA_	cpxA	-1.252837175	0.02745661	Sensor histidine kinase C	2.7.13.3	cpxA	PhoQ Sensor
MNLKPGEA_	mdtH_2	-1.253163502	0.17726418	Multidrug resistance pro	NA	mdtH	Multidrug resistance protein md
MNLKPGEA_	iscS	-1.254038544	0.0018687	Cysteine desulfurase IscS	2.8.1.7	iscS	Master enzyme that delivers sul
MNLKPGEA_	MNLKPGEA	-1.254746141	0.29358571	hypothetical protein	NA	0	Transposase
MNLKPGEA_	murQ_1	-1.255038673	NA	N-acetylmuramic acid 6-	4.2.1.126	murQ	Specifically catalyzes the cleava
MNLKPGEA_	pabB	-1.255577488	0.29019677	Aminodeoxychorismate s	2.6.1.85	pabB	Part of a heterotetrameric comp
MNLKPGEA_	add	-1.258585616	0.00317987	Adenosine deaminase	3.5.4.4	add	Catalyzes the hydrolytic deamina
MNLKPGEA_	pdxB	-1.260099257	0.03035983	Erythronate-4-phosphate	1.1.1.290	pdxB	Catalyzes the oxidation of erythr
MNLKPGEA_	MNLKPGEA	-1.26041293	NA	hypothetical protein	NA	0	0
MNLKPGEA_	sbmA	-1.260996923	0.29272892	Peptide antibiotic transp	NA	sbmA	In Escherichia coli SbmA is involv
MNLKPGEA_	yhhJ	-1.261011508	0.38646682	Inner membrane transpo	NA	yhhJ	ABC-type multidrug transport sy
MNLKPGEA_	MNLKPGEA	-1.261900849	0.0467876	hypothetical protein	NA	walW	Lipopolysaccharide biosynthesis
MNLKPGEA_	cfxP	-1.262273336	0.22984555	Phosphoribulokinase, pla	2.7.1.19	prkB	Phosphoribulokinase
MNLKPGEA_	MNLKPGEA	-1.265089746	0.28858231	hypothetical protein	NA	MA20_35	protein conserved in bacteria
MNLKPGEA_	lpxL_2	-1.265135285	0.22802842	Lipid A biosynthesis laur	2.3.1.241	lpxL	Catalyzes the transfer of laurate
MNLKPGEA_	lolD	-1.265338286	NA	Lipoprotein-releasing sys	3.6.3.-	lolD	Part of the ABC transporter com
MNLKPGEA_	wzxE	-1.265495568	0.38910762	Lipid III flippase	NA	wzxE	Mediates the transbilayer move
MNLKPGEA_	sdhD	-1.267819144	0.0134477	Succinate dehydrogenas	NA	sdhD	Succinate dehydrogenase hydrop
MNLKPGEA_	MNLKPGEA	-1.268393345	0.01144325	HTH-type transcriptional	NA	ascG_1	transcriptional regulator
MNLKPGEA_	bisC	-1.268722509	0.29494193	Biotin sulfoxide reductas	1.-.-.-	bisC	Belongs to the prokaryotic molyb

MNLKPGEA_ galR	-1.269390248	0.21441504	HTH-type transcriptional	NA	galR	transcriptional regulator
MNLKPGEA_ mutS	-1.27005509	0.12299617	DNA mismatch repair pr	NA	mutS	that it carries out the mismatch
MNLKPGEA_ adhB	-1.270256965	NA	Alcohol dehydrogenase 2	1.1.1.1	fucO	alcohol dehydrogenase
MNLKPGEA_ MNLKPGEA	-1.270256965	NA	hypothetical protein	NA	yfdR	5'-deoxynucleotidase activity
MNLKPGEA_ alaA	-1.270404959	0.03012006	Glutamate-pyruvate ami	2.6.1.2	alaA	in Corynebacterium glutamicum
MNLKPGEA_ yajC	-1.271247767	0.01451897	Sec translocon accessory	NA	yajC	Preprotein translocase subunit
MNLKPGEA_ MNLKPGEA	-1.272644336	0.07053055	hypothetical protein	NA	yfgM	protein conserved in bacteria
MNLKPGEA_ norB_1	-1.273195401	NA	Quinolone resistance pro	NA	norB	Quinolone resistance protein
MNLKPGEA_ ydiM	-1.27415516	0.38276043	Inner membrane transpo	NA	ydiM	transport protein
MNLKPGEA_ yohK_1	-1.275468304	0.28232673	Inner membrane protein	NA	yohK	effector of murein hydrolase
MNLKPGEA_ gap_1	-1.27559505	0.03814771	Glyceraldehyde-3-phospl	1.2.1.12	gap	Belongs to the glyceraldehyde-3
MNLKPGEA_ rnt	-1.275929993	0.16397629	Ribonuclease T	3.1.13.-	rnt	Trims short 3' overhangs of a va
MNLKPGEA_ holA	-1.276091423	0.16279405	DNA polymerase III subu	2.7.7.7	holA	dna polymerase III delta subunit
MNLKPGEA_ oxyR_1	-1.277027488	0.21030592	Hydrogen peroxide-induc	NA	0	Transcriptional regulator
MNLKPGEA_ MNLKPGEA	-1.277279777	0.06675065	putative protein	NA	0	periplasmic binding protein
MNLKPGEA_ livF_5	-1.278452615	0.07635036	High-affinity branched-cl	NA	urtE	ABC transporter ATP-binding pro
MNLKPGEA_ hcaT	-1.279141838	0.38276043	putative 3-phenylpropior	NA	hcaT	Major facilitator Superfamily
MNLKPGEA_ aspS	-1.280161596	0.00020304	Aspartate--tRNA ligase	6.1.1.12	aspS	L-aspartate is first activated by A
MNLKPGEA_ fhuB	-1.280788416	0.38276043	Iron(3+)-hydroxamate im	NA	fhuB	Belongs to the binding-protein-d
MNLKPGEA_ ecpR	-1.281996012	NA	HTH-type transcriptional	NA	matA	Part of the ecpRABCDE operon, v
MNLKPGEA_ rsmC	-1.282611487	0.28296255	Ribosomal RNA small su	2.1.1.172	rsmC	Specifically methylates the guar
MNLKPGEA_ ldcC	-1.284125493	0.08987629	Constitutive lysine decar	4.1.1.18	ldcC	decarboxylase
MNLKPGEA_ ompA_3	-1.285169364	2.94E-12	Outer membrane protein	NA	ompA	Belongs to the ompA family
MNLKPGEA_ MNLKPGEA	-1.285472724	0.37992681	hypothetical protein	NA	yfcL	YfcL protein
MNLKPGEA_ arsC_2	-1.286866882	0.1148752	Arsenate reductase	1.20.4.1	arsC	arsenate reductase
MNLKPGEA_ der	-1.289273186	0.00297378	GTPase Der	NA	der	GTPase that plays an essential r
MNLKPGEA_ rcnR	-1.289906232	0.38589145	Transcriptional repressor	NA	rcnR	protein conserved in bacteria
MNLKPGEA_ cysS	-1.290463461	0.00283195	Cysteine--tRNA ligase	6.1.1.16	cysS	Belongs to the class-I aminoacyl
MNLKPGEA_ secA	-1.290958376	0.0002712	Protein translocase subu	NA	secA	Part of the Sec protein transloca
MNLKPGEA_ nasR	-1.291219069	0.16800891	Nitrate regulatory protei	NA	nasR	Nitrate and nitrite sensing doma

MNLKPGEA_ feaB_2	-1.294307284	NA	Phenylacetaldehyde deh	1.2.1.39	feaB	belongs to the aldehyde dehydrc
MNLKPGEA_ MNLKPGEA	-1.294739382	0.21466076	hypothetical protein	NA	0	0
MNLKPGEA_ MNLKPGEA	-1.295993898	NA	hypothetical protein	NA	0	methyltransferase
MNLKPGEA_ MNLKPGEA	-1.296359103	NA	hypothetical protein	NA	yhbV	protease
MNLKPGEA_ alsE_1	-1.29641259	NA	D-allulose-6-phosphate 3	5.1.3.-	alsE	3-epimerase
MNLKPGEA_ yejK	-1.298038337	0.20308941	Nucleoid-associated prot	NA	ndpA	Nucleoid-associated protein
MNLKPGEA_ MNLKPGEA	-1.298237717	0.13581689	hypothetical protein	NA	0	SIR2-like domain
MNLKPGEA_ rhtB_1	-1.298652321	0.27303097	Homoserine/homoserine	NA	yrhP	threonine efflux protein
MNLKPGEA_ MNLKPGEA	-1.298706442	NA	NADH oxidase	1.-.-.-	0	COG1902 NADH flavin oxidoredu
MNLKPGEA_ tsaR_1	-1.298929383	0.38276043	HTH-type transcriptional	NA	0	LysR substrate binding domain
MNLKPGEA_ cbiG	-1.30223006	NA	Cobalt-precorrin-5A hydr	3.7.1.12	cbiG	Cobalamin biosynthesis protein (
MNLKPGEA_ fepC	-1.306366816	NA	Ferric enterobactin trans	NA	fepC	(ABC) transporter
MNLKPGEA_ bdhA	-1.308774581	NA	D-beta-hydroxybutyrate (	1.1.1.30	bdhA	COG1028 Dehydrogenases with
MNLKPGEA_ sdhB	-1.309392149	0.00454065	Succinate dehydrogenas(	1.3.5.1	sdhB	Belongs to the succinate dehydr(
MNLKPGEA_ bcsC	-1.310411315	0.37181399	Cellulose synthase operc	NA	bcsC	Cellulose synthase
MNLKPGEA_ guaC	-1.312043262	0.00997262	GMP reductase	1.7.1.7	guaC	Catalyzes the irreversible NADPH
MNLKPGEA_ MNLKPGEA	-1.313139064	NA	hypothetical protein	NA	0	0
MNLKPGEA_ MNLKPGEA	-1.314097008	0.26417825	hypothetical protein	NA	besA	hydrolase of the alpha beta supe
MNLKPGEA_ MNLKPGEA	-1.31590348	NA	hypothetical protein	NA	0	Glutathione S-transferase
MNLKPGEA_ MNLKPGEA	-1.316581649	0.36677274	hypothetical protein	NA	0	0
MNLKPGEA_ ptsG	-1.317003911	0.00016848	PTS system glucose-spec	NA	ptsG	Phosphotransferase System
MNLKPGEA_ kefC_1	-1.318594079	0.36562294	Glutathione-regulated p(	NA	kefB	Belongs to the monovalent catic
MNLKPGEA_ rcsC_2	-1.320358012	0.1418224	Sensor histidine kinase R	2.7.13.3	rcsC	PhoQ Sensor
MNLKPGEA_ rhtC_1	-1.320621299	NA	Threonine efflux protein	NA	0	threonine efflux protein
MNLKPGEA_ srlD	-1.321116411	0.37704134	Sorbitol-6-phosphate 2-d	1.1.1.140	srlD	Belongs to the short-chain dehyc
MNLKPGEA_ carB_3	-1.321747073	NA	Carbamoyl-phosphate sy	NA	bccA	carboxylase
MNLKPGEA_ ribZ_2	-1.323553405	0.36948997	Riboflavin transporter Ri	NA	yebQ	Major facilitator superfamily
MNLKPGEA_ tdh	-1.323634735	0.02365066	L-threonine 3-dehydroge	1.1.1.103	tdh	Catalyzes the NAD( )-dependent
MNLKPGEA_ nudG	-1.324607793	0.36764774	CTP pyrophosphohydrola	3.6.1.65	mutT	belongs to the nudix hydrolase fa
MNLKPGEA_ ulaR	-1.327916832	0.18874176	HTH-type transcriptional	NA	ulaR	transcriptional regulator

MNLKPGEA_	malP_4	-1.327927862	0.03837703	Maltodextrin phosphoryl	2.4.1.1	malP	Phosphorylase is an important a
MNLKPGEA_	mltB	-1.328171255	0.07972181	Membrane-bound lytic n	4.2.2.-	mltB	Lytic murein transglycosylase
MNLKPGEA_	msrC	-1.3316161	0.04573269	Free methionine-R-sulfo	1.8.4.14	yebR	GAF domain-containing protein
MNLKPGEA_	MNLKPGEA	-1.331790981	0.01504677	hypothetical protein	NA	#N/A	#N/A
MNLKPGEA_	sodA	-1.331972902	0.00512051	Superoxide dismutase [M	1.15.1.1	sodA	Destroys radicals which are norr
MNLKPGEA_	avtA	-1.333733361	0.36087314	Valine--pyruvate aminot	2.6.1.66	avtA	Valine--pyruvate aminotransfera
MNLKPGEA_	MNLKPGEA	-1.335300978	NA	hypothetical protein	NA	0	Helix-turn-helix XRE-family like p
MNLKPGEA_	pyrE	-1.335400267	NA	Orotate phosphoribosylt	2.4.2.10	pyrE	Catalyzes the transfer of a ribos
MNLKPGEA_	mutT	-1.338104529	NA	8-oxo-dGTP diphosphata	3.6.1.55	mutT	belongs to the nudix hydrolase fa
MNLKPGEA_	tusC	-1.338423901	NA	Protein TusC	NA	tusC	Belongs to the DsrF TusC family
MNLKPGEA_	umuC_2	-1.338825965	0.19437103	Protein UmuC	NA	umuC	DNA polymerase
MNLKPGEA_	budB	-1.339026627	NA	Acetolactate synthase, c	2.2.1.6	alsS	Belongs to the TPP enzyme fami
MNLKPGEA_	MNLKPGEA	-1.346435285	NA	hypothetical protein	NA	0	Toprim-like
MNLKPGEA_	nuoG	-1.347214369	0.00377658	NADH-quinone oxidoredu	7.1.1.-	nuoG	NADH-quinone oxidoreductase
MNLKPGEA_	hisF	-1.348641265	NA	Imidazole glycerol phosp	4.3.2.10	hisF	IGPS catalyzes the conversion of
MNLKPGEA_	srlR_1	-1.349899163	0.25697006	Glucitol operon represso	NA	gatR	Transcriptional
MNLKPGEA_	sucA	-1.352152277	6.24E-06	2-oxoglutarate dehydrog	1.2.4.2	sucA	Dehydrogenase E1 component
MNLKPGEA_	rpoZ	-1.352713444	0.00542239	DNA-directed RNA polyn	2.7.7.6	rpoZ	Promotes RNA polymerase asse
MNLKPGEA_	glpF_1	-1.353089781	0.17820069	Glycerol uptake facilitato	NA	glpF	Belongs to the MIP aquaporin (T
MNLKPGEA_	MNLKPGEA	-1.353312293	5.64E-06	hypothetical protein	NA	0	0
MNLKPGEA_	MNLKPGEA	-1.353468931	NA	hypothetical protein	NA	0	of the drug metabolite transport
MNLKPGEA_	gsiA_2	-1.356930644	0.13295543	Glutathione import ATP-	7.4.2.10	gsiA	ATPase activity
MNLKPGEA_	yfcG	-1.358655146	0.04670317	Disulfide-bond oxidoredu	1.8.4.-	yfcG	Belongs to the GST superfamily
MNLKPGEA_	surE	-1.359291649	0.13230884	5'/3'-nucleotidase SurE	3.1.3.5	surE	Nucleotidase that shows phosph
MNLKPGEA_	mnmE	-1.360647516	0.35134134	tRNA modification GTPa	3.6.-.-	mnmE	Exhibits a very high intrinsic GTP
MNLKPGEA_	yajR	-1.360760258	0.34989565	Inner membrane transpo	NA	yajR	Major facilitator Superfamily
MNLKPGEA_	mukB	-1.362218831	0.01945821	Chromosome partition p	NA	mukB	Plays a central role in chromoso
MNLKPGEA_	btuD_2	-1.362323325	0.3512609	Vitamin B12 import ATP	7.6.2.8	oppF	Belongs to the ABC transporter s
MNLKPGEA_	rsxB	-1.362586838	0.35088599	Ion-translocating oxidore	7.-.-.-	rnfB	Part of a membrane complex inv
MNLKPGEA_	lsrC	-1.366239079	NA	Autoinducer 2 import sys	NA	lsrC	Belongs to the binding-protein-d

MNLKPGEA_	hmuU_3	-1.368506006	NA	Hemin transport system	NA	btuC	Belongs to the binding-protein-d
MNLKPGEA_	thrA	-1.36859616	0.25364981	Bifunctional aspartokina	NA	thrA	belongs to the aspartokinase far
MNLKPGEA_	rpmA	-1.371081302	0.00028777	50S ribosomal protein L2	NA	rpmA	Belongs to the bacterial ribosom
MNLKPGEA_	MNLKPGEA	-1.37158634	NA	hypothetical protein	NA	#N/A	#N/A
MNLKPGEA_	fre	-1.373408437	0.00499665	NAD(P)H-flavin reductas	1.5.1.41	fre	PFAM Oxidoreductase FAD NAD
MNLKPGEA_	MNLKPGEA	-1.373410175	0.0046951	hypothetical protein	NA	#N/A	#N/A
MNLKPGEA_	MNLKPGEA	-1.374028316	0.01733249	hypothetical protein	NA	yafK	ErfK YbiS YcfS YnhG family prote
MNLKPGEA_	ybgC	-1.375521287	0.03421676	Acyl-CoA thioester hydro	3.1.2.-	ybgC	Thioesterase
MNLKPGEA_	MNLKPGEA	-1.375754424	1.51E-05	Putative tyrosine-protein	2.7.10.-	wzc	protein involved in exopolysacch
MNLKPGEA_	MNLKPGEA	-1.376212924	0.00310713	hypothetical protein	NA	0	acetyltransferase
MNLKPGEA_	ctpF_2	-1.37841439	NA	putative cation-transport	3.6.3.-	ctpF_2	ATPase, P-type (transporting), H
MNLKPGEA_	tyrS	-1.378765089	4.93E-06	Tyrosine--tRNA ligase	6.1.1.1	tyrS	Catalyzes the attachment of tyro
MNLKPGEA_	truA	-1.378772348	0.24124301	tRNA pseudouridine synt	5.4.99.12	truA	Formation of pseudouridine at p
MNLKPGEA_	MNLKPGEA	-1.380117565	0.12445633	IS3 family transposase IS	NA	0	Transposase
MNLKPGEA_	ldh1	-1.382399616	NA	L-lactate dehydrogenase	1.1.1.27	ldh	Belongs to the LDH MDH superfa
MNLKPGEA_	mglA_1	-1.383307059	0.0337843	Galactose/methyl galact	7.5.2.11	mglA	import. Responsible for energy c
MNLKPGEA_	yphB	-1.383879712	NA	putative protein YphB	NA	yphB	Aldose 1-epimerase
MNLKPGEA_	MNLKPGEA	-1.384142304	NA	hypothetical protein	NA	0	PFAM GCN5-related N-acetyltra
MNLKPGEA_	yejF	-1.385127587	0.34150115	putative ABC transporter	NA	yejF	ATPase activity
MNLKPGEA_	pepN	-1.3852973	1.36E-05	Aminopeptidase N	3.4.11.2	pepN	aminopeptidase N
MNLKPGEA_	dmsC_1	-1.385632087	0.3427026	Anaerobic dimethyl sulfo	NA	dmsC	Dimethyl sulfoxide reductase
MNLKPGEA_	ymdB	-1.385786535	0.12533464	O-acetyl-ADP-ribose dea	3.1.1.106	ymdB	Deacetylates O-acetyl-ADP ribos
MNLKPGEA_	ynjE	-1.387720584	NA	Thiosulfate sulfurtransfe	2.8.1.1	ynjE	sulfurtransferase
MNLKPGEA_	ypeA	-1.387955854	0.24433271	Acetyltransferase YpeA	2.3.1.-	ypeA	Belongs to the acetyltransferase
MNLKPGEA_	sbnD_1	-1.388873412	NA	Staphyloferrin B transpo	NA	mdtG	Major facilitator Superfamily
MNLKPGEA_	acpH	-1.391472152	0.34032494	Acyl carrier protein phos	3.1.4.14	acpH	Converts holo-ACP to apo-ACP by
MNLKPGEA_	MNLKPGEA	-1.391789237	NA	ISKra4 family transposas	NA	fimB	FimB is one of the 2 regulatory p
MNLKPGEA_	galU	-1.393477411	5.41E-07	UTP--glucose-1-phospha	2.7.7.9	galU	Utp--glucose-1-phosphate uridyl
MNLKPGEA_	MNLKPGEA	-1.397861075	0.04699549	hypothetical protein	NA	sanA	Vancomycin high temperature e
MNLKPGEA_	hslU	-1.39791102	0.00356279	ATP-dependent protease	NA	hslU	this subunit has chaperone activ

MNLKPGEA_ ycaD_1	-1.400589629	0.01923717	putative MFS-type trans	NA	0	Major facilitator superfamily
MNLKPGEA_ artQ_1	-1.400667428	0.35134134	Arginine transport syste	NA	yecS_2	amino acid ABC transporter
MNLKPGEA_ bcsB_1	-1.401420125	NA	Cyclic di-GMP-binding pr	NA	bcsB	cellulose synthase
MNLKPGEA_ pta	-1.401762835	1.15E-05	Phosphate acetyltransfe	2.3.1.8	pta	belongs to the CobB CobQ famil
MNLKPGEA_ mtfA	-1.403646456	0.00170372	Protein MtfA	NA	mtfA	Belongs to the MtfA family
MNLKPGEA_ serB	-1.403854806	0.23339116	Phosphoserine phosphat	3.1.3.3	serB	phosphoserine phosphatase
MNLKPGEA_ dxr	-1.404809331	0.0528725	1-deoxy-D-xylulose 5-ph	1.1.1.267	dxr	Catalyzes the NADP-dependent r
MNLKPGEA_ selA	-1.405182804	0.33375303	L-seryl-tRNA(Sec) seleni	2.9.1.1	selA	Converts seryl-tRNA(Sec) to sele
MNLKPGEA_ gloA	-1.408278746	0.0009655	Lactoylglutathione lyase	4.4.1.5	gloA	Catalyzes the conversion of hem
MNLKPGEA_ xylH_2	-1.409540481	0.1265265	Xylose transport system	NA	0	Belongs to the binding-protein-d
MNLKPGEA_ gltB	-1.409774973	0.03421676	Glutamate synthase [NA	1.4.1.13	gltB	Glutamate synthase
MNLKPGEA_ rhtA	-1.410017058	0.07972181	Threonine/homoserine e	NA	rhtA	permease DMT superfamily
MNLKPGEA_ cyoD	-1.411155314	0.00181717	Cytochrome bo(3) ubiqui	NA	cyoD	PFAM Cytochrome C oxidase sub
MNLKPGEA_ MNLKPGEA	-1.411809026	0.22802842	hypothetical protein	NA	#N/A	#N/A
MNLKPGEA_ manZ_2	-1.412217896	0.33229626	PTS system mannose-sp	NA	0	PTS system mannose/fructose/s
MNLKPGEA_ suhB_2	-1.412858925	NA	Inositol-1-monophospha	3.1.3.25	0	inositol monophosphatase
MNLKPGEA_ MNLKPGEA	-1.412927287	0.00948678	hypothetical protein	NA	0	Transcriptional regulator
MNLKPGEA_ yfiC	-1.413083219	0.33340067	tRNA1(Val) (adenine(37	2.1.1.223	yfiC	Specifically methylates the ader
MNLKPGEA_ MNLKPGEA	-1.414587071	5.01E-06	hypothetical protein	NA	bax	FlgJ-related protein
MNLKPGEA_ nrdF	-1.415131194	0.01340668	Ribonucleoside-diphosph	1.17.4.1	nrdF	Provides the precursors necessa
MNLKPGEA_ cobD_1	-1.415560893	NA	Threonine-phosphate de	4.1.1.81	cobD	decarboxylates L-threonine-O-3-
MNLKPGEA_ dxs	-1.41691049	0.03788836	1-deoxy-D-xylulose-5-ph	2.2.1.7	dxs	Catalyzes the acyloin condensati
MNLKPGEA_ mtnB	-1.417227023	NA	Methylthioribulose-1-ph	4.2.1.109	mtnB	Catalyzes the dehydration of me
MNLKPGEA_ iolC	-1.417328745	0.33138136	5-dehydro-2-deoxyglucor	2.7.1.92	iolC	5-dehydro-2-deoxygluconokinase
MNLKPGEA_ ribF	-1.418074359	0.00777456	Bifunctional riboflavin ki	NA	ribF	Belongs to the ribF family
MNLKPGEA_ licC_6	-1.420133623	NA	Lichenan permease IIC c	NA	0	The phosphoenolpyruvate-deper
MNLKPGEA_ MNLKPGEA	-1.421306923	NA	hypothetical protein	NA	0	Protein of unknown function (DU
MNLKPGEA_ MNLKPGEA	-1.421782177	0.00212347	hypothetical protein	NA	0	Domain of unknown function (DU
MNLKPGEA_ ykoT	-1.422548684	0.2235144	putative glycosyltransfer	2.4.-.-	ykoT	Bactoprenol glucosyl transferase
MNLKPGEA_ fhuA_2	-1.425085643	0.0005607	Ferrichrome outer mem	NA	fhuA	Receptor

MNLKPGEA_	MNLKPGEA	-1.425419327	0.00621544	hypothetical protein	NA	0	COG0671 Membrane-associatec
MNLKPGEA_	metL	-1.430350918	0.15625618	Bifunctional aspartokina	NA	metL	belongs to the aspartokinase far
MNLKPGEA_	mlaD	-1.430379615	0.16060559	Intermembrane phosphc	NA	mlaD	ABC-type transport system invol
MNLKPGEA_	rsmI	-1.431817584	0.32406053	Ribosomal RNA small su	2.1.1.198	rsmI	Catalyzes the 2'-O-methylation c
MNLKPGEA_	sapD	-1.433104764	0.15308374	Peptide transport systen	NA	sapD	ATPase activity
MNLKPGEA_	MNLKPGEA	-1.433933391	0.00051304	hypothetical protein	NA	0	glycosyl transferase family
MNLKPGEA_	hemN	-1.433979063	0.00231386	Oxygen-independent cop	1.3.98.3	hemN	Belongs to the anaerobic coprop
MNLKPGEA_	dld	-1.435269631	0.03731986	Quinone-dependent D-la	1.1.5.12	dld	Catalyzes the oxidation of D-lact
MNLKPGEA_	galE	-1.43584852	0.07191665	UDP-glucose 4-epimeras	5.1.3.2	galE	udp-glucose 4-epimerase
MNLKPGEA_	mlaC	-1.436831831	0.01923366	Intermembrane phosphc	NA	mlaC	ABC-type transport system invol
MNLKPGEA_	pcaK_1	-1.43799883	NA	4-hydroxybenzoate trans	NA	0	Major facilitator Superfamily
MNLKPGEA_	malP_5	-1.438601674	0.21930514	PTS system maltose-spe	NA	0	PTS system
MNLKPGEA_	MNLKPGEA	-1.438950253	NA	hypothetical protein	NA	#N/A	#N/A
MNLKPGEA_	MNLKPGEA	-1.439139532	NA	hypothetical protein	NA	0	helix_turn_helix, Lux Regulon
MNLKPGEA_	rnb	-1.440136642	0.01986449	Exoribonuclease 2	3.1.13.1	rnb	Involved in mRNA degradation. I
MNLKPGEA_	rbsR_2	-1.440779375	0.21838429	Ribose operon repressor	NA	0	transcriptional regulator
MNLKPGEA_	sucB	-1.440815754	0.0010809	Dihydrolipoyllysine-resid	2.3.1.61	sucB	The 2-oxoglutarate dehydrogena
MNLKPGEA_	potA_4	-1.442109697	0.16543319	Spermidine/putrescine i	7.6.2.11	potG	Part of the ABC transporter com
MNLKPGEA_	dgoA_1	-1.442352137	NA	2-dehydro-3-deoxy-6-phc	4.1.2.21	dgoA	KDPG and KHG aldolase
MNLKPGEA_	MNLKPGEA	-1.44239483	0.1231709	hypothetical protein	NA	0	radical SAM
MNLKPGEA_	MNLKPGEA	-1.443738457	0.08374568	Tn3 family transposase I	NA	tnpA	Transposase
MNLKPGEA_	ygdR_2	-1.444094699	0.01863863	putative lipoprotein YgdI	NA	ygdI	Lipoprotein
MNLKPGEA_	murB	-1.448730867	0.21820879	UDP-N-acetylenolpyruvo	1.3.1.98	murB	cell wall formation
MNLKPGEA_	lpxK	-1.452022908	0.15308374	Tetraacyldisaccharide 4'	2.7.1.130	lpxK	Transfers the gamma-phosphate
MNLKPGEA_	MNLKPGEA	-1.454120986	0.00113772	hypothetical protein	NA	wzx1	Membrane protein involved in th
MNLKPGEA_	yafP_1	-1.455023025	NA	putative N-acetyltransfe	2.3.1.-	yjaB_1	N-acetyltransferase
MNLKPGEA_	gatC	-1.457055043	0.12632763	PTS system galactitol-sp	NA	gatC	system Galactitol-specific IIC co
MNLKPGEA_	araC_1	-1.457399885	0.08339795	Arabinose operon regula	NA	araC	transcriptional regulator
MNLKPGEA_	secG	-1.457850552	6.68E-07	Protein-export membrar	NA	secG	Preprotein translocase, subunit S
MNLKPGEA_	yqaB	-1.459107381	0.00347807	Fructose-1-phosphate ph	3.1.3.-	yqaB	Phosphatase

MNLKPGEA_ MNLKPGEA	-1.460414078	NA	hypothetical protein	NA	0	0
MNLKPGEA_ pflD	-1.464386275	NA	Trans-4-hydroxy-L-prolin	4.2.1.172	ybiW	Glycine radical enzyme that cata
MNLKPGEA_ virB8	-1.465496539	0.14470861	Type IV secretion system	NA	ptlE	VirB8 protein
MNLKPGEA_ gapA	-1.466806913	3.36E-10	Glyceraldehyde-3-phospl	1.2.1.12	gapA	Belongs to the glyceraldehyde-3
MNLKPGEA_ modB	-1.467326846	0.2358048	Molybdenum transport s	NA	modB	ABC-type molybdate transport s
MNLKPGEA_ csgD	-1.468408071	0.25398687	CsgBAC operon transcrip	NA	corR	Response regulator containing a
MNLKPGEA_ cspA	-1.470821416	0.00034573	Cold shock protein CspA	NA	cspA	SMART Cold shock protein
MNLKPGEA_ catB	-1.47326702	0.20920979	Muconate cycloisomeras	5.5.1.1	catB	Belongs to the mandelate racem
MNLKPGEA_ repE	-1.474	7.98E-06	Replication initiation prc	NA	0	Initiator Replication protein
MNLKPGEA_ mukE	-1.476687405	0.20631172	Chromosome partition p	NA	mukE	Involved in chromosome conden
MNLKPGEA_ fhuD	-1.476802456	NA	Iron(3+)-hydroxamate-bi	NA	fhuD	ABC-type Fe3 -hydroxamate trar
MNLKPGEA_ nuoH	-1.476875658	0.14253829	NADH-quinone oxidoredu	7.1.1.-	nuoH	NDH-1 shuttles electrons from N
MNLKPGEA_ clpC	-1.478288382	1.74E-05	ATP-dependent Clp prote	NA	clpC	Part of a stress-induced multi-ch
MNLKPGEA_ accB	-1.478833693	0.11463694	Biotin carboxyl carrier pr	NA	accB	first, biotin carboxylase catalyze
MNLKPGEA_ yciF	-1.478835887	0.14609636	Protein YciF	NA	yciF	protein conserved in bacteria
MNLKPGEA_ coaA	-1.481692488	0.00171745	Pantothenate kinase	2.7.1.33	coaA	pantothenic acid kinase
MNLKPGEA_ ascG_3	-1.481882908	NA	HTH-type transcriptional	NA	ascG	Transcriptional regulator
MNLKPGEA_ yeaD	-1.481945054	0.04445667	Putative glucose-6-phosp	5.1.3.15	yeaD	Belongs to the glucose-6-phosph
MNLKPGEA_ diaA	-1.482220931	0.0468358	DnaA initiator-associatir	NA	gmhA	Catalyzes the isomerization of s
MNLKPGEA_ ghxP	-1.482484294	0.2071342	Guanine/hypoxanthine p	NA	yjcD	permease
MNLKPGEA_ yrbG	-1.48287447	0.0042016	Inner membrane protein	NA	yrbG	antiporter
MNLKPGEA_ MNLKPGEA	-1.483564811	NA	hypothetical protein	NA	0	Phage regulatory protein Rha (Ph
MNLKPGEA_ garR	-1.483784137	0.21597641	2-hydroxy-3-oxopropiona	1.1.1.60	garR	Catalyzes the reduction of tatror
MNLKPGEA_ asnS	-1.484245907	4.41E-08	Asparagine--tRNA ligase	6.1.1.22	asnS	Asparaginyl-tRNA synthetase
MNLKPGEA_ ppsR	-1.48455953	0.0255676	Phosphoenolpyruvate syn	2.7.11.33	ydiA	Bifunctional serine threonine kir
MNLKPGEA_ fdhF_1	-1.484834235	0.30455493	Formate dehydrogenase	1.17.1.9	fdhA	Belongs to the prokaryotic molyb
MNLKPGEA_ rarD	-1.48750079	0.03610762	Protein RarD	NA	rarD	Rard protein
MNLKPGEA_ ftsA_2	-1.489311062	0.00799036	Cell division protein FtsA	NA	ftsA	Cell division protein that is involv
MNLKPGEA_ nrdE	-1.489340913	0.00524884	Ribonucleoside-diphosph	1.17.4.1	nrdE	Provides the precursors necessar
MNLKPGEA_ rplS	-1.489366638	3.11E-06	50S ribosomal protein L1	NA	rplS	This protein is located at the 30S

MNLKPGEA_	MNLKPGEA	-1.490186717	NA	hypothetical protein	NA	0	0
MNLKPGEA_	recB	-1.490610789	0.13459464	RecBCD enzyme subunit	3.1.11.5	recB	A helicase nuclease that prepare
MNLKPGEA_	cbiA	-1.491506191	0.21989024	Cobyrinate a,c-diamide s	6.3.5.11	cbiA	Catalyzes the ATP-dependent an
MNLKPGEA_	hemG	-1.495054961	0.20175036	Protoporphyrinogen IX de	1.3.5.3	hemG	Protoporphyrinogen oxidase
MNLKPGEA_	pdhR	-1.495598601	1.84E-06	Pyruvate dehydrogenase	NA	pdhR	pyruvate dehydrogenase comple
MNLKPGEA_	rimI	-1.498552107	0.19900576	[Ribosomal protein S18]	2.3.1.266	rimI	This enzyme acetylates the N-te
MNLKPGEA_	exbD	-1.500198991	0.04371936	Biopolymer transport pro	NA	tolR	Biopolymer transport protein, Ex
MNLKPGEA_	ecpA	-1.500406266	NA	Common pilus major fim	NA	matB	Part of the ecpRABCDE operon, v
MNLKPGEA_	MNLKPGEA	-1.501010152	NA	hypothetical protein	NA	dcm	DNA methylase
MNLKPGEA_	MNLKPGEA	-1.501181435	0.29446288	hypothetical protein	NA	0	0
MNLKPGEA_	MNLKPGEA	-1.501597967	NA	hypothetical protein	NA	pcaC	4-carboxymuconolactone decarb
MNLKPGEA_	yeeA	-1.503224786	0.04446215	Inner membrane protein	NA	yeeA	Membrane
MNLKPGEA_	ydgK	-1.503534514	0.20132077	Inner membrane protein	NA	ydgK	Membrane
MNLKPGEA_	dmlR_7	-1.503610469	NA	HTH-type transcriptional	NA	0	Transcriptional regulator
MNLKPGEA_	MNLKPGEA	-1.505235623	0.06013387	hypothetical protein	NA	0	0
MNLKPGEA_	parC	-1.505895086	0.00716002	DNA topoisomerase 4 su	5.6.2.2	parC	Topoisomerase IV is essential fo
MNLKPGEA_	MNLKPGEA	-1.506555346	NA	hypothetical protein	NA	0	0
MNLKPGEA_	thiS	-1.509426978	NA	Sulfur carrier protein Thi	NA	thiS	thiamine biosynthesis protein Th
MNLKPGEA_	citX	-1.510689531	0.19627378	Apo-citrate lyase phosph	2.7.7.61	citX	Apo-citrate lyase phosphoribosyl
MNLKPGEA_	lacZ	-1.511346888	0.29494193	Beta-galactosidase	3.2.1.23	lacZ	Belongs to the glycosyl hydrolas
MNLKPGEA_	licR	-1.511591083	0.1280864	putative licABCH operon	NA	licR	transcriptional antiterminator
MNLKPGEA_	pyrI	-1.511815165	NA	Aspartate carbamoyltrar	NA	pyrI	Involved in allosteric regulation
MNLKPGEA_	MNLKPGEA	-1.512551006	NA	hypothetical protein	NA	yedA	of the drug metabolite transport
MNLKPGEA_	ilvG	-1.51305605	0.29655182	Acetolactate synthase is	2.2.1.6	ilvG	acetolactate synthase
MNLKPGEA_	hdfR_6	-1.514562071	0.02947794	HTH-type transcriptional	NA	hdfR	Negatively regulates the transcr
MNLKPGEA_	btuF_1	-1.51538318	0.29682534	Vitamin B12-binding pro	NA	0	ABC transporter substrate-bindi
MNLKPGEA_	MNLKPGEA	-1.516885026	0.1238924	hypothetical protein	NA	yoaH	Belongs to the UPF0181 family
MNLKPGEA_	dat	-1.518295673	0.01381683	Diaminobutyrate--2-oxog	2.6.1.76	dat	Belongs to the class-III pyridoxal
MNLKPGEA_	MNLKPGEA	-1.519304566	0.32479671	hypothetical protein	NA	0	PerC transcriptional activator
MNLKPGEA_	araJ	-1.519377058	0.29358571	Putative transporter Ara	NA	araJ	Major facilitator Superfamily

MNLKPGEA_ nhaB	-1.51959301	0.2071342	Na(+)/H(+) antiporter Nl	NA	nhaB	Na( ) H( ) antiporter that extrude
MNLKPGEA_ sad_1	-1.523694144	0.3029838	Succinate semialdehyde	1.2.1.16	yneI	belongs to the aldehyde dehydrc
MNLKPGEA_ mdtL	-1.524892757	NA	Multidrug resistance pro	NA	mdtL	Major facilitator Superfamily
MNLKPGEA_ catC	-1.524997487	0.20000071	Muconolactone Delta-isc	5.3.3.4	catC	Muconolactone delta-isomerase
MNLKPGEA_ ung	-1.525464159	0.02805299	Uracil-DNA glycosylase	3.2.2.27	ung	Excises uracil residues from the
MNLKPGEA_ glyQ	-1.525503658	0.04350341	Glycine--tRNA ligase alp	6.1.1.14	glyQ	glycyl-tRNA synthetase alpha su
MNLKPGEA_ MNLKPGEA	-1.526060415	NA	hypothetical protein	NA	0	(Lipo)protein
MNLKPGEA_ tsaB	-1.527535111	0.28928657	tRNA threonylcarbamoyl	NA	yeaZ	COG1214 Inactive homolog of m
MNLKPGEA_ cbiD	-1.528171115	NA	Cobalt-precorrin-5B C(1)	2.1.1.195	cbiD	Catalyzes the methylation of C-1
MNLKPGEA_ aroG	-1.528971386	0.00037212	Phospho-2-dehydro-3-de	2.5.1.54	aroG	Stereospecific condensation of p
MNLKPGEA_ entE	-1.529299616	0.04005426	Enterobactin synthase cc	6.3.2.14	entE	2,3-dihydroxybenzoate-AMP liga
MNLKPGEA_ ftsZ	-1.531319791	1.63E-05	Cell division protein FtsZ	NA	ftsZ	Essential cell division protein tha
MNLKPGEA_ yieH	-1.532777634	0.05515711	6-phosphogluconate pho	3.1.3.-	yieH	HAD-superfamily hydrolase subf
MNLKPGEA_ cbiC	-1.533332297	NA	Cobalt-precorrin-8 meth	5.4.99.60	cobH	Precorrin-8X methylmutase
MNLKPGEA_ prmB	-1.534074637	0.02447114	50S ribosomal protein L3	2.1.1.298	prmB	Specifically methylates the 50S r
MNLKPGEA_ nimR_2	-1.53422666	0.18501948	HTH-type transcriptional	NA	ripA_2	transcriptional regulator
MNLKPGEA_ perR	-1.534655919	0.28714576	HTH-type transcriptional	NA	0	transcriptional regulator
MNLKPGEA_ rhaS_7	-1.534822236	0.28715815	HTH-type transcriptional	NA	0	transcriptional regulator
MNLKPGEA_ MNLKPGEA	-1.535658884	0.32131698	hypothetical protein	NA	0	Pfam:Phage_holin_3_7
MNLKPGEA_ MNLKPGEA	-1.537181624	0.00378475	hypothetical protein	NA	yciC	UPF0259 membrane protein
MNLKPGEA_ ilvA	-1.538212339	0.18736186	L-threonine dehydratase	4.3.1.19	ilvA	Catalyzes the anaerobic formati
MNLKPGEA_ cyoB	-1.540959643	0.00013394	Cytochrome bo(3) ubiqui	7.1.1.3	cyoB	Cytochrome c oxidase is the com
MNLKPGEA_ MNLKPGEA	-1.542578718	0.00010154	hypothetical protein	NA	0	0
MNLKPGEA_ mlaB	-1.543785709	0.2881126	Intermembrane phosphc	NA	mlaB	NTP binding protein (Contains ST
MNLKPGEA_ pth	-1.544120672	0.04931655	Peptidyl-tRNA hydrolase	3.1.1.29	pth	The natural substrate for this en
MNLKPGEA_ yidH	-1.54492273	0.18542846	Inner membrane protein	NA	yidH	Membrane
MNLKPGEA_ lysN_1	-1.545840994	0.1298702	2-aminoadipate transam	2.6.1.39	lysN	Transcriptional regulators contai
MNLKPGEA_ dauA_3	-1.547454689	NA	C4-dicarboxylic acid tran	NA	0	COG0659 Sulfate permease and
MNLKPGEA_ pcaH	-1.550554887	NA	Protocatechuate 3,4-dio	1.13.11.3	pcaH	protocatechuate 3,4-dioxygenas
MNLKPGEA_ nicS	-1.552497699	0.17919971	HTH-type transcriptional	NA	nicS	transcriptional regulator

MNLKPGEA_ folP_1	-1.552793041	0.2810573	Dihydropteroate synthas	2.5.1.15	folP	Catalyzes the condensation of pa
MNLKPGEA_ rbbA	-1.554229039	0.28206968	Ribosome-associated AT	NA	rbbA	(ABC) transporter
MNLKPGEA_ malT_2	-1.554434518	0.00457619	HTH-type transcriptional	NA	moaR	transcriptional regulator
MNLKPGEA_ licH_1	-1.55464231	NA	putative 6-phospho-beta	3.2.1.86	0	Catalyzes the fromation of N-ac
MNLKPGEA_ fldB	-1.555479766	0.2810573	Flavodoxin 2	NA	fldB	Low-potential electron donor to
MNLKPGEA_ glnS	-1.5570116	0.00037064	Glutamine--tRNA ligase	6.1.1.18	glnS	Catalyzes a two-step reaction, fi
MNLKPGEA_ mqo_2	-1.557530339	0.27850291	Malate:quinone oxidorec	1.1.5.4	mqo	malate quinone oxidoreductase
MNLKPGEA_ rpsQ	-1.557899654	9.00E-08	30S ribosomal protein S1	NA	rpsQ	One of the primary rRNA binding
MNLKPGEA_ argA	-1.55902115	0.03173142	Amino-acid acetyltransfe	2.3.1.1	argA	Belongs to the acetyltransferase
MNLKPGEA_ ligA	-1.559400523	0.04749669	DNA ligase	6.5.1.2	ligA	DNA ligase that catalyzes the fo
MNLKPGEA_ nuoJ	-1.560122775	0.18994644	NADH-quinone oxidored	7.1.1.-	nuoJ	Belongs to the complex I subuni
MNLKPGEA_ nagD	-1.560129129	0.12097131	Ribonucleotide monopho	3.1.3.5	nagD	HAD-superfamily hydrolase, sub
MNLKPGEA_ uvrA	-1.561890065	0.0017404	UvrABC system protein A	NA	uvrA	The UvrABC repair system catal
MNLKPGEA_ cobS	-1.564141168	NA	Adenosylcobinamide-GD	2.7.8.26	cobS	Joins adenosylcobinamide-GDP a
MNLKPGEA_ nfdA_2	-1.564344673	NA	N-substituted formamid	3.5.1.91	nfdA	metal-dependent hydrolase with
MNLKPGEA_ steT	-1.565616491	0.11065773	Serine/threonine exchan	NA	0	amino acid
MNLKPGEA_ rhlB	-1.567346858	0.00376586	ATP-dependent RNA heli	3.6.4.13	rhlB	DEAD-box RNA helicase involved
MNLKPGEA_ hscA	-1.569402114	0.13045112	Chaperone protein HscA	NA	hscA	Chaperone involved in the matur
MNLKPGEA_ mdtB	-1.572770208	0.27370395	Multidrug resistance pro	NA	mdtB	Belongs to the resistance-nodula
MNLKPGEA_ fumA	-1.575263087	0.00139573	Fumarate hydratase clas	4.2.1.2	fumA	Catalyzes the reversible hydratic
MNLKPGEA_ MNLKPGEA	-1.578438213	0.07583094	hypothetical protein	NA	ynaJ	Protein of unknown function (DU
MNLKPGEA_ hupA	-1.578782848	1.45E-08	DNA-binding protein HU-	NA	hupA	Histone-like DNA-binding protein
MNLKPGEA_ bglG	-1.582279746	0.2728419	Cryptic beta-glucoside bg	NA	bglG	antiterminator
MNLKPGEA_ nlpD_2	-1.586203973	3.26E-15	Murein hydrolase activat	NA	nlpD	COG0739 Membrane proteins re
MNLKPGEA_ kdgR_1	-1.58655568	0.2697505	HTH-type transcriptional	NA	ptxS	transcriptional regulator
MNLKPGEA_ btuF_3	-1.588817187	0.26845923	Vitamin B12-binding pro	NA	btuF	Part of the ABC transporter com
MNLKPGEA_ gss	-1.589185917	0.00403251	Bifunctional glutathionyl	NA	gsp	Glutathionylspermidine synthase
MNLKPGEA_ galS	-1.590008685	0.04300936	HTH-type transcriptional	NA	galS	transcriptional regulator
MNLKPGEA_ rsmE	-1.593821522	0.03032291	Ribosomal RNA small su	2.1.1.193	rsmE	Specifically methylates the N3 p
MNLKPGEA_ ureC	-1.595420155	NA	Urease subunit alpha	3.5.1.5	ureC	Belongs to the metallo-depende

MNLKPGEA_ tam	-1.596611066	0.16662352	Trans-aconitate 2-methy	2.1.1.144	tam	Catalyzes the S-adenosylmethio
MNLKPGEA_ MNLKPGEA	-1.59827726	0.00044412	hypothetical protein	NA	0	Pectate lyase superfamily protei
MNLKPGEA_ MNLKPGEA	-1.60252082	NA	hypothetical protein	NA	0	0
MNLKPGEA_ hxpB_2	-1.603656793	0.06898904	Hexitol phosphatase B	3.1.3.68	yniC	HAD-superfamily hydrolase subf
MNLKPGEA_ dam	-1.60370794	0.07553021	DNA adenine methylase	2.1.1.72	dam	Site-specific DNA-methyltransfe
MNLKPGEA_ rhaS_3	-1.604076317	0.1958146	HTH-type transcriptional	NA	pocR	transcriptional regulator AraC fa
MNLKPGEA_ ppiC_1	-1.606214272	NA	Peptidyl-prolyl cis-trans i	5.2.1.8	ppiC	PPIC-type PPIASE domain
MNLKPGEA_ manY	-1.607473224	0.04974389	PTS system mannose-sp	NA	manY	pts system
MNLKPGEA_ MNLKPGEA	-1.607669915	0.10348362	hypothetical protein	NA	hmsT	Diguanylate cyclase
MNLKPGEA_ thlA_1	-1.608140294	0.06292688	Acetyl-CoA acetyltransfe	2.3.1.9	yqeF	Catalyzes the final step of fatty a
MNLKPGEA_ hemA	-1.609446513	0.00019201	Glutamyl-tRNA reductas	1.2.1.70	hemA	Catalyzes the NADPH-dependent
MNLKPGEA_ MNLKPGEA	-1.60974536	6.59E-06	hypothetical protein	NA	0	0
MNLKPGEA_ yjjV	-1.611175946	NA	putative metal-depende	3.1.-.-	yjjV	Deoxyribonuclease
MNLKPGEA_ modE	-1.612440038	0.16811814	DNA-binding transcriptic	NA	modE	Transcriptional regulator
MNLKPGEA_ yihG	-1.613582649	0.10277593	putative acyltransferase	2.3.-.-	yihG	Acyltransferase
MNLKPGEA_ asnA	-1.614970144	0.00706347	Aspartate--ammonia lig	6.3.1.1	asnA	aspartate--ammonia ligase
MNLKPGEA_ zapE_2	-1.615455892	0.17243871	Cell division protein ZapI	NA	0	AFG1-like ATPase
MNLKPGEA_ gcvT	-1.619091587	0.26140329	Aminomethyltransferase	2.1.2.10	gcvT	The glycine cleavage system cat
MNLKPGEA_ MNLKPGEA	-1.61936899	0.25739233	hypothetical protein	NA	#N/A	#N/A
MNLKPGEA_ glcR_3	-1.622060192	0.26376534	HTH-type transcriptional	NA	ygbI	transcriptional regulator
MNLKPGEA_ rstB	-1.623975489	0.09619983	Sensor protein RstB	2.7.13.3	rstB	PhoQ Sensor
MNLKPGEA_ citS	-1.624676116	0.28205319	Citrate-sodium symporte	NA	citS	Uptake of citrate across the bou
MNLKPGEA_ MNLKPGEA	-1.626442685	0.25697006	hypothetical protein	NA	ycsG	Mn2 and Fe2 transporters of the
MNLKPGEA_ hisH	-1.626670569	0.18432114	Imidazole glycerol phosp	4.3.2.10	hisH	IGPS catalyzes the conversion of
MNLKPGEA_ MNLKPGEA	-1.631224082	NA	hypothetical protein	NA	0	Acetyltransferase (GNAT) doma
MNLKPGEA_ MNLKPGEA	-1.634882294	NA	hypothetical protein	NA	0	0
MNLKPGEA_ rsmB	-1.635028841	0.16484976	Ribosomal RNA small su	2.1.1.176	sun	Specifically methylates the cytos
MNLKPGEA_ pstA	-1.635532465	NA	Phosphate transport syst	NA	pstA	phosphate transport system per
MNLKPGEA_ MNLKPGEA	-1.635845096	0.0006659	hypothetical protein	NA	#N/A	#N/A
MNLKPGEA_ pal_1	-1.640222888	0.25313423	Peptidoglycan-associate	NA	yfiB	Belongs to the ompA family

MNLKPGEA_	bglC	-1.640592392	0.25313423	Aryl-phospho-beta-D-glu	3.2.1.86	bglC	Belongs to the glycosyl hydrolas
MNLKPGEA_	panM	-1.640662626	NA	PanD regulatory factor	NA	panZ	Controls both the activation and
MNLKPGEA_	rplT	-1.640665171	7.65E-06	50S ribosomal protein L2	NA	rplT	Binds directly to 23S ribosomal I
MNLKPGEA_	metG	-1.641588986	0.00243684	Methionine--tRNA ligase	6.1.1.10	metG	Is required not only for elongatic
MNLKPGEA_	MNLKPGEA	-1.642165248	0.00948678	hypothetical protein	NA	ychA	Transglutaminase-like superfam
MNLKPGEA_	MNLKPGEA	-1.643089687	0.01317767	hypothetical protein	NA	yadI	IIa component
MNLKPGEA_	yhjX	-1.646332897	0.2556722	putative MFS-type trans	NA	yhjX	Major facilitator superfamily
MNLKPGEA_	potF	-1.646539069	0.00287966	Putrescine-binding perip	NA	potF	Required for the activity of the b
MNLKPGEA_	MNLKPGEA	-1.647890199	0.25380083	hypothetical protein	NA	0	ISSoEn1, terminal inverted repea
MNLKPGEA_	rplQ	-1.648623658	1.61E-08	50S ribosomal protein L1	NA	rplQ	Ribosomal protein L17
MNLKPGEA_	rbsR_3	-1.649417737	0.10273788	Ribose operon repressor	NA	scrR	Periplasmic binding protein LacI
MNLKPGEA_	sbp	-1.651798964	NA	Sulfate-binding protein	NA	sbp	sulfate ABC transporter
MNLKPGEA_	rplI	-1.654733902	6.63E-11	50S ribosomal protein L9	NA	rplI	Binds to the 23S rRNA
MNLKPGEA_	araB_1	-1.656266814	NA	Ribulokinase	2.7.1.16	araB	Belongs to the ribulokinase fami
MNLKPGEA_	ycaD_2	-1.656935253	0.24944565	putative MFS-type trans	NA	ycaD	Major facilitator superfamily
MNLKPGEA_	MNLKPGEA	-1.658787739	0.00026818	hypothetical protein	NA	0	0
MNLKPGEA_	cydB_3	-1.659076899	0.00997262	Cytochrome bd-I ubiquin	7.1.1.7	cydB	cytochrome d ubiquinol oxidase,
MNLKPGEA_	ureD	-1.65912219	NA	Urease accessory protei	NA	ureD	Required for maturation of urea
MNLKPGEA_	mutL	-1.659167855	0.00041449	DNA mismatch repair pr	NA	mutL	This protein is involved in the re
MNLKPGEA_	mpl	-1.65940751	0.15759861	UDP-N-acetylmuramate-	6.3.2.45	mpl	Reutilizes the intact tripeptide L
MNLKPGEA_	lpxT	-1.659484829	0.15313152	Lipid A 1-diphosphate sy	2.7.4.29	lpxT	Involved in the modification of t
MNLKPGEA_	yjjG	-1.659852706	0.09884793	Pyrimidine 5'-nucleotida	3.1.3.5	yjjG	HAD-superfamily hydrolase, sub
MNLKPGEA_	pgrR_3	-1.660574602	NA	HTH-type transcriptional	NA	0	transcriptional regulator
MNLKPGEA_	tyrP	-1.662799388	0.14743253	Tyrosine-specific transpo	NA	tyrP	amino acid
MNLKPGEA_	yqaA	-1.664216223	NA	Inner membrane protein	NA	yqaA	Membrane
MNLKPGEA_	appY	-1.664508545	NA	HTH-type transcriptional	NA	ybcM	transcriptional regulator
MNLKPGEA_	mazG	-1.665488896	0.08796934	Nucleoside triphosphate	3.6.1.8	mazG	nucleoside triphosphate pyropho
MNLKPGEA_	rfaC	-1.6658082	0.24710759	Lipopolysaccharide hepto	2.-.-.-	rfaC	lipopolysaccharide heptosyltrans
MNLKPGEA_	MNLKPGEA	-1.665868991	0.00181717	hypothetical protein	NA	yacC	Type II secretion system pilotin l
MNLKPGEA_	bioP	-1.666374556	NA	Biotin transporter	NA	yigM	COG0697 Permeases of the drug

MNLKPGEA_ MNLKPGEA	-1.666491259	NA	hypothetical protein	NA	yeaL	UPF0756 membrane protein
MNLKPGEA_ MNLKPGEA	-1.666525652	0.00040807	hypothetical protein	NA	wza	Protein involved in polysaccharic
MNLKPGEA_ bepA_1	-1.666555604	NA	Beta-barrel assembly-er	3.4.-.-	bcsC	Cellulose synthase
MNLKPGEA_ lysO	-1.667309005	0.24461686	Lysine exporter LysO	NA	ybjE	membrane
MNLKPGEA_ pal_2	-1.667402801	0.00135973	Peptidoglycan-associate	NA	pal	Belongs to the ompA family
MNLKPGEA_ ade2	-1.672038048	NA	Adenine deaminase 2	3.5.4.2	ade	adenine deaminase
MNLKPGEA_ tagH	-1.674652866	0.02494646	Teichoic acids export AT	7.5.2.4	rfbB	ABC-type polysaccharide polyol
MNLKPGEA_ tcdA	-1.674852263	0.2400879	tRNA threonylcarbamoyl	6.1.-.-	ygdL	Dinucleotide-utilizing enzymes i
MNLKPGEA_ pncB	-1.677958772	0.0271777	Nicotinate phosphoribos	6.3.4.21	pncB	Catalyzes the synthesis of beta-r
MNLKPGEA_ astC_1	-1.678471861	NA	Succinylornithine transa	2.6.1.81	argD	aminotransferase
MNLKPGEA_ yabJ	-1.680844857	0.0921139	2-iminobutanoate/2-imi	3.5.99.10	yoaB	Translation Initiation Inhibitor Yj
MNLKPGEA_ lpxB	-1.683072149	0.14815787	Lipid-A-disaccharide syn	2.4.1.182	lpxB	Condensation of UDP-2,3-diacylg
MNLKPGEA_ MNLKPGEA	-1.684246834	0.02329852	hypothetical protein	NA	yqfA	protein, hemolysin III
MNLKPGEA_ tesA	-1.684307472	0.23720969	Thioesterase 1/protease	3.1.2.2	tesA	COG2755 Lysophospholipase L1
MNLKPGEA_ ribX_2	-1.684592778	NA	Riboflavin transport syst	NA	0	ABC-type nitrate sulfonate bicar
MNLKPGEA_ hcr	-1.685581967	0.24337875	NADH oxidoreductase HC	1.-.-.-	hcr	oxidoreductase
MNLKPGEA_ MNLKPGEA	-1.686079401	NA	hypothetical protein	NA	0	COG0697 Permeases of the drug
MNLKPGEA_ sad_2	-1.689687702	0.00016407	Succinate semialdehyde	1.2.1.16	ssdA	belongs to the aldehyde dehydrc
MNLKPGEA_ bioC	-1.690556139	0.25781244	Malonyl-[acyl-carrier prc	2.1.1.197	bioC	Converts the free carboxyl group
MNLKPGEA_ narG	-1.690812878	0.23936966	Respiratory nitrate reduc	1.7.5.1	narG	Belongs to the prokaryotic molyl
MNLKPGEA_ deoR	-1.693996839	0.01180725	Deoxyribose operon repr	NA	deoR	transcriptional
MNLKPGEA_ azoR_2	-1.694543894	0.03293064	FMN-dependent NADH-a	1.7.1.17	azoR	Catalyzes the reductive cleavage
MNLKPGEA_ cysK	-1.69481444	0.00037015	Cysteine synthase A	2.5.1.47	cysK	Belongs to the cysteine synthase
MNLKPGEA_ alx	-1.695230858	0.05203616	Putative membrane-bou	NA	alx	membrane protein, terc
MNLKPGEA_ alaS	-1.695250795	2.14E-05	Alanine--tRNA ligase	6.1.1.7	alaS	Catalyzes the attachment of ala
MNLKPGEA_ MNLKPGEA	-1.698249413	NA	hypothetical protein	NA	#N/A	#N/A
MNLKPGEA_ argI	-1.699442021	0.11301303	Ornithine carbamoyltran	2.1.3.3	argI	Reversibly catalyzes the transfe
MNLKPGEA_ yehX	-1.70211067	NA	Glycine betaine uptake s	3.6.3.-	yehX	abc transporter atp-binding prot
MNLKPGEA_ topB	-1.702224127	0.13979768	DNA topoisomerase 3	5.6.2.1	topB	Releases the supercoiling and tc
MNLKPGEA_ rplW	-1.711041449	1.06E-05	50S ribosomal protein L2	NA	rplW	One of the early assembly prote

MNLKPGEA_ MNLKPGEA	-1.711047922	0.02077325	hypothetical protein	NA	yghW	response to butan-1-ol
MNLKPGEA_ menE	-1.712073984	NA	2-succinylbenzoate--CoA	6.2.1.26	menE	O-succinylbenzoic acid--CoA liga
MNLKPGEA_ ypjD	-1.713914026	0.04555901	Inner membrane protein	NA	ypjD	cytochrome C assembly protein
MNLKPGEA_ aroK	-1.714409993	0.00102057	Shikimate kinase 1	2.7.1.71	aroK	Catalyzes the specific phosphory
MNLKPGEA_ modA	-1.714654645	0.00026818	Molybdate-binding prote	NA	modA	ABC transporter, periplasmic mo
MNLKPGEA_ pucG	-1.718077032	NA	(S)-ureidoglycine--glyoxy	2.6.1.112	pucG	Serine-pyruvate aminotransfera
MNLKPGEA_ nadB	-1.719738733	0.2360821	L-aspartate oxidase	1.4.3.16	nadB	Catalyzes the oxidation of L-aspa
MNLKPGEA_ seqA	-1.719872128	0.00026615	Negative modulator of i	NA	seqA	Negative regulator of replicatior
MNLKPGEA_ mshA_2	-1.720503066	0.00023292	D-inositol-3-phosphate g	2.4.1.250	0	glycosyl transferase group 1
MNLKPGEA_ MNLKPGEA	-1.72065267	0.16183828	hypothetical protein	NA	0	chitinase activity
MNLKPGEA_ rpsE	-1.720763945	3.14E-06	30S ribosomal protein S5	NA	rpsE	Located at the back of the 30S su
MNLKPGEA_ yhhT_1	-1.722662392	0.23108886	Putative transport protei	NA	yhhT	permease
MNLKPGEA_ ybjJ	-1.724319286	0.2261918	Inner membrane protein	NA	ybjJ	Major facilitator superfamily
MNLKPGEA_ amiC_1	-1.725537064	0.22677051	N-acetylmuramoyl-L-ala	3.5.1.28	amiC	N-acetylmuramoyl-L-alanine am
MNLKPGEA_ ffh	-1.725845272	1.63E-05	Signal recognition partic	NA	ffh	Involved in targeting and insertio
MNLKPGEA_ rsfS	-1.727998818	0.0302422	Ribosomal silencing fact	NA	rsfS	Functions as a ribosomal silenci
MNLKPGEA_ btsR	-1.729067643	0.22455143	Transcriptional regulator	NA	yehT	Response regulator of the LytR A
MNLKPGEA_ yciI	-1.730008001	0.01806533	Protein YciI	NA	yciI	YciI from Haemophilus influenza
MNLKPGEA_ MNLKPGEA	-1.730272467	0.13504227	hypothetical protein	NA	yfdQ	Uncharacterized conserved prote
MNLKPGEA_ ybdO_2	-1.73434838	NA	putative HTH-type transc	NA	ybdO	transcriptional regulator
MNLKPGEA_ nrdG	-1.737389649	NA	Anaerobic ribonucleoside	1.97.1.-	nrdG	Activation of anaerobic ribonucle
MNLKPGEA_ lysS	-1.738980616	0.00588659	Lysine--tRNA ligase	6.1.1.6	lysS	Belongs to the class-II aminoacy
MNLKPGEA_ exoX	-1.739009211	0.13979768	Exodeoxyribonuclease 10	3.1.11.-	exoX	3'-5' exonuclease activity on sing
MNLKPGEA_ dsbD_2	-1.74158821	0.22385713	Thiol:disulfide interchan	1.8.1.8	dsbD	Required to facilitate the formal
MNLKPGEA_ rapZ	-1.743009541	0.00231009	RNase adapter protein R	NA	rapZ	Modulates the synthesis of GlmS
MNLKPGEA_ yedF	-1.743310516	0.22906669	Putative sulfur carrier pr	NA	yedF	Belongs to the sulfur carrier prot
MNLKPGEA_ yadH	-1.74344018	0.12627488	Inner membrane transpo	NA	yadH	Transport Permease Protein
MNLKPGEA_ mtgA	-1.744915689	0.12903044	Biosynthetic peptidoglyc	2.4.1.129	mtgA	Peptidoglycan polymerase that c
MNLKPGEA_ qseB	-1.749780097	NA	Transcriptional regulator	NA	qseB	response regulator
MNLKPGEA_ fabD_2	-1.755377625	0.01266235	Malonyl CoA-acyl carrier	2.3.1.39	fabD	malonyl CoA-acyl carrier protein

MNLKPGEA_ cycA_1	-1.759946043	NA	D-serine/D-alanine/glyci	NA	cycA	amino acid
MNLKPGEA_ bioD1_2	-1.760463089	NA	ATP-dependent dethiobi	6.3.3.3	bioD	Catalyzes a mechanistically unus
MNLKPGEA_ eutL	-1.760504045	NA	Ethanolamine utilization	NA	eutL	Carboxysome structural protein i
MNLKPGEA_ ybiO	-1.761218708	0.03012166	Moderate conductance r	NA	ybiO	mechanosensitive ion channel
MNLKPGEA_ tamB	-1.761922743	2.00E-06	Translocation and assem	NA	ytfN	protein conserved in bacteria
MNLKPGEA_ leuS	-1.76201607	2.67E-08	Leucine--tRNA ligase	6.1.1.4	leuS	Belongs to the class-I aminoacyl
MNLKPGEA_ nuoN	-1.76327922	0.04829829	NADH-quinone oxidored	7.1.1.-	nuoN	NDH-1 shuttles electrons from N
MNLKPGEA_ pcaR_1	-1.765344242	0.21597328	Pca regulon regulatory p	NA	0	transcriptional regulator
MNLKPGEA_ minD	-1.767531435	0.00287966	Septum site-determining	NA	minD	Belongs to the ParA family
MNLKPGEA_ ygaZ_1	-1.767707909	NA	Inner membrane protein	NA	ygaZ	branched-chain amino acid
MNLKPGEA_ dinF	-1.767826625	NA	DNA damage-inducible p	NA	dinF	COG0534 Na -driven multidrug e
MNLKPGEA_ MNLKPGEA	-1.768349827	NA	hypothetical protein	NA	yhhL	Membrane
MNLKPGEA_ mraZ	-1.770045288	0.00020433	Transcriptional regulator	NA	mraZ	Negatively regulates its own exp
MNLKPGEA_ rimM	-1.770401977	1.72E-05	Ribosome maturation fa	NA	rimM	An accessory protein needed dur
MNLKPGEA_ ilvE	-1.772018714	0.21491423	Branched-chain-amino-a	2.6.1.42	ilvE	Belongs to the class-IV pyridoxal
MNLKPGEA_ narY	-1.773479326	NA	Respiratory nitrate reduc	1.7.5.1	narH	Nitrate reductase beta subunit
MNLKPGEA_ thpA_3	-1.774885014	0.04023985	D-threitol-binding protei	NA	0	PFAM Periplasmic binding prote
MNLKPGEA_ sorC_2	-1.776279571	0.02412582	Sorbitol operon regulato	NA	deoR_1	transcriptional regulator
MNLKPGEA_ osmY_1	-1.776494639	0.06884793	Osmotically-inducible pr	NA	yraP	Periplasmic or secreted lipoprot
MNLKPGEA_ yfcJ_1	-1.776841424	0.12006999	putative MFS-type trans	NA	yfcJ	Major facilitator Superfamily
MNLKPGEA_ cydA_2	-1.778796021	0.01685151	Cytochrome bd-I ubiquin	7.1.1.7	cydA	oxidase, subunit
MNLKPGEA_ kdgK_2	-1.781536935	0.21068909	2-dehydro-3-deoxyglucor	2.7.1.45	kdgK	COG0524 Sugar kinases, ribokina
MNLKPGEA_ lpoA	-1.782502752	0.00025977	Penicillin-binding protein	NA	lpoA	Regulator of peptidoglycan syntl
MNLKPGEA_ psd	-1.78254282	0.01534469	Phosphatidylserine deca	4.1.1.65	psd	Catalyzes the formation of phos
MNLKPGEA_ MNLKPGEA	-1.782555003	0.03625331	hypothetical protein	NA	0	0
MNLKPGEA_ MNLKPGEA	-1.782703379	NA	hypothetical protein	NA	0	membrane transporter protein
MNLKPGEA_ hmuU_1	-1.78274524	0.2235144	Hemin transport system	NA	hmuU	Belongs to the binding-protein-d
MNLKPGEA_ creC	-1.786905288	NA	Sensor protein CreC	2.7.13.3	creC	PhoQ Sensor
MNLKPGEA_ lplT	-1.786952379	NA	Lysophospholipid transpo	NA	lplT	Catalyzes the facilitated diffusio
MNLKPGEA_ lpxD_1	-1.788139647	2.24E-07	UDP-3-O-(3-hydroxymyri	2.3.1.191	lpxD	as the acyl donor. Is involved in t

MNLKPGEA_	lrp_3	-1.789774431	8.99E-09	Leucine-responsive regul	NA	lrp	Transcriptional regulator
MNLKPGEA_	rpoB	-1.790814977	1.87E-21	DNA-directed RNA polyn	2.7.7.6	rpoB	DNA-dependent RNA polymeras
MNLKPGEA_	glnH_1	-1.791211481	0.00661112	Glutamine-binding perip	NA	glnH	ABC transporter substrate-bindi
MNLKPGEA_	ddlA	-1.793053904	0.1148752	D-alanine--D-alanine lig	6.3.2.4	ddl	Belongs to the D-alanine--D-ala
MNLKPGEA_	astE_1	-1.793222917	NA	Succinylglutamate desuc	3.5.1.96	astE	Belongs to the AspA AstE family
MNLKPGEA_	cysJ	-1.793683218	NA	Sulfite reductase [NADP	1.8.1.2	cysJ	Component of the sulfite reduct
MNLKPGEA_	atpD	-1.79372873	2.84E-08	ATP synthase subunit be	7.1.2.2	atpD	Produces ATP from ADP in the p
MNLKPGEA_	rbsK_4	-1.793950086	0.00488196	Ribokinase	2.7.1.15	rbsK	Catalyzes the phosphorylation of
MNLKPGEA_	MNLKPGEA	-1.796339727	0.11428674	hypothetical protein	NA	#N/A	#N/A
MNLKPGEA_	iolU_1	-1.798200473	0.01296843	scyllo-inositol 2-dehydro	1.1.1.371	ygjR	oxidoreductase
MNLKPGEA_	MNLKPGEA	-1.798387834	0.01442163	hypothetical protein	NA	0	Polysaccharide pyruvyl transfera
MNLKPGEA_	gdx_1	-1.799073744	0.12850938	Guanidinium exporter	NA	sugE	multidrug resistance protein
MNLKPGEA_	trmH	-1.799270073	NA	tRNA (guanosine(18)-2'-	2.1.1.34	trmH	Catalyzes the 2'-O methylation o
MNLKPGEA_	lpxA	-1.799280738	4.93E-06	Acyl-[acyl-carrier-protein	2.3.1.129	lpxA	involved in the biosynthesis of li
MNLKPGEA_	zinT	-1.800964417	6.75E-07	Metal-binding protein Zi	NA	zinT	periplasmic or secreted protein
MNLKPGEA_	MNLKPGEA	-1.800981069	NA	hypothetical protein	NA	cII	Phage regulatory protein CII (CP
MNLKPGEA_	aceE	-1.803330258	2.87E-09	Pyruvate dehydrogenase	1.2.4.1	aceE	Component of the pyruvate dehy
MNLKPGEA_	uhpA	-1.804891312	NA	Transcriptional regulator	NA	uhpA	response regulator
MNLKPGEA_	rpoS	-1.809383785	1.96E-28	RNA polymerase sigma f	NA	rpoS	RNA polymerase sigma
MNLKPGEA_	MNLKPGEA	-1.810101255	NA	hypothetical protein	NA	0	Ead/Ea22-like protein
MNLKPGEA_	acrA	-1.810898348	5.22E-05	Multidrug efflux pump su	NA	acrA	Belongs to the membrane fusion
MNLKPGEA_	ydhC	-1.811475962	0.20447563	Inner membrane transpo	NA	ydhC	Member of the major facilitator
MNLKPGEA_	fimG	-1.815613745	NA	Protein FimG	NA	fimG	Fimbrial protein
MNLKPGEA_	recJ	-1.816111816	0.03419172	Single-stranded-DNA-spe	3.1.-.-	recJ	Single-stranded-DNA-specific ex
MNLKPGEA_	modF	-1.82338876	0.20053526	ABC transporter ATP-bin	NA	modF	ABC-type molybdenum transport
MNLKPGEA_	hisM	-1.8234702	0.20132077	Histidine transport syste	NA	hisM	ABC transporter (permease)
MNLKPGEA_	MNLKPGEA	-1.824818828	NA	IS6 family transposase IS	NA	0	Transposase IS66 family
MNLKPGEA_	adeP	-1.825603669	0.05903628	Adenine permease AdeP	NA	purP	permease
MNLKPGEA_	waaA	-1.834404608	0.10411839	3-deoxy-D-manno-octulo	2.4.99.12	kdtA	Transferase
MNLKPGEA_	murD	-1.836465602	0.10649471	UDP-N-acetylmuramoyla	6.3.2.9	murD	Cell wall formation. Catalyzes th

MNLKPGEA_ ahpF	-1.837052288	0.00880656	Alkyl hydroperoxide redu	1.8.1.-	ahpF	alkyl hydroperoxide reductase
MNLKPGEA_ ais	-1.838127747	NA	Aconitate isomerase	5.3.3.7	0	ABC transporter substrate-bindi
MNLKPGEA_ cusC_1	-1.841357316	NA	Cation efflux system pro	NA	mdtP	RND efflux system, outer memb
MNLKPGEA_ betI_2	-1.841697578	0.19837822	HTH-type transcriptional	NA	uidR	transcriptional regulator
MNLKPGEA_ gyrA	-1.843853059	3.07E-05	DNA gyrase subunit A	5.6.2.2	gyrA	A type II topoisomerase that neg
MNLKPGEA_ dut	-1.847835624	0.19430908	Deoxyuridine 5'-triphosp	3.6.1.23	dut	This enzyme is involved in nucle
MNLKPGEA_ pqqC	-1.849308222	NA	Pyrroloquinoline-quinone	1.3.3.11	pqqC	Ring cyclization and eight-electr
MNLKPGEA_ tilS	-1.851256583	NA	tRNA(Ile)-lysidine syntha	6.3.4.19	tilS	Ligates lysine onto the cytidine p
MNLKPGEA_ mdaB	-1.851815541	0.10067966	NADPH:quinone oxidorec	1.6.5.10	mdaB	modulator of drug activity B
MNLKPGEA_ guaA	-1.856791159	0.00023461	GMP synthase [glutamir	6.3.5.2	guaA	Catalyzes the synthesis of GMP f
MNLKPGEA_ yggX	-1.860109229	0.09770416	putative Fe(2+)-trafficki	NA	yggX	Could be a mediator in iron trans
MNLKPGEA_ mmsB	-1.860354002	0.19193357	putative 3-hydroxyisobut	1.1.1.31	yfjR	Dehydrogenase
MNLKPGEA_ recD	-1.861023803	NA	RecBCD enzyme subunit	3.1.11.5	recD	A helicase nuclease that prepare
MNLKPGEA_ recG	-1.863717196	0.19033486	ATP-dependent DNA heli	3.6.4.12	recG	Critical role in recombination an
MNLKPGEA_ secD	-1.864926068	0.00050616	Protein translocase subu	NA	secD	Part of the Sec protein transloca
MNLKPGEA_ MNLKPGEA	-1.865281104	0.18418837	hypothetical protein	NA	0	YqaJ-like viral recombinase dom
MNLKPGEA_ yejM	-1.867442144	0.00328989	Inner membrane protein	NA	yejM	Hydrolase of alkaline phosphatas
MNLKPGEA_ rplV	-1.867561712	2.00E-07	50S ribosomal protein L2	NA	rplV	The globular domain of the prot
MNLKPGEA_ aas	-1.868048643	0.09898097	Bifunctional protein Aas	NA	aas	Plays a role in lysophospholipid a
MNLKPGEA_ MNLKPGEA	-1.869084001	NA	IS66 family transposase	NA	0	Transposase IS66 family
MNLKPGEA_ comM	-1.86993096	0.18827155	Competence protein Com	NA	comM	ATPase with chaperone activity
MNLKPGEA_ MNLKPGEA	-1.874616959	0.13079323	hypothetical protein	NA	0	outer membrane
MNLKPGEA_ MNLKPGEA	-1.87478691	0.04967077	hypothetical protein	NA	yqiA	esterase
MNLKPGEA_ yejE	-1.876757079	NA	Inner membrane ABC tra	NA	yejE	ABC transporter (Permease
MNLKPGEA_ MNLKPGEA	-1.877219871	0.06398774	Putative thiamine biosyr	NA	thiY	COG0715 ABC-type nitrate sulfo
MNLKPGEA_ miaB	-1.879156086	0.00822951	tRNA-2-methylthio-N(6)	2.8.4.3	miaB	Catalyzes the methylthiolation o
MNLKPGEA_ fldC	-1.88107965	NA	(R)-phenyllactyl-CoA deh	4.2.1.-	yjiM	cellular response to DNA damag
MNLKPGEA_ MNLKPGEA	-1.892837504	0.17431353	hypothetical protein	NA	0	0
MNLKPGEA_ MNLKPGEA	-1.894733029	NA	hypothetical protein	NA	0	Transcriptional regulatory protei
MNLKPGEA_ nudI	-1.896705347	0.17919609	Nucleoside triphosphata	3.6.1.9	nudI	Catalyzes the hydrolysis of nucle

MNLKPGEA_ MNLKPGEA	-1.898923736	0.15551533	hypothetical protein	NA	0	Pfam:Phage_holin_8
MNLKPGEA_ oppB	-1.899407654	0.18014587	Oligopeptide transport s	NA	oppB	ABC-type dipeptide oligopeptide
MNLKPGEA_ jefA_1	-1.903324263	0.01223846	Drug efflux pump JefA	NA	0	Major facilitator Superfamily
MNLKPGEA_ MNLKPGEA	-1.907638628	0.17664401	hypothetical protein	NA	0	acetyltransferase
MNLKPGEA_ MNLKPGEA	-1.909161946	0.08835791	hypothetical protein	NA	0	endonuclease
MNLKPGEA_ rfbD	-1.909839923	0.00383623	UDP-galactopyranose mu	5.4.99.9	glf	UDP-galactopyranose mutase
MNLKPGEA_ MNLKPGEA	-1.91012536	0.02612784	hypothetical protein	NA	#N/A	#N/A
MNLKPGEA_ aroC	-1.912657182	0.05127389	Chorismate synthase	4.2.3.5	aroC	Catalyzes the anti-1,4-eliminatic
MNLKPGEA_ tyrA	-1.917148379	0.02574165	T-protein	NA	tyrA	T-protein
MNLKPGEA_ ftnA_2	-1.919644184	0.12533464	Bacterial non-heme ferri	1.16.3.2	ftnB	Iron-storage protein
MNLKPGEA_ yjjP	-1.919964871	0.01376961	Inner membrane protein	NA	yjjP	Membrane
MNLKPGEA_ argB	-1.920208474	0.058033	Acetylglutamate kinase	2.7.2.8	argB	Catalyzes the ATP-dependent ph
MNLKPGEA_ MNLKPGEA	-1.923780626	NA	hypothetical protein	NA	0	Replication protein P
MNLKPGEA_ mdlB	-1.925125217	0.1742685	Multidrug resistance-like	7.6.2.2	mdlB	Involved in lipid A export and po
MNLKPGEA_ MNLKPGEA	-1.930216565	0.17173679	hypothetical protein	NA	0	nucleobase-containing compoun
MNLKPGEA_ MNLKPGEA	-1.930437231	NA	hypothetical protein	NA	com1	Dsba oxidoreductase
MNLKPGEA_ murE	-1.930697175	0.08374568	UDP-N-acetylmuramoyl-	6.3.2.13	murE	Catalyzes the addition of meso-d
MNLKPGEA_ hisG	-1.930764306	0.18827155	ATP phosphoribosyltrans	2.4.2.17	hisG	Catalyzes the condensation of A
MNLKPGEA_ MNLKPGEA	-1.933207842	NA	hypothetical protein	NA	yaiW	Lipoprotein
MNLKPGEA_ sbcB	-1.933666335	0.08374568	Exodeoxyribonuclease I	3.1.11.1	sbcB	Exonucleolytic cleavage in the 3'
MNLKPGEA_ mltA	-1.933830367	0.00374642	Membrane-bound lytic n	4.2.2.-	mltA	Murein-degrading enzyme. May
MNLKPGEA_ tolB	-1.936031467	1.28E-06	Tol-Pal system protein T	NA	tolB	involved in the tonB-independen
MNLKPGEA_ pglJ_2	-1.936399874	0.0006706	N-acetylgalactosamine-I	2.4.1.291	0	transferase activity, transferring
MNLKPGEA_ MNLKPGEA	-1.939932902	0.16963513	hypothetical protein	NA	0	0
MNLKPGEA_ MNLKPGEA	-1.942099581	0.00061144	hypothetical protein	NA	0	PFAM glycoside hydrolase famil
MNLKPGEA_ ppiB	-1.944658817	0.00048173	Peptidyl-prolyl cis-trans i	5.2.1.8	ppiB	PPIases accelerate the folding o
MNLKPGEA_ hutH	-1.945738561	0.16800891	Histidine ammonia-lyase	4.3.1.3	hutH	PFAM Phenylalanine histidine ar
MNLKPGEA_ MNLKPGEA	-1.949521039	0.16800891	hypothetical protein	NA	#N/A	#N/A
MNLKPGEA_ MNLKPGEA	-1.949778922	0.00052996	hypothetical protein	NA	0	Domain of unknown function DU
MNLKPGEA_ MNLKPGEA	-1.950169802	0.04222084	hypothetical protein	NA	yicH	AsmA Family

MNLKPGEA_	MNLKPGEA	-1.954653577	0.02042828	hypothetical protein	NA	0	0
MNLKPGEA_	MNLKPGEA	-1.956360987	NA	hypothetical protein	NA	hofM	Pilus assembly protein
MNLKPGEA_	hrpB	-1.958640775	NA	ATP-dependent RNA heli	3.6.4.13	hrpB	ATP-dependent helicase
MNLKPGEA_	bioD1_1	-1.962539386	0.16731153	ATP-dependent dethiobi	6.3.3.3	ynfK	Catalyzes a mechanistically unus
MNLKPGEA_	tolR	-1.969082843	0.16345314	Tol-Pal system protein T	NA	tolR	biopolymer transport protein
MNLKPGEA_	lipB	-1.975186861	0.07616093	Octanoyltransferase	2.3.1.181	lipB	Catalyzes the transfer of endoge
MNLKPGEA_	yggS	-1.975310234	0.07556013	Pyridoxal phosphate hom	NA	yggS	Pyridoxal 5'-phosphate (PLP)-bin
MNLKPGEA_	emrD	-1.97788906	NA	Multidrug resistance pro	NA	emrD	Major facilitator Superfamily
MNLKPGEA_	ydgT	-1.980346914	0.01895642	Transcription modulator	NA	cnu	positive regulation of protein co
MNLKPGEA_	MNLKPGEA	-1.983536644	NA	hypothetical protein	NA	0	0
MNLKPGEA_	rplY	-1.983552102	0.00062199	50S ribosomal protein L2	NA	ctc	This is one of the proteins that b
MNLKPGEA_	MNLKPGEA	-1.985517674	0.00911553	IS6 family transposase IS	NA	0	Transposase IS66 family
MNLKPGEA_	apt	-1.986383538	0.01751925	Adenine phosphoribosylt	2.4.2.7	apt	Catalyzes a salvage reaction res
MNLKPGEA_	rpsN	-1.991442142	1.51E-11	30S ribosomal protein S1	NA	rpsN	Binds 16S rRNA, required for the
MNLKPGEA_	ibpB_2	-1.993333823	4.39E-28	Small heat shock proteir	NA	ibp	Belongs to the small heat shock
MNLKPGEA_	MNLKPGEA	-1.995680703	0.07246475	hypothetical protein	NA	yaeR	glyoxalase bleomycin resistance
MNLKPGEA_	cspD	-2.000871621	1.87E-21	Cold shock-like protein C	NA	cspD	Cold shock
MNLKPGEA_	aphA	-2.006007392	NA	Class B acid phosphatase	3.1.3.2	aphA	Belongs to the class B bacterial
MNLKPGEA_	MNLKPGEA	-2.006449879	0.14480255	hypothetical protein	NA	0	0
MNLKPGEA_	MNLKPGEA	-2.009279588	0.07124446	hypothetical protein	NA	yfeH	Bile acid sodium symporter
MNLKPGEA_	yhaI	-2.009723665	NA	Inner membrane protein	NA	0	Protein of unknown function (DU
MNLKPGEA_	yccF	-2.011399087	0.15313152	Inner membrane protein	NA	yccF	Membrane
MNLKPGEA_	cysI	-2.011465641	0.15308374	Sulfite reductase [NADPI	1.8.1.2	cysI	Component of the sulfite reducta
MNLKPGEA_	trpR	-2.011653995	0.06905289	Trp operon repressor	NA	trpR	This protein is an aporepressor.
MNLKPGEA_	poxB	-2.013342621	0.0020912	Pyruvate dehydrogenase	1.2.5.1	poxB	Belongs to the TPP enzyme fami
MNLKPGEA_	mdtA_1	-2.015097944	NA	Multidrug resistance pro	NA	mdtA	Belongs to the membrane fusion
MNLKPGEA_	argS	-2.019237352	0.01978674	Arginine--tRNA ligase	6.1.1.19	argS	Arginyl-tRNA synthetase
MNLKPGEA_	murI	-2.028224842	0.01105798	Glutamate racemase	5.1.1.3	murI	Provides the (R)-glutamate requ
MNLKPGEA_	rplR	-2.039835764	1.40E-06	50S ribosomal protein L1	NA	rplR	This is one of the proteins that b
MNLKPGEA_	MNLKPGEA	-2.042658366	0.06506667	hypothetical protein	NA	yecA	Belongs to the UPF0149 family

MNLKPGEA_	btuD_3	-2.046362166	0.06445579	Vitamin B12 import ATP	7.6.2.8	btuD	Part of the ABC transporter com
MNLKPGEA_	znuB	-2.050796315	0.06884793	High-affinity zinc uptake	NA	znuB	COG1108 ABC-type Mn2 Zn2 tra
MNLKPGEA_	ttcA	-2.05118165	0.01381683	tRNA-cytidine(32) 2-sulf	2.8.1.-	ttcA	Catalyzes the ATP-dependent 2-
MNLKPGEA_	MNLKPGEA	-2.052274042	0.14527734	hypothetical protein	NA	yebY	Protein of unknown function (DU
MNLKPGEA_	MNLKPGEA	-2.05552617	0.00903224	hypothetical protein	NA	tolA	Membrane protein involved in co
MNLKPGEA_	hemW	-2.057624471	NA	Heme chaperone HemW	NA	yggW	Involved in the biosynthesis of p
MNLKPGEA_	dapA_1	-2.059664507	5.39E-09	4-hydroxy-tetrahydrodipi	4.3.3.7	dapA	Catalyzes the condensation of (S
MNLKPGEA_	nuoL	-2.060003889	0.00533118	NADH-quinone oxidoredu	7.1.1.-	nuoL	NADH ubiquinone
MNLKPGEA_	MNLKPGEA	-2.060010478	1.10E-06	hypothetical protein	NA	ycbK	protein conserved in bacteria
MNLKPGEA_	rplF	-2.061441772	7.41E-10	50S ribosomal protein L6	NA	rplF	This protein binds to the 23S rRN
MNLKPGEA_	ftsW	-2.062917239	0.02947794	putative peptidoglycan g	2.4.1.129	ftsW	Peptidoglycan polymerase that i
MNLKPGEA_	rlpA	-2.064147406	0.14095085	Endolytic peptidoglycan t	4.2.2.-	rlpA	Lytic transglycosylase with a stro
MNLKPGEA_	proB	-2.065829369	0.02975297	Glutamate 5-kinase	2.7.2.11	proB	Catalyzes the transfer of a phosp
MNLKPGEA_	norR_4	-2.067158674	0.14089926	Anaerobic nitric oxide re	NA	0	transcriptional regulator
MNLKPGEA_	usg	-2.068515657	NA	USG-1 protein	NA	usg	Catalyzes the NADPH-dependent
MNLKPGEA_	potB	-2.070249258	NA	Spermidine/putrescine t	NA	potB	ABC-type spermidine putrescine
MNLKPGEA_	MNLKPGEA	-2.070624953	0.13943795	hypothetical protein	NA	0	Terminase small subunit
MNLKPGEA_	MNLKPGEA	-2.072223047	NA	hypothetical protein	NA	0	cellulase activity
MNLKPGEA_	rpmG	-2.073601854	1.45E-07	50S ribosomal protein L3	NA	rpmG	Belongs to the bacterial ribosom
MNLKPGEA_	pntA	-2.07366495	0.07335604	NAD(P) transhydrogenas	7.1.1.1	pntA	The transhydrogenation betwee
MNLKPGEA_	trmJ	-2.074695693	0.00766968	tRNA (cytidine/uridine-2	2.1.1.200	trmJ	Catalyzes the formation of 2'O-r
MNLKPGEA_	MNLKPGEA	-2.076483697	0.08735517	hypothetical protein	NA	#N/A	#N/A
MNLKPGEA_	gltS	-2.078562877	0.03286177	Sodium/glutamate symp	NA	gltS	Catalyzes the sodium-dependent
MNLKPGEA_	thiH	-2.07892169	0.02522942	2-iminoacetate synthase	4.1.99.19	thiH	In Escherichia coli this enzyme f
MNLKPGEA_	rbtD	-2.081315116	NA	Ribitol 2-dehydrogenase	1.1.1.56	rbtD	COG4221 Short-chain alcohol de
MNLKPGEA_	ridA_1	-2.08162213	1.74E-06	2-iminobutanoate/2-imi	3.5.99.10	yjgF	Endoribonuclease
MNLKPGEA_	stpA	-2.082961737	0.06301367	DNA-binding protein Stp	NA	stpA	Belongs to the histone-like prote
MNLKPGEA_	mukF	-2.083088398	0.0080514	Chromosome partition p	NA	mukF	Involved in chromosome conden
MNLKPGEA_	MNLKPGEA	-2.083433725	0.02745661	hypothetical protein	NA	asmA	Protein involved in outer membr
MNLKPGEA_	bcr_2	-2.090677757	0.1418224	Bicyclomycin resistance	NA	bcr	Major facilitator Superfamily

MNLKPGEA_	mepA	-2.092399349	NA	Penicillin-insensitive mu	3.4.24.-	mepA	Murein endopeptidase that clea
MNLKPGEA_	arnA	-2.094634167	0.13845526	Bifunctional polymyxin r	NA	arnA	Bifunctional enzyme that catalyz
MNLKPGEA_	dusB	-2.09618021	0.00390926	tRNA-dihydrouridine syn	1.3.1.-	dusB	Catalyzes the synthesis of 5,6-di
MNLKPGEA_	rimL	-2.096710017	NA	Ribosomal-protein-serin	2.3.1.-	rimL	COG1670 Acetyltransferases, inc
MNLKPGEA_	rpmF	-2.097544567	4.41E-09	50S ribosomal protein L3	NA	rpmF	Belongs to the bacterial ribosom
MNLKPGEA_	yfbR	-2.097829233	0.05789915	5'-deoxynucleotidase Yfb	3.1.3.89	yfbR	Catalyzes the strictly specific de
MNLKPGEA_	sra	-2.098330294	2.36E-09	Stationary-phase-induce	NA	rpsV	30S ribosomal protein subunit S
MNLKPGEA_	mreC	-2.099544523	NA	Cell shape-determining p	NA	mreC	Involved in formation and maint
MNLKPGEA_	ileS	-2.101288684	4.46E-06	Isoleucine--tRNA ligase	6.1.1.5	ileS	amino acids such as valine, to av
MNLKPGEA_	pcaK_2	-2.102067485	0.01499852	4-hydroxybenzoate trans	NA	0	transporter
MNLKPGEA_	xerC_2	-2.102803455	NA	Tyrosine recombinase Xe	NA	xerC	Belongs to the 'phage' integrase
MNLKPGEA_	MNLKPGEA	-2.104002172	0.13305339	hypothetical protein	NA	yiiQ	Protein of unknown function (DU
MNLKPGEA_	MNLKPGEA	-2.10419434	2.15E-05	hypothetical protein	NA	0	Initiator Replication protein
MNLKPGEA_	feoA	-2.106078339	0.05541725	Fe(2+) transport protein	NA	feoA	Fe2 transport system protein A
MNLKPGEA_	mdtI	-2.10614424	NA	Spermidine export prote	NA	mdtI	Catalyzes the excretion of sperm
MNLKPGEA_	nuoM	-2.108260957	0.01683751	NADH-quinone oxidoredu	7.1.1.-	nuoM	NADH ubiquinone oxidoreductas
MNLKPGEA_	glnH_2	-2.110233141	8.97E-12	Glutamine-binding perip	NA	glnH	belongs to the bacterial solute-b
MNLKPGEA_	rpsO	-2.11047755	1.69E-13	30S ribosomal protein S1	NA	rpsO	Forms an intersubunit bridge (br
MNLKPGEA_	rpsU	-2.110746406	2.11E-10	30S ribosomal protein S2	NA	rpsU	Belongs to the bacterial ribosom
MNLKPGEA_	pheS	-2.116573167	0.13179585	Phenylalanine--tRNA liga	6.1.1.20	pheS	Belongs to the class-II aminoacy
MNLKPGEA_	malP_2	-2.123056572	NA	PTS system maltose-spe	NA	aglA	PTS system
MNLKPGEA_	MNLKPGEA	-2.126909597	NA	hypothetical protein	NA	0	nuclease activity
MNLKPGEA_	MNLKPGEA	-2.126974565	0.02697431	hypothetical protein	NA	0	nucleotidyltransferase activity
MNLKPGEA_	frcA_1	-2.135134202	0.13085124	Fructose import ATP-bin	7.5.2.-	0	Part of the ABC transporter com
MNLKPGEA_	MNLKPGEA	-2.142316657	0.0936547	hypothetical protein	NA	0	Domain of unknown function (DU
MNLKPGEA_	trpS2	-2.143634527	0.00825977	Tryptophan--tRNA ligase	6.1.1.2	trpS	Tryptophanyl-tRNA synthetase
MNLKPGEA_	rplU	-2.149140782	6.12E-12	50S ribosomal protein L2	NA	rplU	This protein binds to 23S rRNA in
MNLKPGEA_	MNLKPGEA	-2.149160585	NA	ISKra4 family transposas	NA	fimE	FimE is one of the 2 regulatory p
MNLKPGEA_	rsmG	-2.149759974	0.12718005	Ribosomal RNA small su	2.1.1.170	rsmG	Specifically methylates the N7 p
MNLKPGEA_	murC	-2.150727748	0.02329852	UDP-N-acetylmuramate-	6.3.2.8	murC	Belongs to the MurCDEF family

MNLKPGEA_ rplN	-2.152603225	3.90E-15	50S ribosomal protein L1	NA	rplN	Binds to 23S rRNA. Forms part c
MNLKPGEA_ udk	-2.153701574	0.12367207	Uridine kinase	2.7.1.48	udk	Cytidine monophosphokinase
MNLKPGEA_ rpsD	-2.154549285	1.22E-17	30S ribosomal protein S4	NA	rpsD	One of the primary rRNA binding
MNLKPGEA_ rplE	-2.160328985	5.66E-19	50S ribosomal protein L5	NA	rplE	This is 1 of the proteins that bin
MNLKPGEA_ thiB	-2.160486677	0.05171103	Thiamine-binding peripla	NA	tbpA	thiamine ABC transporter
MNLKPGEA_ MNLKPGEA	-2.161460152	NA	hypothetical protein	NA	yraN	Belongs to the UPF0102 family
MNLKPGEA_ pcaI	-2.16265903	NA	3-oxoadipate CoA-transf	2.8.3.6	pcaI	COG1788 Acyl CoA acetate 3-ket
MNLKPGEA_ slmA	-2.164775411	0.12445633	Nucleoid occlusion facto	NA	slmA	Required for nucleoid occlusion
MNLKPGEA_ basS	-2.167348013	0.12065656	Sensor protein BasS	2.7.13.3	basS	Sensor protein basS
MNLKPGEA_ syd	-2.169281367	0.02035413	Protein Syd	NA	syd	regulation of protein complex as
MNLKPGEA_ dctD	-2.171899133	0.12006999	C4-dicarboxylate transpc	NA	pgtA	Response regulator containing C
MNLKPGEA_ rpmC	-2.174054261	2.18E-10	50S ribosomal protein L2	NA	rpmC	Belongs to the universal riboson
MNLKPGEA_ MNLKPGEA	-2.175102663	3.87E-06	hypothetical protein	NA	#N/A	#N/A
MNLKPGEA_ melY	-2.177288657	NA	Melibiose permease	NA	rafB	Major facilitator superfamily
MNLKPGEA_ rpoA	-2.179649052	6.16E-20	DNA-directed RNA polyn	2.7.7.6	rpoA	DNA-dependent RNA polymeras
MNLKPGEA_ dsbC	-2.186321051	0.1184109	Thiol:disulfide interchan	NA	dsbC	Required for disulfide bond form
MNLKPGEA_ MNLKPGEA	-2.188527611	6.38E-05	hypothetical protein	NA	wbbM	Glycosyl Transferase
MNLKPGEA_ deaD	-2.189990399	0.00432309	ATP-dependent RNA heli	3.6.4.13	deaD	DEAD-box RNA helicase involvec
MNLKPGEA_ treB	-2.190534011	NA	PTS system trehalose-sp	NA	treB	pts system
MNLKPGEA_ hpaC	-2.191268177	0.00096336	4-hydroxyphenylacetate	1.5.1.36	hpaC	4-hydroxyphenylacetate 3-mono
MNLKPGEA_ MNLKPGEA	-2.192206858	NA	hypothetical protein	NA	0	Belongs to the WXG100 family
MNLKPGEA_ atpA	-2.199986343	5.59E-08	ATP synthase subunit alp	7.1.2.2	atpA	Produces ATP from ADP in the pr
MNLKPGEA_ emtA	-2.202359581	NA	Endo-type membrane-bo	4.2.2.-	emtA	Murein-degrading enzyme. May
MNLKPGEA_ coaBC	-2.204949765	0.11396973	Coenzyme A biosynthesis	NA	coaBC	Catalyzes two steps in the biosy
MNLKPGEA_ MNLKPGEA	-2.205735957	0.07053055	hypothetical protein	NA	0	Psort location Cytoplasmic, score
MNLKPGEA_ lgt	-2.208552213	0.04416445	Phosphatidylglycerol--pr	2.5.1.145	lgt	Transfers the N-acyl diglyceride
MNLKPGEA_ dnaT_1	-2.210600535	0.12989878	Primosomal protein 1	NA	0	0
MNLKPGEA_ pxpA_1	-2.213289611	NA	5-oxoprolinase subunit A	3.5.2.9	ybgL	Belongs to the UPF0271 (lamB)
MNLKPGEA_ glsA2	-2.216771219	NA	Glutaminase 2	3.5.1.2	glsA	Belongs to the glutaminase fam
MNLKPGEA_ nhaA_1	-2.224735597	0.03364408	Na(+)/H(+) antiporter NI	NA	nhaA	Na( ) H( ) antiporter that extrude

MNLKPGEA_ paaK	-2.225064205	2.81E-06	Phenylacetate-coenzyme	6.2.1.30	paaK	Catalyzes the activation of phen
MNLKPGEA_ msbA_1	-2.225879392	0.00078359	Lipid A export ATP-bindi	7.5.2.6	msbA	Involved in lipid A export and po
MNLKPGEA_ dppB_1	-2.24008679	NA	Dipeptide transport syste	NA	dppB	PFAM binding-protein-depender
MNLKPGEA_ lolC	-2.241127137	NA	Lipoprotein-releasing sy	NA	lolC	Lipoprotein releasing system tra
MNLKPGEA_ feoB	-2.241396443	0.01137513	Fe(2+) transporter FeoB	NA	feoB	Transporter of a GTP-driven Fe(2
MNLKPGEA_ efeU	-2.241539989	0.00270149	Ferrous iron permease E	NA	efeU	Iron Permease
MNLKPGEA_ rsxA	-2.243003921	0.04388371	Ion-translocating oxidore	7.-.-.-	rnfA	Part of a membrane complex inv
MNLKPGEA_ MNLKPGEA	-2.243868846	0.0411687	hypothetical protein	NA	0	DNA metabolic process
MNLKPGEA_ nfo	-2.245268124	NA	Endonuclease 4	3.1.21.2	nfo	Endonuclease IV plays a role in D
MNLKPGEA_ hmuV	-2.245736998	0.09934943	Hemin import ATP-bindi	3.6.3.-	hmuV	Part of the ABC transporter com
MNLKPGEA_ rpmB	-2.249475648	4.90E-11	50S ribosomal protein L2	NA	rpmB	Belongs to the bacterial ribosom
MNLKPGEA_ ybiT	-2.250494453	0.00658386	putative ABC transporter	NA	ybiT	COG0488 ATPase components o
MNLKPGEA_ hmuT	-2.254911578	0.05573951	Hemin-binding periplasm	NA	hmuT	ABC-type hemin transport syster
MNLKPGEA_ prfA	-2.25560169	0.10576674	Peptide chain release fa	NA	prfA	Peptide chain release factor 1 di
MNLKPGEA_ MNLKPGEA	-2.256821247	0.09502366	hypothetical protein	NA	0	0
MNLKPGEA_ ybjI	-2.257643186	NA	5-amino-6-(5-phospho-D	3.1.3.104	ybjI	Hydrolase
MNLKPGEA_ queG	-2.259513094	0.00259638	Epoxyqueuosine reducta	1.17.99.6	queG	Catalyzes the conversion of epox
MNLKPGEA_ nlpI	-2.26025962	9.80E-08	Lipoprotein NlpI	NA	nlpI	May be involved in cell division
MNLKPGEA_ ydjF	-2.261186665	0.10369888	putative HTH-type transc	NA	fucR	transcriptional regulator
MNLKPGEA_ MNLKPGEA	-2.263333676	0.00054978	hypothetical protein	NA	0	0
MNLKPGEA_ infA	-2.267961231	0.0002008	Translation initiation fac	NA	infA	One of the essential component
MNLKPGEA_ astD_2	-2.268241052	0.09507475	N-succinylglutamate 5-s	1.2.1.71	astD	Catalyzes the NAD-dependent re
MNLKPGEA_ puuA	-2.26931306	0.06861947	Gamma-glutamylputres	6.3.1.11	puuA	glutamine synthetase
MNLKPGEA_ pdxJ	-2.270933306	NA	Pyridoxine 5'-phosphate	2.6.99.2	pdxJ	Catalyzes the complicated ring c
MNLKPGEA_ cyoA	-2.272196405	3.22E-13	Cytochrome bo(3) ubiqui	NA	cyoA	Subunits I and II form the functio
MNLKPGEA_ lldP	-2.272948439	0.10154474	L-lactate permease	NA	lldP	L-lactate permease
MNLKPGEA_ rbsB_2	-2.282285897	0.04643718	Ribose import binding pr	NA	0	Periplasmic binding protein LacI
MNLKPGEA_ MNLKPGEA	-2.284884905	NA	Histone deacetylase-like	3.5.1.-	hdaH	COG0123 Deacetylases, includin
MNLKPGEA_ atpF	-2.284973303	5.29E-05	ATP synthase subunit b	NA	atpF	Component of the F(0) channel,
MNLKPGEA_ bioB	-2.286058166	0.01788841	Biotin synthase	2.8.1.6	bioB	Catalyzes the conversion of deth

MNLKPGEA_ cycA_2	-2.287017024	0.00017995	D-serine/D-alanine/glyci	NA	cycA	amino acid
MNLKPGEA_ glnQ_5	-2.292372604	0.00109422	Glutamine transport ATF	NA	glnQ	(ABC) transporter
MNLKPGEA_ nqrA	-2.299683769	0.0844538	Na(+)-translocating NAD	7.2.1.1	nqrA	NQR complex catalyzes the redu
MNLKPGEA_ dsbB	-2.302577892	0.00085848	Disulfide bond formatior	NA	dsbB	Required for disulfide bond form
MNLKPGEA_ mtnD	-2.304246964	0.08157046	Acireductone dioxygenas	1.13.11.54	mtnD	Catalyzes 2 different reactions b
MNLKPGEA_ aspC	-2.307470616	2.08E-05	Aspartate aminotransfer	2.6.1.1	aspC	aminotransferase
MNLKPGEA_ rsuA	-2.31042037	0.09802187	Ribosomal small subunit	5.4.99.19	rsuA	Belongs to the pseudouridine sy
MNLKPGEA_ yhbY	-2.315543467	2.69E-07	RNA-binding protein Yhb	NA	yhbY	CRS1 / YhbY (CRM) domain
MNLKPGEA_ zapE_1	-2.319278777	0.09459378	Cell division protein ZapI	NA	zapE	Reduces the stability of FtsZ pol
MNLKPGEA_ mrdA_2	-2.320787034	0.07859769	Peptidoglycan D,D-transp	3.4.16.4	mrdA	Catalyzes cross-linking of the pe
MNLKPGEA_ yncE_1	-2.330899537	0.00622534	putative protein YncE	NA	yncE	DNA binding
MNLKPGEA_ MNLKPGEA	-2.331621655	0.00034722	hypothetical protein	NA	wbpY	Glycosyl transferases group 1
MNLKPGEA_ tyrB_2	-2.339726484	0.0320224	Tyrosine aminotransfera	2.6.1.5	tyrB	aminotransferase
MNLKPGEA_ yqeG	-2.342238996	0.034503	Inner membrane transpo	NA	yqeG	transporter
MNLKPGEA_ thpA_1	-2.349327012	0.07576016	D-threitol-binding protei	NA	0	ABC-type sugar transport system
MNLKPGEA_ zitB	-2.350910099	0.03262587	Zinc transporter ZitB	NA	zitB	cation diffusion facilitator famil
MNLKPGEA_ ybhC	-2.351472518	0.01396671	Putative acyl-CoA thioes	3.1.2.-	ybhC	Pectinesterase
MNLKPGEA_ tig	-2.352683693	8.75E-12	Trigger factor	5.2.1.8	tig	Involved in protein export. Acts a
MNLKPGEA_ rpsH	-2.353481536	1.00E-12	30S ribosomal protein S8	NA	rpsH	One of the primary rRNA bindin
MNLKPGEA_ MNLKPGEA	-2.354411886	0.00056278	hypothetical protein	NA	0	lipoprotein nlpC
MNLKPGEA_ rdgC	-2.355234235	0.03027926	Recombination-associat	NA	rdgC	May be involved in recombinatic
MNLKPGEA_ fruA_1	-2.355581742	0.0736371	PTS system fructose-spe	NA	0	Phosphotransferase system, EIIC
MNLKPGEA_ fbaB	-2.356945553	6.71E-09	Fructose-bisphosphate a	4.1.2.13	fbaB	Catalyzes the formation of glyce
MNLKPGEA_ ptrA	-2.357330934	0.00032679	Protease 3	3.4.24.55	ptrA	Belongs to the peptidase M16 fa
MNLKPGEA_ trpC	-2.360943334	0.00700906	Tryptophan biosynthesis	NA	trpC	Belongs to the TrpC family
MNLKPGEA_ MNLKPGEA	-2.361903213	0.06386009	hypothetical protein	NA	0	0
MNLKPGEA_ entA	-2.364818892	0.01759851	2,3-dihydro-2,3-dihydrox	1.3.1.28	entA	PFAM Short-chain dehydrogenas
MNLKPGEA_ MNLKPGEA	-2.365497185	0.04931655	hypothetical protein	NA	0	0
MNLKPGEA_ groL	-2.366532123	4.84E-05	60 kDa chaperonin	NA	groL	Prevents misfolding and promot
MNLKPGEA_ MNLKPGEA	-2.367470202	0.07347293	hypothetical protein	NA	yfdP	0

MNLKPGEA_ aroQ	-2.3712672	0.00414774	3-dehydroquinate dehyd	4.2.1.10	aroQ	Catalyzes a trans-dehydration vi
MNLKPGEA_ rlmC	-2.376160084	0.07057298	23S rRNA (uracil(747)-C(	2.1.1.189	rlmC	Catalyzes the formation of 5-me
MNLKPGEA_ thiF	-2.37628555	0.03772974	Sulfur carrier protein Thi	2.7.7.73	thiF	COG0476 Dinucleotide-utilizing
MNLKPGEA_ purE	-2.377045269	0.07424211	N5-carboxyaminoimidaz	5.4.99.18	purE	Catalyzes the conversion of N5-c
MNLKPGEA_ rplJ	-2.382315982	5.99E-24	50S ribosomal protein L1	NA	rplJ	Forms part of the ribosomal sta
MNLKPGEA_ MNLKPGEA	-2.38447051	0.09307332	hypothetical protein	NA	0	DNA replication initiation
MNLKPGEA_ sucC	-2.388460589	0.00522636	Succinate--CoA ligase [A	6.2.1.5	sucC	Succinyl-CoA synthetase functio
MNLKPGEA_ ldcA	-2.388578575	0.06949353	Murein tetrapeptide carl	3.4.17.13	ldcA	proteins, homologs of microcin
MNLKPGEA_ yceD	-2.391171297	2.82E-20	Large ribosomal RNA sul	NA	yceD	metal-binding, possibly nucleic a
MNLKPGEA_ mdfA	-2.393662635	0.08336397	Multidrug transporter M	NA	mdfA	multi-drug
MNLKPGEA_ purN	-2.397843842	0.08374568	Phosphoribosylglycinami	2.1.2.2	purN	Catalyzes the transfer of a form
MNLKPGEA_ murA	-2.397986412	0.08253351	UDP-N-acetylglucosamir	2.5.1.7	murA	Belongs to the EPSP synthase fa
MNLKPGEA_ trpA	-2.399171586	0.08735517	Tryptophan synthase alp	4.2.1.20	trpA	The alpha subunit is responsible
MNLKPGEA_ hpcD	-2.405002959	0.00039092	5-carboxymethyl-2-hydrc	5.3.3.10	hpcD	5-carboxymethyl-2-hydroxymucc
MNLKPGEA_ cytR_1	-2.405263406	0.06857278	HTH-type transcriptional	NA	cscR	Transcriptional
MNLKPGEA_ MNLKPGEA	-2.406590612	0.0411687	hypothetical protein	NA	recT	COG3723 Recombinational DNA
MNLKPGEA_ yicL	-2.407139835	0.08301768	putative inner membran	NA	yicL	transporter
MNLKPGEA_ dacB	-2.411886717	0.02605323	D-alanyl-D-alanine carbc	3.4.16.4	dacB	D-alanyl-D-alanine carboxypepti
MNLKPGEA_ mreB	-2.413675663	0.0271777	Cell shape-determining p	NA	mreB	TIGRFAM Cell shape determinin
MNLKPGEA_ radA	-2.41710747	0.08103702	DNA repair protein RadA	3.6.4.-	radA	DNA-dependent ATPase involvec
MNLKPGEA_ cmoM	-2.418337929	0.0037802	tRNA 5-carboxymethoxy	2.1.1.-	cmoM	Catalyzes the methylation of 5-c
MNLKPGEA_ lon_1	-2.418655722	0.08021684	Lon protease	3.4.21.53	ycbZ	Belongs to the peptidase S16 fa
MNLKPGEA_ glyS	-2.434803449	0.00055743	Glycine--tRNA ligase bet	6.1.1.14	glyS	Glycyl-tRNA synthetase beta sub
MNLKPGEA_ MNLKPGEA	-2.436710427	0.06675065	hypothetical protein	NA	0	peptidase activity
MNLKPGEA_ queA	-2.437888192	0.06295562	S-adenosylmethionine:tF	2.4.99.17	queA	Transfers and isomerizes the rib
MNLKPGEA_ MNLKPGEA	-2.444382831	0.0244967	hypothetical protein	NA	0	HD superfamily
MNLKPGEA_ bioA	-2.446494382	0.07972181	Adenosylmethionine-8-a	2.6.1.62	bioA	Catalyzes the transfer of the alp
MNLKPGEA_ pcnB	-2.446983485	0.00912202	Poly(A) polymerase I	2.7.7.19	pcnB	Adds poly(A) tail to the 3' end of
MNLKPGEA_ rpmI	-2.450974168	9.32E-10	50S ribosomal protein L3	NA	rpmI	Belongs to the bacterial ribosom
MNLKPGEA_ iutA	-2.451316429	0.00147143	Ferric aerobactin recept	NA	iutA	Receptor

MNLKPGEA_	MNLKPGEA	-2.459410264	0.06013387	hypothetical protein	NA	0	filamentation induced by cAMP
MNLKPGEA_	MNLKPGEA	-2.462166705	0.05839097	hypothetical protein	NA	0	GtrA-like protein
MNLKPGEA_	dauA_1	-2.469983426	0.05762654	C4-dicarboxylic acid tran	NA	ychM	COG0659 Sulfate permease and
MNLKPGEA_	nuoK	-2.47824774	0.06131121	NADH-quinone oxidored	7.1.1.-	nuoK	NDH-1 shuttles electrons from N
MNLKPGEA_	MNLKPGEA	-2.478387757	0.00654784	Magnesium transporter	NA	mgtE	Acts as a magnesium transporte
MNLKPGEA_	MNLKPGEA	-2.480574667	3.66E-06	hypothetical protein	NA	radC	Belongs to the UPF0758 family
MNLKPGEA_	rplA	-2.482061953	1.29E-22	50S ribosomal protein L1	NA	rplA	Binds directly to 23S rRNA. The
MNLKPGEA_	yjcH	-2.483031	0.05892215	Inner membrane protein	NA	yjcH	Membrane
MNLKPGEA_	skp	-2.483789706	7.49E-11	Chaperone protein Skp	NA	skp	Belongs to the skp family
MNLKPGEA_	yhhS_1	-2.484722394	0.0564614	putative MFS-type trans	NA	yhhS	MFS-type transporter
MNLKPGEA_	cysD	-2.494544258	0.05573951	Sulfate adenylyltransfera	2.7.7.4	cysD	sulfate adenylyltransferase), sub
MNLKPGEA_	hutU	-2.496056727	0.06942633	Urocanate hydratase	4.2.1.49	hutU	Catalyzes the conversion of uroc
MNLKPGEA_	tusD	-2.497927225	0.06953784	Sulfurtransferase TusD	2.8.1.-	tusD	Part of a sulfur-relay system req
MNLKPGEA_	cysH_1	-2.498879621	0.05534759	Phosphoadenosine phosp	1.8.4.8	cysH	Belongs to the PAPS reductase f
MNLKPGEA_	trxB	-2.499515042	0.00026452	Thioredoxin reductase	1.8.1.9	trxB	Belongs to the class-II pyridine r
MNLKPGEA_	glpT_2	-2.500729688	0.05401431	Glycerol-3-phosphate tra	NA	0	transporter
MNLKPGEA_	hpaB	-2.502991978	0.00048077	4-hydroxyphenylacetate	1.14.14.9	hpaB	4-hydroxyphenylacetate 3-hydro
MNLKPGEA_	MNLKPGEA	-2.50369848	0.00021206	hypothetical protein	NA	0	Glycosyltransferases involved in
MNLKPGEA_	rho	-2.506961954	1.67E-18	Transcription terminatio	3.6.4.-	rho	Facilitates transcription termina
MNLKPGEA_	pcpR_1	-2.508185015	0.05321963	PCP degradation transcri	NA	0	transcriptional regulator
MNLKPGEA_	rlmH	-2.509612986	0.0528725	Ribosomal RNA large su	2.1.1.177	rlmH	Specifically methylates the pseu
MNLKPGEA_	actP_2	-2.513188766	0.07124446	Cation/acetate symporte	NA	actP	Belongs to the sodium solute sy
MNLKPGEA_	mzrA	-2.516997401	0.05573951	Modulator protein MzrA	NA	mzrA	Modulates the activity of the En
MNLKPGEA_	MNLKPGEA	-2.5225512	0.05205836	Inulin fructotransferase	4.2.2.17	0	Periplasmic copper-binding prot
MNLKPGEA_	ispB	-2.538556147	0.00024591	Octaprenyl diphosphate	2.5.1.90	ispB	Belongs to the FPP GGPP syntha
MNLKPGEA_	MNLKPGEA	-2.539921864	0.03985262	hypothetical protein	NA	0	0
MNLKPGEA_	MNLKPGEA	-2.556376428	0.04974389	hypothetical protein	NA	ykgJ	Fe-S-cluster oxidoreductase
MNLKPGEA_	sdaB	-2.564105147	0.04784602	L-serine dehydratase 2	4.3.1.17	sdaB	l-serine dehydratase
MNLKPGEA_	MNLKPGEA	-2.568383079	0.04770155	hypothetical protein	NA	yhaM	Belongs to the UPF0597 family
MNLKPGEA_	ogl	-2.570387697	0.04691278	Oligogalacturonate lyase	4.2.2.6	ogl	oligogalacturonate lyase

MNLKPGEA_ ipdC	-2.57476466	1.48E-10	Indole-3-pyruvate decarb	4.1.1.74	ipdC	Belongs to the TPP enzyme fami
MNLKPGEA_ aceK	-2.577520472	0.03029369	Isocitrate dehydrogenase	2.7.11.5	aceK	Bifunctional enzyme which can p
MNLKPGEA_ ssuB_2	-2.579513245	0.04931655	Aliphatic sulfonates imp	3.6.3.-	ssuB	ABC-type nitrate sulfonate bicar
MNLKPGEA_ MNLKPGEA	-2.58130619	0.06013387	hypothetical protein	NA	yggT	integral membrane protein
MNLKPGEA_ rcsF	-2.585038325	0.06013387	Outer membrane lipopro	NA	rcsF	colanic acid biosynthetic process
MNLKPGEA_ dacA	-2.585685486	0.00591844	D-alanyl-D-alanine carbo	3.4.16.4	dacA	Belongs to the peptidase S11 fa
MNLKPGEA_ cdaR_2	-2.589798168	0.04563195	Carbohydrate diacid regu	NA	cdaR	regulator
MNLKPGEA_ proV	-2.594896841	0.04784602	Glycine betaine/proline I	NA	proV	glycine, betaine
MNLKPGEA_ ydgJ_2	-2.599205002	0.04416443	putative oxidoreductase	1.-.-.-	ydgJ	oxidoreductase
MNLKPGEA_ nrdB	-2.607943254	0.00110765	Ribonucleoside-diphosph	1.17.4.1	nrdB	Provides the precursors necessa
MNLKPGEA_ gsk	-2.61386494	0.05621214	Inosine-guanosine kinase	2.7.1.73	gsk	COG0524 Sugar kinases, ribokina
MNLKPGEA_ yfcA	-2.614479842	0.04332909	putative membrane tran	NA	yfcA	membrane transporter protein
MNLKPGEA_ rpsM	-2.61608709	1.27E-21	30S ribosomal protein S1	NA	rpsM	Located at the top of the head o
MNLKPGEA_ purH	-2.618712651	0.04347903	Bifunctional purine biosy	NA	purH	bifunctional purine biosynthesis
MNLKPGEA_ rplP	-2.619757588	3.56E-16	50S ribosomal protein L1	NA	rplP	Binds 23S rRNA and is also seen
MNLKPGEA_ gatY	-2.623144933	0.04219086	D-tagatose-1,6-bisphosp	4.1.2.40	gatY	Aldolase
MNLKPGEA_ gatZ	-2.623650729	0.04805217	D-tagatose-1,6-bisphosp	NA	gatZ	that is required for full activity a
MNLKPGEA_ MNLKPGEA	-2.626227326	2.36E-06	hypothetical protein	NA	ygiM	sh3 domain protein
MNLKPGEA_ atpE	-2.628385591	0.00010571	ATP synthase subunit c	NA	atpE	F(1)F(0) ATP synthase produces
MNLKPGEA_ ugd	-2.630422886	0.00025157	UDP-glucose 6-dehydrog	1.1.1.22	ugd	Belongs to the UDP-glucose GDF
MNLKPGEA_ MNLKPGEA	-2.632619479	0.03788836	hypothetical protein	NA	0	Bifunctional PTS system fructose
MNLKPGEA_ atpH	-2.635702029	1.87E-05	ATP synthase subunit de	NA	atpH	F(1)F(0) ATP synthase produces
MNLKPGEA_ bla_2	-2.636159771	6.87E-08	Beta-lactamase SHV-2	3.5.2.6	penP	Beta-lactamase
MNLKPGEA_ ddpA_2	-2.637597099	0.04098881	putative D,D-dipeptide-b	NA	ddpA	Extracellular solute-binding prot
MNLKPGEA_ metB	-2.638324245	0.04219086	Cystathionine gamma-sy	2.5.1.48	metB	Catalyzes the formation of L-hor
MNLKPGEA_ MNLKPGEA	-2.645711636	0.04056612	hypothetical protein	NA	thiP	with TbpA and ThiQ functions in
MNLKPGEA_ rpsP	-2.655164046	6.17E-09	30S ribosomal protein S1	NA	rpsP	Belongs to the bacterial ribosom
MNLKPGEA_ rplX	-2.656152243	4.43E-15	50S ribosomal protein L2	NA	rplX	One of the proteins that surroun
MNLKPGEA_ rpsR	-2.663993256	2.43E-10	30S ribosomal protein S1	NA	rpsR	Binds as a heterodimer with pro
MNLKPGEA_ groS	-2.666452931	0.00010767	10 kDa chaperonin	NA	groS	Binds to Cpn60 in the presence o

MNLKPGEA_	proA_2	-2.672768099	0.05106827	Gamma-glutamyl phosp	1.2.1.41	proA	Catalyzes the NADPH-dependent
MNLKPGEA_	yhjE	-2.677792803	0.03889543	Inner membrane metab	NA	yhjE	Major facilitator superfamily
MNLKPGEA_	MNLKPGEA	-2.681149402	0.03779894	hypothetical protein	NA	0	0
MNLKPGEA_	melR	-2.683307206	0.03883905	Melibiose operon regula	NA	melR	melibiose operon regulatory pro
MNLKPGEA_	licC_1	-2.691430575	0.00306904	Lichenan permease IIC c	NA	celB	The phosphoenolpyruvate-deper
MNLKPGEA_	MNLKPGEA	-2.69463188	0.04158675	hypothetical protein	NA	#N/A	#N/A
MNLKPGEA_	ppa_2	-2.701628646	2.86E-08	Inorganic pyrophosphata	3.6.1.1	ppa	Catalyzes the hydrolysis of inorg
MNLKPGEA_	cra_1	-2.703767051	0.03670179	Catabolite repressor/act	NA	scrR	Sucrose operon repressor
MNLKPGEA_	tenA_1	-2.707317583	0.00306604	Aminopyrimidine aminol	3.5.99.2	tenA	Catalyzes an amino-pyrimidine h
MNLKPGEA_	efeO	-2.72505033	0.05037778	Iron uptake system com	NA	efeO	periplasmic lipoprotein involved
MNLKPGEA_	lspA	-2.731162653	0.01118505	Lipoprotein signal peptic	3.4.23.36	lspA	This protein specifically catalyze
MNLKPGEA_	trpGD	-2.732847987	0.01704039	Bifunctional protein Trp(	NA	trpD	Catalyzes the transfer of the phc
MNLKPGEA_	mraY	-2.733313567	0.0467876	Phospho-N-acetylmuram	2.7.8.13	mraY	First step of the lipid cycle react
MNLKPGEA_	betB_3	-2.735400758	1.41E-06	NAD/NADP-dependent b	1.2.1.8	hpaE	Belongs to the aldehyde dehydrc
MNLKPGEA_	zapC	-2.736867687	0.00137135	Cell division protein Zap(	NA	zapC	Contributes to the efficiency of t
MNLKPGEA_	trpB	-2.741996369	0.01499852	Tryptophan synthase bet	4.2.1.20	trpB	The beta subunit is responsible f
MNLKPGEA_	rhaS_10	-2.742088081	0.03386157	HTH-type transcriptional	NA	0	PAS fold
MNLKPGEA_	MNLKPGEA	-2.747306136	0.03287654	hypothetical protein	NA	#N/A	#N/A
MNLKPGEA_	holD	-2.753396585	0.04388918	DNA polymerase III subu	2.7.7.7	holD	DNA polymerase III is a complex
MNLKPGEA_	MNLKPGEA	-2.754353006	0.03439416	hypothetical protein	NA	yjaH	Protein of unknown function (DU
MNLKPGEA_	ybdG_2	-2.761250453	0.03508713	Miniconductance mecha	NA	ybdG	Mechanosensitive Ion channel
MNLKPGEA_	yfdH	-2.763938929	1.13E-08	Prophage bactoprenol gl	2.4.1.-	yfdH	Bactoprenol glucosyl transferase
MNLKPGEA_	gppA	-2.772781366	0.01061282	Guanosine-5'-triphospha	3.6.1.40	gppA	Catalyzes the conversion of pppG
MNLKPGEA_	purL	-2.77372146	0.00444903	Phosphoribosylformylgly	6.3.5.3	purL	Phosphoribosylformylglycinamid
MNLKPGEA_	rplD	-2.778422522	1.18E-10	50S ribosomal protein L4	NA	rplD	Forms part of the polypeptide ex
MNLKPGEA_	trmO	-2.790254304	0.0302422	tRNA (adenine(37)-N6)-I	2.1.1.-	yaeB	PFAM Uncharacterised protein f
MNLKPGEA_	mnmA	-2.793122607	0.04068849	tRNA-specific 2-thiourid	2.8.1.13	mnmA	Catalyzes the 2-thiolation of uric
MNLKPGEA_	yfdG	-2.800025722	1.50E-09	Prophage bactoprenol-li	NA	0	Involved in O antigen modificati
MNLKPGEA_	entB	-2.805817525	0.01161449	Enterobactin synthase co	6.3.2.14	entB	Phosphopantetheine attachment
MNLKPGEA_	rpsC	-2.812485656	1.97E-21	30S ribosomal protein S3	NA	rpsC	Binds the lower part of the 30S s

MNLKPGEA_ mdtJ	-2.829034948	0.04411898	Spermidine export prote	NA	mdtJ	Catalyzes the excretion of sperm
MNLKPGEA_ ftsI_2	-2.830525327	1.08E-15	Peptidoglycan D,D-transp	3.4.16.4	ftsI	Catalyzes cross-linking of the pe
MNLKPGEA_ atpI	-2.84709648	9.49E-08	ATP synthase protein I	NA	atpI	Produces ATP from ADP in the pr
MNLKPGEA_ nadA	-2.849561487	0.02596038	Quinolinate synthase A	2.5.1.72	nadA	Catalyzes the condensation of in
MNLKPGEA_ htpX_2	-2.864978525	0.02685481	Protease HtpX	3.4.24.-	0	Peptidase M48
MNLKPGEA_ carB_1	-2.865580722	0.00010774	Carbamoyl-phosphate sy	6.3.5.5	carB	Carbamoyl-phosphate synthetas
MNLKPGEA_ rpsS	-2.877238099	2.44E-07	30S ribosomal protein S1	NA	rpsS	Protein S19 forms a complex wit
MNLKPGEA_ lldD_1	-2.88417387	0.02936018	L-lactate dehydrogenase	1.1.-.-	lldD	Catalyzes the conversion of L-lac
MNLKPGEA_ MNLKPGEA	-2.884453116	0.01982332	hypothetical protein	NA	0	Bacteriophage head to tail conn
MNLKPGEA_ ndk	-2.887233125	2.20E-06	Nucleoside diphosphate	2.7.4.6	ndk	Major role in the synthesis of nu
MNLKPGEA_ lacC_1	-2.888771459	0.02359809	Tagatose-6-phosphate ki	2.7.1.144	0	Belongs to the carbohydrate kina
MNLKPGEA_ bamC	-2.891274337	9.64E-10	Outer membrane protein	NA	bamC	Part of the outer membrane pro
MNLKPGEA_ MNLKPGEA	-2.895203014	1.59E-05	hypothetical protein	NA	0	membrane
MNLKPGEA_ MNLKPGEA	-2.900191202	0.0244967	hypothetical protein	NA	0	Phosphate-starvation-inducible I
MNLKPGEA_ hpcH	-2.904183257	0.0077635	4-hydroxy-2-oxo-heptane	4.1.2.52	hpaI	Belongs to the HpcH HpaI aldola
MNLKPGEA_ livJ_2	-2.912121852	0.02462536	Leu/Ile/Val/Thr-binding	NA	livJ	With LivFGHM is involved in the
MNLKPGEA_ rpsJ	-2.923261316	2.53E-14	30S ribosomal protein S1	NA	rpsJ	Involved in the binding of tRNA t
MNLKPGEA_ pepD	-2.925282711	1.46E-06	Cytosol non-specific dipe	3.4.13.18	pepD	aminoacyl-histidine dipeptidase
MNLKPGEA_ yciK	-2.933164223	0.03193632	putative oxidoreductase	1.-.-.-	yciK	COG1028 Dehydrogenases with
MNLKPGEA_ MNLKPGEA	-2.949128241	0.02315513	hypothetical protein	NA	0	Bacteriophage replication protei
MNLKPGEA_ hisB	-2.951232701	0.03185464	Histidine biosynthesis bi	NA	hisB	Histidine biosynthesis bifunction
MNLKPGEA_ prs	-2.959357154	1.04E-11	Ribose-phosphate pyrop	2.7.6.1	prs	Involved in the biosynthesis of th
MNLKPGEA_ fimH	-2.96418261	0.02176275	Type 1 fimbrin D-manno	NA	fimH	Fimbrial protein
MNLKPGEA_ rhaR_4	-2.966281516	0.00125456	HTH-type transcriptional	NA	hpaA	4-hydroxyphenylacetate catabolic
MNLKPGEA_ glyA	-2.966679543	0.00032446	Serine hydroxymethyltra	2.1.2.1	glyA	Catalyzes the reversible intercor
MNLKPGEA_ amiB	-2.976816739	0.00531542	N-acetylmuramoyl-L-ala	3.5.1.28	amiB	N-acetylmuramoyl-L-alanine am
MNLKPGEA_ uvrD	-2.986073541	0.02936142	DNA helicase II	3.6.4.12	uvrD	it can initiate unwinding at a nic
MNLKPGEA_ MNLKPGEA	-3.009175044	0.0271777	hypothetical protein	NA	#N/A	#N/A
MNLKPGEA_ pyrH	-3.023826442	0.00429349	Uridylate kinase	2.7.4.22	pyrH	Catalyzes the reversible phospho
MNLKPGEA_ yidC	-3.024558212	7.47E-09	Membrane protein inser	NA	yidC	Required for the insertion and or

MNLKPGEA_ atpB	-3.02584318	3.24E-08	ATP synthase subunit a	NA	atpB	it plays a direct role in the transl
MNLKPGEA_ yhdE	-3.02743842	0.0271777	dTTP/UTP pyrophosphat	3.6.1.9	maf	Maf-like protein
MNLKPGEA_ puuE	-3.029271716	0.00720283	4-aminobutyrate aminot	2.6.1.19	gabT	Belongs to the class-III pyridoxal
MNLKPGEA_ ibaG	-3.042611515	0.01582035	Acid stress protein IbaG	NA	yrbA	Belongs to the BolA IbaG family
MNLKPGEA_ MNLKPGEA	-3.053859286	0.01649511	hypothetical protein	NA	rfaZ	lipopolysaccharide core region b
MNLKPGEA_ MNLKPGEA	-3.069939442	0.00835339	hypothetical protein	NA	recE	PDDEXK-like domain of unknowr
MNLKPGEA_ ilvB_1	-3.07649649	0.01759851	Acetolactate synthase is	2.2.1.6	ilvB	acetolactate synthase
MNLKPGEA_ aceA	-3.07745924	0.00742116	Isocitrate lyase	4.1.3.1	aceA	Isocitrate lyase
MNLKPGEA_ hemB	-3.089142245	0.01427254	Delta-aminolevulinic aci	4.2.1.24	hemB	Belongs to the ALAD family
MNLKPGEA_ celA_1	-3.097562157	0.01381004	PTS system cellobiose-sp	2.7.1.205	celA	Phosphotransferase system, lact
MNLKPGEA_ xylB_4	-3.123197438	0.01293658	Xylulose kinase	2.7.1.17	0	xylulose kinase
MNLKPGEA_ rplC	-3.125667165	5.53E-17	50S ribosomal protein L3	NA	rplC	One of the primary rRNA binding
MNLKPGEA_ hpcE_1	-3.132436387	1.41E-08	Homoprotocatechuate ca	NA	hpaG1	isomerase
MNLKPGEA_ MNLKPGEA	-3.138654192	0.00706607	hypothetical protein	NA	0	viral capsid
MNLKPGEA_ rnpA	-3.140388931	0.00308267	Ribonuclease P protein c	3.1.26.5	rnpA	RNaseP catalyzes the removal o
MNLKPGEA_ fklB	-3.154004042	0.01180336	FKBP-type 22 kDa peptid	5.2.1.8	fklB	Peptidyl-prolyl cis-trans
MNLKPGEA_ MNLKPGEA	-3.156709383	0.0073335	hypothetical protein	NA	0	0
MNLKPGEA_ paaH	-3.168551144	1.23E-06	3-hydroxyadipyl-CoA deh	1.1.1.-	paaH	3-hydroxyacyl-CoA dehydrogenas
MNLKPGEA_ maeA	-3.204734088	0.0103901	NAD-dependent malic en	1.1.1.38	maeA	Malic enzyme
MNLKPGEA_ argC	-3.216393837	0.0033083	N-acetyl-gamma-glutam	1.2.1.38	argC	Catalyzes the NADPH-dependent
MNLKPGEA_ hscB	-3.22569032	0.00997262	Co-chaperone protein Hs	NA	hscB	Co-chaperone involved in the ma
MNLKPGEA_ adk	-3.242758363	5.98E-05	Adenylate kinase	2.7.4.3	adk	Catalyzes the reversible transfer
MNLKPGEA_ srlR_5	-3.256417412	0.00915346	Glucitol operon represso	NA	yciT	transcriptional regulator
MNLKPGEA_ ahpC_2	-3.287081003	3.29E-10	Alkyl hydroperoxide redu	1.11.1.15	ahpC	alkyl hydroperoxide reductase
MNLKPGEA_ fepA_1	-3.288699927	8.82E-05	Ferrienterobactin recept	NA	fepA	Receptor
MNLKPGEA_ cirA	-3.317981281	6.39E-05	Colicin I receptor	NA	cirA	Receptor
MNLKPGEA_ mdoD	-3.351214266	0.01293658	Glucans biosynthesis pro	NA	mdoD	Involved in the biosynthesis of os
MNLKPGEA_ ansP2	-3.358929872	0.00710635	L-asparagine permease 1	NA	ansP	Involved in the transporte of L-as
MNLKPGEA_ murF	-3.365052588	0.00693534	UDP-N-acetylmuramoyl-	6.3.2.10	murF	Involved in cell wall formation. C
MNLKPGEA_ dgkA	-3.379237756	0.00636591	Diacylglycerol kinase	2.7.1.107	dgkA	Recycling of diacylglycerol produ

MNLKPGEA_ mltD	-3.381495005	2.65E-08	Membrane-bound lytic n	4.2.2.-	mltD	COG0741 Soluble lytic murein tr
MNLKPGEA_ hemS	-3.397138382	0.01354082	Hemin transport protein	NA	hmuS	hemin transport protein
MNLKPGEA_ ilvD	-3.397708169	0.00612772	Dihydroxy-acid dehydrat	4.2.1.9	ilvD	Belongs to the IlvD Edd family
MNLKPGEA_ rplK	-3.399226577	1.29E-22	50S ribosomal protein L1	NA	rplK	Forms part of the ribosomal stal
MNLKPGEA_ proQ	-3.418995699	7.05E-17	RNA chaperone ProQ	NA	proQ	RNA chaperone with significant
MNLKPGEA_ btuD_6	-3.452658403	0.0054477	Vitamin B12 import ATP	7.6.2.8	modC	Part of the ABC transporter com
MNLKPGEA_ fimC_1	-3.475237685	0.01072253	Chaperone protein FimC	NA	fimC	chaperone
MNLKPGEA_ thiD	-3.4782709	0.00624218	Hydroxymethylpyrimidin	2.7.1.49	thiD	phosphomethylpyrimidine kinase
MNLKPGEA_ mioC	-3.489647869	5.23E-05	Protein MioC	NA	mioC	flavodoxin binds one FMN molec
MNLKPGEA_ ansA	-3.496507932	0.00452904	L-asparaginase 1	3.5.1.1	ansA	COG0252 L-asparaginase archae
MNLKPGEA_ paaZ	-3.501450867	4.48E-07	Bifunctional protein Paa	NA	paaN	MaoC like domain
MNLKPGEA_ priB	-3.513857407	1.66E-07	Primosomal replication p	NA	priB	Binds single-stranded DNA at th
MNLKPGEA_ pdeH_2	-3.519873303	0.00417132	Cyclic di-GMP phosphodi	3.1.4.52	0	EAL domain
MNLKPGEA_ dnaB	-3.535345218	0.00420358	Replicative DNA helicase	3.6.4.12	dnaB	it exhibits DNA-dependent ATPa
MNLKPGEA_ purM	-3.536630608	0.00542239	Phosphoribosylformylgly	6.3.3.1	purM	Phosphoribosylformylglycinamid
MNLKPGEA_ thiG	-3.539860353	0.00477185	Thiazole synthase	2.8.1.10	thiG	Catalyzes the rearrangement of
MNLKPGEA_ MNLKPGEA	-3.55001323	0.00403188	hypothetical protein	NA	yicN	Protein of unknown function (DU
MNLKPGEA_ paaG	-3.550261192	5.29E-05	1,2-epoxyphenylacetyl-C	5.3.3.18	paaG	Enoyl-CoA hydratase/isomerase
MNLKPGEA_ alaE	-3.552503598	2.22E-06	L-alanine exporter AlaE	NA	alaE	L-alanine exporter AlaE
MNLKPGEA_ rne	-3.561550124	8.66E-13	Ribonuclease E	3.1.26.12	rne	Endoribonuclease that plays a ce
MNLKPGEA_ oatA	-3.582564465	1.82E-10	O-acetyltransferase Oat	2.3.1.-	0	Acyltransferase family
MNLKPGEA_ kgtP_2	-3.640290465	0.00354875	Alpha-ketoglutarate per	NA	citH	Is involved in the uptake of citra
MNLKPGEA_ murG	-3.656302425	0.00299968	UDP-N-acetylglucosamir	2.4.1.227	murG	Cell wall formation. Catalyzes th
MNLKPGEA_ aceB	-3.67669744	0.00069465	Malate synthase A	2.3.3.9	aceB	Involved in the glycolate utilizati
MNLKPGEA_ ampD	-3.757653157	0.00197988	1,6-anhydro-N-acetylmu	3.5.1.28	ampD	Negative regulator of beta-lacta
MNLKPGEA_ trpE	-3.801302797	0.00215768	Anthranilate synthase cc	4.1.3.27	trpE	Part of a heterotetrameric comp
MNLKPGEA_ purB	-3.834030412	0.00163181	Adenylosuccinate lyase	4.3.2.2	purB	Belongs to the lyase 1 family. Ac
MNLKPGEA_ paaJ	-3.848095794	1.75E-06	3-oxoadipyl-CoA/3-oxo-5	2.3.1.174	paaJ	Catalyzes the final step of fatty a
MNLKPGEA_ glnP_1	-3.853624435	0.00376586	Glutamine transport syst	NA	glnP	(ABC) transporter
MNLKPGEA_ cysZ	-3.890055555	0.00136736	Sulfate transporter CysZ	NA	cysZ	High affinity, high specificity pro

MNLKPGEA_ htpG	-3.901528629	0.00033651	Chaperone protein HtpG	NA	htpG	Molecular chaperone. Has ATPas
MNLKPGEA_ paaB	-3.909473791	9.17E-07	1,2-phenylacetyl-CoA ep	NA	paaB	Phenylacetate-CoA oxygenase
MNLKPGEA_ rpsF	-3.974723745	1.11E-10	30S ribosomal protein S	NA	rpsF	Binds together with S18 to 16S r
MNLKPGEA_ thiE	-3.996017195	0.00113772	Thiamine-phosphate syn	2.5.1.3	thiE	Condenses 4-methyl-5-(beta-hyc
MNLKPGEA_ maoA	-4.002497171	0.00297822	Primary amine oxidase	1.4.3.21	tynA	amine oxidase
MNLKPGEA_ hpcG	-4.026437295	0.00260766	2-oxo-hept-4-ene-1,7-di	4.2.1.163	hpaH	2-oxohepta-3-ene-1,7-dioic acid
MNLKPGEA_ MNLKPGEA	-4.031872512	0.00080868	hypothetical protein	NA	yfiR	bacterial-type flagellum-depend
MNLKPGEA_ hpcB	-4.037367228	1.04E-07	3,4-dihydroxyphenylacet	1.13.11.15	hpaD	Catalytic LigB subunit of aromat
MNLKPGEA_ ispE	-4.087624534	2.30E-07	4-diphosphocytidyl-2-C-r	2.7.1.148	ispE	Catalyzes the phosphorylation of
MNLKPGEA_ paaE	-4.087671801	4.36E-13	1,2-phenylacetyl-CoA ep	1.-.-.-	paaE	COG1018 Flavodoxin reductases
MNLKPGEA_ dppA_1	-4.13123109	2.17E-09	Periplasmic dipeptide tra	NA	dppA	ABC-Type Dipeptide Transport S
MNLKPGEA_ ttuB_5	-4.261284829	3.70E-05	Putative tartrate transpc	NA	0	Major facilitator superfamily
MNLKPGEA_ hpcE_2	-4.317631967	2.83E-05	Homoprotocatechuate ca	NA	hpaG	4-hydroxyphenylacetate degrada
MNLKPGEA_ pglA	-4.346274925	0.00027133	N,N'-diacetylbacillosami	2.4.1.290	wbpU	glycosyl transferase group 1
MNLKPGEA_ lpfA_1	-4.52761547	0.00020426	putative major fimbrial s	NA	fimA_1	Fimbrial protein
MNLKPGEA_ mepS_1	-4.622847792	6.71E-12	Murein DD-endopeptidas	3.4.-.-	spr	COG0791 Cell wall-associated hy
MNLKPGEA_ pckA_2	-4.638084602	3.00E-11	Phosphoenolpyruvate ca	4.1.1.49	pckA	Involved in the gluconeogenesis.
MNLKPGEA_ paaI	-4.8017384	5.40E-05	Acyl-coenzyme A thioest	3.1.2.-	paaI	Phenylacetic acid degradation pr
MNLKPGEA_ paaC	-4.822169851	1.11E-13	1,2-phenylacetyl-CoA ep	NA	paaC	Phenylacetate-CoA oxygenase, P
MNLKPGEA_ mtr	-4.921608703	4.06E-08	Tryptophan-specific tran	NA	mtr	Amino Acid
MNLKPGEA_ thiC	-4.959540709	1.80E-06	Phosphomethylpyrimidir	4.1.99.17	thiC	Catalyzes the synthesis of the hy
MNLKPGEA_ fim	-5.000335507	8.28E-20	Fimbrial subunit type 1	NA	fimA	Fimbrial protein
MNLKPGEA_ paaA	-5.021250704	1.42E-25	1,2-phenylacetyl-CoA ep	1.14.13.149	paaA	Phenylacetate-CoA oxygenase
MNLKPGEA_ paaF	-5.086207109	9.94E-05	2,3-dehydroadipyl-CoA h	4.2.1.17	paaF	Enoyl-CoA hydratase/isomerase
MNLKPGEA_ sdaC_1	-5.240737347	9.63E-06	Serine transporter	NA	sdaC	Serine transporter
MNLKPGEA_ paaD	-5.989823644	3.73E-07	Putative 1,2-phenylacety	NA	paaD	Iron-sulfur cluster assembly prot

ara-aminobenzoate (pABA) with 6-hydroxymethyl-7,8-dihydropterin diphosphate (DHPt-PP) to form 7,8-dihydropteroate (H2Pte), the immediate pr
ogenase family

JF1471)
ein
porter SgrT

family
sine at position 1962 (m5C1962) of 23S rRNA

nally produced within the cells and which are toxic to biological systems
(UPF0370)
ily protein

de (NO), protecting several 4Fe-4S NO-sensitive enzymes. Has at least 2 reductase partners, only one of which (NorW, flavorubredoxin reductase)

of toxin-antitoxin stability system

UF1127)

oteins for anaerobic nitric oxide (NO) reductase. Reduces the rubredoxin moiety of NO reductase

n of Enterobacteriaceae

ein
high affinity leucine transport

n protein (MFP) (TC 8.A.1) family
tase and related Zn-dependent oxidoreductases
ssociated, stress protein produced under conditions of nutrient deprivation, osmotic shock and oxidative stress
JF2525)
ermease (2.A.39) family
d in tellurite resistance
sociated peptidase family

binding protein 3 family

JF1778)

UF4111)

be 1 subfamily
JF1471)

ɔcation (Tat) system that transports large folded proteins containing a characteristic twin-arginine motif in their signal peptide across membranes.

·eplication, recombination and repair. Binds to ssDNA and to an array of partner proteins to recruit them to their sites of action during DNA metab

ı ImpK

r NADP-dependent dehydrogenation of L-aspartate to iminoaspartate

JF2559)

equence and methylates the N-terminal (generally Phe) residue
rotein PhnG

thway signal

stem (T2SS, formerly general secretion pathway, GSP) for the export of proteins

JF2509)
hydrolase, YfhB

ino acid cation symporter (DAACS) (TC 2.A.23) family
inase activity

nase muconate lactonizing enzyme family
family
pper homeostasis
lator

s GTP, GDP and possibly (p)ppGpp with moderate affinity, with high nucleotide exchange rates and a fairly low GTP hydrolysis rate. Plays a role in

nit family

l-phosphate-dependent aminotransferase family

mily
JF1471)
sport system / permease component

f D-fructose 6-phosphate, the first committing step of glycolysis. Uses inorganic phosphate (PPi) as phosphoryl donor instead of ATP like common A
ase (SRAP)

, large subunit

thimet oligopeptidase F

isters to apo- ferredoxin. Multiple cycles of 2Fe2S cluster formation and transfer are observed, suggesting that IscA acts catalytically. Recruits intra
m
ino-2-methyl-5- hydroxymethylpyrimidine pyrophosphate (HMP-PP) to 4-amino-2- methyl-5-hydroxymethylpyrimidine phosphate (HMP-P)
sport
n

ertain denaturated proteins, including DnaA, during heat shock stress

JF2884)
rom Escherichia coli forms a dimer and binds zinc ions for catalytic activity and catalyzes the conversion of allantoate to (S)-ureidoglycolate and a

droxy-2-methyl-2-(E)- butenyl 4-diphosphate (HMBPP) into a mixture of isopentenyl diphosphate (IPP) and dimethylallyl diphosphate (DMAPP). Act
orotidine 5'- monophosphate (OMP) to uridine 5'-monophosphate (UMP)

PP-GlcNAc-ManNAcA (Lipid II), the second lipid-linked intermediate involved in enterobacterial common antigen (ECA) synthesis

zation-deamination of glucosamine 6-phosphate (GlcN6P) to form fructose 6-phosphate (Fru6P) and ammonium ion

lease complex

ɔcation (Tat) system that transports large folded proteins containing a characteristic twin-arginine motif in their signal peptide across membranes.

ɔrotein

ein, family 3

type-1 family

ɔn of fumarate to (S)- malate
ɜpecificities (Related to short-chain alcohol dehydrogenases)

ɪn BhsA

hione into 5-oxo-L- proline and a Cys-Gly dipeptide. Acts specifically on glutathione, but not on other gamma-glutamyl peptides

ɲitin. ChbG is essential for growth on the acetylated chitooligosaccharides chitobiose and chitotriose but is dispensable for growth on cellobiose ar

osylase activity

which encodes the E.coli common pilus (ECP). ECP is found in both commensal and pathogenic strains and plays a dual role in early-stage biofilm c

tor protein YcgZ
perfamily
JF406)

drogenases reductases (SDR) family
tein (AlpA)

degrades murein glycan strands and insoluble, high-molecular weight murein sacculi, with the concomitant formation of a 1,6-anhydromuramoyl p
t sugar phosphotransferase system, EIIA 2

e protein
plexes LivFGHMJ and LivFGHMK involved in the high-affinity transport of branched-chain amino acids
mbined with SAM (S- adenosylmethionine) represses the expression of the methionine regulon and of enzymes involved in SAM synthesis
tein (AlpA)

transacylase

ctivator SoxR

ehyde-activating

e boundary membrane with the concomitant transport of protons into the cell (symport system)

different specificities (related to short-chain alcohol dehydrogenases)
the N-terminal Met of newly synthesized proteins. Requires at least a dipeptide for an efficient rate of reaction. N-terminal L-methionine is a pre
te-sugar pyrophosphorylase involved in lipopolysaccharide biosynthesis translation initiation factor 2B, gamma epsilon subunits eIF-2Bgamma eIF-
specificities (Related to short-chain alcohol dehydrogenases)
the OLD family
ansporter
ylpropionate dioxygenase
in
ne ligase which exhibits weak glutamate--cysteine ligase activity

ase

plexes LivFGHMJ and LivFGHMK involved in the high-affinity transport of branched-chain amino acids
which encodes the E.coli common pilus (ECP). ECP is found in both commensal and pathogenic strains and plays a dual role in early-stage biofilm c
talyzes the synthesis of the prenylated FMN cofactor (prenyl-FMN) for 4-hydroxy-3- polyprenylbenzoic acid decarboxylase UbiD. The prenyltransfera
e 13 family

domain protein
JF1435)

stem, permease component

ɔgenase family
volved in the response to DNA damage (SOS response), including recA and lexA. Binds to the 16 bp palindromic sequence 5'-CTGTATATATATACAG
ocess
:ose and maltodextrins

JF2755)

equence, suggesting that its expression is purine-regulated
antitoxin (TA) module
-arabinose- phosphoundecaprenol (alpha-L-Ara4N-phosphoundecaprenol) from the cytoplasmic to the periplasmic side of the inner membrane
lcohol dehydrogenase family. Class-III subfamily

rmease transports the degraded pectin products into the bacterial cell, where they serve as carbon and energy sources. This is a hydrogen coupled
ɔrotein A family

t formation of L-aspartate- semialdehyde (L-ASA) by the reductive dephosphorylation of L- aspartyl-4-phosphate
B component

ıate-dependent decarboxylation of 2-oxoglutarate and the subsequent addition of the resulting succinic semialdehyde-thiamine pyrophosphate ani

to (8S)-3',8-cyclo-7,8- dihydroguanosine 5'-triphosphate
high affinity leucine transport

ion of vitamin B12 (cyanocobalamin) across the outer membrane to the periplasmic space. It derives its energy for transport by interacting with th

ases (PHP family)
purine and pyrimidine nucleosides. Driven by a proton motive force
tive tail-component
se 6-phosphate to 6- phosphogluconolactone

galactanase

e
e 1 family
n. Catalyzes an essential reaction for de novo glycine and purine synthesis, and for DNA precursor synthesis

salvage pathway of pyridoxal 5'-phosphate (PLP). Catalyzes the phosphorylation of pyridoxal to PLP

nannonate
JF2756)
_3

n
, multichain enzyme responsible for most of the replicative synthesis in bacteria. The epsilon subunit contain the editing function and is a proofrea

epairs oxidized periplasmic proteins containing methionine sulfoxide residues (Met-O), using respiratory chain electrons. Thus protects these prote

djacent adenosines (A1518 and A1519) in the loop of a conserved hairpin near the 3'-end of 16S rRNA in the 30S particle. May play a critical role in

ven potassium transport (or Kdp) system, which catalyzes the hydrolysis of ATP coupled with the electrogenic transport of potassium into the cytop
bdopterin-containing oxidoreductase family
dependent transport system permease family
-acetylcytidine (ac(4)C) at the wobble position of tRNA(Met), by using acetyl-CoA as an acetyl donor and ATP (or GTP)

sport system / permease component

dependent transport system permease family

ccinyl-L,L- diaminopimelic acid (SDAP), forming succinate and LL-2,6- diaminoheptanedioate (DAP), an intermediate involved in the bacterial biosy

e 43 family
hospho-AI-2, thereby terminating induction of the lsr operon and closing the AI-2 signaling cycle. Catalyzes the conversion of (4S)-4-hydroxy-5- pho
bonate transport system permease component
ed in the repair of iron-sulfur clusters
cific IIA component
nase muconate lactonizing enzyme family
signaling pathway, periplasmic inhibitor zinc-resistance associated protein

JF2810)

te-binding protein

ırD

oreductase family
ic semialdehyde to 3- hydroxypropionic acid, which is excreted
phatidyltransferase class-I family

ining a DNA-binding HTH domain and an aminotransferase domain (MocR family) and their eukaryotic orthologs

E-RelB toxin-antitoxin system transcriptional repressor

ermease (2.A.39) family
e 13 family

er

te transporter (DMT) superfamily

to 2,5-diamino-6- ribosylamino-4(3H)-pyrimidinone 5'-phosphate (DARP), formate and pyrophosphate

ihydroxy-2-naphthoyl- CoA (DHNA-CoA) to 1,4-dihydroxy-2-naphthoate (DHNA)
ichia coli led to effects on biofilm formation, alteration in expression of a number of genes and mutations in bssS led to defects in indole transpor

superfamily
tabolism

cleoside transporter (CNT) (TC 2.A.41) family

ses, including glyoxylases
binding protein 9 family

ein

itrate to isocitrate via cis-aconitate

l-binding methyltransferase superfamily. RNA methyltransferase TrmH family

n protein (MFP) (TC 8.A.1) family

family
f ribose 1,5-bisphosphate to 5-phospho-D-ribosyl alpha-1-diphosphate (PRPP)

matine from arginine

ehalose 6-phosphate to produce free trehalose
UF1833)
ıdent sugar phosphotransferase system (PTS), a major carbohydrate active - transport system, catalyzes the phosphorylation of incoming sugar sul

ase PfkB family

dependent transport system permease family
coupling to the transport system

ters
udouridine from uracil
ivatives
nt epimerase dehydratase family. dTDP-glucose dehydratase subfamily

family
4-hydroxy-4-methyl-2- oxoglutarate (HMG) into 2 molecules of pyruvate. Also contains a secondary oxaloacetate (OAA) decarboxylase activity due t
ily. Monothiol subfamily
e specificity of the ClpAP-mediated ATP-dependent protein degradation

bdopterin-containing oxidoreductase family

nannonate
apolipoprotein N-acyltransferase
oglycan synthesis and outer membrane constriction during cell division
mporter (SSF) (TC 2.A.21) family

n of some genes transcripts potentially through selective RNA binding

terial toxin-antitoxin system
JF533)

hodiesterase

to remove the methyl group introduced by BioC when the pimeloyl moiety is complete. It allows to synthesize pimeloyl-ACP via the fatty acid synt

protein, lambda gpK
ansporter activity

pimerases

family. ArgE subfamily
ocess

ng protein
ignal transduction systems periplasmic component domain
e 8 (cellulase D) family

ase PfkB family

r activity

ator
aldehyde to acetyl-CoA, using NAD( ) and coenzyme A. Is the final enzyme in the meta- cleavage pathway for the degradation of aromatic compou

dependent transport system permease family

hodiesterase
processing of the antibiotic Microcin B17 and in sensitivity to the DNA gyrase inhibitor LetD

tein erpA
JF2502)

o form functional DNA pol V (UmuD'2UmuC)

presence of ATP renatures cruciform structure in supercoiled DNA with palindromic sequence, indicating that it may promote strand exchange reac
purine and pyrimidine nucleosides. Driven by a proton motive force

maltose receptor)

specific IIA subunit

droperoxidase activity. Required for the reduction of the AhpC active site cysteine residues and for the regeneration of the AhpC enzyme activity

te-binding protein
processing of the 5'-end of pre-16S rRNA

JF1480)

n

ulator of UbiI activity which is involved in aerobic coenzyme Q (ubiquinone) biosynthesis

rocessing of various precursor tRNAs. Initiates hydrolysis at the 3'-terminus of an RNA molecule and releases 5'-mononucleotides
(ferredoxin-NADPH reductases) family 1
JF1471)
ein
on of acetaldehyde and ammonia from ethanolamine

JF3302)

. Catalyzes the conversion of oxaloacetate (OAA) to phosphoenolpyruvate (PEP) through direct phosphoryl transfer between the nucleoside triphosp
to stretch forces in the membrane lipid bilayer. May participate in the regulation of osmotic pressure changes within the cell

samine and N-acetylglucosamine by acting as a repressor of the nagEBACD operon and both a repressor and activator of the glmSU operon

a-hydroxybenzoate (PHB) with an all-trans polyprenyl group. Mediates the second step in the final reaction sequence of ubiquinone-8 (UQ-8) biosy
uction of ubiquinone-1 to ubiquinol by two successive reactions, coupled with the transport of Na( ) ions from the cytoplasm to the periplasm. The
of DNA damaged by oxidation or by mutagenic agents. Acts as DNA glycosylase that recognizes and removes damaged bases. Has a preference for
orin family

bunits of integration host factor, a specific DNA-binding protein that functions in genetic recombination as well as in transcriptional and translatic
osomal dipeptidase

sport system inner membrane component

e of L-rhamnulose-1- phosphate to dihydroxyacetone phosphate (DHAP) and L-lactaldehyde

n protein (MFP) (TC 8.A.1) family

oxylation of meso- diaminopimelate (meso-DAP) to L-lysine

clase
resulting in DNA looping between the operators
ribose at O-5 in a reaction requiring ATP and magnesium. The resulting D-ribose-5- phosphate can then be used either for sythesis of nucleotides
naturation of the E. coli pMccB17 plasmid-encoded microcin B17, an exported protein that targets the essential topoisomerase II DNA gyrase

tR family
ate-requiring enzymes acetolactate synthase, pyruvate dehydrogenase (cytochrome), glyoxylate carboligase, phosphonopyruvate decarboxylase

-6-phosphate (ManNAc-6-P) to N-acetylglucosamine-6-phosphate (GlcNAc-6-P)

ecarboxylation and detoxification of phenolic derivatives under both aerobic and anaerobic conditions. It is able to catalyze the reversible decarboxy
-terminal domain
dehydrogenase

rbohydrate metabolic process

ein

JF1107)
ivatives

binding directly to the RNA polymerase (RNAP). Required for negative regulation of rRNA expression and positive regulation of several amino acid

istance protein dioxygenase

dependent transport system permease family

of toxin-antitoxin stability system

lpha-1,6-glucosidic linkages in glycogen by scission of a 1,4-alpha-linked oligosaccharide from growing alpha-1,4-glucan chains and the subsequen

phorylates phosphatidylglycerophosphate (PGP) to phosphatidylglycerol (PG)

acilitator (CDF) transporter (TC 2.A.4) family
ation reaction of D- cysteine and of several D-cysteine derivatives. It could be a defense mechanism against D-cysteine

which encodes the E.coli common pilus (ECP). ECP is found in both commensal and pathogenic strains and plays a dual role in early-stage biofilm c

mporter (SSF) (TC 2.A.21) family

in-NADPH reductases) family 1

y to utilize trehalose at high osmolarity by splitting it into glucose molecules that can subsequently be taken up by the phosphotransferase-mediat
grS under glucose- phosphate stress conditions as well as yfdZ. Represses its own transcription under both stress and non-stress conditions. Might

UF4186)
dependent transport system permease family

ne and attachment of the murein lipoprotein to the peptidoglycan tetrapeptide chain

acid oxidation in which acetyl-CoA is released and the CoA ester of a fatty acid two carbons shorter is formed

genase
ctase
se family

UF4222)

e 1 family

nine in position 966 of 16S rRNA in the assembled 30S particle

ease

o the corresponding ketose L-fuculose
HypB

6 hairpin glycosidase domain

ne in position 2552 of 23S rRNA at the 2'-O position of the ribose in the fully assembled 50S ribosomal subunit

ein
plex NikABCDE involved in nickel import. Responsible for energy coupling to the transport system

(DUF891)

. Succinylglutamate desuccinylase subfamily
(AMP-forming) AMP-acid ligases II

oration of the urease nickel metallocenter. This process requires GTP hydrolysis, probably effectuated by UreG
nsferase

odopterin-containing oxidoreductase family
mporter (SSF) (TC 2.A.21) family
-phosphate-dependent aminotransferase family

droxy- tetrahydrodipicolinate (HTPA) to tetrahydrodipicolinate

reaction from putrescine to 2-oxoglutarate, leading to glutamate and 4-aminobutanal, which spontaneously cyclizes to form 1-pyrroline. Is also ab

loramphenicol resistance in bacteria
ıate racemases family

se 8-oxoguanine DNA glycosylase
S-adenosylmethionine to S-adenosylmethioninamine (dcAdoMet), the propylamine donor required for the synthesis of the polyamines spermine a

tress response pathway which occurs via periplasmic interactions with CpxA

ıding protein

regulatory RNA (sRNAs) and mRNAs to facilitate mRNA translational regulation in response to envelope stress, environmental stress and change

amine synthase
dependent transport system permease family
r (TC 2.A.52) family
ein H-NS family
ter, YdcZ

protein dioxygenase

A-carboxylase ligase and a biotin-operon repressor. In the presence of ATP, BirA activates biotin to form the BirA-biotinyl-5'-adenylate (BirA-bio- 5

e

rotein

:he sulfur from L- cysteine to yield L-alanine, an essential step in sulfur metabolism for biosynthesis of a variety of sulfur-containing biomolecules.
n protein (MFP) (TC 8.A.1) family
e cystathionine beta- synthase family
rolase fold

ase PfkB family

JF2612)

iptional activator
hydrouridine (D), a modified base found in the D-loop of most tRNAs, via the reduction of the C5-C6 double bond in target uridines. Specifically mc
e family
component

dependent transport system permease family

ein
ter malic acid transport protein

different specificities (related to short-chain alcohol dehydrogenases)
JF1482)

JF2500)

al regulatory protein PhoB
ase
: of PQQ or its precursor to the periplasm

dependent transport system permease family
IIA component

y

er
toacid CoA transferase, alpha subunit

ex accessory protein

damaging agents
the inhibition of FtsZ GTPase activity, therefore promoting FtsZ assembly into bundles of protofilaments necessary for the formation of the divisi
TP in the presence of single-stranded DNA, the ATP-dependent uptake of single-stranded DNA by duplex DNA, and the ATP-dependent hybridizatior

es dGTP over the other canonical NTPs

te transporter (DMT) superfamily

bunits of integration host factor, a specific DNA-binding protein that functions in genetic recombination as well as in transcriptional and translatic
different specificities (related to short-chain alcohol dehydrogenases)
nit
his gene affects biofilm maturation, stress response, and motility

ein
ydrolases (invasion-associated proteins)

A synthetase beta subunit family. Type 1 subfamily
JF3574)
n TIM barrel

salvage pathway of pyridoxal 5'-phosphate (PLP). Catalyzes the phosphorylation of pyridoxal to PLP

tose cellobiose-specific IIB subunit

nthase RsuA family

ndary membrane with the concomitant uptake of a sodium ion (symport system)

both the DnaJ-like co- chaperone activity and the DNA binding activity of CbpA. Together with CbpA, modulates the activity of the DnaK chaperone

t reduction of glyoxylate and hydroxypyruvate into glycolate and glycerate, respectively

antitoxin (TA) module

n YhjU

ase, nitrogen specific
superfamily

gma S factor (RpoS) by promoting its proteolysis in exponentially growing cells. Acts by binding and delivering RpoS to the ClpXP protease. RssB is

family
er and related transporters

damaging agents
ulating RssB activity, thereby increasing the stability of the sigma stress factor RpoS during magnesium starvation
me utilization or adhesion
e 1 family

lent swarming motility
np subunit AaeA

binding methyltransferase superfamily. RNA methyltransferase RlmE family. RlmM subfamily

-phosphate dehydrogenase family

te transporter (DMT) superfamily

cation uptake system

system, which controls transcription of numerous genes. RcsB is the response regulator that binds to regulatory DNA regions

udouridine from uracil
actarate to form 5- dehydro-4-deoxy-D-glucarate

ormation. May be involved in regulation of gene expression, nucleoid organization and DNA protection

e
se
f thiamine to thiamine phosphate
JF1471)
nease

JF1488)

he sulfur from L- cysteine to yield L-alanine, an essential step in sulfur metabolism for biosynthesis of a variety of sulfur-containing biomolecules.

uired for 2-thiolation of 5-methylaminomethyl-2-thiouridine (mnm(5)s(2)U) at tRNA wobble positions
dependent transport system permease family

IIC subunit

hesis that is essential for the function of penicillin-binding protein 1B (PBP1b)
l-deoxy-4-formamido-L- arabinose-phosphoundecaprenol to 4-amino-4-deoxy-L-arabinose- phosphoundecaprenol. The modified arabinose is attacl
nal protein bL36 family
om the sn-1 position of a phospholipid to the N-linked hydroxymyristate on the proximal unit of lipid A or its precursors

of lipoproteins from the inner membrane to the outer membrane. Only forms a complex with a lipoprotein if the residue after the N-terminal Cys
or (ECF) transporter complex CbiMNOQ involved in cobalt import

oxidase center binds Fe(2) ions, oxidizes them by dioxygen to Fe(3), and participates in the subsequent Fe(3) oxide mineral core formation withi
se activity
protection, which is important for survival of enteric bacteria in the acidic environment of the host stomach. Exhibits a chaperone-like activity at a
e release of the substrate protein, thus completing the reaction cycle. Several rounds of ATP-dependent interactions between DnaJ, DnaK and GrpE
e kinase family
JF2002)
ted SufE
AP) that modifies Der EngA GTPase function. May play a role in ribosome biogenesis
nase and related beta-hydroxyacid dehydrogenases

JF1176)

ein, family 5

JF1418)
JF1073)

four acetate groups of uroporphyrinogen-III to yield coproporphyrinogen-III
n of the terminus region of the chromosome (Ter macrodomain) during the cell cycle. Prevents early segregation of duplicated Ter macrodomains

ım efflux system that confers protection against electrophiles. Required for full activity of KefB

JF1471)

yase under anaerobic conditions by generation of an organic free radical, using S- adenosylmethionine and reduced flavodoxin as cosubstrates to p

of a CheY-like receiver domain and a winged-helix DNA-binding domain

embrane protein

ein

peron negative regulatory protein

ıain
or YidZ

eduction of succinylglutamate semialdehyde into succinylglutamate

horing of the catalytic components of the fumarate reductase complex to the cytoplasmic membrane

il, which can arise by alkylation or deamination of cytosine, respectively, from the corresponding mispairs with guanine in ds-DNA. It is capable of

n

n periplasmic component
kin system, parDE
(UPF0257)

ein, pilin FimA
JF1778)

y charged Gln-tRNA(Gln) through the transamidation of misacylated Glu-tRNA(Gln) in organisms which lack glutaminyl-tRNA synthetase. The rea
y, this DNA polymerase exhibits 5'-3' exonuclease activity

shape of the cell. May also contribute to regulation of formation of penicillin-binding proteins
ting swimming and swarming in a bis-(3'-5') cyclic diguanylic acid (c-di-GMP)- dependent manner. Binds 1 c-di-GMP dimer per subunit. Increasing

odiesterase activity

binding protein 3 family
yme family

gopeptide nickel transport systems permease components

ntaining CheY-like receiver, AAA-type ATPase, and DNA-binding domains

JF1471)

catalase and broad- spectrum peroxidase activity
ated lyases

y
f the 3'-hydroxyl group of dephosphocoenzyme A to form coenzyme A
3
mate and GltJLP, DctA and DcuAB for aspartate is involved in the transport of glutamate and aspartate

esis of molybdopterin
ation-cell division (RND) (TC 2.A.6) family

ydratase family
iday junction intermediates made during homologous genetic recombination and DNA repair. Exhibits sequence and structure-selective cleavage o

r (TC 2.A.52) family
te-sugar epimerases

otein
JF1778)
zes the stereospecific interconversion of fumarate to L-malate
e

rotein PaaY
ng protein involved in DNA uptake

ogenase family. UxaB subfamily
nvolved in the processing of primary rRNA transcript to yield the immediate precursors to the large and small rRNAs (23S and 16S). Processes som
nsport systems permease components
ted sulfate

ndent N5,N10-methylene tetrahydromethanopterin reductase and related flavin-dependent oxidoreductases

osomal translocation step during translation elongation. During this step, the ribosome changes from the pre-translocational (PRE) to the post- tr
n dTDP in both de novo and salvage pathways of dTTP synthesis

on control protein

ogenase family

JF3313)

amily
C 1.A.8) family

s of DNA gyrase by preventing its interaction with DNA. Acts by binding directly to the C-terminal domain of GyrB, which probably disrupts DNA bir

dependent transport system permease family

phatase
inducer 2 (AI-2) which is secreted by bacteria and is used to communicate both the cell density and the metabolic potential of the environment. Th

3-keto-L-gulonate-6-P into L-xylulose-5-P. Is involved in the anaerobic L-ascorbate utilization
ase regulating citrate malate metabolism
NA polymerase involved in untargeted mutagenesis. Copies undamaged DNA at stalled replication forks, which arise in vivo from mismatched or n

e 1 family

ndent N5,N10-methylene tetrahydromethanopterin reductase and related flavin-dependent oxidoreductases
ein
rotein

family
JF2526)

nination of UTP to CTP with either L-glutamine or ammonia as the source of nitrogen. Regulates intracellular CTP levels through interactions with
s - catabolite gene activator and regulatory subunit of cAMP-dependent protein kinases
dent zinc metallopeptidase for both cytoplasmic and membrane proteins. Plays a role in the quality control of integral membrane proteins
port
antitoxin (TA) module

J
genase

ns B, D, E, and G on adenosylcobyrinic A,C-diamide. NH(2) groups are provided by glutamine, and one molecule of ATP is hydrogenolyzed for each a
ydratase 2-oxohepta-3-ene-1,7-dioic acid hydratase (catechol pathway)
nily
regulator, winged helix family

eaction that results in 2,5-elimination of pyruvate from 2-succinyl-5-enolpyruvyl-6- hydroxy-3-cyclohexene-1-carboxylate (SEPHCHC) and the format

it transports di- and tripeptides
gation, termination and antitermination

sport system / permease component

bdopterin-containing oxidoreductase family
perfamily
tase
drogenases reductases (SDR) family
s essential for cell wall elongation

es involved in the multiple antibiotic resistance (Mar) phenotype

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

ge of the D-lactyl ether substituent of MurNAc 6-phosphate, producing GlcNAc 6- phosphate and D-lactate
transfer of electrons from pyruvate to flavodoxin
n the assembly of lipopolysaccharide (LPS) at the surface of the outer membrane
gF Family

rane lipoprotein
enase nickel cofactor insertion step
ne hypC hupF

to the periplasm for the biogenesis of c-type cytochromes
ess

sport systems inner membrane component
ist in the late maturation steps of the functional core of the 30S ribosomal subunit. Helps release RbfA from mature subunits. May play a role in th
atidyl group transfer from one phosphatidylglycerol molecule to another to form cardiolipin (CL) (diphosphatidylglycerol) and glycerol

sociated
olase superfamily

acid oxidation in which acetyl-CoA is released and the CoA ester of a fatty acid two carbons shorter is formed
ansferase

e
nate aminotransferase

family
line to tRNA(Pro) in a two-step reaction proline is first activated by ATP to form Pro- AMP and then transferred to the acceptor end of tRNA(Pro). A
sport systems inner membrane component

sport systems inner membrane component

zation of glycolate and propanediol
at

at

nikABCDE operon. Is active in the presence of excessive concentrations of intracellular nickel
gF family

-glucose, from dTTP and glucose 1-phosphate, as well as its pyrophosphorolysis

ein CusF
gopeptide nickel transport systems permease components
se PulE Tfp pilus assembly pathway, ATPase PilB
ng protein

lta
ivated derivatives
echanism carboxysome shell protein

ain

family
dependent transport system permease family
y

ein

ng protein
ven potassium transport (or Kdp) system, which catalyzes the hydrolysis of ATP coupled with the electrogenic transport of potassium into the cytop

csR
UF1889)

lator

mily
haperone system, it is involved in the recovery of the cell from heat-induced damage, in cooperation with DnaK, DnaJ and GrpE

ion of ribose-5- phosphate to ribulose 5-phosphate

:NAc-1-phosphate moiety from UDP-GlcNAc onto the carrier lipid undecaprenyl phosphate (C55-P), yielding GlcNAc-pyrophosphoryl-undecaprenyl (
obutyrate hydrolase
us and endogenous cytidine and 2'-deoxycytidine for UMP synthesis

ribosomal subunits
orbose family IID component

ted flavoproteins
ndent sugar phosphotransferase system (PTS), a major carbohydrate active - transport system, catalyzes the phosphorylation of incoming sugar sul

ning an amidase domain and an AraC-type DNA-binding HTH domain

JF1471)

protein
D-fructose (SF) to 6- deoxy-6-sulfo-D-fructose 1-phosphate (SFP)
that mediates the selective degradation of mutant and abnormal proteins as well as certain short-lived regulatory proteins. Required for cellular h

dependent transport system permease family
:he conversion of demethylmenaquinol (DMKH2) to menaquinol (MKH2) and the conversion of 2-polyprenyl-6-methoxy-1,4-benzoquinol (DDMQH2)

l in the assembly of the 50S ribosomal subunit at low temperature. Exhibits RNA-stimulated ATP hydrolysis and RNA unwinding activity

oisomerase
n-canonical purine nucleotides such as XTP and ITP to their respective diphosphate derivatives. Probably excludes non-canonical purines from DNA

ase YfiH RL5 family

ndoribonuclease involved in late-stage 70S ribosome quality control and in maturation of the 3' terminus of the 16S rRNA
taining a Zn-ribbon domain
and by acivicin (a glutamine analog)
·succinylarginine into N(2)-succinylornithine, ammonia and CO(2)

mily
nase (FDH) activity. Acts as a sulfur carrier protein that transfers sulfur from IscS to the molybdenum cofactor prior to its insertion into FDH

r (TC 2.A.52) family

genase
nate bicarbonate transport systems periplasmic components

genes involved in the phosphotransferase and phosphoenolpyruvate systems, regulates genes involved in the uptake of sugars
way component PulK

bonate transport system permease component

dependent transport system permease family

dependent transport system permease family. FecCD subfamily

plex MetNIQ involved in methionine import. Responsible for energy coupling to the transport system

JF3168)
on protein HypE

JF1471)
ane biogenesis
s FtsZ-ring assembly. Directly interacts with FtsZ and promotes bundling of FtsZ protofilaments, with a reduction in FtsZ GTPase activity

oxy-2-hydroxy-4- methylpentanoate (3-isopropylmalate) to 3-carboxy-4-methyl-2- oxopentanoate. The product decarboxylates to 4-methyl-2 oxop

ision factor that is required for proper Z-ring formation. It is recruited early to the divisome by direct interaction with FtsZ, stimulating Z-ring asse

ate reductase, flavoprotein subunit

JF1131)
eron protein PhnA
e 1 family

TP to Mo-molybdopterin (Mo- MPT) cofactor (Moco or molybdenum cofactor) to form Mo- molybdopterin guanine dinucleotide (Mo-MGD) cofacto

nt hydrolases superfamily. NagA family

n regulation of membrane protease activity

rotein

y-4-formamido-L- arabinose from UDP to undecaprenyl phosphate. The modified arabinose is attached to lipid A and is required for resistance to p
ptidoglycan cell wall at the division septum

ase HPA2 and related acetyltransferases
transcriptional regulator
ine ligase type 1 family. Type 1 subfamily
chain in fatty acid biosynthesis
family
ter, YdcZ
JF1097)
ein translocation channel SecYEG. Clamps together the 2 halves of SecY. May contact the channel plug during translocation

cetylases of ribosomal proteins

sport systems inner membrane component

ng)

3

ng protein
epair enzyme for proteins that have been inactivated by oxidation. Catalyzes the reversible oxidation-reduction of methionine sulfoxide in proteins
ntaining CheY-like receiver, AAA-type ATPase, and DNA-binding domains

n, C terminal

n and for the maintenance of normal septation
rom Escherichia coli forms a dimer and binds zinc ions for catalytic activity and catalyzes the conversion of allantoate to (S)-ureidoglycolate and a

lcohol dehydrogenase family. Quinone oxidoreductase subfamily
notransferase

carbon ketol group from a ketose donor to an aldose acceptor, via a covalent intermediate with the cofactor thiamine pyrophosphate

JF1380)

es sodium in exchange for external protons

protein dioxygenase
inding protein 3 family
4-epimerase and related epimerases and aldolases

type-1 family

e

ıt transport systems inner membrane component
e transport system, permease component
mily

ter (DMT) superfamily

UF1833)

ein C
JF2950)
ble-stranded beta-helix domain

ivatives
TAC

ltransferase family

ɔinding protein 3 family
r of the essential 3'- terminal CCA sequence in tRNAs without using a nucleic acid template. Adds these three nucleotides in the order of C, C, and

ıdent sugar phosphotransferase system

acetylases of ribosomal proteins

ın of malate to oxaloacetate

n system
plex PotABCD involved in spermidine putrescine import. Responsible for energy coupling to the transport system
which encodes the E.coli common pilus (ECP). ECP is found in both commensal and pathogenic strains and plays a dual role in early-stage biofilm c

volved in electron transport

ıg protein

n of the polyhedral organelles involved in propanediol degradation
it IID

ıdent N5,N10-methylene tetrahydromethanopterin reductase and related flavin-dependent oxidoreductases

cid to aminoacrylate. Required to remove a toxic intermediate produce by the pyrimidine nitrogen degradation

family

plex TauABC involved in taurine import. Responsible for energy coupling to the transport system
erone, PapD N-terminal domain

ase, it is an acyl carrier protein to which acetyl and malonyl thioester residues are bound via a 2'-(5''-phosphoribosyl)-3'-dephospho-CoA prosthetic

nd related metal-dependent hydrolases

stem (T2SS, formerly general secretion pathway, GSP) for the export of proteins
ein

ısD, EvfM, TssJ, VC_A0113
JF4089)
JF1471)

ent
JF2878)

dependent transport system permease family

ein
ctase

eutN

amily

rotein PhnK
embrane protein ydjZ

plex MetNIQ involved in methionine import. Responsible for energy coupling to the transport system

nate ABC transport system, membrane component PhnV

otion of the maltose regulon whose gene products are responsible for uptake and catabolism of malto-oligosaccharides. Binds and recognizes a DN

family

drogenases reductases (SDR) family
se
dependent transport system permease family
ng protein

nit
threonylcarbamoyl group on adenosine at position 37 (t(6)A37) in tRNAs that read codons beginning with adenine. Catalyzes the conversion of L-th
osomal peptide biosynthetic process
ic intermediate to pyrroloquinoline quinone

e family

specific IIB subunit

ion of 2- phosphoglycerate into phosphoenolpyruvate. It is essential for the degradation of carbohydrates via glycolysis

etyl-D-glucosamine and N-acetyl-D-glucosamine-6-phosphate from diacetylchitobiose-6-phosphate
dependent transport system permease family
-phosphate-dependent aminotransferase family. PhnW subfamily
ubunit of the Holliday junction resolvase
UF4177)

n

f methylthioribose into methylthioribose-1-phosphate

JF968)
dependent oxidative cleavage of 2,3-dihydroxyphenylpropionic acid and 2,3- dihydroxicinnamic acid into 2-hydroxy-6-ketononadienedioate and 2- h

se PulE Tfp pilus assembly pathway, ATPase PilB
ıt transport systems inner membrane component

B
rotein PhnH
antitoxin N-terminal domain
es involved in the de novo synthesis of purine nucleotides, regulating purB, purC, purEK, purF, purHD, purL, purMN and guaBA expression. PurR is a

nd related ring-hydroxylating dioxygenases large terminal subunit

otection via the biosynthesis of trehalose. Catalyzes the transfer of glucose from UDP-glucose (UDP-Glc) to D-glucose 6-phosphate (Glc-6-P) to for

M-like domain

echanism carboxysome shell protein

ɜe
ependent oxidoreductase family
ɹcation (Tat) system that transports large folded proteins containing a characteristic twin-arginine motif in their signal peptide across membranes.
FtsE
ɜion elongation in a specialized subset of operons that encode extracytoplasmic components. RfaH is recruited into a multi-component RNA polym

ɹmily

ɜenase
ɲ protein (MFP) (TC 8.A.1) family

icotinamidase

ɜ mutase family

ɜ in intracellular peptide degradation
ɔn of nascent membrane proteins into the cytoplasmic membrane. Acts as a receptor for the complex formed by the signal recognition particle (SF

ɹble DNA replication during SOS response. It forms, in concert with dnaB protein and other prepriming proteins dnaC, N, N', N'' a prepriming protei
ay a role in metal insertion (metal-chelatase) or as a chaperone
abinose to L-ribulose

ɹily

JF3343)
P bond in alpha-D-ribose 1-methylphosphonate 5-phosphate (PRPn) forming alpha-D-ribose
B component

ıt decarboxylation of aspartate to produce beta-alanine
Thought to form the channel of an arsenite pump

ses 5'-nucleoside monophosphates and is involved in maturation of structured RNAs

and related acetyltransferases

ıily III
ın
ate from myristoyl-acyl carrier protein (ACP) to Kdo(2)-(lauroyl)-lipid IV(A) to form Kdo(2)-lipid A

cluding N-acetylases of ribosomal proteins
maltose receptor)

ıate aminotransferase
Gpp to ppGpp. Guanosine pentaphosphate (pppGpp) is a cytoplasmic signaling molecule which together with ppGpp controls the stringent respons
that cleaves unmethylated GATC sequences. It is involved in DNA mismatch repair
ase and thioredoxins
bonate transport system, ATPase component

JF1656)

ugar-metabolising enzyme

superfamily
ivatives
to FMNH2 which is used to reduce pyrimidine by RutA via the Rut pathway

drogenases reductases (SDR) family
different specificities (related to short-chain alcohol dehydrogenases)

e
family

F5375)
peptide transport permease C
otein c

e

ors that promote the attachment of RNA polymerase to specific initiation sites and are then released. This sigma factor is the primary sigma factc
rmyltetrahydrofolate (formyl-FH4) to formate and tetrahydrofolate (FH4)
metal-dependent hydrolases
permease component
droperoxidase activity. Required for the reduction of the AhpC active site cysteine residues and for the regeneration of the AhpC enzyme activity

neous hydrolysis of aminoacrylate to malonic semialdehyde. Required to remove a toxic intermediate produce in the pyrimidine nitrogen degradat
he TIM-barrel fold
superfamily

at
ta-lysylation step of the post-translational modification of translation elongation factor P (EF-P). Catalyzes the ATP-dependent activation of (R)-be
ining a DNA-binding HTH domain and an aminotransferase domain (MocR family) and their eukaryotic orthologs
rotein

ate to dihydroxyacetone. Uses fumarate or nitrate as electron acceptor

l in the assembly of the 50S ribosomal subunit. Has an RNA-dependent ATPase activity, which is specific for 23S rRNA, and a 3' to 5' RNA helicase

er of a propylamine group from the amino donor S-adenosylmethioninamine (decarboxy- AdoMet) to putrescine (1,4-diaminobutane) to yield sperı
JF3833)
to the periplasm for the biogenesis of c-type cytochromes
-eliminating lyase threonine aldolase

JF3225)

ım efflux system that confers protection against electrophiles. Required for full activity of KefC. Shows redox enzymatic activity, but this enzymatic
ally associated with flavoprotein oxygenases DIM6 NTAB family

›rotein A family

ımponent

ɗrogenases reductases (SDR) family
ɛquence and methylates the N-terminal (generally Phe) residue

ɡlycerol-3-phosphate dehydrogenase family

›genase family
tion of fatty acid synthesis by the addition to an acyl acceptor of two carbons from malonyl-ACP
ɛase

UF5107)
specific IIB subunit

/l phosphate from acetate and ATP. Can also catalyze the reverse reaction
threonylcarbamoyl group on adenosine at position 37 (t(6)A37) in tRNAs that read codons beginning with adenine. Is involved in the transfer of the
ation-cell division (RND) (TC 2.A.6) family

e3 -siderophores transport systems, ATPase components

›tein

l domain protein
stem permease component

lication origin oriC
resulting in DNA looping between the operators
lucosamine N-acyltransferase

e-specific transporter subunit IIA HPr protein

specifically activate or repress expression of target genes
es involved in arginine and lysine metabolism
sport systems inner membrane component

nally produced within the cells and which are toxic to biological systems

ide bond formation

nily III
plex comprises of a formate dehydrogenase, unidentified electron carriers and hydrogenase-3

2-hydroxyacid dehydrogenase family

ation-cell division (RND) (TC 2.A.6) family

tor superfamily

deacylase
family. Type 1 subfamily
clic radical-mediated conversion of 6-carboxy-5,6,7,8-tetrahydropterin (CPH4) to 7- carboxy-7-deazaguanine (CDG), a step common to the biosynthe
e 31 family
actin out of the cell
rase, MAPEG superfamily
der gluconeogenic growth conditions
ivatives

ofB
ation-cell division (RND) (TC 2.A.6) family

f autoinducer-2 (AI-2) to phospho-AI-2, which subsequently inactivates the transcriptional regulator LsrR and leads to the transcription of the lsr op

ith DnaJ, but functions under different conditions, probably acting as a molecular chaperone in an adaptive response to environmental stresses oth
the TIM-barrel fold
ngle-stranded DNA and RNA. May play a role in the H(2)O(2)-induced DNA damage repair

oxidoreductase 2 family. FRD SDH subfamily

in RcnB
protein

nto protoporphyrin IX

ing protein

ocatechuate from 4-hydroxybenzoate
ein
uction of ubiquinone-1 to ubiquinol by two successive reactions, coupled with the transport of Na( ) ions from the cytoplasm to the periplasm. NqrA

saccharide poly-beta- 1,6-N-acetyl-D-glucosamine (PGA) across the outer membrane. The PGA transported seems to be partially N-deacetylated s
enzymes involved in molybdopterin and thiamine biosynthesis family 2
way of protein degradation where it conjugates Leu, Phe and, less efficiently, Met from aminoacyl-tRNAs to the N-termini of proteins containing a

protein, PSIF

nily. Type
at

nd lipid transport
ndent sugar phosphotransferase system (sugar PTS), a major carbohydrate active transport system, catalyzes the phosphorylation of incoming suga
plexes LivFGHMJ and LivFGHMK involved in the high-affinity transport of branched-chain amino acids

plex NikABCDE involved in nickel import. Responsible for energy coupling to the transport system

ndent sugar phosphotransferase system (PTS), a major carbohydrate active - transport system, catalyzes the phosphorylation of incoming sugar sul
lase, UbiH UbiF VisC COQ6

se
2-phosphoglycerate and 3-phosphoglycerate
transport other divalent cations
mporter (SSF) (TC 2.A.21) family
-CoA oxaloacetate decarboxylase, beta subunit

protein N

epair by recognizing RNA polymerase (RNAP) stalled at DNA lesions. Mediates ATP-dependent release of RNAP and its truncated transcript from t

ınce by binding to RNase E (Rne) and regulating its endonucleolytic activity. Can modulate Rne action in a substrate-dependent manner by altering
the synthesis of short RNA molecules used as primers for DNA polymerase during DNA replication

ved in bacteria (DUF2255)
e 31 family
enase

ein
a-anomer

te hydrogenlyase system which is involved in the cleaving of formate to dihydrogen and carbon dioxide
ting swimming and swarming in a bis-(3'-5') cyclic diguanylic acid (c-di-GMP)- dependent manner. Binds 1 c-di-GMP dimer per subunit. Increasing

(TC 2.A.15) family

at stabilizes the FtsZ protofilaments by cross-linking them and that serves as a cytoplasmic membrane anchor for the Z ring. Also required for the
e 3 family
, subunit
ein (DUF2280)
kyphenol hydroxylase and related FAD-dependent oxidoreductases

plex PotABCD involved in spermidine putrescine import. Responsible for energy coupling to the transport system

protein dioxygenase
e 1 family

aining sensor and EAL
eductase (NAP). Only expressed at high levels during aerobic growth. NapAB complex receives electrons from the membrane-anchored tetraheme

protein PhoH
ein

ng family. YbaK EbsC subfamily
ivity and metabolic process
er and related transporters

ate reductase, flavoprotein subunit

S YhfK family

he chromosome non- specifically, forming a highly ordered and stable dps-DNA co- crystal within which chromosomal DNA is condensed and prote
mponent
MobC)

ranched-chain amino acids (BCAA). Catalyzes an alkyl-migration followed by a ketol- acid reduction of (S)-2-acetolactate (S2AL) to yield (R)-2,3- di

M-like domain

dependent transport system permease family
ase and desuccinylase that specifically removes acetyl and succinyl groups on target proteins. Modulates the activities of several proteins which are

glycerol uptake and metabolism. Catalyzes the phosphorylation of glycerol to yield sn- glycerol 3-phosphate
yde dehydrogenases

romosome partitioning
genase-like hydrolases superfamily and Cof family of proteins

in that could be required for efficient cell constriction
tor protein AriR
e
mily
PP-GlcNAc-ManNAcA-Fuc4NAc (Lipid III), the third lipid-linked intermediate involved in ECA synthesis
coupling to the transport system
ein, family 1

system, which controls transcription of numerous genes. RcsD is a phosphotransfer intermediate between the sensor kinase RcsC and the respons

JF969)

\ invertase Pin homologs
lependent transport system permease family

rotein PhnL
n PhnM

ı EutJ
ase HPA2 and related acetyltransferases
rC possibly involved in tellurium resistance

f utilization of gamma- aminobutyric acid
3-O-myristoyl-N- acetylglucosamine to form UDP-3-O-myristoylglucosamine and acetate, the committed step in lipid A biosynthesis

droxylase and related flavodoxin oxidoreductases

te transport system periplasmic component
in

ichia coli led to effects on biofilm formation, alteration in expression of a number of genes and mutations in bssS led to defects in indole transpor

vates transcription by stimulating RNA polymerase (RNAP) recycling in case of stress conditions such as supercoiled DNA or high salt concentratio
ly protein
rotein hflD homolog

ydrolases (invasion-associated proteins)

com of molecular oxygen into position 2 of the phenyl ring of 3-(3- hydroxyphenyl)propionate (3-HPP) and hydroxycinnamic acid (3HCl)

ory transposon protein

ependent oxidoreductase family

in cobalt-precorrin-6Y to form cobalt-precorrin-7W-a
n protein

e stimulus
orter activity

sport

carboxy-lyase
tch superfamily
nickel transport systems, permease components

·PD) degradation by catalyzing the conversion of propanoyl-CoA to propanoyl-phosphate

›acterial periplasmic transport system of putrescine
phate isomerase type 1 family
in

gion
l-3-phosphate acyltransferase family
t oxidation of 4- (phosphohydroxy)-L-threonine (HTP) into 2-amino-3-oxo-4- (phosphohydroxy)butyric acid which spontaneously decarboxylates to fo
ıma chain

cid of tripeptides
olase, subfamily IA, variant 3

sphate (Ap4A) hydrolase and other HIT family hydrolases
nponent of the phosphoenolpyruvate-dependent sugar phosphotransferase system (sugar PTS). This major carbohydrate active-transport system ca

onent of the Clp protease. It directs the protease to specific substrates. Can perform chaperone functions in the absence of ClpP
ocess

tion between acetaldehyde and D-glyceraldehyde 3-phosphate to generate 2-deoxy- D-ribose 5-phosphate
g N-terminal aspartate residues. May play a role in allowing the cell to use peptide aspartate to spare carbon otherwise required for the synthesis
ıt transports di- and tripeptides

lator
ily C, member 28, conserved domain

potassium in exchange for external protons and maintains the internal concentration of potassium under toxic levels

tor N-terminus

related transporters (MFS superfamily)

carbon ketol group from a ketose donor to an aldose acceptor, via a covalent intermediate with the cofactor thiamine pyrophosphate

alyzes the degradation of glycine. The H protein shuttles the methylamine group of glycine from the P protein to the T protein
protein
oreductase activity in the presence of NADPH and glutathione reductase. Reduces low molecular weight disulfides and proteins
ein
tase Thiol specific antioxidant Mal allergen

d in colicin E2 resistance
specificities (Related to short-chain alcohol dehydrogenases)

JF541)
onsisting of a CheY-like receiver domain and a winged-helix DNA-binding domain
mily
ide reductase family

dehydrogenase

dependent transport system permease family. FecCD subfamily
ain

er and related transporters

family

strate-binding protein
nase muconate lactonizing enzyme family

ven potassium transport (or Kdp) system, which catalyzes the hydrolysis of ATP coupled with the electrogenic transport of potassium into the cytop

a subunit
tase and related Zn-dependent oxidoreductases

sidue in the C- terminal position
sion of L-fucose
n, C terminal
dependent transport system permease family
ter (DMT) superfamily

superfamily
r assembly. Binds nickel. Probably functions as a nickel donor during metallocenter assembly

JF4035)
bonate transport systems, periplasmic components
or
superfamily
tin-NADPH reductases) family 1
rotein
ily
se superfamily. PhnX family
ase
ge of 4-hydroxy-2- oxopentanoate to pyruvate and acetaldehyde. Is involved in the meta-cleavage pathway for the degradation of aromatic compou
hospho-AI-2, thereby terminating induction of the lsr operon and closing the AI-2 signaling cycle. Catalyzes the transfer of an acetyl moiety from 3-
on of acetaldehyde and ammonia from ethanolamine

dent
nsfer protein
P-binding protein

nine in position 2445 (m2G2445) and the guanine in position 2069 (m7G2069) of 23S rRNA
t reduction of ketopantoate into pantoic acid
plex AraFGH involved in arabinose import. Responsible for energy coupling to the transport system

ıding
erase
e 43 family

istance protein dioxygenase

er and related transporters

coupling to the transport system
orane usher protein
ı chorismate, with concomitant aromatization of the ring, to provide 4- hydroxybenzoate (4HB) for the ubiquinone pathway

ivatives
ase PfkB family
ıbstrate specificity for short-chain acyl-CoA thioesters with the activity decreasing when the length of the carboxylic acid chain exceeds four carbor
ıt transports di- and tripeptides
xylamine to form NH(3) and H(2)O

operon from a sigma-70 promoter
bonate transport systems periplasmic components

p

mily
Fe-S) clusters to target apoproteins. Can hydrolyze ATP
t system. Interacts with trk system potassium uptake protein TrkA

ıcetylases of ribosomal proteins
lator

lase, UbiH UbiF VisC COQ6
r termination of DNA replication. Binds to DNA replication terminator sequences (terA to terF) to prevent the passage of replication forks. The terr
ımino)-4(3h)-pyrimidinone 5'-phosphate into 5-amino-6-(ribosylamino)-2,4(1h,3h)- pyrimidinedione 5'-phosphate
lase, HD

ːnase
ːconcentration in the cell, thus reducing its toxicity
cell wall biogenesis
plex MetNIQ involved in methionine import. Responsible for energy coupling to the transport system

ɔgenase family. UxaB subfamily
ıeine moiety from coenzyme A to a Ser of acyl-carrier-protein

ː family
ːein

r and related permeases

JF2492)
ismate to isochorismate

ne osmoprotectant glycine betaine. Catalyzes the oxidation of choline to betaine aldehyde and betaine aldehyde to glycine betaine at the same rat

at

e family
glycerol-3-phosphate dehydrogenase family
eins in a process that requires ATP hydrolysis. Has a chymotrypsin-like activity. Plays a major role in the degradation of misfolded proteins
PhzF
synthase enzyme
gO

cific

onal repair of damaged DNA

JF1479)
ning an amidase domain and an AraC-type DNA-binding HTH domain

ıily. 5-hydroxyisourate hydrolase subfamily
dependent transport system permease family. FecCD subfamily
C 1.A.8) family
dehydrogenase

ters
-arabinose- phosphoundecaprenol (alpha-L-Ara4N-phosphoundecaprenol) from the cytoplasmic to the periplasmic side of the inner membrane
he repair of deaminated bases. Selectively cleaves double-stranded DNA at the second phosphodiester bond 3' to a deoxyinosine leaving behind th
dependent binding of aminoacyl-tRNA to the A-site of ribosomes during protein biosynthesis

YSE YGGA)

ɔinding protein 3 family
erase

acid oxidation in which acetyl-CoA is released and the CoA ester of a fatty acid two carbons shorter is formed
llosteric enzyme in carbohydrate metabolism. Enzymes from different sources differ in their regulatory mechanisms and in their natural substrate
ein

ɹrane lipoprotein

ı eutQ

MobC)
tem
bonate transport
ygenase and related ring-hydroxylating dioxygenases, large terminal subunit

-3',8-cyclo-7,8- dihydroguanosine 5'-triphosphate to cyclic pyranopterin monophosphate (cPMP)

A transcriptional activator to the activator sequence of hyc operon
(OSB-CoA) to 1,4- dihydroxy-2-naphthoyl-CoA (DHNA-CoA)

l domain

ype 2

ino acid cation symporter (DAACS) (TC 2.A.23) family
against the biological effects of O6-methylguanine (O6-MeG) and O4-methylthymine (O4-MeT) in DNA. Repairs the methylated nucleobase in DN
binding methyltransferase superfamily. C5-methyltransferase family
genase family
(AMP-forming) AMP-acid ligases II

. Catalyzes stereospecifically the conversion of dihydroxyacetone phosphate (DHAP) to D-glyceraldehyde-3-phosphate (G3P)
toacid CoA transferase beta subunit

galactonate to 2-keto-3- deoxy-D-galactonate
plex LsrABCD involved in autoinducer 2 (AI-2) import. Responsible for energy coupling to the transport system

ding
volved in electron transport

n the assembly of lipopolysaccharide (LPS) at the surface of the outer membrane. Required for the proper assembly of LptD. Binds LPS and may se

n

or facilitator superfamily

amily

yl group to IIB which then transfers the phosphoryl group to the sugar

se
he biosynthesis of 5- methylaminomethyl-2-thiouridine (mnm(5)s(2)U) at the wobble position (U34) in tRNA. Catalyzes the FAD-dependent demo
ation-cell division (RND) (TC 2.A.6) family

ogenase family

/l phosphate from acetate and ATP. Can also catalyze the reverse reaction
orin family

drogenase

tide biosynthesis protein

degrades murein glycan strands and insoluble, high-molecular weight murein sacculi, with the concomitant formation of a 1,6-anhydromuramoyl p

e
toacid CoA transferase, beta subunit
ily
genase family

JF3300)

e, central domain
ane protein

udouridine from uracil- 55 in the psi GC loop of transfer RNAs
UF4760)
is seems not to be the case, but its exact role is uncertain. Responsible for energy coupling to the transport system

A. Could function as a metabolic relief valve, allowing to eliminate certain compounds when they accumulate to high levels in the cell

gulatory system

e mutase family

UF386)
y
ein SseB

NAD binding domain

atase, YffH AdpP family

ivatives
n DsbC
on of alpha-ketobutyrate and ammonia from threonine in a two-step reaction. The first step involved a dehydration of threonine and a production

nding proteins, family 5 Middle

npetence protein ComEC Rec2
against the biological effects of O6-methylguanine (O6-MeG) and O4-methylthymine (O4-MeT) in DNA. Repairs the methylated nucleobase in DN

e methyltransferase

bosomal translocation step during translation elongation. During this step, the ribosome changes from the pre-translocational (PRE) to the post- tr

se via the functional incorporation of the urease nickel metallocenter
ng protein
dehydratase family. DsdA subfamily
nding protein

EutP

nide by the addition of aminopropanol on the F carboxylic group
ubunits stomatin prohibitin homologs

bdopterin-containing oxidoreductase family
rminase that cleaves nascent peptidoglycan strands endolytically to terminate their elongation

ine-binding (lipo)protein of an ABC-type transport system (osmoprotectant binding protein)

in CsiE
tion site

mily
e phosphoribosyltransferase family

family. ECF subfamily
or

sport
tase and related Zn-dependent oxidoreductases

e protein, TolC

amily

protein (HSP20) family

nation in some periplasmic proteins. Acts by transferring its disulfide bond to other proteins and is reduced in the process

nslocation of the substrate across the membrane

JF1656)

e family
F72
gatively supercoils closed circular double-stranded (ds) DNA in an ATP-dependent manner to modulate DNA topology and maintain chromosomes i
il and 5-phospho-alpha- D-ribose 1-diphosphate (PRPP) to UMP and diphosphate
t oxidation of 4- (phosphohydroxy)-L-threonine (HTP) into 2-amino-3-oxo-4- (phosphohydroxy)butyric acid which spontaneously decarboxylates to fo

is. Catalyzes the aerobic oxidative decarboxylation of propionate groups of rings A and B of coproporphyrinogen-III to yield the vinyl groups in protc

rotein
rase
unt for an outwardly- directed proton pump that is linked to amino acid decarboxylation, as part of the extreme acid resistance (XAR) response

P from Y. pestis shows phosphodiesterase activity which is required for the inhibition of biofilm formation
dehydrogenases, class III

stem permease component
stem involved in resistance to organic solvents, permease component
ain length of enterobacterial common antigen (ECA)
bdopterin-containing oxidoreductase family
plex PotABCD involved in spermidine putrescine import. Responsible for energy coupling to the transport system

ved in bacteria (DUF2345)

n system
ucleotide-disulfide oxidoreductase family

ılcohol dehydrogenase family

JF3302)
ine and serine into the cell, with the concomitant import of a proton (symport system)

nthase RsuA family

drogenases reductases (SDR) family
dependent transport system permease family

diverse nucleosides, yielding D-ribose 1-phosphate and the respective free bases. Can use uridine, adenosine, guanosine, cytidine, thymidine, inosi

liphatic sulfonates

rase
ivatives

f ribose at O-5 in a reaction requiring ATP and magnesium. The resulting D-ribose-5- phosphate can then be used either for sythesis of nucleotides
e biogenesis of c-type cytochromes. Transiently binds heme delivered by CcmC and transfers the heme to apo-cytochromes in a process facilitated

ation-cell division (RND) (TC 2.A.6) family
gulation of the bet genes

xylation of 6- phosphogluconate to ribulose 5-phosphate and CO(2), with concomitant reduction of NADP to NADPH
smic substrate-binding protein
l related proteins, alkaline phosphatase superfamily
l-glycosidic bond of AMP to form adenine and ribose 5-phosphate. Involved in regulation of AMP concentrations
lose 1-phosphate to glycerone phosphate and L-lactaldehyde
ses, including glyoxylases

ges N4 and lambda

- and N(8)-acetylspermidine from spermidine

-ribulose 5-phosphate to D-xylulose 5-phosphate
ng protein

om selenide and ATP
ining a DNA-binding HTH domain and an aminotransferase domain (MocR family) and their eukaryotic orthologs

tR family
ne chorismate, which leads to the biosynthesis of aromatic amino acids. Catalyzes the reversible NADPH linked reduction of 3-dehydroshikimate (D

ıe acetyl group of acetyl-CoA with 3-methyl-2-oxobutanoate (2-oxoisovalerate) to form 3-carboxy-3-hydroxy-4-methylpentanoate (2-isopropylmala
R operon in response to L-rhamnose
different specificities (related to short-chain alcohol dehydrogenases)

JF2955)

nination. Required for transcription of ribosomal RNA (rRNA) genes. Binds specifically to the boxA antiterminator sequence of the ribosomal RNA
of a CheY-like receiver domain and a winged-helix DNA-binding domain
a number of redox enzymes
ative DNA transfer

type-1 family
(DUF1323)

robic degradation of long-chain fatty acids via beta-oxidation cycle. Catalyzes the formation of 3-oxoacyl-CoA from enoyl-CoA via L-3-hydroxyacyl-C
cation (Tat) system that transports large folded proteins containing a characteristic twin-arginine motif in their signal peptide across membranes.

ependent oxidoreductase family

ose and maltodextrins
ein

family

amily
onsisting of a CheY-like receiver domain and a winged-helix DNA-binding domain
ystems
inding protein 9 family

beta-lactamase fold

JF2754)
C4-dicarboxylates from the periplasm across the inner membrane
ystem Periplasmic Component

edoheptulose 7-phosphate in D-glycero-D-manno-heptose 7-phosphate
in
and related acetyltransferases

ly of DMSO reductase, but not for the interaction of the DmsA signal peptide with the Tat system. May be part of a chaperone cascade complex th

ween 2-isopropylmalate and 3-isopropylmalate, via the formation of 2-isopropylmaleate

ogenase fumarate reductase iron-sulfur protein family
er and related transporters

euridylylation, the PII regulatory proteins (GlnB and homologs), in response to the nitrogen status of the cell that GlnD senses through the glutamir
5'-end of 16S rRNA

mily

dratase
dependent transport system permease family. FecCD subfamily

ors that promote the attachment of RNA polymerase to specific initiation sites and are then released. This sigma factor is involved in regulation of

ubunit family

50S ribosomal subunit and may have a role during protein synthesis or ribosome biogenesis

ter
r Thr protein kinase)

ocess
UF1971)
lenosyl-L-methionine (SAM) to carboxy-S-adenosyl-L-methionine (Cx-SAM)
class II
ivatives
and related acetyltransferases

maltose receptor)
ation-cell division (RND) (TC 2.A.6) family

ening between N-3 and C- 4 by an unusual flavin hydroperoxide-catalyzed mechanism to yield ureidoacrylate peracid. It cleaves pyrmidine rings dir
egrades the RNA of RNA- DNA hybrids
in LacI transcriptional regulator
yl group from 5- methyltetrahydrofolate to homocysteine resulting in methionine formation
mily
droorotate to orotate with quinone as electron acceptor
se of guanosine 2251 in 23S rRNA

to 2-nitropropane dioxygenase

ng protein

bon sugar) for incorporation into bacterial lipopolysaccharide in Gram-negative bacteria

detoxification of formaldehyde

plex ThiBPQ involved in thiamine import. Responsible for energy coupling to the transport system
methylated cytidine (Cm32) or 2'O-methylated uridine (Um32) at position 32 in tRNA
ain amino acid transport systems, periplasmic component
t transport systems inner membrane component
-alcohol dehydrogenases)
different specificities (related to short-chain alcohol dehydrogenases)
sis. Alleviates ribosome stalling that occurs when 3 or more consecutive Pro residues or the sequence PPG is present in a protein, possibly by augm
unt for an outwardly- directed proton pump that is linked to amino acid decarboxylation, as part of the extreme acid resistance (XAR) response

tase NADH

tems permease components
oreductase family
rom Escherichia coli forms a dimer and binds zinc ions for catalytic activity and catalyzes the conversion of allantoate to (S)-ureidoglycolate and a

lase
sulfur trafficking in the cell. Part of a sulfur-relay system required for 2-thiolation during synthesis of 2-thiouridine of the modified wobble base 5

-terminal domain

ntaining CheY-like receiver, AAA-type ATPase, and DNA-binding domains

nversion of 7-carboxy-7- deazaguanine (CDG) to 7-cyano-7-deazaguanine (preQ(0))
ociated region
ous penultimate amino acid residues except L-proline
group from ATP to 4'- phosphopantetheine, yielding dephospho-CoA (dPCoA) and pyrophosphate
acilitator (CDF) transporter (TC 2.A.4) family
bdopterin-containing oxidoreductase family

on dicarboxylic acid source for the tricarboxylic acid cycle
bonate transport system permease component

kR family

egrades the RNA of RNA- DNA hybrids
e catalyzes the transcription of DNA into RNA using the four ribonucleoside triphosphates as substrates

ve mutations in essential genes by modulating rho-dependent transcription termination
)S ribosome and the 50S ribosomal subunit in a nucleotide-independent manner

ation-cell division (RND) (TC 2.A.6) family

ng protein

AD superfamily, subfamily IC
pendent hydrolase
UF1833)

ptor subunit CsdE
lase
hamnose (6-deoxy-L- mannose). Catalyzes the transfer of the gamma-phosphate group from ATP to the 1-hydroxyl group of L-rhamnulose to yield
n protein (MFP) (TC 8.A.1) family
ivatives

ugar-metabolising enzyme

nvolved in the transport of proline across the inner membrane
oxin, Type IV TA system

family

plex PhnCDE involved in phosphonates import. Responsible for energy coupling to the transport system

ne balance of metabolites in the pentose-phosphate pathway

nily

h DNA N-glycosylase activity and AP-lyase activity. The DNA N-glycosylase activity releases various damaged pyrimidines from DNA by cleaving the
ily
nidase
in
y driven movement of water in both directions. It is involved in the osmoregulation and in the maintenance of cell turgor during volume expansion

sterase lipase family

nponent

nvolved in cell wall biogenesis
ase family
e of citrate lyase

roline-5-carboxylate (PCA) to L-proline
n, RelE StbE family

ivatives

drogenases reductases (SDR) family

JF2724)
accelerates covalent attachment of the cofactor into other proteins. Plays an essential role in the assembly of succinate dehydrogenase (SDH, res

transferase MdcG
Prophage Related)

tyltransferase family
ns in the citric acid cycle (TCA), coupling the hydrolysis of succinyl-CoA to the synthesis of either ATP or GTP and thus represents the only step of su

ogenesis. Binds a 4Fe- 4S cluster, can transfer this cluster to apoproteins, and thereby intervenes in the maturation of Fe S proteins. Could also act

s for the initiation of protein synthesis. Protects formylmethionyl-tRNA from spontaneous hydrolysis and promotes its binding to the 30S ribosoma

bdopterin-containing oxidoreductase family

at
ng protein

3-octaprenyl-4-hydroxy benzoate to 2-octaprenylphenol, an intermediate step in ubiquinone biosynthesis

superfamily
ure protein
amily

yltransferase

:tures. These structures can inhibit DNA replication and are intermediates in certain DNA recombination reactions. The complex acts as a 3'- 5' dou

:-terminal domain
of mitomycin antibiotics polyketide fumonisin
system, periplasmic component
ısion by the F plasmid
JF3277)
JF2543)
methylenetetrahydrofolate to 5,10-methenyltetrahydrofolate and then the hydrolysis of 5,10-methenyltetrahydrofolate to 10- formyltetrahydrofola

ıyl group from 5- methyltetrahydrofolate to homocysteine resulting in methionine formation
nickel transport systems, permease components
UF1869)

stranded DNA into large acid-insoluble oligonucleotides, which are then degraded further into small acid-soluble oligonucleotides
ficiency, the sulfur transfer reaction from thiosulfate to cyanide

different specificities (related to short-chain alcohol dehydrogenases)
; with AAA ATPase

ınd a metalloprotease. Maintains the integrity of the outer membrane by promoting either the assembly or the elimination of outer membrane pro
NADH, via FMN and iron- sulfur (Fe-S) centers, to quinones in the respiratory chain
e

ys an important regulatory role in modulating the intracellular concentration of cAMP, thereby influencing cAMP-dependent processes

dependent binding of aminoacyl-tRNA to the A-site of ribosomes during protein biosynthesis

X involved in cellular division
RNA polymerase, activating expression of sigma-S-regulated genes. Stimulates RNA polymerase holoenzyme formation and may bind to several c

2 of adenine 2503 in 23S rRNA and position 2 of adenine 37 in tRNAs

m MacAB-TolC. MacB is a non-canonical ABC transporter that contains transmembrane domains (TMD), which form a pore in the inner membran
enase activity

me 1

plex FbpABC involved in Fe(3) ions import. Responsible for energy coupling to the transport system
drogenases reductases (SDR) family
damaging agents

ween 2-isopropylmalate and 3-isopropylmalate, via the formation of 2-isopropylmaleate
indirectly, cGMP

of a CheY-like receiver domain and a winged-helix DNA-binding domain

no acids

sose (2-keto-myo- inositol, 2KMI or 2,4,6 3,5-pentahydroxycyclohexanone) to 3D- (3,5 4)-trihydroxycyclohexane-1,2-dione (D-2,3-diketo-4-deoxy-ep

atidyl group transfer from one phosphatidylglycerol molecule to another to form cardiolipin (CL) (diphosphatidylglycerol) and glycerol
kidase family
inding protein
-inositol (MI) to 2- keto-myo-inositol (2KMI or 2-inosose)

n and normal SOS inducibility. RecF binds preferentially to single-stranded, linear DNA. It also seems to bind ATP

bdopterin-containing oxidoreductase family
cell
against the biological effects of O6-methylguanine (O6-MeG) and O4-methylthymine (O4-MeT) in DNA. Repairs the methylated nucleobase in DN
ne balance of metabolites in the pentose-phosphate pathway

genase

lator

n
lated enzymes

sport systems inner membrane component

ıethylthio-cis-ribozeatin in tRNA
e of azo bond in aromatic azo compounds to the corresponding amines. Requires NADH, but not NADPH, as an electron donor for its activity
e family

ate into acetyl-CoA (AcCoA), an essential intermediate at the junction of anabolic and catabolic pathways. AcsA undergoes a two-step reaction. In
JF4054)
epairs oxidized periplasmic proteins containing methionine sulfoxide residues (Met-O), using respiratory chain electrons. Thus protects these prote

csF

to the periplasm for the biogenesis of c-type cytochromes
hodiesterase

liphatic sulfonates

nc finger

plex PstSACB involved in phosphate import

on proton antiporter 2 (CPA2) transporter (TC 2.A.37) family
in
amily

-hydrolyzing

ist in the late maturation steps of the functional core of the 30S ribosomal subunit. Associates with free 30S ribosomal subunits (but not with 30S
JF499)

se family
ocess

ining a DNA-binding HTH domain and an aminotransferase domain (MocR family) and their eukaryotic orthologs
-terminal domain

nslation factor GTPase superfamily. Classic translation factor GTPase family. CysN NodQ subfamily
essing and regular turnover of intracellular proteins. Catalyzes the removal of unsubstituted N-terminal amino acids from various peptides

naged PFL and possibly other radical proteins
y acid metabolism

different specificities (related to short-chain alcohol dehydrogenases)
horing of the catalytic components of the fumarate reductase complex to the cytoplasmic membrane

4-amino-4,6-dideoxy-D- galactose (dTDP-Fuc4N) from dTDP-4-keto-6-deoxy-D-glucose (dTDP-D- Glc4O) and L-glutamate

cific
family

ng protein

me 1
JF2732)

ıding
e 1 family

e porin

; the transfer of the FMN moiety of FAD and its covalent binding to the hydroxyl group of a threonine residue in a target flavoprotein

uction of ubiquinone-1 to ubiquinol by two successive reactions, coupled with the transport of Na( ) ions from the cytoplasm to the periplasm. NqrA
thesis protein E

tamate to tRNA(Glu) in a two-step reaction glutamate is first activated by ATP to form Glu-AMP and then transferred to the acceptor end of tRNA

sport protein (AzlD)

inding protein 3 family
beta-pyran and beta- furan forms of D-ribose

tive antigen OMA87

containing CBS domains

ino acid cation symporter (DAACS) (TC 2.A.23) family
UF4222)
sport systems inner membrane component

sport system inner membrane component
nthesis enzymes

transport system, permease component I

ide reductase function

nate kinase
ct folding and assembly of outer membrane proteins. Recognizes specific patterns of aromatic residues and the orientation of their side chains, wh
ogenase

ndent sugar phosphotransferase system (PTS), a major carbohydrate active - transport system, catalyzes the phosphorylation of incoming sugar sub
beta-lactamase fold
e 13 family
otic resistance protein

C4-dicarboxylates from the periplasm across the inner membrane
se
thylallyl group onto the adenine at position 37 in tRNAs that read codons beginning with uridine, leading to the formation of N6-(dimethylallyl)ade

ransport signal transduction systems periplasmic component domain

AD superfamily, subfamily IC

ɔmain protein
ɔgenase family

ɲO
lk which helps the ribosome interact with GTP-bound translation factors. Is thus essential for accurate translation

nd an inhibitor of cell division. Accumulation of SulA causes rapid cessation of cell division and the appearance of long, non-septate filaments. In t
ɣmerase transcription elongation past template-encoded arresting sites. The arresting sites in DNA have the property of trapping a certain fraction

ulator

ulator SirB
ɲ protein (MFP) (TC 8.A.1) family

to the transport system
ese efflux pump
ation-cell division (RND) (TC 2.A.6) family
iosynthesis. Catalyzes the transfer of formate to 5-phospho-ribosyl-glycinamide (GAR), producing 5-phospho-ribosyl-N-formylglycinamide (FGAR).
dromonapterin triphosphate from dihydroneopterin triphosphate
ɔgenase family

tor protein

otein CcmA involved in cell shape determination
ɨivated derivatives IS5 family

mily

udouridine from uracil
dehydrogenases family

succinylarginine into N(2)-succinylornithine, ammonia and CO(2)
cleoside transporter (CNT) (TC 2.A.41) family
ıily
phodiester linkages between 5'-phosphoryl and 3'-hydroxyl groups in double-stranded DNA using NAD as a coenzyme and as the energy source for

a lesser extent hypoxanthine

subunits
ivatives

er

sporter substrate-binding protein

biogenesis protein
aining sensor and EAL

e protein/Dioxygenase superfamily
phatidyltransferase class-I family
and threonine into the cell, with the concomitant import of sodium (symport system)

he initiation point. It is needed to translate mRNA with a short Shine-Dalgarno (SD) purine-rich sequence
ons

n NADH and NADP is coupled to respiration and ATP hydrolysis and functions as a proton pump across the membrane
JF1090)
e 43 family

tase and related Zn-dependent oxidoreductases

the cytoplasmic membrane of D-alanine, D-serine and glycine'

eonine to tRNA(Thr) in a two-step reaction L-threonine is first activated by ATP to form Thr-AMP and then transferred to the acceptor end of tRNA

rmimidoyl-L-glutamate to L-glutamate and formamide
ein

carbon ketol group from a ketose donor to an aldose acceptor, via a covalent intermediate with the cofactor thiamine pyrophosphate
lay link together the upstream cell division proteins, which are predominantly cytoplasmic, with the downstream cell division proteins, which are p
3-like protein
in LacI transcriptional regulator

on of bacterial ribonucleotide reductase nrd genes and operons by binding to NrdR- boxes
toxic effects of hydrogen peroxide
of the terminal phosphate of ATP to form a long-chain polyphosphate (polyP)

rization of enterobacterial common antigen (ECA) trisaccharide repeat units

t transports di- and tripeptides

olase superfamily
ree amino group of methionyl-tRNA(fMet). The formyl group appears to play a dual role in the initiator identity of N-formylmethionyl-tRNA by pro

ter (DMT) superfamily

ulon, which plays a key role in phosphate homeostasis. PhoU is essential for the repression of the Pho regulon at high phosphate conditions
methylthioribose-1- phosphate (MTR-1-P) into methylthioribulose-1-phosphate (MTRu-1- P)
permease component

: 2-hydroxyacid dehydrogenase family
e protein/Dioxygenase superfamily

UF4312)

ptosyltransferase)

2-(5''-phosphoribosyl)- 3'-dephosphocoenzyme-A) of the gamma subunit of citrate lyase

of genes involved in protecting the cell against nitrosative stress. May require iron for activity
family
JF2770)
conversion of molybdopterin precursor Z to molybdopterin

JF2498)

JF1349)
of DNA damaged by oxidation or by mutagenic agents. Acts as DNA glycosylase that recognizes and removes damaged bases. Has a preference for
the normal export of preproteins out of the cell cytoplasm. It is a molecular chaperone that binds to a subset of precursor proteins, maintaining th

ily. MTOX subfamily

inding protein 3 family
ase FtsK SpoIIIE and related proteins

During DNA replication, flap endonucleases cleave the 5'-overhanging flap structure that is generated by displacement synthesis when DNA polyme

mily
-ribulose 5-phosphate to D-xylulose 5-phosphate

plex MetNIQ involved in methionine import. Responsible for energy coupling to the transport system

isters to apo- ferredoxin. Multiple cycles of 2Fe2S cluster formation and transfer are observed, suggesting that IscA acts catalytically. Recruits intra
ided DNA at a 9 bp consensus (dnaA box) 5'-TTATC CA A CA A-3'. DnaA binds to ATP and to acidic phospholipids
es of the 16S rRNA that are involved in tRNA selection in the A site and with the mRNA backbone. Located at the interface of the 30S and 50S sub
opyrrole PBG into the hydroxymethylbilane pre-uroporphyrinogen in several discrete steps
bunit

e synthase family. Type
athway, periplasmic inhibitor zinc-resistance associated protein

membrane lipoproteins

sport

group from acyl- phosphate (acyl-PO(4)) to glycerol-3-phosphate (G3P) to form lysophosphatidic acid (LPA). This enzyme utilizes acyl-phosphate a
both GDP and GTP, with rapid nucleotide exchange. Plays a role in 16S rRNA processing and 30S ribosomal subunit biogenesis and possibly also in
ining a DNA-binding HTH domain and an aminotransferase domain (MocR family) and their eukaryotic orthologs

doxin

reductase 4Fe-4S domain family

protein PtsN
ng protein

actarate to form 5- dehydro-4-deoxy-D-glucarate

ntaining a CheY-like receiver domain and an HTH DNA-binding domain
t transports di- and tripeptides

seems to be involved in an RecBC-independent recombinational process of DNA repair. It may act with RecF and RecO

ivatives
zes the 2 O-methylation steps in the ubiquinone biosynthetic pathway
rotein
plex PstSACB involved in phosphate import. Responsible for energy coupling to the transport system

volved in electron transport
glucose, a sugar donor used in elongation reactions on alpha-glucans
ion of 3- phosphohydroxypyruvate to phosphoserine and of 3-hydroxy-2-oxo-4- phosphonooxybutanoate to phosphohydroxythreonine

YdiB remains unclear, nor is it known whether 3-dehydroshikimate or quinate represents the natural substrate. Catalyzes the reversible NAD-depe

antibiotic exporters, contain an N-terminal double-glycine peptidase domain

tein assembly complex, which is involved in assembly and insertion of beta-barrel proteins into the outer membrane
xidoreductase
JF3383)

JF2919)
inal non-reducing alpha-D-galactose residues in alpha-D-galactosides
protein PtsN
n

ted with the inner membrane in Escherichia coli

f cross-linked peptidoglycan from the lipid intermediates. The enzyme has a penicillin-insensitive transglycosylase N-terminal domain (formation c

t reduction of ketopantoate into pantoic acid
acid oxidation in which acetyl-CoA is released and the CoA ester of a fatty acid two carbons shorter is formed

ressor
droperoxidase activity. Required for the reduction of the AhpC active site cysteine residues and for the regeneration of the AhpC enzyme activity

F5347)
otein

nthase RsuA family
transporters

family
of DNA gyrase. Acts by inhibiting DNA gyrase at an early step, prior to (or at the step of) binding of DNA by the gyrase. It protects cells against tox
lation of the 3-hydroxyl group of shikimic acid using ATP as a cosubstrate
-phosphate dehydrogenase family
uction of ubiquinone-1 to ubiquinol by two successive reactions, coupled with the transport of Na( ) ions from the cytoplasm to the periplasm. NqrA
naride (LPS) levels by regulating LpxC, which is involved in lipid A biosynthesis. May act by modulating the proteolytic activity of FtsH towards LpxC.
of a CheY-like receiver domain and a winged-helix DNA-binding domain
ved in lysophospholipase L1 biosynthesis permease component

se
NADH, via FMN and iron- sulfur (Fe-S) centers, to quinones in the respiratory chain. The immediate electron acceptor for the enzyme in this species
stranded DNA into large acid-insoluble oligonucleotides, which are then degraded further into small acid-soluble oligonucleotides

JF2560)
ntaining CheY-like receiver, AAA-type ATPase, and DNA-binding domains

-phosphate-dependent aminotransferase family. Histidinol-phosphate aminotransferase subfamily
3'-diphosphate 5-' diphosphate) is a mediator of the stringent response that coordinates a variety of cellular activities in response to changes in n
junction intermediates in genetic recombination. Cleaves the cruciform structure in supercoiled DNA by nicking to strands with the same polarity a
of a CheY-like receiver domain and a winged-helix DNA-binding domain

toplasmic function (ECF) sigma factor sigma-E (RpoE). ECF sigma factors are held in an inactive form by an anti-sigma factor until released by reg

ıponent
C7 resistance protein MccF

ıdent sugar phosphotransferase system (PTS), a major carbohydrate active - transport system, catalyzes the phosphorylation of incoming sugar sul

ɡene expression by modulating the protein level of the anti sigma factor FlgM upon sensing ring completion or hook elongation. Flk could inhibit Flg
displays some tRNA 3'- processing endonuclease activity. Probably involved in tRNA maturation, by removing a 3'-trailer from precursor tRNA
'abA

JF2554)

ns of the de novo folate biosynthetic pathway. Catalyzes the addition of a glutamate residue to dihydropteroate (7,8-dihydropteroate or H2Pte) to

UF4862)

'ivatives
ıine in position 1835 (m2G1835) of 23S rRNA
abB, involved in unsaturated fatty acid (UFA) biosynthesis. By controlling UFA production, FabR directly influences the physical properties of the m
periplasmic component

ıctases, Old Yellow Enzyme family

ıily

ɔsphogluconolactone to 6-phosphogluconate
different specificities (related to short-chain alcohol dehydrogenases)

lioxide

acid oxidation in which acetyl-CoA is released and the CoA ester of a fatty acid two carbons shorter is formed

ıtalyzes the reduction of hydrogen peroxide and organic hydroperoxides to water and alcohols, respectively. Plays a role in cell protection against o

superfamily
ɔhoribosylamino)methylideneamino imidazole-4-carboxamide isomerase
ein

ı termination and antitermination
ein
sport systems inner membrane component

ıerone. Protects both thermally unfolding and oxidatively damaged proteins from irreversible aggregation. Plays an important role in the bacterial
Catalyzes the phosphorolysis of single-stranded polyribonucleotides processively in the 3'- to 5'-direction

in 70 family
binding protein 3 family
from lauroyl-acyl carrier protein (ACP) to Kdo(2)-lipid IV(A) to form Kdo(2)- (lauroyl)-lipid IV(A)
4-cyclohexadiene-1- carboxylate (SHCHC) to 2-succinylbenzoate (OSB)

ycling by cleaving the terminal beta-1,4-linked N-acetylglucosamine (GlcNAc) from peptide-linked peptidoglycan fragments, giving rise to free Glc
coupling to the transport system
orin family

activity

ne acetyl group of acetyl-CoA with 3-methyl-2-oxobutanoate (2-oxoisovalerate) to form 3-carboxy-3-hydroxy-4-methylpentanoate (2-isopropylmala
nydrolysis reaction at the C5' of the pyrimidine moiety of thiamine compounds, a reaction that is part of a thiamine salvage pathway. Thus, catalyz

chorismate pathway, which leads to the biosynthesis of aromatic amino acids. Catalyzes the cis-dehydration of 3-dehydroquinate (DHQ) and introc

st glucose residue to the LPS core

orin family

gulate a protease
pA, BimE, VC_A0119, VasJ

popolysaccharides (LPSs). Catalyzes the hydrolysis of 3-deoxy-D-manno-octulosonate 8-phosphate (KDO 8-P) to 3-deoxy-D-manno-octulosonate (KD
ansfer of a sulfur to tRNA to produce 4-thiouridine in position 8 of tRNAs, which functions as a near-UV photosensor. Also catalyzes the transfer of

LL-2,6- diaminoheptanedioate (L,L-DAP) to meso-diaminoheptanedioate (meso- DAP), a precursor of L-lysine and an essential component of the b
ondensation of pimeloyl- acyl-carrier protein and L-alanine to produce 8-amino-7- oxononanoate (AON), acyl-carrier protein , and carbon dioxide

xylase

ogenase family
yzes the recognition and processing of DNA lesions. UvrC both incises the 5' and 3' sides of the lesion. The N-terminal half is responsible for the 3'
) to heme O by substitution of the vinyl group on carbon 2 of heme B porphyrin ring with a hydroxyethyl farnesyl side group

lioxide

fide bond formation
tein assembly complex, which is involved in assembly and insertion of beta-barrel proteins into the outer membrane

amily

sport systems inner membrane component
of a CheY-like receiver domain and a winged-helix DNA-binding domain

e cystathionine beta- synthase family
in LacI transcriptional regulator

tautomerase family

bitor of c-type lysozyme

ıine in position 2030 of 23S rRNA

ning protein

tase

JF2633)
ired for growth during stress conditions. May be involved in protecting or stabilizing the divisomal assembly under conditions of stress
in regulating the level of ATP-DnaA and in the modification of some tRNAs. It is probably a key factor in regulatory networks that act via tRNA mod

hamnonate to 2-keto-3- deoxy-L-rhamnonate (KDR)
cleoside transporter (CNT) (TC 2.A.41) family
on
coupling to the transport system

f D-fructose 6-phosphate to fructose 1,6-bisphosphate by ATP, the first committing step of glycolysis

II

ein

natic compounds catabolism

(TC 2.A.15) family
t oxidation of 4- (phosphohydroxy)-L-threonine (HTP) into 2-amino-3-oxo-4- (phosphohydroxy)butyric acid which spontaneously decarboxylates to fo

n structurally related to pyridoxine 5'-phosphate oxidase

n
anic pyrophosphate (PPi) forming two phosphate ions

n of undecaprenyl diphosphate (UPP). Confers resistance to bacitracin
alyzes the SAM-dependent methylations of uroporphyrinogen III at position C-2 and C-7 to form precorrin-2 via precorrin-1. Then it catalyzes the N
limethyl-8- ribityllumazine by condensation of 5-amino-6-(D- ribitylamino)uracil with 3,4-dihydroxy-2-butanone 4-phosphate. This is the penultima

tion of fatty acid synthesis by the addition to an acyl acceptor of two carbons from malonyl-ACP. Catalyzes the first condensation reaction which ir

lates RpoD-mediated transcription activation by preventing the interaction between the primary sigma factor RpoD with the catalytic core of the R
intracellular balance of NAD and NADP, and is a key enzyme in the biosynthesis of NADP. Catalyzes specifically the phosphorylation on 2'-hydroxyl
r use as a carbon and nitrogen source
reversible phosphorolysis of pyrimidine nucleosides are involved in the degradation of these compounds and in their utilization as carbon and ene

transcripts by removing pyrophosphate from the 5'-end of triphosphorylated RNA, leading to a more labile monophosphorylated state that can stim
racellular sulfur reduction
dihydroneopterin to 6- hydroxymethyl-7,8-dihydropterin

se, AIG2-like

phate isomerase type 2 family
novo pathway of purine nucleotide biosynthesis. Catalyzes the first committed step in the biosynthesis of AMP from IMP

s

zation at C-2 of UDP-N- acetylglucosamine (UDP-GlcNAc) and thereby provides bacteria with UDP-N-acetylmannosamine (UDP-ManNAc), the activ

synthesis of the CN ligands of the active site iron of NiFe -hydrogenases using carbamoylphosphate as a substrate. It functions as a carbamoyl tra
ily
lenosine to inosine at the wobble position 34 of tRNA(Arg2)

cine radical
f cis unsaturation into fatty acids. Catalyzes the dehydration of (3R)-3-hydroxydecanoyl- ACP to E-(2)-decenoyl-ACP and then its isomerization to Z-
ond of UDP-2,3- diacylglucosamine to yield 2,3-diacylglucosamine 1-phosphate (lipid X) and UMP by catalyzing the attack of water at the alpha-P a
molysin expression

nslocation of the substrate across the membrane
ent protein synthesis under certain stress conditions. May act as a fidelity factor of the translation reaction, by catalyzing a one-codon backward tr
tein assembly complex, which is involved in assembly and insertion of beta-barrel proteins into the outer membrane

on of acyl-phosphate (acyl-PO(4)) from acyl- acyl-carrier-protein (acyl-ACP). This enzyme utilizes acyl-ACP as fatty acyl donor, but not acyl-CoA

ion of carbamoyl aspartate to dihydroorotate

ors that promote the attachment of RNA polymerase to specific initiation sites and are then released
ation-cell division (RND) (TC 2.A.6) family

in
ein
UF1989)
itution of periplasmic glucans. Could catalyze the transfer of succinyl residues from the cytoplasmic side of the membrane to the nascent glucan b
play a role in recycling of muropeptides during cell elongation and or cell division

te 3-epimerase family
ter (DMT) superfamily

coupling to the transport system

coupling to the transport system
-ribazole-5'-phosphate from nicotinate mononucleotide (NAMN) and 5,6- dimethylbenzimidazole (DMB)

superfamily
nate bicarbonate transport systems, periplasmic components
tion of nicotinate mononucleotide (NaMN) to nicotinic acid adenine dinucleotide (NaAD)
s - catabolite gene activator and regulatory subunit of cAMP-dependent protein kinases
transport system, permease component II

hat catalyzes the oxidative cleavage of substituted catechols

olved in lipopolysaccharide synthesis

Direct interaction between DnaK and DjlA is needed for the induction of the wcaABCDE operon, involved in the synthesis of a colanic acid polysacch
rotein

ide bond formation

cleotide 34 wobble position in the two leucyl isoacceptors tRNA(Leu)(CmAA) and tRNA(Leu)(cmnm5UmAA). Catalyzes the methyl transfer from S-
periplasmic component surface adhesin
rotease

volved in electron transport

pendent hydrolase

lated to metalloendopeptidases
hosphohydrolase class 1
r
everal operons and genes involved in the biogenesis of Fe-S clusters and Fe-S-containing proteins
me A carboxylase (ACC) complex. Biotin carboxylase (BC) catalyzes the carboxylation of biotin on its carrier protein (BCCP) and then the CO(2) grou
2,4-cyclodiphosphate (ME-2,4cPP) into 1-hydroxy-2-methyl-2-(E)-butenyl 4-diphosphate
anslational coupling of the secM secA operon. Translational pausing at a specific Pro residue 5 residues before the end of the protein may allow di
resence of a proton gradient across the membrane. The gamma chain is believed to be important in regulating ATPase activity and the flow of pro

se family
thesis. Transports lipid-linked peptidoglycan precursors from the inner to the outer leaflet of the cytoplasmic membrane
d by peripheral catabolic pathways, to NADH, which can enter the respiratory chain for energy generation
ein, family 5

nidation of deamido-NAD to form NAD. Uses ammonia as a nitrogen source
otein A
hosphatidylserine from CDP-diacylglycerol and L-serine which leads eventually to the production of phosphatidylethanolamine
e mutase family. BPG- dependent PGAM subfamily

teins, together with IbpB, to stabilize and protect them from irreversible denaturation and extensive proteolysis during heat shock and oxidative st
n TIM barrel

hosphatase
smoregulated periplasmic glucans (OPGs)
n in which hydroxymethyl group from 5,10-methylenetetrahydrofolate is transferred onto alpha-ketoisovalerate to form ketopantoate

luctase

olpyruvyl moiety of phosphoenolpyruvate (PEP) to the 5-hydroxyl of shikimate-3- phosphate (S3P) to produce enolpyruvyl shikimate-3-phosphate an
phodiester to an RNA 2'- phosphomonoester

ino acid cation symporter (DAACS) (TC 2.A.23) family

round one UvrB monomer. DNA wrap is dependent on ATP binding by UvrB and probably causes local melting of the DNA helix, facilitating insertio

JF1073)

teins, together with IbpA, to stabilize and protect them from irreversible denaturation and extensive proteolysis during heat shock and oxidative st
csE
sine at position 1407 (m5C1407) of 16S rRNA

lates Ser and Thr residues. Probably acts to suppress the effects of stress linked to accumulation of reactive oxygen species. Probably involved in th
ine 5'-phosphate (IMP) to xanthosine 5'-phosphate (XMP), the first committed and rate- limiting step in the de novo synthesis of guanine nucleotic

ase regulating citrate malate metabolism

nickel transport systems, permease

se that catalyzes the formation of 5-methyluridine at position 54 (m5U54) in all tRNAs, and that of position 341 (m5U341) in tmRNA (transfer-mR
oulose 5-phosphate to formate and 3,4-dihydroxy-2-butanone 4-phosphate

ogenase family

ase and related Zn-dependent dehydrogenases
tremities of branched DNA structures

from lauroyl-acyl carrier protein (ACP) to Kdo(2)-lipid IV(A) to form Kdo(2)- (lauroyl)-lipid IV(A)
ains using ADP-glucose

idase
es dsDNA breaks (DSB) for recombinational DNA repair. Binds to DSBs and unwinds DNA via a highly rapid and processive ATP-dependent bidirecti

uC
sation of isopentenyl diphosphate (IPP) with (2E,6E)-farnesyl diphosphate (E,E-FPP) to yield (2Z,6Z,10Z,14Z,18Z,22Z,26Z,30Z,34E,38E)-undecapren
elated to metalloendopeptidases

g proteins, it binds directly to 16S rRNA where it nucleates assembly of the head domain of the 30S subunit. Is located at the subunit interface clos
on of motility
hosphocoenzyme-A synthase
alyzing the conversion of glyoxal to glycolate
dependent transport system permease family
biotin carboxylase subunit of the acetyl CoA carboxylase, an enzyme that catalyzes the formation of malonyl-CoA, which in turn controls the rate of
JF979)
rects the termination of translation in response to the peptide chain termination codons UGA and UAA
f an aspartic acid residue of ribosomal protein S12
peptide repeat family
family. NudJ subfamily
ogenase family
ily
pathway recombination

amily
mma-phosphate of ATP to D-galactose to form alpha-D-galactose-1-phosphate (Gal-1-P)
l phosphate from acetate and ATP. Can also catalyze the reverse reaction
which encodes the E.coli common pilus (ECP). ECP is found in both commensal and pathogenic strains and plays a dual role in early-stage biofilm c
yme with beta-cystathionase and maltose regulon repressor activities
ctivity

erase (Dam)

orin family

robic degradation of long-chain fatty acids via beta-oxidation cycle. Catalyzes the formation of 3-oxoacyl-CoA from enoyl-CoA via L-3-hydroxyacyl-C
tate to pyruvate. Is coupled to the respiratory chain
l reactions in the de novo biosynthetic pathway for UDP-N-acetylglucosamine (UDP- GlcNAc). The C-terminal domain catalyzes the transfer of ace
NADH, via FMN and iron- sulfur (Fe-S) centers, to quinones in the respiratory chain. The immediate electron acceptor for the enzyme in this species
transport system, permease component II

es involved in the de novo synthesis of purine nucleotides, regulating purB, purC, purEK, purF, purHD, purL, purMN and guaBA expression. PurR is a

ATP to D-glycero-beta-D- manno-heptose 1-phosphate, yielding ADP-D-glycero-beta-D-manno- heptose
ra4N moiety of the glycolipid undecaprenyl phosphate-alpha-L-Ara4N to lipid A. The modified arabinose is attached to lipid A and is required for re

phosphoenolpyruvate (PEP) and D-erythrose-4-phosphate (E4P) giving rise to 3-deoxy-D- arabino-heptulosonate-7-phosphate (DAHP)
n an aerobic process, termed nitric oxide dioxygenase (NOD) reaction that utilizes O(2) and NAD(P)H to convert NO to nitrate, which protects the l
ubunit ArtQ

in

; the transfer of the FMN moiety of FAD and its covalent binding to the hydroxyl group of a threonine residue in a target flavoprotein
UF386)
bonate transport system permease component
regulatory system ZraS ZraR. May function as a membrane-associated protein kinase that phosphorylates ZraR in response to high concentrations
horylation of adenosylcobinamide and addition of GMP to adenosylcobinamide phosphate
sose (2-keto-myo- inositol, 2KMI or 2,4,6 3,5-pentahydroxycyclohexanone) to 3D- (3,5 4)-trihydroxycyclohexane-1,2-dione (D-2,3-diketo-4-deoxy-ep
oration of lipoproteins in the outer membrane after they are released by the LolA protein
nocysteine from O- succinyl-L-homoserine (OSHS) and hydrogen sulfide
or chromosome segregation. It relaxes supercoiled DNA. Performs the decatenation events required during the replication of a circular DNA molecu

o avoid such errors, it has a posttransfer editing activity that hydrolyzes mischarged Thr-tRNA(Val) in a tRNA-dependent manner

esis of the corrin ring for the assimilation of exogenous corrinoids. Participates in the adenosylation of a variety of incomplete and complete corrir
genase

ter (DMT) superfamily

JF2560)

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

7K

bosomes from messenger RNA at the termination of protein biosynthesis. May increase the efficiency of translation by recycling ribosomes from

ase
me A carboxylase (ACC) complex. First, biotin carboxylase catalyzes the carboxylation of biotin on its carrier protein (BCCP) and then the CO(2) gro
presence of ATP renatures cruciform structure in supercoiled DNA with palindromic sequence, indicating that it may promote strand exchange reac

ase, NADP-dependent

ıte

nine ligase family
plex MalEFGK involved in maltose maltodextrin import. Responsible for energy coupling to the transport system
f the hydroxyl group of 4-methyl-5-beta-hydroxyethylthiazole (THZ)
y

smoregulated periplasmic glucans (OPGs)

t reduction of 7-cyano-7- deazaguanine (preQ0) to 7-aminomethyl-7-deazaguanine (preQ1)
se complex. Interacts with the SecYEG preprotein conducting channel. SecDF uses the proton motive force (PMF) to complete protein translocatio

plex BtuCDF involved in vitamin B12 import. Involved in the translocation of the substrate across the membrane

nt component of the zinc- balancing mechanism

oyl-CoA and pNP-butyrate in vitro

dependent transport system permease family. FecCD subfamily

ndent sugar phosphotransferase system (PTS), a major carbohydrate active transport system, catalyzes the phosphorylation of incoming sugar subs
ivatives
resence of a proton gradient across the membrane
JF1062)
tures. These structures can inhibit DNA replication and are intermediates in certain DNA recombination reactions. The complex acts as a 3'- 5' dou
ain protein
phosphoenolpyruvate (PEP) and D-erythrose-4-phosphate (E4P) giving rise to 3-deoxy-D- arabino-heptulosonate-7-phosphate (DAHP)

n
of a CheY-like receiver domain and a winged-helix DNA-binding domain
JF1471)
se family

ge of the glycosidic bond in both 5'-methylthioadenosine (MTA) and S- adenosylhomocysteine (SAH AdoHcy) to adenine and the corresponding thio

transferase family
superfamily
omerase family
replication forks. Recognizes and binds the arrested nascent DNA chain at stalled replication forks. It can open the DNA duplex, via its helicase act

amily
nase family

protein PtsN

olysaccharide (LPS). Required for the translocation of LPS from the inner membrane to the outer membrane. Facilitates the transfer of LPS from t

ase regulating citrate malate metabolism
drogenases reductases (SDR) family

natic amino acids metabolism

toxin-antitoxin (TA) system. Neutralizes the toxic effect of cognate toxin HipA. Also neutralizes the toxic effect of non- cognate toxin YjjJ. Binds to

NADH, via FMN and iron- sulfur (Fe-S) centers, to quinones in the respiratory chain. The immediate electron acceptor for the enzyme in this species
opentenyl diphosphate (IPP) and dimethylallyl diphosphate (DMAPP), two major building blocks of isoprenoid compounds. Catalyzes the conversion
antoate with beta-alanine in an ATP-dependent reaction via a pantoyl-adenylate intermediate
r from carboxy-S- adenosyl-L-methionine (Cx-SAM) to 5-hydroxyuridine (ho5U) to form 5-carboxymethoxyuridine (cmo5U) at position 34 in tRNAs
ng protein

phoribosylamine from phosphoribosylpyrophosphate (PRPP) and glutamine

cetyltransferases, isoleucine patch superfamily
plex ZnuABC involved in zinc import. Responsible for energy coupling to the transport system
4-epimerase and related epimerases and aldolases
ining a DNA-binding HTH domain and an aminotransferase domain (MocR family) and their eukaryotic orthologs

family. ArgE subfamily
-ribazole-5'-phosphate from nicotinate mononucleotide (NAMN) and 5,6- dimethylbenzimidazole (DMB)

ductase laccase
enosylmethionine (AdoMet) from methionine and ATP. The overall synthetic reaction is composed of two sequential steps, AdoMet formation and
ily

f proteins. It catalyzes the cis-trans isomerization of proline imidic peptide bonds in oligopeptides

n which is capable of wrapping DNA to stabilize it, and thus to prevent its denaturation under extreme environmental conditions
cific
te hydrogenlyase system which is involved in the cleaving of formate to dihydrogen and carbon dioxide

ase HPA2 and related acetyltransferases

ily

pendent hydrolase

ein
lioxide

tween ADP-D-glycero- beta-D-manno-heptose and ADP-L-glycero-beta-D-manno-heptose via an epimerization at carbon 6 of the heptose
nation in some periplasmic proteins. Acts by transferring its disulfide bond to other proteins and is reduced in the process

alginate biosynthesis
nal protein uS9 family

tion of fatty acid synthesis by the addition to an acyl acceptor of two carbons from malonyl-ACP

ivatives
gement of the homoallylic substrate isopentenyl (IPP) to its highly electrophilic allylic isomer, dimethylallyl diphosphate (DMAPP)
e. Important to control the intracellular level of arginine and the correct balance between arginine and lysine

protein dioxygenase

rsional tension of DNA, which is introduced during the DNA replication and transcription, by transiently cleaving and rejoining one strand of the DN

phores transport systems, ATPase components

ent site

ıctases, Old Yellow Enzyme family
transcriptional regulator

ıhosphocytidyl-2-C- methyl-D-erythritol from CTP and 2-C-methyl-D-erythritol 4- phosphate (MEP)
L and C5 carbon atoms of pentose
ɔrylytic cleavage of uridine and deoxyuridine to uracil and ribose- or deoxyribose-1- phosphate. The produced molecules are then utilized as carbon

ım from selenophosphate for conversion of 2-thiouridine to 2-selenouridine at the wobble position in tRNA

ıferase TrmD family
te-sugar epimerases

cific
synthase family

e 8 (cellulase D) family
natic function

lay link together the upstream cell division proteins, which are predominantly cytoplasmic, with the downstream cell division proteins, which are p
tamine synthetase GlnA, a key enzyme in the process to assimilate ammonia. When cellular nitrogen levels are high, the C-terminal adenylyl trans
ase family

ıte reductase family

nate aldolase
ion by proteins MinC and MinD at internal division sites while permitting inhibition at polar sites. This ensures cell division at the proper site by res
rminal domain
sporter substrate-binding protein
amine metabolism, converting fructose-6P into glucosamine-6P using glutamine as a nitrogen source
tion of 2'-deoxyuridine- 5'-monophosphate (dUMP) to 2'-deoxythymidine-5'-monophosphate (dTMP) while utilizing 5,10-methylenetetrahydrofolat
pyridoxine 5'- phosphate (PNP) or pyridoxamine 5'-phosphate (PMP) into pyridoxal 5'-phosphate (PLP)
dehydrogenases family
anscription, elongation
se superfamily
ylase and related regulatory proteins (some contain LysM invasin domains)

n protein (MFP) (TC 8.A.1) family

e family
f N-acetyl-D-glucosamine (GlcNAc) derived from cell-wall degradation, yielding GlcNAc-6-P

IIA component
ion of L-isoaspartyl residues in peptides and proteins that result from spontaneous decomposition of normal L-aspartyl and L-asparaginyl residues.
ine (Q) precursors, required for Q precursor salvage

ethyl-uridine at position 1939 (m5U1939) in 23S rRNA
mily

rase
ivated derivatives IS5 family
on proton antiporter 2 (CPA2) transporter (TC 2.A.37) family
rane lipoprotein
mplex catalyzes the overall conversion of pyruvate to acetyl-CoA and CO(2)

ter (DMT) superfamily
o transfer from one phosphatidylglycerol molecule to another to form cardiolipin (CL) (diphosphatidylglycerol) and glycerol
t sugar phosphotransferase system
2-hydroxyacid dehydrogenase family
JF4056)

regulation

ransporter complex to transport maltose into the cell by using ATP hydrolysis
stem, permease component

n of O-acetyl groups into the enterobacterial common antigen (ECA) trisaccharide repeat units

at
rofolate cyclo-ligase family
xidase family

oles Fe-S clusters. It is likely that Fe-S cluster coordination is flexible as the role of this complex is to build and then hand off Fe-S clusters

lay link together the upstream cell division proteins, which are predominantly cytoplasmic, with the downstream cell division proteins, which are p
em for branched-chain amino acids

superfamily
l family
ry for DNA synthesis. Catalyzes the biosynthesis of deoxyribonucleotides from the corresponding ribonucleotides
septation
ymerase transcription elongation past template-encoded arresting sites. The arresting sites in DNA have the property of trapping a certain fraction
k in the DNA. It binds to the single-stranded DNA and acts in a progressive fashion along the DNA in the 3' to 5' direction

e
Thought to form the channel of an arsenite pump
-mannose dehydrogenase family
JF2946)

bosomes mediated by trans-translation. Binds to transfer-messenger RNA (tmRNA), required for stable association of tmRNA with ribosomes. tm

osphorylation of L- homoserine to L-homoserine phosphate
ly

a guanine (G) residue with the queuine precursor 7-aminomethyl-7-deazaguanine (PreQ1) at position 34 (anticodon wobble position) in tRNAs wit
the formation of polar Z ring septums. Rapidly oscillates between the poles of the cell to destabilize FtsZ filaments that have formed before they

otake of glycerol-3-phosphate

n protein (MFP) (TC 8.A.1) family

l-tRNA synthetase family
JF2594)
family

n detecting D-amino acids in the active site. By recycling D-aminoacyl-tRNA to D-amino acids and free tRNA molecules, this enzyme counteracts tl

zes the epimerization of the S- and R-forms of NAD(P)HX and the dehydration of the S-form of NAD(P)HX at the expense of ADP, which is converte
NADH, via FMN and iron- sulfur (Fe-S) centers, to quinones in the respiratory chain. The immediate electron acceptor for the enzyme in this species
on termination release factors RF1 PrfA and RF2 PrfB on the glutamine residue of the universally conserved GGQ motif
yme family
hydrouridine (D), a modified base found in the D-loop of most tRNAs, via the reduction of the C5-C6 double bond in target uridines. Specifically mc

plex SsuABC involved in aliphatic sulfonates import. Responsible for energy coupling to the transport system
AD and rhaT operons
L-alanine and D- alanine. May also act on other amino acids
ne-like degradation complex believed to be a general protein degrading machinery
nosine in position 1516 of 16S rRNA
ansport of beta-methylgalactoside

methylguanine at position 46 (m7G46) in tRNA

iH operons and other genes involved in the transport and catabolism of L-arabinose
ine to tRNA(Ser). Is also able to aminoacylate tRNA(Sec) with serine, to form the misacylated tRNA L-seryl-tRNA(Sec), which will be further conve
dependent transport system permease family. FecCD subfamily
ng domain protein
complex and induces the exchange of GDP to GTP. It remains bound to the aminoacyl-tRNA.EF- Tu.GTP complex up to the GTP hydrolysis stage on
superfamily
omal termination complexes and stimulates activities of RF-1 and RF-2. It binds guanine nucleotides and has strong preference for UGA stop codc

inding protein 3 family

L-alanine and D- alanine. May also act on other amino acids
in synthesis. Acts as a proofreading enzyme that prevents EntB misacylation by hydrolyzing the thioester bound existing between EntB and wrongl
that removes nucleotide residues following the -CCA terminus of tRNA and adds nucleotides to the ends of RNA molecules by using nucleoside dip

n YhjQ
ining a DNA-binding HTH domain and an aminotransferase domain (MocR family) and their eukaryotic orthologs
sporters with duplicated ATPase domains

the hydrolysis of nucleoside triphosphates to their monophosphate derivatives, with a high preference for the non-canonical purine nucleotides XT

ily. 5-hydroxyisourate hydrolase subfamily

P-fucosamine (dTDP-4- amino-4,6-dideoxy-D-galactose) to dTDP-Fuc4NAc, which is utilized in the biosynthesis of the enterobacterial common ant

binding protein 3 family
n

eriplasmic molybdate-binding protein
IF87
protection, which is important for survival of enteric bacteria in the acidic environment of the host stomach. Exhibits a chaperone-like activity at a

t activation of glutamate in presence of ATP and the subsequent transfer of glutamate onto a tRNA(Asp). Glutamate is transferred on the 2-aminc
cule, which serves as a redox-active prosthetic group

oxy-D-arabino- heptulosonate 7-phosphate (DAHP) to dehydroquinate (DHQ)
avy metals
ved in cell-shape control through regulation of the length of the long axis

A protein (GPA)
amily
t contain T G mispairs resulting from m5C-deamination

ɔgenase family

domain
ɪnt activation of exogenously supplied lipoate to lipoyl-AMP and the transfer of the activated lipoyl onto the lipoyl domains of lipoate-dependent er

osamine-6-phosphate to glucosamine-1-phosphate
e, 20
ɛin-NADPH reductases) family 1

ɔosition of cytidine in position 1402 (C1402) of 16S rRNA
ɔndensation of pimeloyl- acyl-carrier protein and L-alanine to produce 8-amino-7- oxononanoate (AON), acyl-carrier protein , and carbon dioxide

ɲe balance of metabolites in the pentose-phosphate pathway
y to utilize trehalose at high osmolarity by splitting it into glucose molecules that can subsequently be taken up by the phosphotransferase-mediat
ɔolysaccharide (LPS). Required for the translocation of LPS from the inner membrane to the outer membrane. May form a bridge between the inne
ʂpecificities (Related to short-chain alcohol dehydrogenases)
transcriptional regulator
ɪmily

ʏlation of 1,6-anhydro-N- acetylmuramic acid (anhMurNAc) with the simultaneous cleavage of the 1,6-anhydro ring, generating MurNAc-6-P. Is req
ɔr (ECF) transporter complex CbiMNOQ involved in cobalt import

uction of ubiquinone-1 to ubiquinol by two successive reactions, coupled with the transport of Na( ) ions from the cytoplasm to the periplasm. NqrA

3'-diphosphate 5-' diphosphate) is a mediator of the stringent response that coordinates a variety of cellular activities in response to changes in n
for small oligoribonucleotides

ining a DNA-binding HTH domain and an aminotransferase domain (MocR family) and their eukaryotic orthologs
in

polysaccharide (LPS)

ved in bacteria (DUF2184)
ine in position 1618 of 23S rRNA
rt protein
f pyruvate to phosphoenolpyruvate

tion between acetaldehyde and D-glyceraldehyde 3-phosphate to generate 2-deoxy- D-ribose 5-phosphate

receptor proteins that carry out high-affinity binding and energy dependent uptake into the periplasmic space of specific substrates. It could act to

ygenase and related ring-hydroxylating dioxygenases, large terminal subunit

ription. Plays a direct role in upstream activation of rRNA promoters
n metabolic process

te dehydrogenase complex, dihydrolipoamide dehydrogenase (E3) component, and related enzymes
tein assembly complex, which is involved in assembly and insertion of beta-barrel proteins into the outer membrane
in
ivatives
te and the transport of protons into the cell
ptosyltransferase)
sion of L-rhamnose

insertion of two sulfur atoms into the C-6 and C-8 positions of the octanoyl moiety bound to the lipoyl domains of lipoate-dependent enzymes, ther
that catalyzes intramembrane proteolysis

s of L-ascorbate-6-P into 3-keto-L-gulonate-6-P. Is essential for L-ascorbate utilization under anaerobic conditions
binding protein 3 family

system, which controls transcription of numerous genes. Binds, with RcsB, to the RcsAB box to regulate expression of genes
oxiredoxin

nase muconate lactonizing enzyme family
tase family

nsmembrane protein
dependent transport system permease family

denine ring of phosphoribosyl-AMP
ethyldihydropteridine pyrophosphokinase

ein (DUF2164)
dependent transport system permease family
tion of fatty acid synthesis by the addition to an acyl acceptor of two carbons from malonyl-ACP
, multichain enzyme responsible for most of the replicative synthesis in bacteria. This DNA polymerase also exhibits 3' to 5' exonuclease activity
hydrolysis of S-D- lactoyl-glutathione to form glutathione and D-lactic acid
g proteins. Required for association of the 30S and 50S subunits to form the 70S ribosome, for tRNA binding and peptide bond formation. It has be

keto-L-gulonate in the presence of NADH, to form 3-keto-L-gulonate

into sirohydrochlorin
alyzes the SAM-dependent methylations of uroporphyrinogen III at position C-2 and C-7 to form precorrin-2 via precorrin-1. Then it catalyzes the N
ssembly proteins of the 50S ribosomal subunit, although it is not seen to bind rRNA by itself. It is important during the early stages of 50S assemb

reductase 4Fe-4S domain family
L,P4-tetraphosphate to yield ADP
JF1176)

oxidoreductase 2 family. FRD SDH subfamily
imerases
ng protein
ein
ase family

ent of type IV transporter system

ds biosynthesis. Catalyzes the dehydration of short chain beta-hydroxyacyl-ACPs and long chain saturated and unsaturated beta-hydroxyacyl-ACPs
tein assembly complex, which is involved in assembly and insertion of beta-barrel proteins into the outer membrane
cofactor assembly chaperone
family
-ribulose 5-phosphate to D-xylulose 5-phosphate
onse to hyperosmotic and heat shock by preventing the aggregation of stress-denatured proteins, in association with DnaK and GrpE. It is the nucle
subunit and shifts the equilibrum between 70S ribosomes and their 50S and 30S subunits in favor of the free subunits, thus enhancing the availabi

c genes

ulating RssB activity, thereby increasing the stability of the sigma stress factor RpoS especially during phosphate starvation, but also in stationary p
e 13 family
se
1 IS1096 IS1165
d region
JF2496)
JF1382)
ptidoglycan cell wall
ng protein

se family

succinyl-CoA to L- homoserine, forming succinyl-L-homoserine

alyzes the degradation of glycine. The P protein binds the alpha-amino group of glycine through its pyridoxal phosphate cofactor
ıtion of the intracellular concentration of adenosylhomocysteine
domain
high affinity leucine transport

at activates septal peptidoglycan synthesis and constriction of the cell. Acts on both sides of the membrane, via interaction with FtsA in the cytopla
ydroperoxidase activity. Required for the reduction of the AhpC active site cysteine residues and for the regeneration of the AhpC enzyme activity
ansferase
JF416)

n translocation channel SecYEG. Consists of two halves formed by TMs 1-5 and 6-10. These two domains form a lateral gate at the front which op
udouridine from uracil- 13 in transfer RNAs

concentration in the cell, thus reducing its toxicity
coupling to the transport system
genes
lator

replication inititator protein DnaA with DNA polymerase subunit beta sliding clamp (dnaN). Stimulates hydrolysis of ATP-DnaA to ADP-DnaA, renc
ependent oxidations of L- histidinol to L-histidinaldehyde and then to L-histidine

e that releases amino acids sequentially from the C-terminus, including neutral, aromatic, polar and basic residues

olases including oxidative damage repair enzymes

nversion of 5- aminoimidazole ribonucleotide (AIR) and HCO(3)(-) to N5- carboxyaminoimidazole ribonucleotide (N5-CAIR)
ocess

erine proteases inhibits chymotrypsin, trypsin, elastases, factor X, kallikrein as well as a variety of other proteases

JF2766)
essivity to DNA polymerases and other proteins. Acts as a clamp, forming a ring around DNA (a reaction catalyzed by the clamp-loading complex) v

plex CysAWTP involved in sulfate thiosulfate import. Responsible for energy coupling to the transport system

on. Could contribute to adhesion to various surfaces in specific environmental niches. Increases adhesion to eukaryotic T24 bladder epithelial cells
ndent sugar phosphotransferase system (sugar PTS), a major carbohydrate active transport system, catalyzes the phosphorylation of incoming suga
ssibly also in glycerophospholipid export and for biogenesis of the outer membrane. Transmembrane domains (TMD) form a pore in the inner mer

tein assembly complex, which is involved in assembly and insertion of beta-barrel proteins into the outer membrane
e protein/Dioxygenase superfamily
ng protein

JF554)
n protein

zes the enolization of 2,3-diketo-5-methylthiopentyl-1-phosphate (DK-MTP-1-P) into the intermediate 2-hydroxy-3-keto-5-methylthiopentenyl-1-ph

ltH
fur to a number of partners involved in Fe-S cluster assembly, tRNA modification or cofactor biosynthesis. Catalyzes the removal of elemental sulf

ge of the D-lactyl ether substituent of MurNAc 6-phosphate, producing GlcNAc 6- phosphate and D-lactate. Together with AnmK, is also required f
olex that catalyzes the two-step biosynthesis of anthranilate, an intermediate in the biosynthesis of L-tryptophan. In the first step, the glutamine- b
ation of adenine to hypoxanthine. Plays an important role in the purine salvage pathway and in nitrogen catabolism
onate-4-phosphate to 3- hydroxy-2-oxo-4-phosphonooxybutanoate

ved in uptake of microcin J25
stem, permease component
protein

from lauroyl-acyl carrier protein (ACP) to Kdo(2)-lipid IV(A) to form Kdo(2)- (lauroyl)-lipid IV(A)
plex LolCDE involved in the translocation of
ment of Und-PP-GlcNAc- ManNAcA-Fuc4NAc (lipid III) from the inner to the outer leaflet of the cytoplasmic membrane during the assembly of en
ohobic membrane anchor subunit

bdopterin-containing oxidoreductase family

recognition step. This protein has a weak ATPase activity

this protein can use glutamate, 2-aminobutyrate, and aspartate as amino donors and pyruvate as the acceptor'

-phosphate dehydrogenase family
riety of RNA species, leaving a one or two nucleotide 3' overhang. Responsible for the end-turnover of tRNA specifically removes the terminal AM

otein

ATP to form Asp-AMP and then transferred to the acceptor end of tRNA(Asp)
dependent transport system permease family. FecCD subfamily
which encodes the E.coli common pilus (ECP). ECP is found in both commensal and pathogenic strains and plays a dual role in early-stage biofilm c
ine in position 1207 of 16S rRNA in the 30S particle

ole in the late steps of ribosome biogenesis

-tRNA synthetase family
se complex. Interacts with the SecYEG preprotein conducting channel. Has a central role in coupling the hydrolysis of ATP to the transfer of proteir
ain protein

ɔgenase family

ıctases, Old Yellow Enzyme family

CbiG

different specificities (related to short-chain alcohol dehydrogenases)
ogenase fumarate reductase iron-sulfur protein family

H-dependent deamination of GMP to IMP. It functions in the conversion of nucleobase, nucleoside and nucleotide derivatives of G to A nucleotides,

erfamily

ɔn proton antiporter 2 (CPA2) transporter (TC 2.A.37) family

drogenases reductases (SDR) family

oxidation of L-threonine to 2-amino-3-ketobutyrate
amily

llosteric enzyme in carbohydrate metabolism. Enzymes from different sources differ in their regulatory mechanisms and in their natural substrate

nally produced within the cells and which are toxic to biological systems
ase
proteins
yl phosphate group from 5-phosphoribose 1-diphosphate to orotate, leading to the formation of orotidine monophosphate (OMP)
amily

ily

PRFAR and glutamine to IGP, AICAR and glutamate. The HisF subunit catalyzes the cyclization activity that produces IGP and AICAR from PRFAR u

mbly. Latches the N- and C- terminal regions of the beta' subunit thereby facilitating its interaction with the beta and alpha subunits
C 1.A.8) family

ter (DMT) superfamily

natase activity on nucleoside 5'-monophosphates
Pase hydrolysis rate. Involved in the addition of a carboxymethylaminomethyl (cmnm) group at the wobble position (U34) of certain tRNAs, formin

me condensation, segregation and cell cycle progression. Functions as a homodimer, which is essential for chromosome partition. Involved in nega
superfamily
volved in electron transport
dependent transport system permease family

dependent transport system permease family. FecCD subfamily
mily
nal protein bL27 family

(P)-binding

ein

aride biosynthesis

AD superfamily, subfamily IC
osine to tRNA(Tyr) in a two-step reaction tyrosine is first activated by ATP to form Tyr- AMP and then transferred to the acceptor end of tRNA(Tyr)
positions 38, 39 and 40 in the anticodon stem and loop of transfer RNAs

amily
coupling to the transport system

nsferase

e. Down-regulates ribonuclease 3 (RNase III) activity. Acts by interacting directly with the region of the ribonuclease that is required for dimerizat

e family. YpeA subfamily

y hydrolytic cleavage of the phosphopantetheine prosthetic group from ACP
proteins which control the phase variation of type 1 fimbriae in E.coli. These proteins mediate the periodic inversion of a 300bp DNA segment that
yltransferase
xclusion protein
ity. The binding of ATP and its subsequent hydrolysis by HslU are essential for unfolding of protein substrates subsequently hydrolyzed by HslV. Hsl

y

rearrangement and reduction of 1-deoxy-D-xylulose-5-phosphate (DXP) to 2-C-methyl-D-erythritol 4-phosphate (MEP)
enocysteinyl-tRNA(Sec) required for selenoprotein biosynthesis
imercaptal, formed from methylglyoxal and glutathione, to S-lactoylglutathione
dependent transport system permease family

unit IV

sorbose family IID component

nine in position 37 of tRNA(1)(Val) (anticodon cmo5UAC)

ry for DNA synthesis. Catalyzes the biosynthesis of deoxyribonucleotides from the corresponding ribonucleotides
phosphate to yield (R)-1-amino-2-propanol O-2-phosphate, the precursor for the linkage between the nucleotide loop and the corrin ring in cobala
ion reaction between C atoms 2 and 3 of pyruvate and glyceraldehyde 3-phosphate to yield 1-deoxy-D-xylulose-5-phosphate (DXP)
thylthioribulose-1- phosphate (MTRu-1-P) into 2,3-diketo-5-methylthiopentyl-1- phosphate (DK-MTP-1-P)
e

ndent sugar phosphotransferase system (PTS), a major carbohydrate active - transport system, catalyzes the phosphorylation of incoming sugar sul
UF3156)
UF4041)
e

d phospholipid phosphatase
mily
ved in resistance to organic solvents periplasmic component
of the ribose of cytidine 1402 (C1402) in 16S rRNA

orphyrinogen-III oxidase family
ate to pyruvate

ved in resistance to organic solvents auxiliary component

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

se complex catalyzes the overall conversion of 2-oxoglutarate to succinyl-CoA and CO(2)
plex PotABCD involved in spermidine putrescine import. Responsible for energy coupling to the transport system

e of ATP to the 4'-position of a tetraacyldisaccharide 1-phosphate intermediate (termed DS-1- P) to form tetraacyldisaccharide 1,4'-bis-phosphate
ne export of O-antigen and teichoic acid

mponent

SecG

alyzes the cleavage of a C-N bond in choline, producing trimethylamine (TMA) and acetaldehyde

-phosphate dehydrogenase family
ystem, permease component
CheY-like receiver domain and an HTH DNA-binding domain

nase muconate lactonizing enzyme family

sation, segregation and cell cycle progression. May participate in facilitating chromosome segregation by condensation DNA from both sides of a c
nsport system, periplasmic component
NADH, via FMN and iron- sulfur (Fe-S) centers, to quinones in the respiratory chain. The immediate electron acceptor for the enzyme in this species
naperone system, it is involved in the recovery of the cell from heat-induced damage, in cooperation with DnaK, DnaJ and GrpE
s the carboxylation of the carrier protein and then the transcarboxylase transfers the carboxyl group to form malonyl-CoA

nate 1-epimerase family
edoheptulose 7-phosphate in D-glycero-D-manno-heptose 7-phosphate

hage_pRha)
nate semialdehyde to D- glycerate

nase and phosphorylase involved in the regulation of the phosphoenolpyruvate synthase (PEPS) by catalyzing its phosphorylation dephosphorylation
bdopterin-containing oxidoreductase family

ved in the assembly of the Z ring. May serve as a membrane anchor for the Z ring
ry for DNA synthesis. Catalyzes the biosynthesis of deoxyribonucleotides from the corresponding ribonucleotides
S-50S ribosomal subunit interface and may play a role in the structure and function of the aminoacyl-tRNA binding site

es dsDNA breaks (DSB) for recombinational DNA repair. Binds to DSBs and unwinds DNA via a highly rapid and processive ATP-dependent bidirecti
nidation of the two carboxylate groups at positions a and c of hydrogenobyrinate, using either L-glutamine or ammonia as the nitrogen source

x
rminal alanine of ribosomal protein S18
cbD
which encodes the E.coli common pilus (ECP). ECP is found in both commensal and pathogenic strains and plays a dual role in early-stage biofilm c

oxylase

r chromosome segregation. It relaxes supercoiled DNA. Performs the decatenation events required during the replication of a circular DNA molecu

niS
l-dephospho-CoA transferase
e 2 family

of aspartate carbamoyltransferase
ter (DMT) superfamily

iption of the flagellar master operon flhDC by binding to the upstream region of the operon
ng protein

l-phosphate-dependent aminotransferase family

es sodium in exchange for external protons
ɔgenase family

DNA which can arise as a result of misincorporation of dUMP residues by DNA polymerase or due to deamination of cytosine
bunit

ıetal-dependent proteases
. in cobalt-precorrin-5B to form cobalt-precorrin-6A
ɔhosphoenolpyruvate (PEP) and D-erythrose-4-phosphate (E4P) giving rise to 3-deoxy-D- arabino-heptulosonate-7-phosphate (DAHP)
se
at forms a contractile ring structure (Z ring) at the future cell division site. The regulation of the ring assembly controls the timing and the location
amily IA, variant 3

ribosomal protein L3 on a specific glutamine residue

on of alpha-ketobutyrate and ammonia from threonine in a two-step reaction. The first step involved a dehydration of threonine and a production
ıponent of the respiratory chain that catalyzes the reduction of oxygen to water. Subunits 1- 3 form the functional core of the enzyme complex. CO

TAS domain)
ızyme may be peptidyl- tRNAs which drop off the ribosome during protein synthesis

ining a DNA-binding HTH domain and an aminotransferase domain (MocR family) and their eukaryotic orthologs
related transporters (MFS superfamily)
e

ara-aminobenzoate (pABA) with 6-hydroxymethyl-7,8-dihydropterin diphosphate (DHPt-PP) to form 7,8-dihydropteroate (H2Pte), the immediate pr

etyl-D-glucosamine and N-acetyl-D-glucosamine-6-phosphate from diacetylchitobiose-6-phosphate
a number of redox enzymes
irst charging a glutamine molecule by linking its carboxyl group to the alpha-phosphate of ATP, followed by transfer of the aminoacyl-adenylate to

g proteins, it binds specifically to the 5'-end of 16S ribosomal RNA
e family. ArgA subfamily
rmation of phosphodiester linkages between 5'-phosphoryl and 3'-hydroxyl groups in double-stranded DNA using NAD as a coenzyme and as the er
t 6 family
family IIA
yzes the recognition and processing of DNA lesions. UvrA is an ATPase and a DNA-binding protein. A damage recognition complex composed of 2 U
and alpha-ribazole to generate adenosylcobalamin (Ado-cobalamin). Also synthesizes adenosylcobalamin 5'-phosphate from adenosylcobinamide-
n the TIM-barrel fold

d in
ration of iron-sulfur cluster-containing proteins. Has a low intrinsic ATPase activity which is markedly stimulated by HscB. Involved in the maturatic
ation-cell division (RND) (TC 2.A.6) family
on of fumarate to (S)- malate
UF2534)
n which is capable of wrapping DNA to stabilize it, and thus to prevent its denaturation under extreme environmental conditions

elated to metalloendopeptidases

plex BtuCDF involved in vitamin B12 import. Binds vitamin B12 and delivers it to the periplasmic surface of BtuC
e

osition of the uracil ring of uridine 1498 (m3U1498) in 16S rRNA. Acts on the fully assembled 30S ribosomal subunit
nt hydrolases superfamily. Urease alpha subunit family

nine monomethyl esterification of trans-aconitate
n

amily IA, variant 3
rase (Adenine-specific)
mily

acid oxidation in which acetyl-CoA is released and the CoA ester of a fatty acid two carbons shorter is formed
t reduction of glutamyl- tRNA(Glu) to glutamate 1-semialdehyde (GSA)

alyzes the degradation of glycine

ndary membrane with the concomitant uptake of a sodium ion (symport system)
e NRAMP family
PRFAR and glutamine to IGP, AICAR and glutamate. The HisH subunit provides the glutamine amidotransferase activity that produces the ammor
in

sine at position 967 (m5C967) of 16S rRNA
mease

e 1 family
catalytic activity of PanD in a coenzyme A (CoA)-dependent fashion
RNA and is necessary for the in vitro assembly process of the 50S ribosomal subunit. It is not involved in the protein synthesizing functions of that
on of protein synthesis but also for the initiation of all mRNA translation through initiator tRNA(fMet) aminoacylation
ily

bacterial periplasmic transport system of putrescine
at

transcriptional regulator

ily

subunit
se via the functional incorporation of the urease nickel metallocenter
pair of mismatches in DNA. It is required for dam-dependent methyl-directed DNA mismatch repair. May act as a molecular matchmaker , a prote
-alanyl-gamma-D- glutamyl-meso-diaminopimelate by linking it to UDP-N- acetylmuramate
he lipid A domain of lipopolysaccharides (LPS). Transfers a phosphate group from undecaprenyl pyrophosphate (C55-PP) to lipid A to form lipid A 1
family IA, variant 3

osphohydrolase
sferase I
lipoprotein (PulS_OutS)
g metabolite transporter (DMT) superfamily

de

phosphate transport system ATPase component
nvolved in molybdopterin and thiamine biosynthesis family 1
nicotinate D- ribonucleotide from nicotinate and 5-phospho-D-ribose 1-phosphate at the expense of ATP

gF Family
glucosamine and 2,3- diacylglucosamine-1-phosphate to form lipid A disaccharide, a precursor of lipid A, a phosphorylated glycolipid that anchors t

and related esterases
bonate transport system permease component

g metabolite transporter (DMT) superfamily
ogenase family
of a malonyl-thioester to its methyl ester by transfer of a methyl group from S-adenosyl- L-methionine (SAM). It allows to synthesize pimeloyl-AC
bdopterin-containing oxidoreductase family

e of azo bond in aromatic azo compounds to the corresponding amines. Requires NADH, but not NADPH, as an electron donor for its activity
e cystathionine beta- synthase family

nine to tRNA(Ala) in a two-step reaction alanine is first activated by ATP to form Ala- AMP and then transferred to the acceptor end of tRNA(Ala).

r of the carbamoyl group from carbamoyl phosphate (CP) to the N(epsilon) atom of ornithine (ORN) to produce L-citrulline
ein
orsional tension of DNA, which is introduced during the DNA replication and transcription, by transiently cleaving and rejoining one strand of the DN
ins it binds 23S rRNA. One of the proteins that surrounds the polypeptide exit tunnel on the outside of the ribosome. Forms the main docking site f

se

ylation of the 3-hydroxyl group of shikimic acid using ATP as a cosubstrate
olybdate-binding protein
se archaeal aspartate aminotransferase
artate to iminoaspartate
n initiation, which contributes to regulation of DNA replication and ensures that replication initiation occurs exactly once per chromosome per cell c

ubunit body where it stabilizes the conformation of the head with respect to the body

nidase
on of nascent membrane proteins into the cytoplasmic membrane. Binds to the hydrophobic signal sequence of the ribosome-nascent chain (RNC)
ng factor. Interacts with ribosomal protein L14 (rplN), blocking formation of intersubunit bridge B8. Prevents association of the 30S and 50S riboso
AlgR family
ne presents crystal structure similarity to a muconolactone isomerase, but does not seem to catalyze any of the
ein (DUF2303)

eoside-triphosphate reductase under anaerobic conditions by generation of an organic free radical, using S-adenosylmethionine and reduced flavoc
yl-tRNA synthetase family
gle or double-strand DNA
tion of correct disulfide bonds in some periplasmic proteins and for the assembly of the periplasmic c-type cytochromes. Acts by transferring elect
S, by affecting the processing and stability of the regulatory small RNA GlmZ. When glucosamine-6-phosphate (GlcN6P) concentrations are high ir
tein TusA family

catalyzes glycan chain elongation from lipid-linked precursors

transacylase

sual reaction, the ATP- dependent insertion of CO2 between the N7 and N8 nitrogen atoms of 7,8-diaminopelargonic acid (DAPA) to form an ureid
involved in ethanolamine utilization

l-tRNA synthetase family
NADH, via FMN and iron- sulfur (Fe-S) centers, to quinones in the respiratory chain. The immediate electron acceptor for the enzyme in this species

efflux pump

pression and that of the subsequent genes in the proximal part of the division and cell wall (dcw) gene cluster. Acts by binding directly to DNA. Ma
ring the final step in the assembly of 30S ribosomal subunit, possibly for assembly of the head region. Probably interacts with S19. Essential for ef
l-phosphate-dependent aminotransferase family

in LacI transcriptional regulator

ein

ase family
hesis that is essential for the function of penicillin-binding protein 1A (PBP1a)
phatidylethanolamine (PtdEtn) from phosphatidylserine (PtdSer)

dependent transport system permease family. FecCD subfamily

n of 2-acyl-glycero-3- phosphoethanolamine (2-acyl-GPE) into the cell
the biosynthesis of lipid A, a phosphorylated glycolipid that anchors the lipopolysaccharide to the outer membrane of the cell

e catalyzes the transcription of DNA into RNA using the four ribonucleoside triphosphates as substrates
ng protein
nine ligase family
. Succinylglutamate desuccinylase subfamily
ase complex that catalyzes the 6-electron reduction of sulfite to sulfide. This is one of several activities required for the biosynthesis of L- cysteine
resence of a proton gradient across the membrane. The catalytic sites are hosted primarily by the beta subunits
f ribose at O-5 in a reaction requiring ATP and magnesium. The resulting D-ribose-5- phosphate can then be used either for sythesis of nucleotides

se

of guanosine at position 18 in tRNA
pid A, a phosphorylated glycolipid that anchors the lipopolysaccharide to the outer membrane of the cell

76)
ydrogenase (PDH) complex, that catalyzes the overall conversion of pyruvate to acetyl-CoA and CO(2)

n protein (MFP) (TC 8.A.1) family
superfamily (MFS)

conuclease
t system ATPase component photorepair protein PhrA

ne addition of glutamate to the nucleotide precursor UDP-N-acetylmuramoyl-L-alanine (UMA)

ng protein
rane lipoprotein

gatively supercoils closed circular double-stranded (ds) DNA in an ATP-dependent manner to modulate DNA topology and maintain chromosomes i
otide metabolism it produces dUMP, the immediate precursor of thymidine nucleotides and it decreases the intracellular concentration of dUTP so
on oxidation of 3a-(2- amino-2-carboxyethyl)-4,5-dioxo-4,5,6,7,8,9-hexahydroquinoline- 7,9-dicarboxylic-acid to PQQ
present at position 34 of the AUA codon-specific tRNA(Ile) that contains the anticodon CAU, in an ATP-dependent manner. Cytidine is converted to

from XMP
sactions between iron acquisition and iron-requiring processes, such as synthesis and or repair of Fe-S clusters in biosynthetic enzymes

es dsDNA breaks (DSB) for recombinational DNA repair. Binds to DSBs and unwinds DNA via a highly rapid and processive ATP-dependent bidirecti
d DNA repair. Helps process Holliday junction intermediates to mature products by catalyzing branch migration. Has a DNA unwinding activity char
se complex. Interacts with the SecYEG preprotein conducting channel. SecDF uses the proton motive force (PMF) to complete protein translocatio
ain
se superfamily
ein is located near the polypeptide exit tunnel on the outside of the subunit, while an extended beta-hairpin is found that lines the wall of the exit
acylation. Transfers fatty acids to the 1-position via an enzyme-bound acyl-ACP intermediate in the presence of ATP and magnesium. Its physiologi

nate bicarbonate transport systems periplasmic components
f N6- (dimethylallyl)adenosine (i(6)A), leading to the formation of 2- methylthio-N6-(dimethylallyl)adenosine (ms(2)i(6)A) at position 37 in tRNAs
e stimulus

n, C terminal
oside triphosphates, with a preference for pyrimidine deoxynucleoside triphosphates (dUTP, dTTP and dCTP)

nickel transport systems, permease components

on of the C-3 phosphate and the C-6 proR hydrogen from 5-enolpyruvylshikimate-3-phosphate (EPSP) to yield chorismate, which is the branch point

iosphorylation of N-acetyl- L-glutamate

ssibly also in glycerophospholipid export and for biogenesis of the outer membrane. Transmembrane domains (TMD) form a pore in the inner mem
id metabolic process

diaminopimelic acid to the nucleotide precursor UDP-N-acetylmuramoyl-L-alanyl-D-glutamate (UMAG) in the biosynthesis of bacterial cell-wall pe
TP and 5-phosphoribose 1- diphosphate to form N'-(5'-phosphoribosyl)-ATP (PR-ATP). Has a crucial role in the pathway because the rate of histidir

- to 5'-direction to yield nucleoside 5'-phosphates
play a role in recycling of muropeptides during cell elongation and or cell division
it uptake of proteins
glycosyl groups

y 39
f proteins. It catalyzes the cis-trans isomerization of proline imidic peptide bonds in oligopeptides
mmonia-lyase

IF87

sual reaction, the ATP- dependent insertion of CO2 between the N7 and N8 nitrogen atoms of 7,8-diaminopelargonic acid (DAPA) to form an ureid

enously produced octanoic acid from octanoyl-acyl-carrier-protein onto the lipoyl domains of lipoate-dependent enzymes. Lipoyl-ACP can also act a
ding protein, which is involved in PLP homeostasis

mplex disassembly

binds to the 5S RNA in the ribosome where it forms part of the central protuberance

ulting in the formation of AMP, that is energically less costly than de novo synthesis
e assembly of 30S particles and may also be responsible for determining the conformation of the 16S rRNA at the A site
protein (HSP20) family
protein dioxygenase

acid phosphatase family

JF805)

ase complex that catalyzes the 6-electron reduction of sulfite to sulfide. This is one of several activities required for the biosynthesis of L- cysteine
When complexed with L- tryptophan it binds the operator region of the trp operon (5'- ACTAGT-'3') and prevents the initiation of transcription. The
ily
n protein (MFP) (TC 8.A.1) family

ired for cell wall biosynthesis
binds and probably mediates the attachment of the 5S RNA into the large ribosomal subunit, where it forms part of the central protuberance

plex BtuCDF involved in vitamin B12 import. Responsible for energy coupling to the transport system
nsport systems permease components
thiolation of cytidine in position 32 of tRNA, to form 2-thiocytidine (s(2)C32). The sulfur atoms are provided by the cysteine cysteine desulfurase (I
JF2511)
olicin uptake
orphyrin-containing compound
S)-aspartate-beta- semialdehyde (S)-ASA and pyruvate to 4-hydroxy- tetrahydrodipicolinate (HTPA)

NA, and is important in its secondary structure. It is located near the subunit interface in the base of the L7 L12 stalk, and near the tRNA binding si
s essential for cell division
ong preference for naked glycan strands that lack stem peptides
ohate group to glutamate to form L-glutamate 5-phosphate

t formation of L-aspartate- semialdehyde (L-ASA) by the reductive dephosphorylation of L- aspartyl-4-phosphate
transport system, permease component I

nal protein bL33 family
n NADH and NADP is coupled to respiration and ATP hydrolysis and functions as a proton pump across the membrane
methylated cytidine (Cm32) or 2'O-methylated uridine (Um32) at position 32 in tRNA

t transport of glutamate
unctions in thiamine biosynthesis along with thiFSGI and iscS
hydrogenase of

ein H-NS family
sation, segregation and cell cycle progression. May participate in facilitating chromosome segregation by condensation DNA from both sides of a
ane biogenesis

ves the D-alanyl-meso-2,6- diamino-pimelyl amide bond that connects peptidoglycan strands. Likely plays a role in the removal of murein from the
zes the oxidative decarboxylation of UDP-glucuronic acid (UDP-GlcUA) to UDP-4-keto- arabinose (UDP-Ara4O) and the addition of a formyl group t
hydrouridine (D), a modified base found in the D-loop of most tRNAs, via the reduction of the C5-C6 double bond in target uridines
cluding N-acetylases of ribosomal proteins
ıal protein bL32 family
phosphorylation of 2'- deoxyribonucleoside 5'-monophosphates
22 family
enance of cell shape
void such errors it has two additional distinct tRNA(Ile)-dependent editing activities. One activity is designated as 'pretransfer' editing and involves

e family. XerC subfamily
JF1454)

ıidine
e subunit
inding protein 3 family
ridge B4) with the 23S rRNA of the 50S subunit in the ribosome
ıal protein bS21 family
l-tRNA synthetase family. Phe-tRNA synthetase alpha subunit type 1 subfamily

plex RbsABC involved in ribose import. Responsible for energy coupling to the transport system
UF1852)

n the presence of protein L20
proteins which control the phase variation of type 1 fimbriae in E.coli. These proteins mediate the periodic inversion of a 300bp DNA segment that
osition of guanine in position 527 of 16S rRNA

of two intersubunit bridges in the 70S ribosome

g proteins, it binds directly to 16S rRNA where it nucleates assembly of the body of the 30S subunit
ds and probably mediates the attachment of the 5S RNA into the large ribosomal subunit, where it forms part of the central protuberance. In the 7

toacid CoA transferase, alpha subunit
(NO) phenomenon, which prevents Z-ring formation and cell division over the nucleoid. Acts as a DNA-associated cell division inhibitor that binds s

ssembly
CheY-like receiver AAA-type ATPase and DNA-binding domains
nal protein uL29 family

e catalyzes the transcription of DNA into RNA using the four ribonucleoside triphosphates as substrates
nation in some periplasmic proteins. Acts by transferring its disulfide bond to other proteins and is reduced in the process

d in various cellular processes at low temperature, including ribosome biogenesis, mRNA degradation and translation initiation

oxygenase, reductase subunit

resence of a proton gradient across the membrane. The alpha chain is a regulatory subunit
play a role in recycling of muropeptides during cell elongation and or cell division. Preferentially cleaves at a distance of more than two disacchari
nthesis of coenzyme A. In the first step cysteine is conjugated to 4'-phosphopantothenate to form 4-phosphopantothenoylcysteine, in the latter cor
e 8.96
group on what will become the N-terminal cysteine of membrane lipoproteins

family
ily
es sodium in exchange for external protons

ylacetic acid (PA) to phenylacetyl-CoA (PA-CoA)
ssibly also in glycerophospholipid export and for biogenesis of the outer membrane. Transmembrane domains (TMD) form a pore in the inner mer
ıt transport systems inner membrane component
nsmembrane protein
2) uptake system

volved in electron transport

DNA repair. It cleaves phosphodiester bonds at apurinic or apyrimidinic sites (AP sites) to produce new 5'-ends that are base-free deoxyribose 5-ph
plex HmuTUV involved in hemin import. Responsible for energy coupling to the transport system
ıal protein bL28 family
f ABC transporters with duplicated ATPase domains
m, periplasmic component
rects the termination of translation in response to the peptide chain termination codons UAG and UAA

cyqueuosine (oQ) to queuosine (Q), which is a hypermodified base found in the wobble positions of tRNA(Asp), tRNA(Asn), tRNA(His) and tRNA(Ty

s for the initiation of protein synthesis. Stabilizes the binding of IF-2 and IF-3 on the 30S subunit to which N-formylmethionyl-tRNA(fMet) subsequ
eduction of succinylglutamate semialdehyde into succinylglutamate

closure reaction between the two acyclic compounds 1-deoxy-D-xylulose-5-phosphate (DXP) and 3-amino-2-oxopropyl phosphate (1-amino-acetone
onal core of the enzyme complex. Electrons originating in cytochrome c are transferred via heme a and Cu(A) to the binuclear center formed by he

transcriptional regulator
g yeast histone deacetylase and acetoin utilization protein
it forms part of the peripheral stalk, linking F(1) to F(0)
iobiotin (DTB) to biotin by the insertion of a sulfur atom into dethiobiotin via a radical- based mechanism

uction of ubiquinone-1 to ubiquinol by two successive reactions, coupled with the transport of Na( ) ions from the cytoplasm to the periplasm. NqrA
nation in some periplasmic proteins. Acts by oxidizing the DsbA protein
between oxygene and the acireductone 1,2-dihydroxy-3-keto-5-methylthiopentene (DHK-MTPene) depending upon the metal bound in the active sit

nthase RsuA family

ymers in the presence of ATP
ptidoglycan cell wall

n periplasmic component
y transporter

as a chaperone by maintaining the newly synthesized protein in an open conformation. Functions as a peptidyl-prolyl cis-trans isomerase
g proteins, it binds directly to 16S rRNA central domain where it helps coordinate assembly of the platform of the 30S subunit

on
rone phosphate and D-glyceraldehyde 3-phosphate from D-fructose 1,6-bisphosphate
amily

se reductase SDR

es the refolding and proper assembly of unfolded polypeptides generated under stress conditions

a an enolate intermediate
ethyl-uridine at position 747 (m5U747) in 23S rRNA
enzymes involved in molybdopterin and thiamine biosynthesis family 2
carboxyaminoimidazole ribonucleotide (N5-CAIR) to 4-carboxy-5-aminoimidazole ribonucleotide (CAIR)
lk, playing a central role in the interaction of the ribosome with GTP-bound translation factors

ns in the citric acid cycle (TCA), coupling the hydrolysis of succinyl-CoA to the synthesis of either ATP or GTP and thus represents the only step of su
C7 resistance protein MccF
acid-binding protein

yl group from 10- formyltetrahydrofolate to 5-phospho-ribosyl-glycinamide (GAR), producing 5-phospho-ribosyl-N-formylglycinamide (FGAR) and t
mily. MurA subfamily
for the aldol cleavage of indoleglycerol phosphate to indole and glyceraldehyde 3- phosphate
onate isomerase

repair protein (RecE pathway)

dase
g protein MreB Mrl
d in processing of recombination intermediates, plays a role in repairing DNA breaks. Stimulates the branch migration of RecA-mediated strand tra
carboxymethoxyuridine (cmo5U) to form 5-methoxycarbonylmethoxyuridine (mcmo5U) at position 34 in tRNAs
mily
ounit

ose moiety from AdoMet to the 7-aminomethyl group of 7-deazaguanine (preQ1-tRNA) to give epoxyqueuosine (oQ-tRNA)

ha-amino group from S- adenosyl-L-methionine (SAM) to 7-keto-8-aminopelargonic acid (KAPA) to form 7,8-diaminopelargonic acid (DAPA). It is t
f many RNAs, which usually targets these RNAs for decay. Plays a significant role in the global control of gene expression, through influencing the
al protein bL35 family

related transporters (MFS superfamily)
NADH, via FMN and iron- sulfur (Fe-S) centers, to quinones in the respiratory chain. The immediate electron acceptor for the enzyme in this species
er

L1 stalk is quite mobile in the ribosome, and is involved in E site tRNA release

ounit 2
anate to 4-imidazolone- 5-propionate
quired for 2-thiolation of 5-methylaminomethyl-2-thiouridine (mnm(5)s(2)U) at tRNA wobble positions. Accepts sulfur from TusA and transfers it i
amily. CysH subfamily
nucleotide-disulfide oxidoreductase family

xylase C terminal
cell wall biogenesis
tion by a mechanism that involves Rho binding to the nascent RNA, activation of Rho's RNA-dependent ATPase activity, and release of the mRNA

idouridine at position 1915 (m3Psi1915) in 23S rRNA
mporter (SSF) (TC 2.A.21) family
vZ OmpR two-component regulatory system, probably by directly modulating EnvZ enzymatic activity and increasing stability of phosphorylated Or
ein (NosD)
se family

ily
phosphorylate or dephosphorylate isocitrate dehydrogenase (IDH) on a specific serine residue. This is a regulatory mechanism which enables bacte
bonate transport system ATPase component

;
mily

ry for DNA synthesis. Catalyzes the biosynthesis of deoxyribonucleotides from the corresponding ribonucleotides
ase family

f the 30S subunit, it contacts several helices of the 16S rRNA. In the 70S ribosome it contacts the 23S rRNA (bridge B1a) and protein L5 of the 50S
protein purh
to make contacts with the A and possibly P site tRNAs

nd stability of the Y subunit. Could have a chaperone-like function for the proper and stable folding of

ATP from ADP in the presence of a proton or sodium gradient. F-type ATPases consist of two structural domains, F(1) containing the extramembra
P-mannose dehydrogenase family
e-specific transporter subunit IIA HPr protein
ATP from ADP in the presence of a proton or sodium gradient. F-type ATPases consist of two structural domains, F(1) containing the extramembra

ein, family 5
mocysteine from O- succinyl-L-homoserine (OSHS) and hydrogen sulfide
transport of thiamine and thiamine pyrophosphate into the cell
nal protein bS16 family
ds the polypeptide exit tunnel on the outside of the subunit
tein S6 to the central domain of the 16S rRNA, where it helps stabilize the platform of the 30S subunit
of Mg-ATP and suppresses the ATPase activity of the latter

t reduction of L-glutamate 5-phosphate into L-glutamate 5-semialdehyde and phosphate. The product spontaneously undergoes cyclization to form

tein
ndent sugar phosphotransferase system (PTS), a major carbohydrate active - transport system, catalyzes the phosphorylation of incoming sugar sul

anic pyrophosphate (PPi) forming two phosphate ions

ydrolysis reaction at the C5' of the pyrimidine moiety of thiamine compounds, a reaction that is part of a thiamine salvage pathway
in iron transport
s the removal of signal peptides from prolipoproteins
osphoribosyl group of 5- phosphorylribose-1-pyrophosphate (PRPP) to anthranilate to yield N-(5'-phosphoribosyl)-anthranilate (PRA)
ions in the biosynthesis of the cell wall peptidoglycan
ogenase family
he cell division process by stabilizing the polymeric form of the cell division protein FtsZ. Acts by promoting interactions between FtsZ protofilame
for the synthesis of L- tryptophan from indole and L-serine

, multichain enzyme responsible for most of the replicative synthesis in bacteria. This DNA polymerase also exhibits 3' to 5' exonuclease activity. T
JF1481)

e
Gpp to ppGpp. Guanosine pentaphosphate (pppGpp) is a cytoplasmic signaling molecule which together with ppGpp controls the stringent respons
line synthase involved in the purines biosynthetic pathway. Catalyzes the ATP-dependent conversion of formylglycinamide ribonucleotide (FGAR) a
kit tunnel
amily UPF0066
line at the wobble position (U34) of tRNA, leading to the formation of s(2)U34
on. Involved in the translocation of bactoprenol-linked glucose across the cytoplasmic membrane
t site
subunit head. Binds mRNA in the 70S ribosome, positioning it for translation

ıidine
ptidoglycan cell wall at the division septum
resence of a proton gradient across the membrane. Subunit I associates with the membrane and may be involved with cation translocation
ninoaspartate with dihydroxyacetone phosphate to form quinolinate

e ammonia chain
th S13 that binds strongly to the 16S ribosomal RNA
:tate to pyruvate. Is coupled to the respiratory chain
ecting protein
ıcleoside triphosphates other than ATP. The ATP gamma phosphate is transferred to the NDP beta phosphate via a ping-pong mechanism, using a
ase PfkB family
tein assembly complex, which is involved in assembly and insertion of beta-barrel proteins into the outer membrane

E
se family
high affinity leucine transport
to the ribosomes

different specificities (related to short-chain alcohol dehydrogenases)
in O
ıal protein HisB
ne central metabolite phospho-alpha-D-ribosyl-1-pyrophosphate (PRPP) via the transfer of pyrophosphoryl group from ATP to 1-hydroxyl of ribose-5

ism regulatory protein hpaA
ıversion of serine and glycine with tetrahydrofolate (THF) serving as the one-carbon carrier. This reaction serves as the major source of one-carbor
ıidase
:k in the DNA. It binds to the single-stranded DNA and acts in a progressive fashion along the DNA in the 3' to 5' direction

orylation of UMP to UDP
r proper folding and or complex formation of integral membrane proteins into the membrane. Involved in integration of membrane proteins that i

location of protons across the membrane

-phosphate-dependent aminotransferase family

iosynthetic process
function (DUF3799)

tose cellobiose-specific IIB subunit

g proteins, it binds directly near the 3'-end of the 23S rRNA, where it nucleates assembly of the 50S subunit

f the 5'-leader sequence from pre-tRNA to produce the mature 5'-terminus. It can also cleave other RNA substrates such as 4.5S RNA. The protein

se

t reduction of N-acetyl-5- glutamyl phosphate to yield N-acetyl-L-glutamate 5-semialdehyde
aturation of iron-sulfur cluster-containing proteins. Seems to help targeting proteins to be folded toward HscA
of the terminal phosphate group between ATP and AMP. Plays an important role in cellular energy homeostasis and in adenine nucleotide metab

smoregulated periplasmic glucans (OPGs)
sparagine
Catalyzes the final step in the synthesis of UDP-N-acetylmuramoyl-pentapeptide, the precursor of murein
uced during the turnover of membrane phospholipid

ansglycosylase and related regulatory proteins (some contain LysM invasin domains)

lk which helps the ribosome interact with GTP-bound translation factors
RNA binding, RNA strand exchange and RNA duplexing activities
plex ModABC involved in molybdenum import. Responsible for energy coupling to the transport system

e
cule, which serves as a redox-active prosthetic group
eal Glu-tRNAGln amidotransferase subunit D

e primosome assembly site (PAS)

se activity and contains distinct active sites for ATP binding, DNA binding, and interaction with DnaC protein, primase, and other prepriming protei
line cyclo-ligase
1-deoxy-D-xylulose 5- phosphate (DXP) to produce the thiazole phosphate moiety of thiamine. Sulfur is provided by the thiocarboxylate moiety of t
JF1198)

entral role in RNA processing and decay. Required for the maturation of 5S and 16S rRNAs and the majority of tRNAs. Also involved in the degrada

te and the transport of protons into the cell
ne transfer of a GlcNAc subunit on undecaprenyl-pyrophosphoryl-MurNAc-pentapeptide (lipid intermediate I) to form undecaprenyl-pyrophosphoryl
ion. Catalyzes the condensation and subsequent hydrolysis of acetyl-coenzyme A (acetyl-CoA) and glyoxylate to form malate and CoA
mase expression
plex that catalyzes the two-step biosynthesis of anthranilate, an intermediate in the biosynthesis of L-tryptophan. In the first step, the glutamine- b
denylosuccinate lyase subfamily
acid oxidation in which acetyl-CoA is released and the CoA ester of a fatty acid two carbons shorter is formed

ton-dependent sulfate transporter, which mediates sulfate uptake. Provides the sulfur source for the cysteine synthesis pathway

se activity

ribosomal RNA
droxyethyl)thiazole monophosphate (THZ-P) and 2-methyl-4-amino-5-hydroxymethyl pyrimidine pyrophosphate (HMP-PP) to form thiamine monopl

hydratase
lent swarming motility
ic ring-opening dioxygenase
f the position 2 hydroxy group of 4-diphosphocytidyl-2C-methyl-D-erythritol
(ferredoxin-NADPH reductases) family 1
ystem Periplasmic Component

ıtion bifunctional isomerase

ydrolases (invasion-associated proteins)
. Catalyzes the conversion of oxaloacetate (OAA) to phosphoenolpyruvate (PEP) through direct phosphoryl transfer between the nucleoside triphosp
rotein PaaD
'aaI subunit

ydroxymethylpyrimidine phosphate (HMP-P) moiety of thiamine from aminoimidazole ribotide (AIR) in a radical S-adenosyl-L-methionine (SAM)-de

tein

ecursor of folate derivatives

has been identified. NO probably binds to the di-iron center

. TatE shares overlapping functions with TatA

olism

control of the cell cycle, stress response, ribosome biogenesis and in those bacteria that undergo differentiation, in morphogenesis control

ATP-dependent phosphofructokinases (ATP-PFKs), which renders the reaction reversible, and can thus function both in glycolysis and gluconeogene

acellular free iron so as to provide iron for the assembly of transient iron-sulfur cluster in IscU in the presence of IscS, L-cysteine and the thioredox

mmonia

ts in the terminal step of the DOXP MEP pathway for isoprenoid precursor biosynthesis

. TatA could form the protein-conducting channel of the Tat system

ıd chitosan dimer, the deacetylated form of chitobiose. Deacetylation of chitobiose-6-P and chitotriose-6-P is necessary for both the activation of t

levelopment and host cell recognition (By similarity)

ɔroduct. Lytic transglycosylases (LTs) play an integral role in the metabolism of the peptidoglycan (PG) sacculus. Their lytic action creates space wi

:requisite for activity but the enzyme has broad specificity at other positions
-2Bepsilon

levelopment and host cell recognition. Tip pilus adhesin, which is required for assembly of EcpA into fibers (By similarity)
ase is metal-independent and links a dimethylallyl moiety from dimethylallyl monophosphate (DMAP) to the flavin N5 and C6 atoms of FMN

-3'. In the presence of single-stranded DNA, RecA interacts with LexA causing an autocatalytic cleavage which disrupts the DNA-binding part of Le

transport system

on to isochorismate to yield 2-succinyl-5-enolpyruvyl-6-hydroxy-3- cyclohexene-1-carboxylate (SEPHCHC)

e trans-periplasmic membrane protein TonB

ading 3'-5' exonuclease

eins from oxidative-stress damage caused by reactive species of oxygen and chlorine generated by the host defense mechanisms. MsrPQ is essenti

biogenesis of 30S subunits

plasm. This subunit binds and transports the potassium across the cytoplasmic membrane

nthesis of lysine and meso-diaminopimelic acid, an essential component of bacterial cell walls

sphonooxypentane-2,3-dione (P-DPD) to 3-hydroxy-5- phosphonooxypentane-2,4-dione (P-HPD)

t and autoinducer-2 uptake and processing

ɔstrates concomitant with their translocation across the cell membrane

to the common pyruvate enolate transition state formed following C-C bond cleavage in the retro-aldol and decarboxylation reactions

hetic pathway through the hydrolysis of the ester bonds of pimeloyl-ACP esters

ınds

:tions in homologous recombination. RuvAB is a helicase that mediates the Holliday junction migration by localized denaturation and reannealing

ɔhate and OAA

nthesis, which is the condensation of the polyisoprenoid side chain with PHB, generating the first membrane-bound Q intermediate 3- octaprenyl-
first step is catalyzed by NqrF, which accepts electrons from NADH and reduces ubiquinone-1 to ubisemiquinone by a one-electron transfer pathw
· oxidized pyrimidines, such as thymine glycol, 5,6-dihydrouracil and 5,6-dihydrothymine. Has AP (apurinic apyrimidinic) lyase activity and introduce

ɔnal control

, histidine, and tryptophan, or as a component of the pentose phosphate pathway

/lation of 4-hydroxybenzoate and vanillate

d biosynthesis promoters. Also required for regulation of fis expression

ıt attachment of the oligosaccharide to the alpha-1,6 position

levelopment and host cell recognition (By similarity)

:ed uptake system
act as a sensor of the intracellular accumulation of phosphoglucose by binding these molecules in its C-terminal solute-binding domain

ole to transaminate cadaverine and, in lower extent, spermidine, but not ornithine

and spermidine from the diamine putrescine

s in metabolite concentrations. Also binds with high specificity to tRNAs

'-AMP or holoBirA) complex. HoloBirA can either transfer the biotinyl moiety to the biotin carboxyl carrier protein (BCCP) subunit of acetyl-CoA car

Component of the suf operon, which is activated and required under specific conditions such as oxidative stress and iron limitation. Acts as a pote

odifies U20 and U20a in tRNAs

on Z ring. It is recruited early at mid-cell but it is not essential for cell division
ı of homologous single-stranded DNAs. It interacts with LexA causing its activation and leading to its autocatalytic cleavage

ɔnal control

system. Does not inhibit the co-chaperone activity of DnaJ

not co- degraded with RpoS, but is released from the complex and can initiate a new cycle of RpoS recognition and degradation

Component of the suf operon, which is activated and required under specific conditions such as oxidative stress and iron limitation. Acts as a pote

ned to lipid A and is required for resistance to polymyxin and cationic antimicrobial peptides

is not an aspartate (The Asp acts as a targeting signal to indicate that the lipoprotein should stay in the inner membrane)

n the central cavity of the protein complex

icidic pH by preventing the aggregation of many different periplasmic proteins
are required for fully efficient folding. Also involved, together with DnaK and GrpE, in the DNA replication of plasmids through activation of initiat

during cell division. Binds specifically to matS, which is a 13 bp signature motif repeated within the Ter macrodomain

›roduce 5'-deoxy-adenosine

hydrolyzing the carbon-nitrogen bond between the sugar-phosphate backbone of the DNA and the mispaired base. The complementary strand gua

ction takes place in the presence of glutamine and ATP through an activated gamma-phospho-Glu-tRNA(Gln)

levels of c-di-GMP lead to decreased motility

f four-way DNA junctions, where it introduces symmetrical nicks in two strands of the same polarity at the 5' side of dinucleotides. Corrects the de

e mRNAs, and tRNAs when they are encoded in the rRNA operon. Processes pre- crRNA and tracrRNA of type II CRISPR loci if present in the organi

anslocational (POST) state as the newly formed A-site-bound peptidyl-tRNA and P-site-bound deacylated tRNA move to the P and E sites, respecti

ıding by the gyrase

ıe regulation of gene expression in response to changes in cell density is called quorum sensing. Catalyzes the transformation of S-ribosylhomocys

ınisaligned primer ends. These misaligned primers can be extended by PolIV. Exhibits no 3'-5' exonuclease (proofreading) activity. May be involved

the four ribonucleotide triphosphates

midation

tion of 2-succinyl-6-hydroxy-2,4-cyclohexadiene-1-carboxylate (SHCHC)

ıe assembly of ribosomal proteins into the subunit. Circularly permuted GTPase that catalyzes slow GTP hydrolysis, GTPase activity is stimulated b

As ProRS can inadvertently accommodate and process non-cognate amino acids such as alanine and cysteine, to avoid such errors it has two additi

ɔlasm. This subunit acts as a catalytic chaperone that increases the ATP- binding affinity of the ATP-hydrolyzing subunit KdpB by the formation of a

GlcNAc-PP- C55)

ɔstrates concomitant with their translocation across the cell membrane

ıomeostasis and for survival from DNA damage and developmental changes induced by stress. Degrades polypeptides processively to yield small p

to 2- polyprenyl-3-methyl-6-methoxy-1,4-benzoquinol (DMQH2)

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

entanoate

mbly and thereby promoting cell division earlier in the cell cycle. Its recruitment to the Z-ring requires functional FtsA or ZipA

ır

olymyxin and cationic antimicrobial peptides

; to methionine

mmonia

A to the tRNA nucleotide-73, using CTP and ATP as substrates and producing inorganic pyrophosphate. Also shows phosphatase, 2'- nucleotidase a

levelopment and host cell recognition (By similarity)

: group and turn over during the catalytic mechanism

NA motif (called the malT box) 5'-GGA TG GA-3'

ıreonine, HCO(3)(-) CO(2) and ATP to give threonylcarbamoyl-AMP (TC-AMP) as the acyladenylate intermediate, with the release of diphosphate

ıydroxy-6-ketononatrienedioate, respectively

llosterically activated to bind its cognate DNA by binding the purine corepressors, hypoxanthine or guanine, thereby effecting transcription repressi

m trehalose-6-phosphate. Acts with retention of the anomeric configuration of the UDP-sugar donor

. Together with TatC, TatB is part of a receptor directly interacting with Tat signal peptides. TatB may form an oligomeric binding site that transie

erase complex by the ops element, which is a short conserved DNA sequence located downstream of the main promoter of these operons. Once b

RP) and the ribosome-nascent chain (RNC). Interaction with SRP-RNC leads to the transfer of the RNC complex to the Sec translocase for insertion

n complex on the specific site of the template DNA recognized by protein N'

e , an adaptive process that allows bacteria to respond to amino acid starvation, resulting in the coordinated regulation of numerous cellular activ

ɔr during exponential growth

ion

ta-lysine produced by EpmB, forming a lysyl-adenylate, from which the beta- lysyl moiety is then transferred to the epsilon-amino group of a cons

activity that uses the energy of ATP hydrolysis to destabilize and unwind short rRNA duplexes

midine

activity is not required for activation of KefC

e threonylcarbamoyl moiety of threonylcarbamoyl-AMP (TC-AMP) to the N6 group of A37, together with TsaE and TsaB. TsaD likely plays a direct c

ɛtic pathways of all 7-deazapurine-containing compounds

ɔeron. Phosphorylates the ring-open form of (S)-4,5-dihydroxypentane-2,3- dione (DPD), which is the precursor to all AI-2 signaling molecules, at th

ıer than heat shock. Lacks autonomous chaperone activity

A to NqrE are probably involved in the second step, the conversion of ubisemiquinone to ubiquinol

ince N- deacetylation of PGA by PgaB is needed for PGA export through the PgaA porin

an N-terminal arginine or lysine

ar substrates concomitantly with their translocation across the cell membrane. The enzyme II UlaABC PTS system is involved in ascorbate transpor

ostrates concomitant with their translocation across the cell membrane

he DNA, and recruitment of nucleotide excision repair machinery to the damaged site

the composition of the degradosome

levels of c-di-GMP lead to decreased motility

recruitment to the septal ring of downstream cell division proteins

protein NapC. Essential function for nitrate assimilation and may have a role in anaerobic metabolism

cted from diverse damages. It protects DNA from oxidative damage by sequestering intracellular Fe(2) ion and storing it in the form of Fe(3) oxy

hydroxy-isovalerate. In the isomerase reaction, S2AL is rearranged via a Mg-dependent methyl migration to produce 3- hydroxy-3-methyl-2-ketobu

e inactive in their acylated form

e regulator RcsB. It acquires a phosphoryl group from RcsC and transfers it to RcsB

t and autoinducer-2 uptake and processing

ns. Probably acts by releasing the RNAP, when it is trapped or immobilized on tightly supercoiled DNA. Does not activate transcription on linear DN

ɔrm 3-amino-2-oxopropyl phosphate (AHAP)

atalyzes the phosphorylation of incoming sugar substrates concomitantly with their translocation across the cell membrane. Enzyme I transfers the

of the aspartate family of amino acids

)lasm. This subunit is responsible for energy coupling to the transport system

ınds

·hydroxy-5-phosphonooxypentane-2,4-dione to CoA to form glycerone phosphate and acetyl-CoA

ıs

nination efficiency will be affected by the affinity of this protein for the terminator sequence

e

ıe intact lesion on the nicked DNA

s. However, all known phosphorylases share catalytic and structural properties

A by stoichiometrically transferring the methyl group to a cysteine residue in the enzyme. This is a suicide reaction the enzyme is irreversibly inacti

erve as the LPS recognition site at the outer membrane

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

ɔroduct. Lytic transglycosylases (LTs) play an integral role in the metabolism of the peptidoglycan (PG) sacculus. Their lytic action creates space wi

of enamine intermediates (aminocrotonate), which tautomerizes to its imine form (iminobutyrate). Both intermediates are unstable and short- liv

A by stoichiometrically transferring the methyl group to a cysteine residue in the enzyme. This is a suicide reaction the enzyme is irreversibly inacti

anslocational (POST) state as the newly formed A-site-bound peptidyl-tRNA and P-site-bound deacylated tRNA move to the P and E sites, respecti

n an underwound state. Negative supercoiling favors strand separation, and DNA replication, transcription, recombination and repair, all of which

ɔrm 3-amino-2-oxopropyl phosphate (AHAP)

›porphyrinogen-IX

ne and xanthosine as substrates. Also catalyzes the reverse reactions

, histidine, and tryptophan, or as a component of the pentose phosphate pathway

l by CcmF and CcmH

)HSA) to yield shikimate (SA)

te)

(rrn) operons

CoA. It can also use D-3-hydroxyacyl-CoA and cis-3-enoyl-CoA as substrate
. Together with TatB, TatC is part of a receptor directly interacting with Tat signal peptides

ıat facilitates a folding-maturation pathway for the substrate protein

ne level. Under low glutamine levels, catalyzes the conversion of the PII proteins and UTP to PII-UMP and PPi, while under higher glutamine levels,

f expression of heat shock genes

rectly by adding oxygen atoms, making a toxic ureidoacrylate peracid product which can be spontaneously reduced to ureidoacrylate

ıenting the peptidyl transferase activity of the ribosome. Modification of Lys-34 is required for alleviation

mmonia

- methylaminomethyl-2-thiouridine (mnm(5)s(2)U) in tRNA. Interacts with IscS and stimulates its cysteine desulfurase activity. Accepts an activat

L-rhamnulose 1-phosphate

e N- glycosidic bond, leaving an AP (apurinic apyrimidinic) site. The AP-lyase activity cleaves the phosphodiester bond 3' to the AP site by a beta-eli

in rapidly growing cells. It mediates rapid entry or exit of water in response to abrupt changes in osmolarity

piratory complex II), an enzyme complex that is a component of both the tricarboxylic acid cycle and the electron transport chain, and which couple

ubstrate-level phosphorylation in the TCA. The alpha subunit of the enzyme binds the substrates coenzyme A and phosphate, while succinate bindir

as a scaffold chaperone for damaged Fe S proteins

ıl subunits. Also involved in the hydrolysis of GTP during the formation of the 70S ribosomal complex

ıble strand exonuclease that can open hairpins. It also has a 5' single-strand endonuclease activity

ıte

ɔteins, depending on their folding state

›ther sigma factors, such as sigma-70 and sigma-32

e, and an ATP-binding domain (NBD), which is responsible for energy generation. Confers resistance against macrolides

i- inositol)

ϟ by stoichiometrically transferring the methyl group to a cysteine residue in the enzyme. This is a suicide reaction the enzyme is irreversibly inacti

the first half reaction, AcsA combines acetate with ATP to form acetyl-adenylate (AcAMP) intermediate. In the second half reaction, it can then tr

eins from oxidative-stress damage caused by reactive species of oxygen and chlorine generated by the host defense mechanisms. MsrPQ is essenti

subunits that are part of 70S ribosomes or polysomes). Required for efficient processing of 16S rRNA. May interact with the 5'-terminal helix regi

A to NqrE are probably involved in the second step, the conversion of ubisemiquinone to ubiquinol

(Glu)

ıich are found more frequently in integral outer membrane proteins. May act in both early periplasmic and late outer membrane-associated steps

ɔstrates concomitant with their translocation across the cell membrane

ɛnosine (i(6)A)

:he presence of GTP, binds a polymerization-competent form of FtsZ in a 1 1 ratio, thus inhibiting FtsZ polymerization and therefore preventing it f
ı of elongating RNA polymerases that pass through, resulting in locked ternary complexes. Cleavage of the nascent transcript by cleavage factors s

Formate is provided by PurU via hydrolysis of 10-formyl-tetrahydrofolate

the reaction

(Thr)

predominantly periplasmic. May control correct divisome assembly

moting its recognition by IF2 and preventing the misappropriation of this tRNA by the elongation apparatus

· oxidized purines, such as 7,8-dihydro-8-oxoguanine (8-oxoG). Has AP (apurinic apyrimidinic) lyase activity and introduces nicks in the DNA strand.
ıem in a translocation-competent state. It also specifically binds to its receptor SecA

erase encounters the 5'-end of a downstream Okazaki fragment

acellular free iron so as to provide iron for the assembly of transient iron-sulfur cluster in IscU in the presence of IscS, L-cysteine and the thioredox

units, it traverses the body of the 30S subunit contacting proteins on the other side and probably holding the rRNA structure together. The combin

ıs fatty acyl donor, but not acyl-CoA or acyl-ACP
cell cycle regulation and energy metabolism

endent reduction of both 3-dehydroshikimate (DHSA) and 3-dehydroquinate to yield shikimate (SA) and quinate, respectively. It can use both NAD c

of linear glycan strands) and a penicillin-sensitive transpeptidase C-terminal domain (cross-linking of the peptide subunits)

ins that target DNA gyrase, by inhibiting activity of these toxins and reducing the formation of lethal double-strand breaks in the cell

A to NqrE are probably involved in the second step, the conversion of ubisemiquinone to ubiquinol
May also coordinate assembly of proteins involved in LPS synthesis at the plasma membrane

s is believed to be ubiquinone. Couples the redox reaction to proton translocation (for every two electrons transferred, four hydrogen ions are trans

utritional abundance
t sites symmetrically opposed at the junction in the homologous arms and leaves a 5'-terminal phosphate and a 3'-terminal hydroxyl group

ulated intramembrane proteolysis (RIP). RIP occurs when an extracytoplasmic signal triggers a concerted proteolytic cascade to transmit informat

ɔstrates concomitant with their translocation across the cell membrane

gM secretion by acting as a braking system for the flagellar- associated type III secretion

form dihydrofolate (7,8-dihydrofolate monoglutamate or H2Pte-Glu). Also catalyzes successive additions of L-glutamate to tetrahydrofolate or 10-

embrane bilayer

xidative stress by detoxifying peroxides

defense system toward oxidative stress

NAc, anhydro-N-acetylmuramic acid and anhydro-N-acetylmuramic acid-linked peptides

te)
es the conversion of 4-amino-5-aminomethyl-2-methylpyrimidine to 4-amino- 5-hydroxymethyl-2-methylpyrimidine (HMP)

luces the first double bond of the aromatic ring to yield 3- dehydroshikimate

)O) and inorganic phosphate
sulfur to the sulfur carrier protein ThiS, forming ThiS-thiocarboxylate. This is a step in the synthesis of thiazole, in the thiamine biosynthesis pathv

acterial peptidoglycan

incision and the C-terminal half is responsible for the 5' incision

dification, such as initiation of chromosomal replication

orm 3-amino-2-oxopropyl phosphate (AHAP)

AD- dependent ring dehydrogenation of precorrin-2 to yield sirohydrochlorin. Finally, it catalyzes the ferrochelation of sirohydrochlorin to yield siro
te step in the biosynthesis of riboflavin

ıitiates fatty acid synthesis and may therefore play a role in governing the total rate of fatty acid production. Possesses both acetoacetyl-ACP synth

.NA polymerase and with promoter DNA. May be involved in replacement of the RNA polymerase sigma subunit from RpoD to RpoS during the tra
of the adenosine moiety of NAD to yield NADP

rgy sources, or in the rescue of pyrimidine bases for nucleotide synthesis

ıulate subsequent ribonuclease cleavage

vated donor of ManNAc residues

ansferase using carbamoylphosphate as a substrate and transferring the carboxamido moiety in an ATP-dependent reaction to the thiolate of the C

·(3)- decenoyl-ACP. Can catalyze the dehydratase reaction for beta- hydroxyacyl-ACPs with saturated chain lengths up to 16 0, being most active or
ıtom. Involved in the biosynthesis of lipid A, a phosphorylated glycolipid that anchors the lipopolysaccharide to the outer membrane of the cell

anslocation of tRNAs on improperly translocated ribosomes. Back- translocation proceeds from a post-translocation (POST) complex to a pre-trans

ackbones on the periplasmic side of the membrane

haride capsule, possibly through activation of the RcsB RcsC phosphotransfer signaling pathway. The colanic acid capsule may help the bacterium s

adenosyl-L-methionine to the 2'-OH of the wobble nucleotide

ıp is transferred by the transcarboxylase to acetyl-CoA to form malonyl- CoA

sruption of a mRNA repressor helix that normally suppresses secA translation initiation
ıtons through the CF(0) complex

ress. Aggregated proteins bound to the IbpAB complex are more efficiently refolded and reactivated by the ATP-dependent chaperone systems Clp

ıd inorganic phosphate

ın of UvrB beta-hairpin between the DNA strands. Then UvrB probes one DNA strand for the presence of a lesion. If a lesion is found the UvrA subu

ress. Aggregated proteins bound to the IbpAB complex are more efficiently refolded and reactivated by the ATP-dependent chaperone systems Clp

ıe extracytoplasmic stress response
ɟes, and therefore plays an important role in the regulation of cell growth

ʁNA)

ɔnal helicase activity. Unwinds dsDNA until it encounters a Chi (crossover hotspot instigator) sequence from the 3' direction. Cuts ssDNA a few nuc

yl diphosphate (di-trans,octa-cis-UPP). UPP is the precursor of glycosyl carrier lipid in the biosynthesis of bacterial cell wall polysaccharide compon

se to the decoding center, probably blocks exit of the E-site tRNA

fatty acid metabolism

development and host cell recognition (By similarity)

CoA. It can also use D-3-hydroxyacyl-CoA and cis-3-enoyl-CoA as substrate

tyl group from acetyl coenzyme A to glucosamine-1-phosphate (GlcN-1-P) to produce N-acetylglucosamine-1-phosphate (GlcNAc-1-P), which is co
s is believed to be ubiquinone. Couples the redox reaction to proton translocation (for every two electrons transferred, four hydrogen ions are trans

llosterically activated to bind its cognate DNA by binding the purine corepressors, hypoxanthine or guanine, thereby effecting transcription repressi

esistance to polymyxin and cationic antimicrobial peptides

bacterium from various noxious nitrogen compounds. Therefore, plays a central role in the inducible response to nitrosative stress

of zinc or lead in the medium

i- inositol)

ıle

ıoids

one round of translation to another

up is transferred by the carboxyltransferase to acetyl-CoA to form malonyl-CoA

tions in homologous recombination. RuvAB is a helicase that mediates the Holliday junction migration by localized denaturation and reannealing.

n after the ATP-dependent function of SecA

strates concomitant with their translocation across the cell membrane. The enzyme II complex composed of GatA, GatB and GatC is involved in ga

uble strand exonuclease that can open hairpins. It also has a 5' single-strand endonuclease activity

oribose, 5'-methylthioribose and S-ribosylhomocysteine, respectively

tivity, and promote assembly of the primosome and loading of the major replicative helicase DnaB onto DNA

the inner membrane to the periplasmic protein LptA. Could be a docking site for LptA

) operator sites with the consensus sequence 5-'TATCCN(8)GGATA-3' to repress the hipBA operon promoter

s is believed to be ubiquinone. Couples the redox reaction to proton translocation (for every two electrons transferred, four hydrogen ions are trans
n of 4- diphosphocytidyl-2-C-methyl-D-erythritol 2-phosphate (CDP-ME2P) to 2-C-methyl-D-erythritol 2,4-cyclodiphosphate (ME-CPP) with a corresp

the subsequent tripolyphosphate hydrolysis which occurs prior to release of AdoMet from the enzyme

NA duplex. Introduces a single-strand break via transesterification at a target site in duplex DNA. The scissile phosphodiester is attacked by the cat

and energy sources or in the rescue of pyrimidine bases for nucleotide synthesis

predominantly periplasmic
sferase (AT) inactivates GlnA by covalent transfer of an adenylyl group from ATP to specific tyrosine residue of GlnA, thus reducing its activity. Conv

tricting the formation of a division septum at the midpoint of the long axis of the cell

e (mTHF) as the methyl donor and reductant in the reaction, yielding dihydrofolate (DHF) as a by-product. This enzymatic reaction provides an intr

It plays a role in the repair and or degradation of damaged proteins

predominantly periplasmic

of elongating RNA polymerases that pass through, resulting in locked ternary complexes. Cleavage of the nascent transcript by cleavage factors s

RNA and SmpB together mimic tRNA shape, replacing the anticodon stem-loop with SmpB. tmRNA is encoded by the ssrA gene

th GU(N) anticodons (tRNA-Asp, -Asn, -His and -Tyr). Catalysis occurs through a double-displacement mechanism. The nucleophile active site attac
mature into polar Z rings. Prevents FtsZ polymerization

ne toxicity associated with the formation of D-aminoacyl-tRNA entities in vivo and helps enforce protein L-homochirality

d to AMP. This allows the repair of both epimers of NAD(P)HX, a damaged form of NAD(P)H that is a result of enzymatic or heat-dependent hydrat
s is believed to be ubiquinone. Couples the redox reaction to proton translocation (for every two electrons transferred, four hydrogen ions are trans

odifies U16 in tRNAs

erted into selenocysteinyl-tRNA(Sec)

the ribosome

ons. It may interact directly with the ribosome. The stimulation of RF- 1 and RF-2 is significantly reduced by GTP and GDP, but not by GMP

ly charged molecules
hosphates as substrates

P (xanthosine triphosphate), dITP (deoxyinosine triphosphate) and ITP. Seems to function as a house-cleaning enzyme that removes non-canonical

igen (ECA)

ıcidic pH by preventing the aggregation of many different periplasmic proteins

›-5-(4,5- dihydroxy-2-cyclopenten-1-yl) moiety of the queuosine in the wobble position of the QUC anticodon

ɪzymes

:ed uptake system
ɐr membrane and the outer membrane, via interactions with LptC and LptD, thereby facilitating LPS transfer across the periplasm

|uired for the utilization of anhMurNAc either imported from the medium or derived from its own cell wall murein, and thus plays a role in cell wa

A to NqrE are probably involved in the second step, the conversion of ubisemiquinone to ubiquinol

utritional abundance

transduce energy from the cytoplasmic membrane to specific energy- requiring processes in the outer membrane, resulting in the release into the

reby converting the octanoylated domains into lipoylated derivatives

:en suggested to have peptidyltransferase activity

AD- dependent ring dehydrogenation of precorrin-2 to yield sirohydrochlorin. Finally, it catalyzes the ferrochelation of sirohydrochlorin to yield siroh
ɔly

otide exchange factor for DnaK and may function as a thermosensor. Unfolded proteins bind initially to DnaJ
lity of 30S subunits on which protein synthesis initiation begins

ɔhase and during nitrogen starvation. Its effect on RpoS stability is due to its interaction with RssB, which probably blocks the interaction of RssB v

asm and interaction with the FtsQBL complex in the periplasm. These interactions may induce a conformational switch in both FtsA and FtsQBL, le

en onto the bilayer between TMs 2 and 7, and are clamped together by SecE at the back. The channel is closed by both a pore ring composed of hy

dering DnaA inactive for reinititation, a process called regulatory inhibition of DnaA or RIDA

which diffuses in an ATP-independent manner freely and bidirectionally along dsDNA. Initially characterized for its ability to contact the catalytic su

in the absence of fim operon

ar substrates concomitantly with their translocation across the cell membrane. This system is involved in N-acetylmuramic acid (MurNAc) transpor
nbrane and the ATP-binding domain (NBD) is responsible for energy generation

osphate (HK-MTPenyl-1-P), which is then dephosphorylated to form the acireductone 1,2-dihydroxy-3-keto-5-methylthiopentene (DHK- MTPene)

ur atoms from cysteine to produce alanine. Functions as a sulfur delivery protein for Fe-S cluster synthesis onto IscU, an Fe-S scaffold assembly pr

or the utilization of anhydro-N-acetylmuramic acid (anhMurNAc) either imported from the medium or derived from its own cell wall murein, and t
inding beta subunit (TrpG) of anthranilate synthase (AS) provides the glutamine amidotransferase activity which generates ammonia as a substra

terobacterial common antigen (ECA)

P residue from uncharged tRNA (tRNA-C-C-A). Also appears to be involved in tRNA biosynthesis

levelopment and host cell recognition

ns into and across the cell membrane, serving both as a receptor for the preprotein-SecB complex and as an ATP-driven molecular motor driving th

, and in maintaining the intracellular balance of A and G nucleotides

s. However, all known phosphorylases share catalytic and structural properties

ısing the ammonia provided by the HisH subunit

g tRNA- cmnm(5)s(2)U34

ative DNA supercoiling in vivo, and by this means organize and compact chromosomes. May achieve or facilitate chromosome segregation by cond

ion activation

harbors the promoter for the fimbrial structural gene, fimA. FimB switches fimA on

U recognizes the N-terminal part of its protein substrates and unfolds these before they are guided to HslV for hydrolysis

min

ostrates concomitant with their translocation across the cell membrane

(lipid IVA)

centrally located replisome during cell division. Probably acts via its interaction with MukB and MukF

s is believed to be ubiquinone. Couples the redox reaction to proton translocation (for every two electrons transferred, four hydrogen ions are trans

ɔnal helicase activity. Unwinds dsDNA until it encounters a Chi (crossover hotspot instigator) sequence from the 3' direction. Cuts ssDNA a few nuc

levelopment and host cell recognition. Major subunit of the fimbria

ɹle

ı of cell division. One of the functions of the FtsZ ring is to recruit other cell division proteins to the septum to produce a new cell wall between the

of enamine intermediates (aminocrotonate), which tautomerizes to its imine form (iminobutyrate). Both intermediates are unstable and short- liv
) I is the catalytic subunit of the enzyme. Electrons originating in cytochrome c are transferred via the copper A center of subunit 2 and heme A of s

ecursor of folate derivatives

its tRNA

nergy source for the reaction. It is essential for DNA replication and repair of damaged DNA

JvrA and 2 UvrB subunits scans DNA for abnormalities. When the presence of a lesion has been verified by UvrB, the UvrA molecules dissociate

GDP and alpha-ribazole 5'-phosphate

on of IscU

ıia necessary to HisF for the synthesis of IGP and AICAR

subunit

in that promotes the formation of a stable complex between two or more DNA-binding proteins in an ATP-dependent manner without itself being

- diphosphate. Contributes to the recycling of undecaprenyl phosphate (C55-P)

:he lipopolysaccharide to the outer membrane of the cell

:P via the fatty acid synthetic pathway

Also edits incorrectly charged Ser-tRNA(Ala) and Gly-tRNA(Ala) via its editing domain

NA duplex. Introduces a single-strand break via transesterification at a target site in duplex DNA. The scissile phosphodiester is attacked by the cat
for trigger factor binding to the ribosome

cycle. Binds to pairs of hemimethylated GATC sequences in the oriC region, thus preventing assembly of replication proteins and re- initiation at ne

as it emerges from the ribosomes. The SRP-RNC complex is then targeted to the cytoplasmic membrane where it interacts with the SRP receptor
ɔmal subunits and the formation of functional ribosomes, thus repressing translation

doxin as cosubstrates to produce 5'-deoxy-adenosine

rons from cytoplasmic thioredoxin to the periplasm. This transfer involves a cascade of disulfide bond formation and reduction steps
ɔ the cell, RapZ binds GlmZ and targets it to cleavage by RNase E. Consequently, GlmZ is inactivated and unable to activate GlmS synthesis. Under

o ring

s is believed to be ubiquinone. Couples the redox reaction to proton translocation (for every two electrons transferred, four hydrogen ions are trans

y also regulate the expression of genes outside the dcw cluster
ficient processing of 16S rRNA. May be needed both before and after RbfA during the maturation of 16S rRNA. It has affinity for free ribosomal 30

from sulfate. The flavoprotein component catalyzes the electron flow from NADPH - FAD - FMN to the hemoprotein component

, histidine, and tryptophan, or as a component of the pentose phosphate pathway

n an underwound state. Negative supercoiling favors strand separation, and DNA replication, transcription, recombination and repair, all of which
› that uracil cannot be incorporated into DNA

lysidine, thus changing the amino acid specificity of the tRNA from methionine to isoleucine

›nal helicase activity. Unwinds dsDNA until it encounters a Chi (crossover hotspot instigator) sequence from the 3' direction. Cuts ssDNA a few nuc
·acteristic of a DNA helicase with a 3'- to 5'- polarity. Unwinds branched duplex DNA (Y-DNA)
n after the ATP-dependent function of SecA

tunnel in the center of the 70S ribosome
cal function is to regenerate phosphatidylethanolamine from 2-acyl-glycero-3-phosphoethanolamine (2-acyl-GPE) formed by transacylation reactic

that read codons beginning with uridine

: compound that serves as the starting substrate for the three terminal pathways of aromatic amino acid biosynthesis. This reaction introduces a s

nbrane and the ATP-binding domain (NBD) is responsible for energy generation

ptidoglycan
ıe biosynthesis seems to be controlled primarily by regulation of HisG enzymatic activity

o ring

s a substrate although octanoyl-ACP is likely to be the physiological substrate

from sulfate

e complex also regulates trp repressor biosynthesis by binding to its regulatory region

scS) system

te of the peptidyltransferase center

centrally located replisome during cell division. Not required for mini-F plasmid partitioning. Probably acts via its interaction with MukB and MukE.

e sacculus
o UDP-4- amino-4-deoxy-L-arabinose (UDP-L-Ara4N) to form UDP-L-4-formamido- arabinose (UDP-L-Ara4FN). The modified arabinose is attached

; the hydrolysis of activated Val-AMP. The other activity is designated 'posttransfer' editing and involves deacylation of mischarged Val-tRNA(Ile)

harbors the promoter for the fimbrial structural gene, fimA. FimE switches fimA off

70S ribosome it contacts protein S13 of the 30S subunit (bridge B1b), connecting the 2 subunits

simultaneously chromosomal DNA and FtsZ, and disrupts the assembly of FtsZ polymers. SlmA-DNA-binding sequences (SBS) are dispersed on nor

ide units from the ends of the glycan chain
mpound is decarboxylated to form 4'-phosphopantotheine

nbrane and the ATP-binding domain (NBD) is responsible for energy generation

iosphate residues. It preferentially attacks modified AP sites created by bleomycin and neocarzinostatin

r)

iently binds. Helps modulate mRNA selection, yielding the 30S pre- initiation complex (PIC). Upon addition of the 50S ribosomal subunit IF-1, IF-2 a

-3-phosphate or AAP) to form pyridoxine 5'-phosphate (PNP) and inorganic phosphate
me a3 and Cu(B)

A to NqrE are probably involved in the second step, the conversion of ubisemiquinone to ubiquinol

e. Fe-containing acireductone dioxygenase (Fe-ARD) produces formate and 2-keto-4- methylthiobutyrate (KMTB), the alpha-ketoacid precursor of

ubstrate-level phosphorylation in the TCA. The beta subunit provides nucleotide specificity of the enzyme and binds the substrate succinate, while t

etrahydrofolate

ansfer reactions, allowing the 3' invading strand to extend heteroduplex DNA faster. Binds ssDNA in the presence of ADP but not other nucleotides,

he only animotransferase known to utilize SAM as an amino donor
rate of transcript degradation, and in the general RNA quality control

s is believed to be ubiquinone. Couples the redox reaction to proton translocation (for every two electrons transferred, four hydrogen ions are trans

n turn to TusE

from the DNA template

npR

ria to bypass the Krebs cycle via the glyoxylate shunt in response to the source of carbon. When bacteria are grown on glucose, IDH is fully active a

subunit (bridge B1b), connecting the 2 subunits

aneous catalytic core and F(0) containing the membrane proton channel, linked together by a central stalk and a peripheral stalk. During catalysis, A

aneous catalytic core and F(0) containing the membrane proton channel, linked together by a central stalk and a peripheral stalk. During catalysis, A

ı 1-pyrroline-5- carboxylate

ɔstrates concomitant with their translocation across the cell membrane

ents and suppressing the GTPase activity of FtsZ

The exact function of the psi subunit is

se , an adaptive process that allows bacteria to respond to amino acid starvation, resulting in the coordinated regulation of numerous cellular activ
nd glutamine to yield formylglycinamidine ribonucleotide (FGAM) and glutamate

phosphorylated active-site intermediate

ɔ-phosphate (Rib-5-P)

ı groups required for the biosynthesis of purines, thymidylate, methionine, and other important biomolecules. Also exhibits THF- independent aldo

nsert both dependently and independently of the Sec translocase complex, as well as at least some lipoproteins. Aids folding of multispanning me

ı component plays an auxiliary but essential role in vivo by binding to the 5'-leader sequence and broadening the substrate specificity of the ribozyr

olism

ns

:he carrier protein ThiS. In vitro, sulfur can be provided by H(2)S

tion of most mRNAs

-MurNAc- (pentapeptide)GlcNAc (lipid intermediate II)

)inding beta subunit (TrpG) of anthranilate synthase (AS) provides the glutamine amidotransferase activity which generates ammonia as a substra

hosphate (TMP)

ohate and OAA

ependent reaction

sis. Consistently, PPi-PFK can replace the enzymes of both the forward (ATP-PFK) and reverse (fructose-bisphosphatase (FBPase)) reactions

in reductase system

he chb promoter by the regulatory protein ChbR and the hydrolysis of phosphorylated beta-glucosides by the phospho- beta-glucosidase ChbF. Cata

thin the PG sacculus to allow for its expansion as well as for the insertion of various structures such as secretion systems and flagella

xA, leading to derepression of the SOS regulon and eventually DNA repair

ial for the maintenance of envelope integrity under bleach stress, rescuing a wide series of structurally unrelated periplasmic proteins from methi

4-hydroxybenzoate
ay
s nicks in the DNA strand. Cleaves the DNA backbone by beta-delta elimination to generate a single-strand break at the site of the removed base v

boxylase, or bind to the biotin operator site and inhibit transcription of the operon

nt selenocysteine lyase in vitro, that mobilizes selenium from L-selenocysteine. Selenocysteine lyase activity is however unsure in vivo

ent selenocysteine lyase in vitro, that mobilizes selenium from L-selenocysteine. Selenocysteine lyase activity is however unsure in vivo

ion proteins

nine functions in substrate recognition. Required for DNA damage lesion repair in stationary-phase cells

efects in genetic recombination and DNA repair associated with inactivation of ruvAB or ruvC

ism

vely. Catalyzes the coordinated movement of the two tRNA molecules, the mRNA and conformational changes in the ribosome

teine (RHC) to homocysteine (HC) and 4,5- dihydroxy-2,3-pentadione (DPD)

in translesional synthesis, in conjunction with the beta clamp from PolIII

ɣ the 30S ribosomal subunit

onal distinct editing activities against alanine. One activity is designated as 'pretransfer' editing and involves the tRNA(Pro)-independent hydrolysi

transient KdpB KdpC ATP ternary complex

eptide fragments that are 5 to 10 amino acids long. Binds to DNA in a double-stranded, site-specific manner

and 2',3'-cyclic phosphodiesterase activities. These phosphohydrolase activities are probably involved in the repair of the tRNA 3'-CCA terminus deg

ion

ntly accommodates folded Tat precursor proteins before their translocation

ound, RfaH suppresses pausing and inhibits Rho- dependent and intrinsic termination at a subset of sites. Termination signals are bypassed, which

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

ities

erved specific lysine residue in EF-P

atalytic role in this reaction

ıe C5 position

t

hydroxide mineral, which can be released after reduction. One hydrogen peroxide oxidizes two Fe(2) ions, which prevents hydroxyl radical product

ıtyrate (HMKB). In the reductase reaction, this 2-ketoacid undergoes a metal-dependent reduction by NADPH to yield (R)-2,3-dihydroxy-isovalerate

IA. Probably not involved in DNA repair

e phosphoryl group from phosphoenolpyruvate (PEP) to the phosphoryl carrier protein (HPr)

ivated

m mnm(5)s(2)U34

thin the PG sacculus to allow for its expansion as well as for the insertion of various structures such as secretion systems and flagella

ved. The second step is the nonenzymatic hydrolysis of the enamine imine intermediates to form 2-ketobutyrate and free ammonia. In the low wat

ivated

vely. Catalyzes the coordinated movement of the two tRNA molecules, the mRNA and conformational changes in the ribosome

involve strand separation. Also able to catalyze the interconversion of other topological isomers of dsDNA rings, including catenanes and knotted r

GlnD hydrolyzes PII-UMP to PII and UMP (deuridylylation). Thus, controls uridylylation state and activity of the PII proteins, and plays an important

ed sulfur from IscS, which is then transferred to TusD, and thus determines the direction of sulfur flow from IscS to 2-thiouridine formation. Also a

imination, leaving a 3'-terminal unsaturated sugar and a product with a terminal 5'-phosphate

es the oxidation of succinate to fumarate with the reduction of ubiquinone (coenzyme Q) to ubiquinol. Required for flavinylation (covalent attachm

ŋg and nucleotide specificity is provided by the beta subunit

ivated

ansfer the acetyl group from AcAMP to the sulfhydryl group of CoA, forming the product AcCoA

ial for the maintenance of envelope integrity under bleach stress, rescuing a wide series of structurally unrelated periplasmic proteins from methi

on of 16S rRNA

of protein maturation

from participating in the assembly of the Z ring. This mechanism prevents the premature segregation of damaged DNA to daughter cells during ce
uch as GreA or GreB allows the resumption of elongation from the new 3'terminus. GreB releases sequences of up to 9 nucleotides in length

Cleaves the DNA backbone by beta-delta elimination to generate a single-strand break at the site of the removed base with both 3'- and 5'-phospl

in reductase system

ed cluster of proteins S8, S12 and S17 appears to hold together the shoulder and platform of the 30S subunit

›r NADP for catalysis, however it has higher catalytic efficiency with NAD

located across the cytoplasmic membrane), and thus conserves the redox energy in a proton gradient

ion and elicit cellular responses. The membrane-spanning regulatory substrate protein is first cut periplasmically (site-1 protease, S1P, DegS), the

formyltetrahydrofolate or 5,10-methylenetetrahydrofolate, leading to folylpolyglutamate derivatives

way. The sulfur is donated as persulfide by IscS

heme

ıase and acetyl transacylase activities. Its substrate specificity determines the biosynthesis of branched- chain and or straight-chain of fatty acids

nsition from exponential growth to the stationary phase

C-terminal cysteine of HypE yielding a protein-S-carboxamide

ı intermediate chain length

slocation (PRE) complex, thus giving elongation factor G a second chance to translocate the tRNAs correctly. Binds to ribosomes in a GTP-depende

survive conditions outside the host

B and DnaK DnaJ GrpE. Its activity is ATP- independent

ınits dissociate and the UvrB-DNA preincision complex is formed. This complex is subsequently bound by UvrC and the second UvrB is released. If r

B and DnaK DnaJ GrpE. Its activity is ATP- independent

:leotides 3' to the Chi site. The properties and activities of the enzyme are changed at Chi. The Chi-altered holoenzyme produces a long 3'-ssDNA o

ıents such as peptidoglycan and lipopolysaccharide

nverted into UDP-GlcNAc by the transfer of uridine 5- monophosphate (from uridine 5-triphosphate), a reaction catalyzed by the N-terminal doma
located across the cytoplasmic membrane), and thus conserves the redox energy in a proton gradient

ion

RuvA stimulates, in the presence of DNA, the weak ATPase activity of RuvB

lactitol transport

located across the cytoplasmic membrane), and thus conserves the redox energy in a proton gradient
onding release of cytidine 5-monophosphate (CMP)

alytic tyrosine of the enzyme, resulting in the formation of a DNA-(5'-phosphotyrosyl)-enzyme intermediate and the expulsion of a 3'-OH DNA stra

versely, when nitrogen levels are low, the N-terminal adenylyl removase (AR) activates GlnA by removing the adenylyl group by phosphorolysis, inc

acellular de novo source of dTMP, an essential precursor for DNA biosynthesis

uch as GreA or GreB allows the resumption of elongation from the new 3'terminus. GreA releases sequences of 2 to 3 nucleotides

cks the C1' of nucleotide 34 to detach the guanine base from the RNA, forming a covalent enzyme-RNA intermediate. The proton acceptor active si

tion
located across the cytoplasmic membrane), and thus conserves the redox energy in a proton gradient

purine nucleotides from the nucleotide pool, thus preventing their incorporation into DNA RNA and avoiding chromosomal lesions

ll recycling

e periplasm of ligands bound by these outer membrane proteins

heme

vith RpoS, and the consequent delivery of the RssB-RpoS complex to the ClpXP protein degradation pathway

eading to septal peptidoglycan synthesis by FtsI and associated synthases

ydrophobic SecY resides and a short helix (helix 2A) on the extracellular side of the membrane which forms a plug. The plug probably moves latera

ubunit of DNA polymerase III (Pol III), a complex, multichain enzyme responsible for most of the replicative synthesis in bacteria

t, yielding cytoplasmic MurNAc-6-P. Is

rotein, as well as other S acceptor proteins

thus plays a role in cell wall recycling
ate that, along with chorismate, is used in the second step, catalyzed by the large alpha subunit of AS (TrpE) to produce anthranilate. In the absenc

ıe stepwise translocation of polypeptide chains across the membrane

ensation DNA from both sides of a centrally located replisome during cell division

located across the cytoplasmic membrane), and thus conserves the redox energy in a proton gradient. This subunit may bind ubiquinone

cleotides 3' to the Chi site. The properties and activities of the enzyme are changed at Chi. The Chi-altered holoenzyme produces a long 3'-ssDNA o

e dividing cells. Binds GTP and shows GTPase activity

ved. The second step is the nonenzymatic hydrolysis of the enamine imine intermediates to form 2-ketobutyrate and free ammonia. In the low wat
subunit 1 to the bimetallic center formed by heme A3 and copper B

; part of a final effector complex

alytic tyrosine of the enzyme, resulting in the formation of a DNA-(5'-phosphotyrosyl)-enzyme intermediate and the expulsion of a 3'-OH DNA stra

ewly replicated origins. Repression is relieved when the region becomes fully methylated

· FtsY. Interaction with FtsY leads to the transfer of the RNC complex to the Sec translocase for insertion into the membrane, the hydrolysis of GTP

· low GlcN6P concentrations, RapZ is sequestered and inactivated by an other regulatory small RNA, GlmY, preventing GlmZ degradation and leadi

located across the cytoplasmic membrane), and thus conserves the redox energy in a proton gradient

S subunits but not for 70S ribosomes

involve strand separation. Also able to catalyze the interconversion of other topological isomers of dsDNA rings, including catenanes and knotted r

cleotides 3' to the Chi site. The properties and activities of the enzyme are changed at Chi. The Chi-altered holoenzyme produces a long 3'-ssDNA c

ons or degradation by phospholipase A1

econd double bond into the aromatic ring system

Overexpression results in anucleate cells. It has a calcium binding activity

to lipid A and is required for resistance to polymyxin and cationic antimicrobial peptides

ı-Ter regions of the chromosome, preventing FtsZ polymerization at these regions

and IF-3 are released leaving the mature 70S translation initation complex

methionine in the methionine recycle pathway. Ni-containing acireductone dioxygenase (Ni-ARD) produces methylthiopropionate, carbon monoxid

:he binding sites for coenzyme A and phosphate are found in the alpha subunit

, has ATPase activity that is stimulated by ssDNA and various branched DNA structures, but inhibited by SSB. Does not have RecA's homology-searc

located across the cytoplasmic membrane), and thus conserves the redox energy in a proton gradient

ınd unphosphorylated, but when grown on acetate or ethanol, the activity of IDH declines drastically concomitant with its phosphorylation

ATP synthesis in the catalytic domain of F(1) is coupled via a rotary mechanism of the central stalk subunits to proton translocation

ATP synthesis in the catalytic domain of F(1) is coupled via a rotary mechanism of the central stalk subunits to proton translocation

ities

lase activity toward beta-hydroxyamino acids, producing glycine and aldehydes, via a retro-aldol mechanism

mbrane proteins

ɲe

ate that, along with chorismate, is used in the second step, catalyzed by the large alpha subunit of AS (TrpE) to produce anthranilate. In the absenc

lyzes the removal of only one acetyl group from chitobiose-6-P to yield monoacetylchitobiose-6-P, the inducer of ChbR and the substrate of ChbF

onine oxidation. The catalytic subunit MsrP is non-stereospecific, being able to reduce both (R-) and (S-) diastereoisomers of methionine sulfoxide

with both 3'- and 5'- phosphates

s of activated Ala-AMP. The other activity is designated 'posttransfer' editing and involves deacylation of mischarged Ala-tRNA(Pro). The misacyla

ɡraded by intracellular RNases

ı allows complete synthesis of long RNA chains

:ion by the Fenton reaction

ter environment of the cell, the second step is accelerated by RidA

ings. Type II topoisomerases break and join 2 DNA strands simultaneously in an ATP-dependent manner

: role in the regulation of nitrogen

appears to be involved in sulfur transfer for the biosynthesis of molybdopterin

ıent of FAD) of the flavoprotein subunit SdhA of SDH

onine oxidation. MsrQ provides electrons for reduction to the reductase catalytic subunit MsrP, using the quinone pool of the respiratory chain

ll division

nates

n within the membrane itself (site-2 protease, S2P, RseP), while cytoplasmic proteases finish degrading the anti-sigma factor, liberating sigma-E

nt manner

ıo lesion is found, the DNA wraps around the other UvrB subunit that will check the other stand for damage

verhang and facilitates RecA-binding to the ssDNA for homologous DNA recombination and repair. Holoenzyme degrades any linearized DNA that

in

nd. The free DNA strand then undergoes passage around the unbroken strand, thus removing DNA supercoils. Finally, in the religation step, the DN

creasing its activity. The regulatory region of GlnE binds the signal transduction protein PII (GlnB) which indicates the nitrogen status of the cell

ite deprotonates the incoming PreQ1, allowing a nucleophilic attack on the C1' of the ribose to form the product. After dissociation, two additional

lly to allow the channel to open. The ring and the pore may move independently

ce of TrpG, TrpE can synthesize anthranilate directly from chorismate and high concentrations of ammonia

verhang and facilitates RecA-binding to the ssDNA for homologous DNA recombination and repair. Holoenzyme degrades any linearized DNA that

ter environment of the cell, the second step is accelerated by RidA

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

ng to synthesis of GlmS

ings. Type II topoisomerases break and join 2 DNA strands simultaneously in an ATP-dependent manner

›verhang and facilitates RecA-binding to the ssDNA for homologous DNA recombination and repair. Holoenzyme degrades any linearized DNA that

e and formate, and does not lie on the methionine recycle pathway

ching function

ce of TrpG, TrpE can synthesize anthranilate directly from chorismate and high concentrations of ammonia

ted Cys- tRNA(Pro) is not edited by ProRS

is unable to undergo homologous recombination. In the holoenzyme this subunit recognizes the wild- type Chi sequence, and when added to isolat

IA 3'-OH attacks the covalent intermediate to expel the active-site tyrosine and restore the DNA phosphodiester backbone

enzymatic reactions on the tRNA convert PreQ1 to queuine (Q), resulting in the hypermodified nucleoside queuosine (7-(((4,5-cis-dihydroxy-2- cyc

is unable to undergo homologous recombination. In the holoenzyme this subunit contributes ATPase, 3'-5' helicase, exonuclease activity and loads

IA 3'-OH attacks the covalent intermediate to expel the active-site tyrosine and restore the DNA phosphodiester backbone

is unable to undergo homologous recombination. In the holoenzyme this subunit has ssDNA-dependent ATPase and 5'-3' helicase activity. When a

ted RecB increases its ATP-dependent helicase processivity

:lopenten-1-yl)amino)methyl)-7-deazaguanosine)

RecA onto ssDNA

ıdded to pre-assembled RecBC greatly stimulates nuclease activity and augments holoenzyme processivity. Negatively regulates the RecA-loading

ability of RecBCD