

Table S10 - expression profiles of shared genes between *A. baumannii* AB6870155 and *K. pneumoniae* KP6870155 in coculture vs. monoculture mapped to Biocyc pathways

Full Pathway				KP6870155		AB6870155	
Category	Name	Pathway	ID	gene	log2FC	log2FC	product
Stimulus_F	Proteins	l- Starvation Respo	EG10835	relA	-0.511	0.982	GDP/GTP pyrophosphokinase
Stimulus_F	Proteins	l- Starvation Respo	EG10977	sspA	-0.926	-0.467	stringent starvation protein A
Stimulus_F	Proteins	l- Starvation Respo	EG10966	spoT	-1.098	-0.172	bifunctional (p)ppGpp synthase/hydrolase SpoT
Stimulus_F	Proteins	l- Starvation Respo	EG10572	mazG	-1.665	0.19	nucleoside triphosphate pyrophosphohydrolase
Stimulus_F	Proteins	l- Starvation Respo	EG10167	cstA	0.373	-0.617	carbon starvation protein A
Stimulus_F	Proteins	l- Starvation Respo	EG10735	phoU	-0.423	-0.6	negative regulator of the pho regulon
Stimulus_F	Proteins	l- Starvation Respo	EG11209	psiE	1.457	-0.74	putative phosphate starvation-inducible protein PsiE
Stimulus_F	Proteins	l- Starvation Respo	EG10733	phoR	-0.729	-0.506	sensor histidine kinase PhoR
Stimulus_F	Proteins	l- Starvation Respo	EG10072	argT	-0.554	-0.254	lysine/arginine/ornithine ABC transporter periplasmic binding pr
Stimulus_F	Proteins	l- Starvation Respo	G7038	dcyD	1.114	-0.313	D-cysteine desulfhydrase
Stimulus_F	Proteins	l- Starvation Respo	G6217	tauA	2.153	-2.318	taurine ABC transporter periplasmic binding protein
Stimulus_F	Proteins	l- Starvation Respo	EG10872	rplK	-3.399	2.273	50S ribosomal subunit protein L11
Stimulus_F	Proteins	l- Starvation Respo	G7748	nfuA	-0.202	1.33	iron-sulfur cluster carrier protein NfuA
Stimulus_F	Proteins	l- Starvation Respo	EG11577	leuB	0.548	-0.014	3-isopropylmalate dehydrogenase
Stimulus_F	Proteins	l- Heat Response	EG10896	rpoD	0.399	1.815	RNA polymerase, sigma 70 (sigma D) factor
Stimulus_F	Proteins	l- Heat Response	EG11345	hflD	0.243	-0.753	lysogenization regulator
Stimulus_F	Proteins	l- Heat Response	EG10461	htpG	-3.902	2.793	chaperone protein HtpG
Stimulus_F	Proteins	l- Heat Response	G7744	hslO	-0.552	2.225	molecular chaperone Hsp33
Stimulus_F	Proteins	l- Heat Response	EG10599	groL	-2.367	3.304	chaperonin GroEL
Stimulus_F	Proteins	l- Heat Response	EG10600	groS	-2.666	4.238	cochaperonin GroES
Stimulus_F	Proteins	l- Heat Response	EG11393	dsbB	-2.303	0.749	protein thiol:quinone oxidoreductase DsbBReduced
Stimulus_F	Proteins	l- Heat Response	EG11595	moaA	1.558	0.073	GTP 3',8'-cyclase
Stimulus_F	Proteins	l- Heat Response	EG11144	yfcA	-2.614	0.04	putative transporter YfcA
Stimulus_F	Proteins	l- Heat Response	EG11852	dtd	-1.017	1.039	D-aminoacyl-tRNA deacylase

Stimulus_F Proteins l Heat Response	EG11837	bipA	-0.475	1.467	50S ribosomal subunit assembly factor BipA
Stimulus_F Proteins l Heat Response	EG10743	pnp	-0.553	-1.652	polynucleotide phosphorylase
Stimulus_F Proteins l Heat Response	EG12633	nudF	-1.223	-0.671	ADP-sugar pyrophosphatase
Stimulus_F Proteins l Heat Response	G6477	ssuD	-0.273	-1.791	FMNH2-dependent alkanesulfonate monooxygenase
Stimulus_F Proteins l Heat Response	EG11003	tig	-2.353	0.398	trigger factor
Stimulus_F Proteins l Heat Response	G6463	clpS	1.336	-0.027	specificity factor for ClpA-ClpP chaperone-protease complex
Stimulus_F Proteins l Heat Response	EG10897	rpoH	-0.094	1.082	RNA polymerase, sigma 32 (sigma H) factor
Stimulus_F Proteins l Heat Response	G6362	ybeY	0.573	-0.711	endoribonuclease YbeY
Stimulus_F Proteins l Heat Response	EG10437	hflX	-0.096	-0.265	ribosome rescue factor HflX
Stimulus_F Proteins l Heat Response	EG10416	grpE	-1.164	3.874	nucleotide exchange factor GrpE
Stimulus_F Proteins l Heat Response	EG10240	dnaJ	0.834	3.71	chaperone protein DnaJ
Stimulus_F Proteins l Heat Response	G7647	yhbO	-0.602	0.194	protein/nucleic acid deglycase 2
Stimulus_F Proteins l Heat Response	EG10157	clpB	0.611	1.356	ClpB80
Stimulus_F Proteins l Heat Response	EG10156	clpA	0.392	-0.303	ATP-dependent Clp protease ATP-binding subunit ClpA
Stimulus_F Proteins l Heat Response	EG10735	phoU	-0.423	-0.6	negative regulator of the pho regulon
Stimulus_F Proteins l Heat Response	EG11291	loiP	0.149	0.119	metalloprotease LoiP
Stimulus_F Proteins l Heat Response	EG10595	miaA	-0.344	1.252	tRNA dimethylallyltransferase
Stimulus_F Proteins l Heat Response	G7743	hslR	-0.385	1.371	heat shock protein Hsp15
Stimulus_F Proteins l Cold Response	G7241	lpxP	-0.555	-1.42	palmitoleoyl acyltransferase
Stimulus_F Proteins l Cold Response	EG11178	rbfA	-0.282	0.532	30S ribosome binding factor
Stimulus_F Proteins l Cold Response	EG11259	rnr	0.418	-0.175	RNase R
Stimulus_F Proteins l Cold Response	EG10529	lepA	-0.673	0.031	30S ribosomal subunit biogenesis factor LepA
Stimulus_F Proteins l Cold Response	EG10506	infC	-1.165	0.798	translation initiation factor IF-3
Stimulus_F Proteins l Cold Response	EG11837	bipA	-0.475	1.467	50S ribosomal subunit assembly factor BipA
Stimulus_F Proteins l Cold Response	G6938	ves	0.502	-0.785	HutD family protein Ves
Stimulus_F Proteins l Cold Response	EG12130	hscA	-1.569	0.685	iron-sulfur cluster biosynthesis chaperone HscA
Stimulus_F Proteins l Cold Response	EG10215	deaD	-2.19	-2.847	ATP-dependent RNA helicase DeaD
Stimulus_F Proteins l Cold Response	EG11752	otsB	1.361	2.141	trehalose-6-phosphate phosphatase
Stimulus_F Proteins l Cold Response	EG11751	otsA	0.438	1.798	trehalose-6-phosphate synthase
Stimulus_F Proteins l DNA Damage Re	EG10230	dksA	1.138	0.95	RNA polymerase-binding transcription factor DksA

Stimulus_F Proteins l DNA Damage Re: EG10861	rnhB	-0.146	-0.281	RNase HII
Stimulus_F Proteins l DNA Damage Re: G6115	dinB	0.682	0.6	DNA polymerase IV
Stimulus_F Proteins l DNA Damage Re: G6136	mmuM	0.225	-1.181	CP4-6 prophage; homocysteine S-methyltransferase
Stimulus_F Proteins l DNA Damage Re: EG10834	recR	-0.47	-0.759	DNA repair protein RecR
Stimulus_F Proteins l DNA Damage Re: EG10461	htpG	-3.902	2.793	chaperone protein HtpG
Stimulus_F Proteins l DNA Damage Re: G6256	fsr	-0.868	-0.143	fosmidomycin efflux pump
Stimulus_F Proteins l DNA Damage Re: EG11104	entS	0.344	0.403	enterobactin exporter EntS
Stimulus_F Proteins l DNA Damage Re: EG10736	phr	1.34	-0.289	deoxyribodipyrimidine photolyase
Stimulus_F Proteins l DNA Damage Re: G6489	uup	0.195	1.196	ATP-binding protein Uup
Stimulus_F Proteins l DNA Damage Re: EG11619	mfd	0.305	0.107	transcription-repair coupling factor
Stimulus_F Proteins l DNA Damage Re: EG11314	purB	-3.834	-1.376	adenylosuccinate lyase
Stimulus_F Proteins l DNA Damage Re: G6643	puuP	-0.618	0.221	putrescine:H ⁺ symporter PuuP
Stimulus_F Proteins l DNA Damage Re: EG10668	ogt	-0.261	0.181	methylated-DNA--[protein]-cysteine S-methyltransferase
Stimulus_F Proteins l DNA Damage Re: G6718	paaJ	-3.848	0.427	CE $\leq$ -ketoadipyl-CoA thiolase
Stimulus_F Proteins l DNA Damage Re: EG10030	add	-1.259	-0.114	adenosine deaminase
Stimulus_F Proteins l DNA Damage Re: EG10662	nth	-0.162	0.537	endonuclease III
Stimulus_F Proteins l DNA Damage Re: EG11547	rnt	-1.276	-1.165	RNase T
Stimulus_F Proteins l DNA Damage Re: EG10509	katE	-0.414	1.55	catalase HP1I
Stimulus_F Proteins l DNA Damage Re: EG10663	nadE	-0.718	-0.394	NH ₃ -dependent NAD ⁺ synthetase
Stimulus_F Proteins l DNA Damage Re: G7016	exoX	-1.739	0.797	exonuclease X
Stimulus_F Proteins l DNA Damage Re: RUVA	ruvA	-0.836	0.414	Holliday junction branch migration complex subunit RuvA
Stimulus_F Proteins l DNA Damage Re: EG10925	ruvC	-0.512	-0.508	crossover junction endodeoxyribonuclease RuvC
Stimulus_F Proteins l DNA Damage Re: EG11751	otsA	0.438	1.798	trehalose-6-phosphate synthase
Stimulus_F Proteins l DNA Damage Re: EG11063	uvrC	-0.598	1.971	excision nuclease subunit C
Stimulus_F Proteins l DNA Damage Re: EG10444	hisA	-0.548	0.029	1-(5-phosphoribosyl)-5-[(5-phosphoribosylamino)methylideneam
Stimulus_F Proteins l DNA Damage Re: EG10037	alkB	-0.524	1.243	DNA oxidative demethylase
Stimulus_F Proteins l DNA Damage Re: G7184	alaA	-1.27	-0.396	glutamate--pyruvate aminotransferase AlaA
Stimulus_F Proteins l DNA Damage Re: EG10249	dsdA	0.03	0.826	D-serine ammonia-lyase
Stimulus_F Proteins l DNA Damage Re: EG10534	ligA	-1.559	-0.32	DNA ligase
Stimulus_F Proteins l DNA Damage Re: EG10799	purN	-2.398	0.496	phosphoribosylglycinamide formyltransferase 1

Stimulus_F Proteins l DNA Damage Re: EG10832	recO	-0.769	-0.246	DNA repair protein RecO
Stimulus_F Proteins l DNA Damage Re: EG11058	ung	-1.525	-0.126	uracil-DNA glycosylase
Stimulus_F Proteins l DNA Damage Re: EG10831	recN	0.111	-0.3	DNA repair protein RecN
Stimulus_F Proteins l DNA Damage Re: EG12080	recX	-0.27	1.028	RecA inhibitor RecX
Stimulus_F Proteins l DNA Damage Re: EG10823	recA	0.96	0.456	DNA recombination/repair protein RecA
Stimulus_F Proteins l DNA Damage Re: EG10625	mutS	-1.27	-1.387	DNA mismatch repair protein MutS
Stimulus_F Proteins l DNA Damage Re: EG10826	recD	-1.861	-0.186	exodeoxyribonuclease V subunit RecD
Stimulus_F Proteins l DNA Damage Re: EG10824	recB	-1.491	0.129	exodeoxyribonuclease V subunit RecB
Stimulus_F Proteins l DNA Damage Re: EG10825	recC	-0.755	-0.461	exodeoxyribonuclease V subunit RecC
Stimulus_F Proteins l DNA Damage Re: EG10830	recJ	-1.816	-0.258	ssDNA-specific exonuclease RecJ
Stimulus_F Proteins l DNA Damage Re: G7525	yqgF	1.245	-0.145	ribonuclease H-like domain containing nuclease
Stimulus_F Proteins l DNA Damage Re: EG10627	mutY	-0.902	-0.025	adenine DNA glycosylase
Stimulus_F Proteins l DNA Damage Re: G7647	yhbO	-0.602	0.194	protein/nucleic acid deglycase 2
Stimulus_F Proteins l DNA Damage Re: EG11178	rbfA	-0.282	0.532	30S ribosome binding factor
Stimulus_F Proteins l DNA Damage Re: EG11871	gph	-0.971	-0.101	phosphoglycolate phosphatase
Stimulus_F Proteins l DNA Damage Re: G7742	yrfG	0.76	0.573	purine nucleotidase
Stimulus_F Proteins l DNA Damage Re: EG12102	feoB	-2.241	-1.547	Fe ²⁺ transporter FeoB
Stimulus_F Proteins l DNA Damage Re: EG10986	tag	-0.699	-0.289	3-methyl-adenine DNA glycosylase I, constitutive
Stimulus_F Proteins l DNA Damage Re: EG11961	lldP	-2.273	0.606	lactate/glycolate:H ⁺ symporter LldP
Stimulus_F Proteins l DNA Damage Re: EG10329	mutM	-0.431	0.188	DNA-formamidopyrimidine glycosylase
Stimulus_F Proteins l DNA Damage Re: EG10829	recG	-1.864	-0.102	ATP-dependent DNA helicase RecG
Stimulus_F Proteins l DNA Damage Re: EG10242	dnaN	-1.232	-0.058	Ø ₆₄ sliding clamp
Stimulus_F Proteins l DNA Damage Re: EG10746	polA	0.763	-0.118	DNA polymerase I
Stimulus_F Proteins l DNA Damage Re: EG10398	glpK	0.274	-0.238	glycerol kinase
Stimulus_F Proteins l DNA Damage Re: EG10763	priA	-0.874	-0.533	primosomal protein N'
Stimulus_F Proteins l DNA Damage Re: EG10064	argB	-1.92	0.471	acetylglutamate kinase
Stimulus_F Proteins l DNA Damage Re: EG10792	purD	-0.47	-0.804	phosphoribosylamine--glycine ligase
Stimulus_F Proteins l DNA Damage Re: EG11061	uvrA	-1.562	1.685	excision nuclease subunit A
Stimulus_F Proteins l DNA Damage Re: EG10976	ssb	2.338	1.296	ssDNA-binding protein
Stimulus_F Proteins l DNA Damage Re: EG10357	fumB	1.864	1.605	fumarase B

Stimulus_F Proteins I	DNA Damage Re: EG11281	mutL	-1.659	0.053	DNA mismatch repair protein MutL
Stimulus_F Proteins I	DNA Damage Re: EG10790	purA	-0.652	-1.525	adenylosuccinate synthetase
Stimulus_F Proteins I	DNA Damage Re: EG11296	radA	-2.417	0.217	DNA recombination protein
Stimulus_F Proteins I	Osmotic Stress R EG10269	envZ	-0.232	-0.789	sensor histidine kinase EnvZ
Stimulus_F Proteins I	Osmotic Stress R EG11752	otsB	1.361	2.141	trehalose-6-phosphate phosphatase
Stimulus_F Proteins I	Osmotic Stress R EG11751	otsA	0.438	1.798	trehalose-6-phosphate synthase
Stimulus_F Proteins I	Osmotic Stress R EG10109	betA	0.13	-0.558	choline dehydrogenase
Stimulus_F Proteins I	Osmotic Stress R EG10509	katE	-0.414	1.55	catalase HP1
Stimulus_F Proteins I	Osmotic Stress R EG10418	gshA	0.525	-0.038	glutamate--cysteine ligase
Stimulus_F Proteins I	Osmotic Stress R EG10529	lepA	-0.673	0.031	30S ribosomal subunit biogenesis factor LepA
Stimulus_F Proteins I	Osmotic Stress R EG11143	ubiG	-0.471	0.639	bifunctional 3-demethylubiquinone-8 3-O-methyltransferase and
Stimulus_F Proteins I	Osmotic Stress R EG11291	loiP	0.149	0.119	metalloprotease LoiP
Stimulus_F Proteins I	pH Response EG10529	lepA	-0.673	0.031	30S ribosomal subunit biogenesis factor LepA
Stimulus_F Proteins I	pH Response G7647	yhbO	-0.602	0.194	protein/nucleic acid deglycase 2
Stimulus_F Proteins I	pH Response EG10997	mnmA	-1.361	0.871	5-carboxymethylaminomethyluridine-tRNA synthase GTPase sul
Stimulus_F Proteins I	pH Response EG10735	phoU	-0.423	-0.6	negative regulator of the pho regulon
Stimulus_F Proteins I	pH Response EG11211	epmA	0.395	0.053	EF-P-lysine lysyltransferase
Stimulus_F Detoxifica	Detoxification Pr EG50010	frmA	1.617	0.148	S-(hydroxymethyl)glutathione dehydrogenase
Stimulus_F Detoxifica	Detoxification Pr G6461	macA	-0.357	0.344	ABC-type tripartite efflux pump membrane fusion protein
Stimulus_F Detoxifica	Detoxification Pr G6462	macB	-0.236	0.08	ABC-type tripartite efflux pump ATP binding/membrane subunit
Stimulus_F Detoxifica	Detoxification Pr EG10249	dsdA	0.03	0.826	D-serine ammonia-lyase
Stimulus_F Oxidant D	Oxidant Detoxific G7193	yfcF	-1.17	0.308	glutathione S-transferase YfcF
Stimulus_F Oxidant D	Oxidant Detoxific EG12294	grxC	0.206	2.129	oxidized glutaredoxin 3
Stimulus_F Oxidant D	Oxidant Detoxific EG10108	bcp	0.204	0.571	thiol peroxidase
Stimulus_F Oxidant D	Oxidant Detoxific EG10129	btuE	-0.996	-1.022	thioredoxin/glutathione peroxidase
Stimulus_F Oxidant D	Oxidant Detoxific EG10511	katG	0.743	0.489	catalase/hydroperoxidase HP1
Stimulus_F Oxidant D	Oxidant Detoxific G7553	yghU	0.684	0.026	disulfide reductase / organic hydroperoxide reductase
Stimulus_F Oxidant D	Oxidant Detoxific EG10509	katE	-0.414	1.55	catalase HP1
Stimulus_F Oxidant D	Oxidant Detoxific EG10954	sodB	0.358	1.587	superoxide dismutase (Fe)
Stimulus_F Other Pro	Other EG10011	yaaA	0.062	0.033	DNA binding and peroxide stress response protein YaaA

Stimulus_F Other Pro: Other	EG10492	ileS	-2.101	-0.506	isoleucine--tRNA ligase
Stimulus_F Other Pro: Other	EG10048	apaH	-1.148	0.322	diadenosine tetraphosphatase
Stimulus_F Other Pro: Other	EG10523	rsmA	1.51	-0.022	16S rRNA m62A1518,m62A1519 dimethyltransferase
Stimulus_F Other Pro: Other	EG11569	lptD	0.645	-0.015	lipopolysaccharide assembly protein LptD
Stimulus_F Other Pro: Other	EG11577	leuB	0.548	-0.014	3-isopropylmalate dehydrogenase
Stimulus_F Other Pro: Other	EG12320	yadG	0.736	-0.715	putative ABC transporter ATP-binding protein YadG
Stimulus_F Other Pro: Other	EG10605	mrcB	-0.486	-0.255	PBP1BCE $\geq$
Stimulus_F Other Pro: Other	EG12436	rseP	-0.733	-0.148	intramembrane zinc metalloprotease RseP
Stimulus_F Other Pro: Other	M012	mhpC	0.297	0.646	2-hydroxy-6-ketono-2,4-dienedioate hydrolase
Stimulus_F Other Pro: Other	G6217	tauA	2.153	-2.318	taurine ABC transporter periplasmic binding protein
Stimulus_F Other Pro: Other	EG10928	sbmA	-1.261	-0.708	peptide antibiotic/peptide nucleic acid transporter
Stimulus_F Other Pro: Other	EG10728	phoB	0.981	0.479	Phosphorylated DNA-binding transcriptional dual regulator PhoB
Stimulus_F Other Pro: Other	EG10733	phoR	-0.729	-0.506	sensor histidine kinase PhoR
Stimulus_F Other Pro: Other	EG10812	queA	-2.438	0.39	tRNA preQ134 S-adenosylmethionine ribosyltransferase-isomer
Stimulus_F Other Pro: Other	EG10704	pgpA	1.116	0.276	phosphatidylglycerophosphatase A
Stimulus_F Other Pro: Other	EG11703	acrA	-1.811	-2.56	multidrug efflux pump membrane fusion lipoprotein AcrA
Stimulus_F Other Pro: Other	EG11100	ybaB	0.864	0.453	putative nucleoid-associated protein YbaB
Stimulus_F Other Pro: Other	EG10431	hemH	0.33	-0.099	ferrochelataase
Stimulus_F Other Pro: Other	EG12454	ybaK	0.287	0.552	Cys-tRNA ^{Pro} and Cys-tRNA ^{Cys} deacylase
Stimulus_F Other Pro: Other	G6318	cusS	0.039	-0.296	CusS-N-phospho-L-histidine
Stimulus_F Other Pro: Other	EG10167	cstA	0.373	-0.617	carbon starvation protein A
Stimulus_F Other Pro: Other	EG10517	kdpE	-0.11	-0.977	KdpE-Phosphorylated
Stimulus_F Other Pro: Other	EG10516	kdpD	0.594	-0.207	sensor histidine kinase KdpD
Stimulus_F Other Pro: Other	EG11008	tolB	-1.936	0.239	Tol-Pal system periplasmic protein TolB
Stimulus_F Other Pro: Other	EG12427	modA	-1.715	1.605	molybdate ABC transporter periplasmic binding protein
Stimulus_F Other Pro: Other	G6439	ybjG	0.847	0.701	undecaprenyl pyrophosphate phosphatase
Stimulus_F Other Pro: Other	G6461	macA	-0.357	0.344	ABC-type tripartite efflux pump membrane fusion protein
Stimulus_F Other Pro: Other	G6462	macB	-0.236	0.08	ABC-type tripartite efflux pump ATP binding/membrane subunit
Stimulus_F Other Pro: Other	EG11265	cmk	0.346	0.562	cytidylate kinase
Stimulus_F Other Pro: Other	G6475	gloC	1.386	0.925	hydroxyacylglutathione hydrolase GloC

Stimulus_F Other Pro Other	EG10801	putA	-0.647	-0.46	fused DNA-binding transcriptional repressor / proline dehydroge
Stimulus_F Other Pro Other	EG10890	rpmF	-2.098	0.87	50S ribosomal subunit protein L32
Stimulus_F Other Pro Other	EG50003	acpP	0.524	0.277	octanoyl-ACP
Stimulus_F Other Pro Other	G6569	comR	0.494	1.445	DNA-binding transcriptional repressor ComR
Stimulus_F Other Pro Other	G6577	cobB	0.277	0.032	CobB-S
Stimulus_F Other Pro Other	EG11404	ychF	-0.148	1.8	redox-responsive ATPase YchF
Stimulus_F Other Pro Other	EG11325	acnA	1.373	1.446	aconitate hydratase 1
Stimulus_F Other Pro Other	EG11528	fabI	-0.122	0.666	enoyl-[acyl-carrier-protein] reductase
Stimulus_F Other Pro Other	EG10777	pspB	2.455	-0.968	phage shock protein B
Stimulus_F Other Pro Other	G6708	paaZ	-3.501	0.382	fused 3-oxo-5,6-dehydrosueryl-CoA semialdehyde dehydrogena
Stimulus_F Other Pro Other	G6709	paaA	-5.021	1.126	phenylacetyl-CoA 1,2-epoxidase, monooxygenase subunit
Stimulus_F Other Pro Other	G6710	paaB	-3.909	1.115	phenylacetyl-CoA 1,2-epoxidase subunit B
Stimulus_F Other Pro Other	G6711	paaC	-4.822	1.134	phenylacetyl-CoA 1,2-epoxidase, structural subunit
Stimulus_F Other Pro Other	G6712	paaD	-5.99	1.192	phenylacetate degradation protein
Stimulus_F Other Pro Other	G6713	paaE	-4.088	1.196	phenylacetyl-CoA 1,2-epoxidase, reductase subunit
Stimulus_F Other Pro Other	G6715	paaG	-3.55	0.88	putative ring 1,2-epoxyphenylacetyl-CoA isomerase (oxepin-CoA
Stimulus_F Other Pro Other	G6719	paaK	-2.225	0.205	phenylacetate-CoA ligase
Stimulus_F Other Pro Other	G6720	paaX	0.791	-0.538	DNA-binding transcriptional repressor PaaX
Stimulus_F Other Pro Other	G6864	rstA	-0.512	0.134	Phosphorylated DNA-binding transcriptional regulator RstA
Stimulus_F Other Pro Other	EG10358	fumC	0.721	-1.154	fumarase C
Stimulus_F Other Pro Other	G6889	nemR	0.676	1.872	DNA-binding transcriptional repressor NemR
Stimulus_F Other Pro Other	G6890	nemaA	1.149	0.75	N-ethylmaleimide reductase
Stimulus_F Other Pro Other	G6891	gloA	-1.408	2.349	glyoxalase I
Stimulus_F Other Pro Other	EG10710	pheT	0.937	-0.471	phenylalanine--tRNA ligase subunit Cε
Stimulus_F Other Pro Other	EG10709	pheS	-2.117	-0.528	phenylalanine--tRNA ligase subunit Cε
Stimulus_F Other Pro Other	EG11001	thrS	-0.405	0.37	threonine--tRNA ligase
Stimulus_F Other Pro Other	EG12394	msrB	0.198	0.18	methionine sulfoxide reductase B
Stimulus_F Other Pro Other	G6977	nimT	0.439	0.249	2-nitroimidazole exporter
Stimulus_F Other Pro Other	EG11530	fadD	1.067	-1.658	long-chain-fatty-acid--CoA ligase
Stimulus_F Other Pro Other	EG10760	prc	0.012	-0.244	tail-specific protease

Stimulus_F Other Pro Other	G7014	yobA	-0.39	0.548	CopC domain-containing protein
Stimulus_F Other Pro Other	G7018	znuC	-0.892	0.026	Zn ²⁺ ABC transporter ATP binding subunit
Stimulus_F Other Pro Other	EG12368	znuB	-2.051	0.342	Zn ²⁺ ABC transporter membrane subunit
Stimulus_F Other Pro Other	G7038	dcyD	1.114	-0.313	D-cysteine desulfhydrase
Stimulus_F Other Pro Other	EG11418	dcd	-1.016	0.373	dCTP deaminase
Stimulus_F Other Pro Other	EG11618	baeR	-0.621	-0.351	Phosphorylated DNA-binding transcriptional activator BaeR
Stimulus_F Other Pro Other	EG12006	btsR	-1.729	-0.633	Phosphorylated DNA-binding transcriptional dual regulator BtsR
Stimulus_F Other Pro Other	EG11337	lysP	-0.898	-0.504	lysine:H ⁺ symporter
Stimulus_F Other Pro Other	EG10885	rplY	-1.984	1.618	50S ribosomal subunit protein L25
Stimulus_F Other Pro Other	EG10423	gyrA	-1.844	-0.652	DNA gyrase subunit A
Stimulus_F Other Pro Other	G7167	arnC	0.529	-0.966	undecaprenyl-phosphate 4-deoxy-4-formamido-L-arabinose tran
Stimulus_F Other Pro Other	G7170	arnT	-0.793	-0.084	lipid IVA 4-amino-4-deoxy-L-arabinosyltransferase
Stimulus_F Other Pro Other	EG10072	argT	-0.554	-0.254	lysine/arginine/ornithine ABC transporter periplasmic binding pr
Stimulus_F Other Pro Other	EG10580	mepA	-2.092	-0.477	peptidoglycan DD-endopeptidase/peptidoglycan LD-endopeptida
Stimulus_F Other Pro Other	EG10421	guaB	-0.735	0.68	inosine 5'-monophosphate dehydrogenase
Stimulus_F Other Pro Other	EG12401	rlmN	-0.233	0.183	23S rRNA m2A2503 methyltransferase/tRNA m2A37 methyltra
Stimulus_F Other Pro Other	EG10408	glyA	-2.967	0.691	serine hydroxymethyltransferase
Stimulus_F Other Pro Other	EG10456	hmp	-0.795	1.432	nitric oxide dioxygenase
Stimulus_F Other Pro Other	EG12880	dgcN	-1.174	-0.954	diguanylate cyclase DgcN
Stimulus_F Other Pro Other	EG10952	bamE	-0.48	0.678	outer membrane protein assembly factor BamE
Stimulus_F Other Pro Other	EG10186	cysD	-2.495	1.049	sulfate adenylyltransferase subunit 2
Stimulus_F Other Pro Other	EG10572	mazG	-1.665	0.19	nucleoside triphosphate pyrophosphohydrolase
Stimulus_F Other Pro Other	EG10835	relA	-0.511	0.982	GDP/GTP pyrophosphokinase
Stimulus_F Other Pro Other	EG11002	thyA	-0.966	-0.248	thymidylate synthase
Stimulus_F Other Pro Other	EG12188	ptsP	-1.02	-0.025	PtsP-phosphorylated
Stimulus_F Other Pro Other	EG11324	ubiH	-0.578	-0.571	2-octaprenyl-6-methoxyphenol 4-hydroxylase
Stimulus_F Other Pro Other	EG10687	parE	-0.81	-0.273	DNA topoisomerase IV subunit B
Stimulus_F Other Pro Other	EG11009	tolC	0.015	0.407	outer membrane channel TolC
Stimulus_F Other Pro Other	EG11665	bacA	-0.645	-0.074	undecaprenyl pyrophosphate phosphatase
Stimulus_F Other Pro Other	EG12147	npr	0.022	0.374	Npr phosphorylated

Stimulus_F Other Pro: Other	EG10977	sspA	-0.926	-0.467	stringent starvation protein A
Stimulus_F Other Pro: Other	EG11652	degS	0.495	0.555	serine endoprotease
Stimulus_F Other Pro: Other	EG11311	dusB	-2.096	-0.355	tRNA-dihydrouridine synthase B
Stimulus_F Other Pro: Other	EG10317	fis	-1.11	-0.32	DNA-binding transcriptional dual regulator Fis
Stimulus_F Other Pro: Other	EG10903	rpsD	-2.155	0.66	30S ribosomal subunit protein S4
Stimulus_F Other Pro: Other	EG10904	rpsE	-1.721	1.148	30S ribosomal subunit protein S5
Stimulus_F Other Pro: Other	EG10869	rplF	-2.061	1.375	50S ribosomal subunit protein L6
Stimulus_F Other Pro: Other	EG10916	rpsQ	-1.558	1.906	30S ribosomal subunit protein S17
Stimulus_F Other Pro: Other	EG10882	rplV	-1.868	1.753	50S ribosomal subunit protein L22
Stimulus_F Other Pro: Other	EG10867	rplD	-2.778	2.173	50S ribosomal subunit protein L4
Stimulus_F Other Pro: Other	EG10911	rpsL	-0.447	2.627	30S ribosomal subunit protein S12
Stimulus_F Other Pro: Other	EG10081	aroK	-1.714	-0.25	shikimate kinase 1
Stimulus_F Other Pro: Other	EG10748	mrcA	0.098	-0.227	peptidoglycan glycosyltransferase / peptidoglycan DD-transpept
Stimulus_F Other Pro: Other	G7746	yhgF	-0.142	-0.592	putative RNA-binding protein YhgF
Stimulus_F Other Pro: Other	G7748	nfuA	-0.202	1.33	iron-sulfur cluster carrier protein NfuA
Stimulus_F Other Pro: Other	EG10187	cysE	-0.596	0.366	serine acetyltransferase
Stimulus_F Other Pro: Other	EG12296	gpmM	0.309	-0.191	2,3-bisphosphoglycerate-independent phosphoglycerate mutase
Stimulus_F Other Pro: Other	EG10891	rpmG	-2.074	2.118	50S ribosomal subunit protein L33
Stimulus_F Other Pro: Other	EG10966	spoT	-1.098	-0.172	bifunctional (p)ppGpp synthase/hydrolase SpoT
Stimulus_F Other Pro: Other	EG10424	gyrB	-0.001	-0.399	DNA gyrase subunit B
Stimulus_F Other Pro: Other	EG10375	mnmG	-0.824	0.232	5-carboxymethylaminomethyluridine-tRNA synthase subunit Mr
Stimulus_F Other Pro: Other	EG10093	asnC	0.026	-0.791	DNA-binding transcriptional dual regulator AsnC
Stimulus_F Other Pro: Other	EG11541	kup	-0.26	0.297	K ⁺ :H ⁺ symporter Kup
Stimulus_F Other Pro: Other	EG11479	tatC	-0.067	0.791	twin arginine protein translocation system - TatC protein
Stimulus_F Other Pro: Other	EG11297	dsbA	0.94	1.065	thiol:disulfide oxidoreductase - DsbA _{reduced}
Stimulus_F Other Pro: Other	EG10387	glnL	0.905	-0.845	sensory histidine kinase NtrB
Stimulus_F Other Pro: Other	EG10872	rplK	-3.399	2.273	50S ribosomal subunit protein L11
Stimulus_F Other Pro: Other	EG10894	rpoB	-1.791	-0.953	RNA polymerase subunit β
Stimulus_F Other Pro: Other	EG10895	rpoC	-0.146	-0.827	RNA polymerase subunit β'
Stimulus_F Other Pro: Other	EG10702	pgi	-0.83	0.101	glucose-6-phosphate isomerase

Stimulus_F Other Pro Other	EG11209	psiE	1.457	-0.74	putative phosphate starvation-inducible protein PsiE
Stimulus_F Other Pro Other	EG10224	dgkA	-3.379	-0.259	diacylglycerol kinase
Stimulus_F Other Pro Other	EG10957	soxR	1.744	0.712	DNA-binding transcriptional dual regulator SoxR
Stimulus_F Other Pro Other	EG11613	eptA	-0.706	0.055	phosphoethanolamine transferase EptA
Stimulus_F Other Pro Other	EG11433	msrA	0.515	0.277	methionine sulfoxide reductase A
Stimulus_F Other Pro Other	EG12525	mgtA	-0.154	2.412	Mg2+ importing P-type ATPase
Stimulus_F Other Pro Other	G7924	hypT	-0.596	-0.257	DNA-binding transcriptional dual regulator HypT
Cell_Exteri Transport Transport	EG12168	brnQ	-1.001	-1.911	branched chain amino acid transporter BrnQ
Cell_Exteri Transport Transport	EG10708	pheP	-0.138	-0.776	phenylalanine:H+ symporter PheP
Cell_Exteri Transport Transport	EG12662	gltK	0.737	-1.442	glutamate/aspartate ABC transporter membrane subunit GltK
Cell_Exteri Transport Transport	G6359	gltI	1.292	0.048	glutamate/aspartate ABC transporter periplasmic binding prote
Cell_Exteri Transport Transport	EG10802	putP	1.322	0.007	proline:Na+ symporter
Cell_Exteri Transport Transport	G6934	tcyP	-0.73	0.721	cystine/sulfocysteine:cation symporter
Cell_Exteri Transport Transport	EG11337	lysP	-0.898	-0.504	lysine:H+ symporter
Cell_Exteri Transport Transport	EG10007	hisM	-1.823	-0.423	lysine/arginine/ornithine ABC transporter / histidine ABC transp
Cell_Exteri Transport Transport	EG10072	argT	-0.554	-0.254	lysine/arginine/ornithine ABC transporter periplasmic binding pi
Cell_Exteri Transport Transport	EG12445	eamB	0.213	0.266	cysteine/O-acetylserine exporter EamB
Cell_Exteri Transport Transport	EG11159	argO	-0.925	-6.685	L-arginine exporter
Cell_Exteri Transport Transport	EG12732	sstT	-0.381	-0.389	serine/threonine:Na+ symporter
Cell_Exteri Transport Transport	EG10406	gltS	-2.079	-0.651	glutamate:sodium symporter
Cell_Exteri Transport Transport	EG12183	ampG	-1.149	-0.168	muropeptide:H+ symporter
Cell_Exteri Transport Transport	EG11703	acrA	-1.811	-2.56	multidrug efflux pump membrane fusion lipoprotein AcrA
Cell_Exteri Transport Transport	EG11700	pnuC	1.702	0.91	nicotinamide riboside transporter
Cell_Exteri Transport Transport	G6531	pgaA	0.327	0.158	partially deacetylated poly- α -1,6-N-acetyl-D-glucosamine oute
Cell_Exteri Transport Transport	G6561	murJ	-0.715	0.058	lipid II flippase MurJ
Cell_Exteri Transport Transport	EG11009	tolC	0.015	0.407	outer membrane channel TolC
Cell_Exteri Transport Transport	EG12380	gntT	-0.157	-1.086	high-affinity gluconate transporter
Cell_Exteri Transport Transport	EG10515	kdpC	0.615	1.009	K+ transporting P-type ATPase subunit KdpC
Cell_Exteri Transport Transport	EG10514	kdpB	0.18	0.36	K+ transporting P-type ATPase subunit KdpB
Cell_Exteri Transport Transport	EG10513	kdpA	1.508	-0.323	K+ transporting P-type ATPase subunit KdpA

Cell_Exteri Transport Transport	G7017	znuA	-0.704	-1.053	Zn ²⁺ ABC transporter periplasmic binding protein
Cell_Exteri Transport Transport	G7018	znuC	-0.892	0.026	Zn ²⁺ ABC transporter ATP binding subunit
Cell_Exteri Transport Transport	EG12368	znuB	-2.051	0.342	Zn ²⁺ ABC transporter membrane subunit
Cell_Exteri Transport Transport	EG12102	feoB	-2.241	-1.547	Fe ²⁺ transporter FeoB
Cell_Exteri Transport Transport	EG10783	pstB	-0.471	-0.217	phosphate ABC transporter ATP binding subunit
Cell_Exteri Transport Transport	EG11541	kup	-0.26	0.297	K ⁺ :H ⁺ symporter Kup
Cell_Exteri Transport Transport	EG11463	corA	-0.389	0.726	Ni ²⁺ /Co ²⁺ /Mg ²⁺ transporter
Cell_Exteri Transport Transport	EG12525	mgtA	-0.154	2.412	Mg ²⁺ importing P-type ATPase
Cell_Exteri Transport Transport	EG11104	entS	0.344	0.403	enterobactin exporter EntS
Cell_Exteri Transport Transport	G6461	macA	-0.357	0.344	ABC-type tripartite efflux pump membrane fusion protein
Cell_Exteri Transport Transport	G6462	macB	-0.236	0.08	ABC-type tripartite efflux pump ATP binding/membrane subunit
Cell_Exteri Transport Transport	G6977	nimT	0.439	0.249	2-nitroimidazole exporter
Cell_Exteri Transport Transport	EG11561	caiT	-0.636	-0.096	L-carnitine:Æ [±] -butyrobetaine antiporter
Cell_Exteri Transport Transport	EG11569	lptD	0.645	-0.015	lipopolysaccharide assembly protein LptD
Cell_Exteri Transport Transport	G6206	mhpT	0.287	-0.97	3-hydroxyphenylpropionate/3-hydroxycinnamate:H ⁺ symporter
Cell_Exteri Transport Transport	G6217	tauA	2.153	-2.318	taurine ABC transporter periplasmic binding protein
Cell_Exteri Transport Transport	EG10928	sbmA	-1.261	-0.708	peptide antibiotic/peptide nucleic acid transporter
Cell_Exteri Transport Transport	G6256	fsr	-0.868	-0.143	fosmidomycin efflux pump
Cell_Exteri Transport Transport	EG10855	lptE	0.064	-0.036	lipopolysaccharide assembly protein LptE
Cell_Exteri Transport Transport	EG11380	appC	0.091	1.344	cytochrome bd-II ubiquinol oxidase subunit I
Cell_Exteri Transport Transport	EG11379	appB	1.7	2.186	cytochrome bd-II ubiquinol oxidase subunit II
Cell_Exteri Transport Transport	G6517	rutG	-0.73	0.35	pyrimidine:H ⁺ symporter
Cell_Exteri Transport Transport	G6643	puuP	-0.618	0.221	putrescine:H ⁺ symporter PuuP
Cell_Exteri Transport Transport	G7115	mdtC	0.374	-1.041	multidrug efflux pump RND permease subunit MdtC
Cell_Exteri Transport Transport	EG12038	yejB	-1.107	-0.323	putative oligopeptide ABC transporter membrane subunit YejB
Cell_Exteri Transport Transport	EG12040	yejE	-1.877	-0.033	putative oligopeptide ABC transporter membrane subunit YejE
Cell_Exteri Transport Transport	EG12041	yejF	-1.385	0.072	putative oligopeptide ABC transporter ATP binding subunit YejF
Cell_Exteri Transport Transport	G7330	hcaT	-1.279	0.086	putative 3-phenylpropionate transporter
Cell_Exteri Transport Transport	EG12455	lplT	-1.787	-0.405	lysophospholipid transporter
Cell_Exteri Transport Transport	EG11160	mscS	-0.134	-0.196	small conductance mechanosensitive channel MscS

Cell_Exteri	Transport	Transport	G7664	lptC	-0.879	0.663	lipopolysaccharide transport system protein LptC
Cell_Exteri	Transport	Transport	G7665	lptA	-1.079	0.494	lipopolysaccharide transport system protein LptA
Cell_Exteri	Transport	Transport	EG11180	mscL	1.216	-0.212	large conductance mechanosensitive channel
Cell_Exteri	Transport	Transport	EG11961	lldP	-2.273	0.606	lactate/glycolate:H ⁺ symporter LldP
Cell_Exteri	Transport	Transport	EG11724	adeP	-1.826	-1.362	adenine:H ⁺ symporter
Cell_Exteri	Transport	Transport	G7806	tatA	1.922	0.029	twin arginine protein translocation system - TatA protein
Cell_Exteri	Transport	Transport	G7808	tatB	0.436	0.558	twin arginine protein translocation system - TatB protein
Cell_Exteri	Transport	Transport	EG11479	tatC	-0.067	0.791	twin arginine protein translocation system - TatC protein
Cell_Exteri	Transport	Transport	G7888	lptF	0.749	-0.751	lipopolysaccharide transport system protein LptF
Cell_Exteri	Transport	Transport	G7889	lptG	1.145	-0.732	lipopolysaccharide transport system protein LptG
Cell_Exteri	Cell Wall	Cell Wall Biogen	EG10621	murE	-1.931	-0.95	UDP-N-acetylmuramoyl-L-alanyl-D-glutamate--2,6-diaminopim
Cell_Exteri	Cell Wall	Cell Wall Biogen	EG10622	murF	-3.365	-0.888	D-alanyl-D-alanine-adding enzyme
Cell_Exteri	Cell Wall	Cell Wall Biogen	EG10604	mraY	-2.733	-0.367	phospho-N-acetylmuramoyl-pentapeptide-transferase
Cell_Exteri	Cell Wall	Cell Wall Biogen	EG10620	murD	-1.836	-0.434	UDP-N-acetylmuramoyl-L-alanine--D-glutamate ligase
Cell_Exteri	Cell Wall	Cell Wall Biogen	EG10344	ftsW	-2.063	-0.743	essential cell division protein FtsW
Cell_Exteri	Cell Wall	Cell Wall Biogen	EG10623	murG	-3.656	-0.02	N-acetylglucosaminyl transferase
Cell_Exteri	Cell Wall	Cell Wall Biogen	EG10619	murC	-2.151	-0.568	UDP-N-acetylmuramate--L-alanine ligase
Cell_Exteri	Cell Wall	Cell Wall Biogen	EG10041	ampD	-3.758	-0.593	1,6-anhydro-N-acetylmuramoyl-L-alanine amidase
Cell_Exteri	Cell Wall	Cell Wall Biogen	EG10605	mrcB	-0.486	-0.255	PBP1BCE
Cell_Exteri	Cell Wall	Cell Wall Biogen	G6092	uppS	-0.759	-1.223	ditrans, polycis-undecaprenyl-diphosphate synthase [(2E,6E)-farr
Cell_Exteri	Cell Wall	Cell Wall Biogen	EG12183	ampG	-1.149	-0.168	muropeptide:H ⁺ symporter
Cell_Exteri	Cell Wall	Cell Wall Biogen	EG10201	dacA	-2.586	-0.494	D-alanyl-D-alanine carboxypeptidase DacA
Cell_Exteri	Cell Wall	Cell Wall Biogen	EG10854	rlpA	-2.064	-0.304	rare lipoprotein RlpA
Cell_Exteri	Cell Wall	Cell Wall Biogen	EG10607	mrdb	0.654	2.104	SEDS family protein MrdB
Cell_Exteri	Cell Wall	Cell Wall Biogen	G6439	ybjG	0.847	0.701	undecaprenyl pyrophosphate phosphatase
Cell_Exteri	Cell Wall	Cell Wall Biogen	G6561	murJ	-0.715	0.058	lipid II flippase MurJ
Cell_Exteri	Cell Wall	Cell Wall Biogen	EG11494	mltG	0.025	-0.551	endolytic murein transglycosylase
Cell_Exteri	Cell Wall	Cell Wall Biogen	G6567	nagZ	-0.56	-0.198	CE-N-acetylhexosaminidase
Cell_Exteri	Cell Wall	Cell Wall Biogen	EG11893	dacD	-0.102	0.976	D-alanyl-D-alanine carboxypeptidase DacD
Cell_Exteri	Cell Wall	Cell Wall Biogen	EG10580	mepA	-2.092	-0.477	peptidoglycan DD-endopeptidase/peptidoglycan LD-endopeptida

Cell_Exteri	Cell Wall	Cell Wall Biogen	G7410	mltB	-1.328	-0.087	membrane-bound lytic murein transglycosylase B
Cell_Exteri	Cell Wall	Cell Wall Biogen	EG11665	bacA	-0.645	-0.074	undecaprenyl pyrophosphate phosphatase
Cell_Exteri	Cell Wall	Cell Wall Biogen	EG11553	glmM	-1.071	-0.191	phosphoglucosamine mutase
Cell_Exteri	Cell Wall	Cell Wall Biogen	EG11358	murA	-2.398	-0.867	UDP-N-acetylglucosamine 1-carboxyvinyltransferase
Cell_Exteri	Cell Wall	Cell Wall Biogen	G7668	mtgA	-1.745	0.142	peptidoglycan glycosyltransferase MtgA
Cell_Exteri	Cell Wall	Cell Wall Biogen	EG10748	mrcA	0.098	-0.227	peptidoglycan glycosyltransferase / peptidoglycan DD-transpeptidase
Cell_Exteri	Cell Wall	Cell Wall Biogen	EG11198	glmU	-0.787	-0.277	fused N-acetylglucosamine-1-phosphate uridylyltransferase and glucosyltransferase
Cell_Exteri	Cell Wall	Cell Wall Biogen	EG11204	murI	-2.028	0.738	glutamate racemase
Cell_Exteri	Cell Wall	Cell Wall Biogen	EG11205	murB	-1.449	-1.07	UDP-N-acetylenolpyruvoylglucosamine reductase
Cell_Exteri	Cell Wall	Cell Wall Biogen	EG12440	mpl	-1.659	0.434	UDP-N-acetylmuramate--L-alanyl-CE-D-glutamyl-meso-2,6-diaminocapryloyl transferase
Cell_Exteri	Cell Wall	Cell Wall Biogen	EG10950	slt	-0.969	0.428	soluble lytic murein transglycosylase
Cell_Exteri	Lipopolysaccharide	LPS Metabolism	G7165	ais	-1.838	-0.135	putative lipopolysaccharide core heptose(II)-phosphate phosphatase
Cell_Exteri	Lipopolysaccharide	LPS Metabolism	EG12691	lapB	-0.502	-0.143	lipopolysaccharide assembly protein B
Cell_Exteri	Lipopolysaccharide	LPS Metabolism	G7167	arnC	0.529	-0.966	undecaprenyl-phosphate 4-deoxy-4-formamido-L-arabinose transferase
Cell_Exteri	Lipopolysaccharide	LPS Metabolism	EG11198	glmU	-0.787	-0.277	fused N-acetylglucosamine-1-phosphate uridylyltransferase and glucosyltransferase
Cell_Exteri	Lipopolysaccharide	LPS Metabolism	G7241	lpxP	-0.555	-1.42	palmitoleoyl acyltransferase
Cell_Exteri	Lipopolysaccharide	LPS Metabolism	G7663	kdsC	-0.586	-0.059	3-deoxy-D-manno-octulosonate 8-phosphate phosphatase KdsC
Cell_Exteri	Lipopolysaccharide	LPS Metabolism	G7170	arnT	-0.793	-0.084	lipid IVA 4-amino-4-deoxy-L-arabinosyltransferase
Cell_Exteri	Lipopolysaccharide	LPS Metabolism	EG10519	kdsB	-0.11	0.538	3-deoxy-manno-octulosonate cytidylyltransferase
Cell_Exteri	Lipopolysaccharide	LPS Metabolism	EG10518	kdsA	-0.65	-0.99	3-deoxy-D-manno-octulosonate 8-phosphate synthase
Cell_Exteri	Lipopolysaccharide	LPS Metabolism	G7662	kdsD	-0.507	0.633	D-arabinose 5-phosphate isomerase KdsD
Cell_Exteri	Lipopolysaccharide	LPS Metabolism	EG11613	eptA	-0.706	0.055	phosphoethanolamine transferase EptA
Cell_Exteri	Lipopolysaccharide	LPS Metabolism	EG10520	waaA	-1.834	-0.113	KDO transferase
Cell_Exteri	Lipopolysaccharide	LPS Metabolism	EG11319	galU	-1.393	0.37	UTP--glucose-1-phosphate uridylyltransferase
Cell_Exteri	Lipopolysaccharide	LPS Metabolism	EG11409	lpxK	-1.452	0.473	tetraacyldisaccharide 4'-kinase
Cell_Exteri	Pilus	Pilus	EG10308	fimA	-0.087	0.569	type 1 fimbriae major subunit
Cell_Exteri	Outer Membrane	Outer Membrane	G6437	ylil	0.451	0.014	aldose sugar dehydrogenase Ylil
Cell_Exteri	Outer Membrane	Outer Membrane	EG10854	rlpA	-2.064	-0.304	rare lipoprotein RlpA
Cell_Exteri	Outer Membrane	Outer Membrane	G7665	lptA	-1.079	0.494	lipopolysaccharide transport system protein LptA
Cell_Exteri	Outer Membrane	Outer Membrane	EG11124	ompW	0.706	0.134	outer membrane protein W

Cell_Exteri Outer Membrane	EG11291	loiP	0.149	0.119	metalloprotease LoiP
Cell_Exteri Outer Membrane	EG10855	lptE	0.064	-0.036	lipopolysaccharide assembly protein LptE
Cell_Exteri Outer Membrane	EG11569	lptD	0.645	-0.015	lipopolysaccharide assembly protein LptD
Cell_Exteri Outer Membrane	G6530	pgaB	-0.858	-0.229	poly- ϵ -1,6-N-acetyl-D-glucosamine N-deacetylase and ϵ -1,6
Cell_Exteri Outer Membrane	EG10952	bamE	-0.48	0.678	outer membrane protein assembly factor BamE
Cell_Exteri Outer Membrane	G7352	bamD	-1.241	0.552	outer membrane protein assembly factor BamD
Cell_Exteri Outer Membrane	G7320	bamB	-0.674	-0.58	outer membrane protein assembly factor BamB
Cell_Exteri Outer Membrane	G7410	mltB	-1.328	-0.087	membrane-bound lytic murein transglycosylase B
Cell_Exteri Outer Membrane	EG11293	lolB	-0.809	-0.483	outer membrane lipoprotein LolB
Cell_Exteri Outer Membrane	EG11009	tolC	0.015	0.407	outer membrane channel TolC
Cell_Exteri Outer Membrane	G6531	pgaA	0.327	0.158	partially deacetylated poly- ϵ -1,6-N-acetyl-D-glucosamine oute
Cell_Exteri Plasma Membrane	EG10801	putA	-0.647	-0.46	fused DNA-binding transcriptional repressor / proline dehydroge
Cell_Exteri Plasma Membrane	EG10608	mreB	-2.414	-0.26	dynamic cytoskeletal protein MreB
Cell_Exteri Plasma Membrane	G6977	nimT	0.439	0.249	2-nitroimidazole exporter
Cell_Exteri Plasma Membrane	EG12691	lapB	-0.502	-0.143	lipopolysaccharide assembly protein B
Cell_Exteri Plasma Membrane	G6206	mhpT	0.287	-0.97	3-hydroxyphenylpropionate/3-hydroxycinnamate:H ⁺ symporter
Cell_Exteri Plasma Membrane	EG12799	mlaD	-1.43	0.249	intermembrane phospholipid transport system, substrate bindin
Cell_Exteri Plasma Membrane	EG12800	mleE	-0.022	-0.412	intermembrane phospholipid transport system, integral membr
Cell_Exteri Plasma Membrane	EG11159	argO	-0.925	-6.685	L-arginine exporter
Cell_Exteri Plasma Membrane	EG11403	ppx	0.41	-0.213	exopolyphosphatase
Cell_Exteri Plasma Membrane	EG11096	yajC	-1.271	-0.86	Sec translocon accessory complex subunit YajC
Cell_Exteri Plasma Membrane	EG10224	dggA	-3.379	-0.259	diacylglycerol kinase
Cell_Exteri Plasma Membrane	EG10231	dld	-1.435	0.167	quinone-dependent D-lactate dehydrogenase
Cell_Exteri Plasma Membrane	EG12041	yejF	-1.385	0.072	putative oligopeptide ABC transporter ATP binding subunit YejF
Cell_Exteri Plasma Membrane	EG10104	atpG	-0.713	-0.931	ATP synthase F1 complex subunit ϵ
Cell_Exteri Plasma Membrane	EG10735	phoU	-0.423	-0.6	negative regulator of the pho regulon
Cell_Exteri Plasma Membrane	EG10704	pgpA	1.116	0.276	phosphatidylglycerophosphatase A
Cell_Exteri Plasma Membrane	EG10597	minD	-1.768	-1.011	Z-ring positioning protein MinD
Cell_Exteri Plasma Membrane	G6643	puuP	-0.618	0.221	putrescine:H ⁺ symporter PuuP
Cell_Exteri Plasma Membrane	EG10109	betA	0.13	-0.558	choline dehydrogenase

Cell_Exteri Plasma M Plasma Membrar	EG10100	atpC	-0.863	-0.363	ATP synthase F1 complex subunit C ϵ μ
Cell_Exteri Plasma M Plasma Membrar	EG11665	bacA	-0.645	-0.074	undecaprenyl pyrophosphate phosphatase
Cell_Exteri Plasma M Plasma Membrar	EG11197	yidC	-3.025	-0.122	membrane protein insertase YidC
Cell_Exteri Plasma M Plasma Membrar	G6105	fadE	0.82	-0.591	acyl-CoA dehydrogenase
Cell_Exteri Plasma M Plasma Membrar	EG10760	prc	0.012	-0.244	tail-specific protease
Cell_Exteri Plasma M Plasma Membrar	EG10015	rodZ	-1.064	-0.309	cytoskeleton protein RodZ
Cell_Exteri Plasma M Plasma Membrar	EG10406	gltS	-2.079	-0.651	glutamate:sodium symporter
Cell_Exteri Plasma M Plasma Membrar	EG12128	lgt	-2.209	1.733	phosphatidylglycerol--prolipoprotein diacylglycerol transferase
Cell_Exteri Plasma M Plasma Membrar	EG11144	yfcA	-2.614	0.04	putative transporter YfcA
Cell_Exteri Plasma M Plasma Membrar	EG12320	yadG	0.736	-0.715	putative ABC transporter ATP-binding protein YadG
Cell_Exteri Plasma M Plasma Membrar	EG11370	ubiA	1.207	0.337	4-hydroxybenzoate octaprenyltransferase
Cell_Exteri Plasma M Plasma Membrar	EG11724	adeP	-1.826	-1.362	adenine:H ⁺ symporter
Cell_Exteri Plasma M Plasma Membrar	G6561	murJ	-0.715	0.058	lipid II flippase MurJ
Cell_Exteri Plasma M Plasma Membrar	EG10938	secD	-1.865	-1.123	Sec translocon accessory complex subunit SecD
Cell_Exteri Plasma M Plasma Membrar	EG11529	ftsN	-1.2	-0.122	cell division protein FtsN
Cell_Exteri Plasma M Plasma Membrar	G7424	ftsB	-0.955	-0.98	cell division protein FtsB
Cell_Exteri Plasma M Plasma Membrar	EG11541	kup	-0.26	0.297	K ⁺ :H ⁺ symporter Kup
Cell_Exteri Plasma M Plasma Membrar	G7664	lptC	-0.879	0.663	lipopolysaccharide transport system protein LptC
Cell_Exteri Plasma M Plasma Membrar	EG10740	plsB	-0.655	-0.114	glycerol-3-phosphate 1-O-acyltransferase
Cell_Exteri Plasma M Plasma Membrar	EG11570	djlA	-0.697	0.651	co-chaperone protein DjlA
Cell_Exteri Plasma M Plasma Membrar	G7682	degQ	-0.091	-0.064	periplasmic serine endoprotease
Cell_Exteri Plasma M Plasma Membrar	G6461	macA	-0.357	0.344	ABC-type tripartite efflux pump membrane fusion protein
Cell_Exteri Plasma M Plasma Membrar	EG12168	brnQ	-1.001	-1.911	branched chain amino acid transporter BrnQ
Cell_Exteri Plasma M Plasma Membrar	EG11409	lpxK	-1.452	0.473	tetraacyldisaccharide 4'-kinase
Cell_Exteri Plasma M Plasma Membrar	EG11530	fadD	1.067	-1.658	long-chain-fatty-acid--CoA ligase
Cell_Exteri Plasma M Plasma Membrar	EG10997	mnmE	-1.361	0.871	5-carboxymethylaminomethyluridine-tRNA synthase GTPase sul
Cell_Exteri Plasma M Plasma Membrar	EG11299	rng	-0.09	-0.469	RNase G
Cell_Exteri Plasma M Plasma Membrar	G6489	uup	0.195	1.196	ATP-binding protein Uup
Cell_Exteri Plasma M Plasma Membrar	EG10609	mreC	-2.1	-0.915	cell shape determining protein MreC
Cell_Exteri Plasma M Plasma Membrar	G6242	ppiD	-0.294	-0.629	periplasmic folding chaperone

Cell_Exteri Plasma M Plasma Membrar	EG10269	envZ	-0.232	-0.789	sensor histidine kinase EnvZ
Cell_Exteri Plasma M Plasma Membrar	EG11506	ftsH	0.675	0.469	ATP-dependent zinc metalloprotease FtsH
Cell_Exteri Plasma M Plasma Membrar	EG12321	yadH	-1.743	-0.749	putative ABC transporter membrane subunit YadH
Cell_Exteri Plasma M Plasma Membrar	EG12801	mlaF	-0.511	0.137	intermembrane phospholipid transport system, ATP binding sub
Cell_Exteri Plasma M Plasma Membrar	EG11463	corA	-0.389	0.726	Ni ²⁺ /Co ²⁺ /Mg ²⁺ transporter
Cell_Exteri Plasma M Plasma Membrar	EG10369	gcd	1.48	-1.72	quinoprotein glucose dehydrogenase
Cell_Exteri Plasma M Plasma Membrar	EG10344	ftsW	-2.063	-0.743	essential cell division protein FtsW
Cell_Exteri Plasma M Plasma Membrar	G7330	hcaT	-1.279	0.086	putative 3-phenylpropionate transporter
Cell_Exteri Plasma M Plasma Membrar	G7241	lpxP	-0.555	-1.42	palmitoleoyl acyltransferase
Cell_Exteri Plasma M Plasma Membrar	EG11379	appB	1.7	2.186	cytochrome bd-II ubiquinol oxidase subunit II
Cell_Exteri Plasma M Plasma Membrar	EG10706	pgsA	-0.381	-0.271	CDP-diacylglycerol--glycerol-3-phosphate 3-phosphatidyltransfer
Cell_Exteri Plasma M Plasma Membrar	EG10180	cyoC	-1.184	-0.38	cytochrome bo3 ubiquinol oxidase subunit 3
Cell_Exteri Plasma M Plasma Membrar	EG12272	ghrB	0.916	-0.416	glyoxylate reductase
Cell_Exteri Plasma M Plasma Membrar	EG10686	parC	-1.506	-0.103	DNA topoisomerase IV subunit A
Cell_Exteri Plasma M Plasma Membrar	EG10520	waaA	-1.834	-0.113	KDO transferase
Cell_Exteri Plasma M Plasma Membrar	G7808	tatB	0.436	0.558	twin arginine protein translocation system - TatB protein
Cell_Exteri Plasma M Plasma Membrar	EG11209	psiE	1.457	-0.74	putative phosphate starvation-inducible protein PsiE
Cell_Exteri Plasma M Plasma Membrar	G6934	tcyP	-0.73	0.721	cystine/sulfocysteine:cation symporter
Cell_Exteri Plasma M Plasma Membrar	EG11086	ftsL	-1	-0.881	cell division protein FtsL
Cell_Exteri Plasma M Plasma Membrar	EG11393	dsbB	-2.303	0.749	protein thiol:quinone oxidoreductase DsbBReduced
Cell_Exteri Plasma M Plasma Membrar	G7217	yfdC	1.018	0.777	inner membrane protein YfdC
Cell_Exteri Plasma M Plasma Membrar	EG10529	lepA	-0.673	0.031	30S ribosomal subunit biogenesis factor LepA
Cell_Exteri Plasma M Plasma Membrar	EG10102	atpE	-2.628	-0.936	ATP synthase Fo complex subunit c
Cell_Exteri Plasma M Plasma Membrar	EG10605	mrcB	-0.486	-0.255	PBP1BCE ₂
Cell_Exteri Plasma M Plasma Membrar	G6854	ynfM	1.263	-1.25	putative transporter YnfM
Cell_Exteri Plasma M Plasma Membrar	EG10748	mrcA	0.098	-0.227	peptidoglycan glycosyltransferase / peptidoglycan DD-transpept
Cell_Exteri Plasma M Plasma Membrar	G6517	rutG	-0.73	0.35	pyrimidine:H ⁺ symporter
Cell_Exteri Plasma M Plasma Membrar	EG11011	tolR	-1.969	0.279	Tol-Pal system protein TolR
Cell_Exteri Plasma M Plasma Membrar	EG11337	lysP	-0.898	-0.504	lysine:H ⁺ symporter
Cell_Exteri Plasma M Plasma Membrar	G7115	mdtC	0.374	-1.041	multidrug efflux pump RND permease subunit MdtC

Cell_Exteri Plasma M Plasma Membrar	EG11893	dacD	-0.102	0.976	D-alanyl-D-alanine carboxypeptidase DacD
Cell_Exteri Plasma M Plasma Membrar	EG10201	dacA	-2.586	-0.494	D-alanyl-D-alanine carboxypeptidase DacA
Cell_Exteri Plasma M Plasma Membrar	EG11345	hflD	0.243	-0.753	lysogenization regulator
Cell_Exteri Plasma M Plasma Membrar	EG11652	degS	0.495	0.555	serine endoprotease
Cell_Exteri Plasma M Plasma Membrar	G7018	znuC	-0.892	0.026	Zn ²⁺ ABC transporter ATP binding subunit
Cell_Exteri Plasma M Plasma Membrar	EG10387	glnL	0.905	-0.845	sensory histidine kinase NtrB
Cell_Exteri Plasma M Plasma Membrar	EG10745	pntB	-0.396	2.331	pyridine nucleotide transhydrogenase subunit C _ε
Cell_Exteri Plasma M Plasma Membrar	EG10744	pntA	-2.074	2.717	pyridine nucleotide transhydrogenase subunit C _ε
Cell_Exteri Plasma M Plasma Membrar	EG10649	ndh	-0.631	0.323	NADH:quinone oxidoreductase II
Cell_Exteri Plasma M Plasma Membrar	G7888	lptF	0.749	-0.751	lipopolysaccharide transport system protein LptF
Cell_Exteri Plasma M Plasma Membrar	EG10270	era	-0.458	0.651	30S ribosomal subunit maturation GTPase Era
Cell_Exteri Plasma M Plasma Membrar	EG11479	tatC	-0.067	0.791	twin arginine protein translocation system - TatC protein
Cell_Exteri Plasma M Plasma Membrar	EG12343	ettA	-1.151	0.017	energy-dependent translational throttle protein EttA
Cell_Exteri Plasma M Plasma Membrar	EG10346	ftsY	0.422	0.1	signal recognition particle receptor
Cell_Exteri Plasma M Plasma Membrar	EG10043	cysQ	0.979	-0.124	3'(2'),5'-bisphosphate nucleotidase
Cell_Exteri Plasma M Plasma Membrar	EG11380	appC	0.091	1.344	cytochrome bd-II ubiquinol oxidase subunit I
Cell_Exteri Plasma M Plasma Membrar	G7889	lptG	1.145	-0.732	lipopolysaccharide transport system protein LptG
Cell_Exteri Plasma M Plasma Membrar	G6574	lolD	-1.265	0.151	lipoprotein release complex - ATP binding subunit
Cell_Exteri Plasma M Plasma Membrar	EG11700	pnuC	1.702	0.91	nicotinamide riboside transporter
Cell_Exteri Plasma M Plasma Membrar	EG12709	yedI	2.719	0.135	DUF808 domain-containing inner membrane protein YedI
Cell_Exteri Plasma M Plasma Membrar	EG10178	cyoA	-2.272	-0.588	cytochrome bo3 ubiquinol oxidase subunit 2
Cell_Exteri Plasma M Plasma Membrar	EG10394	glpD	0.381	0.052	aerobic glycerol 3-phosphate dehydrogenase
Cell_Exteri Plasma M Plasma Membrar	EG10940	secF	-0.852	-0.815	Sec translocon accessory complex subunit SecF
Cell_Exteri Plasma M Plasma Membrar	EG10936	secA	-1.291	1.148	protein translocation ATPase
Cell_Exteri Plasma M Plasma Membrar	G7668	mtgA	-1.745	0.142	peptidoglycan glycosyltransferase MtgA
Cell_Exteri Plasma M Plasma Membrar	EG11143	ubiG	-0.471	0.639	bifunctional 3-demethylubiquinone-8 3-O-methyltransferase and
Cell_Exteri Plasma M Plasma Membrar	EG12038	yejB	-1.107	-0.323	putative oligopeptide ABC transporter membrane subunit YejB
Cell_Exteri Plasma M Plasma Membrar	EG10546	lpxB	-1.683	-0.69	lipid A disaccharide synthase
Cell_Exteri Plasma M Plasma Membrar	EG10513	kdpA	1.508	-0.323	K ⁺ transporting P-type ATPase subunit KdpA
Cell_Exteri Plasma M Plasma Membrar	EG10098	atpA	-2.2	-0.798	ATP synthase F1 complex subunit C _ε

Cell_Exteri Plasma M Plasma Membrar	EG11613	eptA	-0.706	0.055	phosphoethanolamine transferase EptA
Cell_Exteri Plasma M Plasma Membrar	EG12416	gatC	-1.457	0.161	galactitol-specific PTS enzyme IIC component
Cell_Exteri Plasma M Plasma Membrar	EG10465	ribB	-0.737	2.272	3,4-dihydroxy-2-butanone-4-phosphate synthase
Cell_Exteri Plasma M Plasma Membrar	EG10182	cyoE	-0.598	-1.288	heme O synthase
Cell_Exteri Plasma M Plasma Membrar	EG12095	secG	-1.458	0.553	Sec translocon subunit SecG
Cell_Exteri Plasma M Plasma Membrar	EG10766	secY	-1.205	0.529	Sec translocon subunit SecY
Cell_Exteri Plasma M Plasma Membrar	EG12150	cobS	-1.564	0.301	cobalamin 5'-phosphate synthase
Cell_Exteri Plasma M Plasma Membrar	G7615	yqjF	-0.196	-0.131	DoxX family protein
Cell_Exteri Plasma M Plasma Membrar	EG11608	clsA	0.636	0.215	cardiolipin synthase A
Cell_Exteri Plasma M Plasma Membrar	EG10783	pstB	-0.471	-0.217	phosphate ABC transporter ATP binding subunit
Cell_Exteri Plasma M Plasma Membrar	EG11104	entS	0.344	0.403	enterobactin exporter EntS
Cell_Exteri Plasma M Plasma Membrar	EG12436	rseP	-0.733	-0.148	intramembrane zinc metalloprotease RseP
Cell_Exteri Plasma M Plasma Membrar	EG12455	lplT	-1.787	-0.405	lysophospholipid transporter
Cell_Exteri Plasma M Plasma Membrar	G6439	ybjG	0.847	0.701	undecaprenyl pyrophosphate phosphatase
Cell_Exteri Plasma M Plasma Membrar	EG10002	modB	-1.467	0.096	molybdate ABC transporter membrane subunit
Cell_Exteri Plasma M Plasma Membrar	EG10514	kdpB	0.18	0.36	K ⁺ transporting P-type ATPase subunit KdpB
Cell_Exteri Plasma M Plasma Membrar	G7167	arnC	0.529	-0.966	undecaprenyl-phosphate 4-deoxy-4-formamido-L-arabinose tran
Cell_Exteri Plasma M Plasma Membrar	EG11180	mscL	1.216	-0.212	large conductance mechanosensitive channel
Cell_Exteri Plasma M Plasma Membrar	EG10928	sbmA	-1.261	-0.708	peptide antibiotic/peptide nucleic acid transporter
Cell_Exteri Plasma M Plasma Membrar	G6861	ydjI	0.856	-0.483	putative arginine:ornithine antiporter
Cell_Exteri Plasma M Plasma Membrar	G7313	hda	-1.214	-0.84	inibitor of reinitiation of DNA replication
Cell_Exteri Plasma M Plasma Membrar	EG10105	atpH	-2.636	-0.803	ATP synthase F1 complex subunit α
Cell_Exteri Plasma M Plasma Membrar	EG11122	yciB	-1.003	-0.178	inner membrane protein
Cell_Exteri Plasma M Plasma Membrar	EG10598	minE	-0.963	-1.013	Z-ring positioning protein MinE
Cell_Exteri Plasma M Plasma Membrar	G7806	tatA	1.922	0.029	twin arginine protein translocation system - TatA protein
Cell_Exteri Plasma M Plasma Membrar	EG10604	mraY	-2.733	-0.367	phospho-N-acetylmuramoyl-pentapeptide-transferase
Cell_Exteri Plasma M Plasma Membrar	EG10530	lepB	0.02	-0.907	signal peptidase I
Cell_Exteri Plasma M Plasma Membrar	EG10103	atpF	-2.285	-0.963	ATP synthase Fo complex subunit b
Cell_Exteri Plasma M Plasma Membrar	G6256	fsr	-0.868	-0.143	fosmidomycin efflux pump
Cell_Exteri Plasma M Plasma Membrar	EG10623	murG	-3.656	-0.02	N-acetylglucosaminyl transferase

Cell_Exteri Plasma M Plasma Membrar	EG10168	Int	-0.456	-0.325	apolipoprotein N-acyltransferase
Cell_Exteri Plasma M Plasma Membrar	G6359	gltI	1.292	0.048	glutamate/aspartate ABC transporter periplasmic binding prote
Cell_Exteri Plasma M Plasma Membrar	EG12662	gltK	0.737	-1.442	glutamate/aspartate ABC transporter membrane subunit GltK
Cell_Exteri Plasma M Plasma Membrar	G6872	rsxB	-1.363	1.308	SoxR [2Fe-2S] reducing system protein RsxB
Cell_Exteri Plasma M Plasma Membrar	EG11494	mltG	0.025	-0.551	endolytic murein transglycosylase
Cell_Exteri Plasma M Plasma Membrar	EG10854	rlpA	-2.064	-0.304	rare lipoprotein RlpA
Cell_Exteri Plasma M Plasma Membrar	EG12666	lpxH	-0.67	-1.62	UDP-2,3-diacylglucosamine diphosphatase
Cell_Exteri Plasma M Plasma Membrar	EG10181	cyoD	-1.411	-0.316	cytochrome bo3 ubiquinol oxidase subunit 4
Cell_Exteri Plasma M Plasma Membrar	EG10198	cysW	-0.283	-0.776	sulfate/thiosulfate ABC transporter inner membrane subunit Cy:
Cell_Exteri Plasma M Plasma Membrar	EG10939	secE	0.521	1.014	Sec translocon subunit SecE
Cell_Exteri Plasma M Plasma Membrar	EG10516	kdpD	0.594	-0.207	sensor histidine kinase KdpD
Cell_Exteri Plasma M Plasma Membrar	EG10461	htpG	-3.902	2.793	chaperone protein HtpG
Cell_Exteri Plasma M Plasma Membrar	EG11961	lldP	-2.273	0.606	lactate/glycolate:H ⁺ symporter LldP
Cell_Exteri Plasma M Plasma Membrar	EG11110	ybgC	-1.376	0.593	esterase/thioesterase
Cell_Exteri Plasma M Plasma Membrar	G6462	macB	-0.236	0.08	ABC-type tripartite efflux pump ATP binding/membrane subunit
Cell_Exteri Plasma M Plasma Membrar	EG10260	entB	-2.806	-6.528	holo EntB
Cell_Exteri Plasma M Plasma Membrar	EG12088	nuoH	-1.477	1.386	NADH:quinone oxidoreductase subunit H
Cell_Exteri Plasma M Plasma Membrar	EG12090	nuoJ	-1.56	1.196	NADH:quinone oxidoreductase subunit J
Cell_Exteri Plasma M Plasma Membrar	EG12091	nuoK	-2.478	1.063	NADH:quinone oxidoreductase subunit K
Cell_Exteri Plasma M Plasma Membrar	EG12092	nuoL	-2.06	0.479	NADH:quinone oxidoreductase subunit L
Cell_Exteri Plasma M Plasma Membrar	EG12093	nuoN	-1.763	-0.195	NADH:quinone oxidoreductase subunit N
Cell_Exteri Plasma M Plasma Membrar	EG12089	nuoI	-0.888	1.472	NADH:quinone oxidoreductase subunit I
Cell_Exteri Plasma M Plasma Membrar	EG12087	nuoG	-1.347	1.469	NADH:quinone oxidoreductase subunit G
Cell_Exteri Plasma M Plasma Membrar	EG11774	nuoF	-0.226	1.858	NADH:quinone oxidoreductase subunit F
Cell_Exteri Plasma M Plasma Membrar	EG12084	nuoC	-1.019	1.447	NADH:quinone oxidoreductase subunit CD
Cell_Exteri Plasma M Plasma Membrar	EG12083	nuoB	-0.509	2.067	NADH:quinone oxidoreductase subunit B
Cell_Exteri Plasma M Plasma Membrar	EG10775	psd	-1.783	-0.244	phosphatidylserine decarboxylase proenzyme
Cell_Exteri Plasma M Plasma Membrar	EG12102	feoB	-2.241	-1.547	Fe ²⁺ transporter FeoB
Cell_Exteri Plasma M Plasma Membrar	EG10733	phoR	-0.729	-0.506	sensor histidine kinase PhoR
Cell_Exteri Plasma M Plasma Membrar	G6217	tauA	2.153	-2.318	taurine ABC transporter periplasmic binding protein

Cell_Exteri Plasma M Plasma Membrar	EG12445	eamB	0.213	0.266	cysteine/O-acetylserine exporter EamB
Cell_Exteri Plasma M Plasma Membrar	EG10932	sdhB	-1.309	1.038	succinate:quinone oxidoreductase, iron-sulfur cluster binding pro
Cell_Exteri Plasma M Plasma Membrar	EG10933	sdhC	-0.367	1.083	succinate:quinone oxidoreductase, membrane protein SdhC
Cell_Exteri Plasma M Plasma Membrar	EG10934	sdhD	-1.268	1.67	succinate:quinone oxidoreductase, membrane protein SdhD
Cell_Exteri Plasma M Plasma Membrar	EG12368	znuB	-2.051	0.342	Zn ²⁺ ABC transporter membrane subunit
Cell_Exteri Plasma M Plasma Membrar	EG12623	ybaL	-0.978	-0.23	putative transporter YbaL
Cell_Exteri Plasma M Plasma Membrar	EG12086	nuoE	-0.112	1.772	NADH:quinone oxidoreductase subunit E
Cell_Exteri Plasma M Plasma Membrar	EG12380	gntT	-0.157	-1.086	high-affinity gluconate transporter
Cell_Exteri Plasma M Plasma Membrar	EG12183	ampG	-1.149	-0.168	muropeptide:H ⁺ symporter
Cell_Exteri Plasma M Plasma Membrar	EG10708	pheP	-0.138	-0.776	phenylalanine:H ⁺ symporter PheP
Cell_Exteri Plasma M Plasma Membrar	EG10607	mrdb	0.654	2.104	SEDS family protein MrdB
Cell_Exteri Plasma M Plasma Membrar	G7258	zipA	0.292	-0.348	cell division protein ZipA
Cell_Exteri Plasma M Plasma Membrar	G6575	lolE	-1.13	0.27	lipoprotein release complex - inner membrane subunit
Cell_Exteri Plasma M Plasma Membrar	EG10007	hisM	-1.823	-0.423	lysine/arginine/ornithine ABC transporter / histidine ABC transp
Cell_Exteri Plasma M Plasma Membrar	EG11466	rarD	-1.488	-0.285	putative transporter RarD
Cell_Exteri Plasma M Plasma Membrar	EG10179	cyoB	-1.541	-0.558	cytochrome bo3 ubiquinol oxidase subunit 1
Cell_Exteri Plasma M Plasma Membrar	EG10342	ftsQ	-0.409	-0.471	cell division protein FtsQ
Cell_Exteri Plasma M Plasma Membrar	EG12525	mgtA	-0.154	2.412	Mg ²⁺ importing P-type ATPase
Cell_Exteri Plasma M Plasma Membrar	EG11160	mscS	-0.134	-0.196	small conductance mechanosensitive channel MscS
Cell_Exteri Plasma M Plasma Membrar	EG11703	acrA	-1.811	-2.56	multidrug efflux pump membrane fusion lipoprotein AcrA
Cell_Exteri Plasma M Plasma Membrar	EG10897	sigma H	-0.094	1.082	RNA polymerase, sigma 32
Cell_Exteri Plasma M Plasma Membrar	G7170	arnT	-0.793	-0.084	lipid IVA 4-amino-4-deoxy-L-arabinosyltransferase
Cell_Exteri Plasma M Plasma Membrar	EG10397	glpG	-1.12	0.415	rhomboid protease GlpG
Cell_Exteri Plasma M Plasma Membrar	EG10931	sdhA	-1.15	1.198	succinate:quinone oxidoreductase, FAD binding protein
Cell_Exteri Plasma M Plasma Membrar	EG10690	pcnB	-2.447	0.164	poly(A) polymerase I
Cell_Exteri Plasma M Plasma Membrar	EG12880	dgcN	-1.174	-0.954	diguanylate cyclase DgcN
Cell_Exteri Plasma M Plasma Membrar	EG12040	yejE	-1.877	-0.033	putative oligopeptide ABC transporter membrane subunit YejE
Cell_Exteri Plasma M Plasma Membrar	EG12732	sstT	-0.381	-0.389	serine/threonine:Na ⁺ symporter
Cell_Exteri Plasma M Plasma Membrar	EG10167	cstA	0.373	-0.617	carbon starvation protein A
Cell_Exteri Plasma M Plasma Membrar	EG10807	pyrD	-0.102	0.623	dihydroorotate dehydrogenase, type 2

Cell_Exteri Plasma M Plasma Membrar	EG10859	rne	-3.562	-0.662	ribonuclease E
Cell_Exteri Plasma M Plasma Membrar	EG10844	rhlB	-1.567	0.352	ATP-dependent RNA helicase RhlB
Cell_Exteri Plasma M Plasma Membrar	EG10743	pnp	-0.553	-1.652	polynucleotide phosphorylase
Cell_Exteri Plasma M Plasma Membrar	EG10258	enolase	0.448	-0.774	enolase
Cell_Exteri Plasma M Plasma Membrar	EG11773	nuoM	-2.108	0.305	NADH:quinone oxidoreductase subunit M
Cell_Exteri Plasma M Plasma Membrar	EG10777	pspB	2.455	-0.968	phage shock protein B
Cell_Exteri Plasma M Plasma Membrar	G6491	pqiB	0.021	-1.357	intermembrane transport protein PqiB
Cell_Exteri Plasma M Plasma Membrar	EG10515	kdpC	0.615	1.009	K ⁺ transporting P-type ATPase subunit KdpC
Cell_Exteri Plasma M Plasma Membrar	EG10235	dnaA	-0.446	-0.998	chromosomal replication initiator protein DnaA
Cell_Exteri Plasma M Plasma Membrar	EG10802	putP	1.322	0.007	proline:Na ⁺ symporter
Cell_Exteri Plasma M Plasma Membrar	EG10099	atpB	-3.026	-0.605	ATP synthase Fo complex subunit a
Cell_Exteri Plasma M Plasma Membrar	G6318	cusS	0.039	-0.296	CusS-N-phospho-L-histidine
Cell_Exteri Plasma M Plasma Membrar	EG11561	caiT	-0.636	-0.096	L-carnitine:Æ [±] -butyrobetaine antiporter
Cell_Exteri Periplasm Periplasm	G6217	tauA	2.153	-2.318	taurine ABC transporter periplasmic binding protein
Cell_Exteri Periplasm Periplasm	G6437	ylil	0.451	0.014	aldose sugar dehydrogenase Ylil
Cell_Exteri Periplasm Periplasm	EG11744	pqqL	-0.315	-0.882	periplasmic metalloprotease
Cell_Exteri Periplasm Periplasm	EG10072	argT	-0.554	-0.254	lysine/arginine/ornithine ABC transporter periplasmic binding p
Cell_Exteri Periplasm Periplasm	EG10399	glpQ	-0.273	0.181	glycerophosphoryl diester phosphodiesterase GlpQ
Cell_Exteri Periplasm Periplasm	EG11703	acrA	-1.811	-2.56	multidrug efflux pump membrane fusion lipoprotein AcrA
Cell_Exteri Periplasm Periplasm	EG12427	modA	-1.715	1.605	molybdate ABC transporter periplasmic binding protein
Cell_Exteri Periplasm Periplasm	EG11337	lysP	-0.898	-0.504	lysine:H ⁺ symporter
Cell_Exteri Periplasm Periplasm	G7665	lptA	-1.079	0.494	lipopolysaccharide transport system protein LptA
Cell_Exteri Periplasm Periplasm	EG11652	degS	0.495	0.555	serine endoprotease
Cell_Exteri Periplasm Periplasm	G6491	pqiB	0.021	-1.357	intermembrane transport protein PqiB
Cell_Exteri Periplasm Periplasm	G6359	gltI	1.292	0.048	glutamate/aspartate ABC transporter periplasmic binding prote
Cell_Exteri Periplasm Periplasm	EG10950	slt	-0.969	0.428	soluble lytic murein transglycosylase
Cell_Exteri Periplasm Periplasm	G7659	mlaC	-1.437	0.429	intermembrane phospholipid transport system - periplasmic bin
Cell_Exteri Periplasm Periplasm	EG10757	ppiA	-0.905	-0.928	peptidyl-prolyl cis-trans isomerase A
Cell_Exteri Periplasm Periplasm	EG10985	surA	-0.337	-0.135	chaperone SurA
Cell_Exteri Periplasm Periplasm	G7410	mltB	-1.328	-0.087	membrane-bound lytic murein transglycosylase B

Cell_Exteri	Periplasm	Periplasm	G6318	cusS	0.039	-0.296	CusS-N-phospho-L-histidine
Cell_Exteri	Periplasm	Periplasm	EG11297	dsbA	0.94	1.065	thiol:disulfide oxidoreductase - DsbA reduced
Cell_Exteri	Periplasm	Periplasm	EG11542	tesA	-1.684	0.281	multifunctional acyl-CoA thioesterase I and protease I and lysop
Cell_Exteri	Periplasm	Periplasm	EG12799	mlaD	-1.43	0.249	intermembrane phospholipid transport system, substrate bindin
Cell_Exteri	Periplasm	Periplasm	G7165	ais	-1.838	-0.135	putative lipopolysaccharide core heptose(II)-phosphate phospho
Cell_Exteri	Periplasm	Periplasm	EG10374	ggt	-0.378	-1.098	glutathione hydrolase, small subunit
Cell_Exteri	Periplasm	Periplasm	EG11008	tolB	-1.936	0.239	Tol-Pal system periplasmic protein TolB
Cell_Exteri	Periplasm	Periplasm	EG11009	tolC	0.015	0.407	outer membrane channel TolC
Cell_Exteri	Periplasm	Periplasm	EG10046	ansB	-0.076	0.21	L-asparaginase 2
Cell_Exteri	Periplasm	Periplasm	EG10855	lptE	0.064	-0.036	lipopolysaccharide assembly protein LptE
Cell_Exteri	Periplasm	Periplasm	EG10627	mutY	-0.902	-0.025	adenine DNA glycosylase
Cell_Exteri	Periplasm	Periplasm	EG10580	mepA	-2.092	-0.477	peptidoglycan DD-endopeptidase/peptidoglycan LD-endopeptida
Cell_Exteri	Periplasm	Periplasm	G6465	lolA	0.838	1.284	outer membrane lipoprotein carrier protein
Cell_Exteri	Periplasm	Periplasm	EG10456	hmp	-0.795	1.432	nitric oxide dioxygenase
Cell_Exteri	Periplasm	Periplasm	G7017	znuA	-0.704	-1.053	Zn ²⁺ ABC transporter periplasmic binding protein
Cell_Exteri	Periplasm	Periplasm	EG10760	prc	0.012	-0.244	tail-specific protease
Cell_Exteri	Periplasm	Periplasm	EG11494	mltG	0.025	-0.551	endolytic murein transglycosylase
Cell_Exteri	Periplasm	Periplasm	G7716	fkpA	-0.055	0.232	peptidyl-prolyl cis-trans isomerase FkpA
Cell_Exteri	Periplasm	Periplasm	G7014	yobA	-0.39	0.548	CopC domain-containing protein
Cell_Exteri	Periplasm	Periplasm	G7682	degQ	-0.091	-0.064	periplasmic serine endoprotease
Cell_Exteri	Periplasm	Periplasm	EG10516	kdpD	0.594	-0.207	sensor histidine kinase KdpD
Cell_Exteri	Periplasm	Periplasm	EG10605	mrcB	-0.486	-0.255	PBP1BCE ₂
Cell_Exteri	Periplasm	Periplasm	G7664	lptC	-0.879	0.663	lipopolysaccharide transport system protein LptC
Cell_Exteri	Periplasm	Periplasm	EG10168	Int	-0.456	-0.325	apolipoprotein N-acyltransferase
Cell_Exteri	Periplasm	Periplasm	EG10269	envZ	-0.232	-0.789	sensor histidine kinase EnvZ
Cell_Exteri	Periplasm	Periplasm	EG11293	lolB	-0.809	-0.483	outer membrane lipoprotein LolB
Cell_Exteri	Periplasm	Periplasm	EG11893	dacD	-0.102	0.976	D-alanyl-D-alanine carboxypeptidase DacD
Cell_Exteri	Periplasm	Periplasm	EG10201	dacA	-2.586	-0.494	D-alanyl-D-alanine carboxypeptidase DacA
Cell_Exteri	Periplasm	Periplasm	EG10129	btuE	-0.996	-1.022	thioredoxin/glutathione peroxidase
Cell_Exteri	Periplasm	Periplasm	EG10369	gcd	1.48	-1.72	quinoprotein glucose dehydrogenase

Cell_Exteri	Periplasm	Periplasm	EG10609	mreC	-2.1	-0.915	cell shape determining protein MreC
Cell_Exteri	Cell Wall	Cell Wall Comp	EG10605	mrcB	-0.486	-0.255	PBP1BCE
Cell_Exteri	Cell Wall	Cell Wall Comp	G7668	mtgA	-1.745	0.142	peptidoglycan glycosyltransferase MtgA
Cell_Exteri	Cell Wall	Cell Wall Comp	EG10950	slt	-0.969	0.428	soluble lytic murein transglycosylase
Cellular_Pr	Cell Cycle	Cell Cycle/Divisio	EG11086	ftsL	-1	-0.881	cell division protein FtsL
Cellular_Pr	Cell Cycle	Cell Cycle/Divisio	EG10621	murE	-1.931	-0.95	UDP-N-acetylmuramoyl-L-alanyl-D-glutamate--2,6-diaminopime
Cellular_Pr	Cell Cycle	Cell Cycle/Divisio	EG10622	murF	-3.365	-0.888	D-alanyl-D-alanine-adding enzyme
Cellular_Pr	Cell Cycle	Cell Cycle/Divisio	EG10604	mraY	-2.733	-0.367	phospho-N-acetylmuramoyl-pentapeptide-transferase
Cellular_Pr	Cell Cycle	Cell Cycle/Divisio	EG10620	murD	-1.836	-0.434	UDP-N-acetylmuramoyl-L-alanine--D-glutamate ligase
Cellular_Pr	Cell Cycle	Cell Cycle/Divisio	EG10344	ftsW	-2.063	-0.743	essential cell division protein FtsW
Cellular_Pr	Cell Cycle	Cell Cycle/Divisio	EG10623	murG	-3.656	-0.02	N-acetylglucosaminyl transferase
Cellular_Pr	Cell Cycle	Cell Cycle/Divisio	EG10619	murC	-2.151	-0.568	UDP-N-acetylmuramate--L-alanine ligase
Cellular_Pr	Cell Cycle	Cell Cycle/Divisio	EG10342	ftsQ	-0.409	-0.471	cell division protein FtsQ
Cellular_Pr	Cell Cycle	Cell Cycle/Divisio	EG10347	ftsZ	-1.531	0.206	cell division protein FtsZ
Cellular_Pr	Cell Cycle	Cell Cycle/Divisio	G6092	uppS	-0.759	-1.223	ditrans, polycis-undecaprenyl-diphosphate synthase [(2E,6E)-farr
Cellular_Pr	Cell Cycle	Cell Cycle/Divisio	EG11003	tig	-2.353	0.398	trigger factor
Cellular_Pr	Cell Cycle	Cell Cycle/Divisio	EG10159	clpX	0.221	0.699	ATP-dependent Clp protease ATP-binding subunit ClpX
Cellular_Pr	Cell Cycle	Cell Cycle/Divisio	EG10461	htpG	-3.902	2.793	chaperone protein HtpG
Cellular_Pr	Cell Cycle	Cell Cycle/Divisio	EG10201	dacA	-2.586	-0.494	D-alanyl-D-alanine carboxypeptidase DacA
Cellular_Pr	Cell Cycle	Cell Cycle/Divisio	EG10854	rlpA	-2.064	-0.304	rare lipoprotein RlpA
Cellular_Pr	Cell Cycle	Cell Cycle/Divisio	EG10607	mrdb	0.654	2.104	SEDS family protein MrdB
Cellular_Pr	Cell Cycle	Cell Cycle/Divisio	EG11011	tolR	-1.969	0.279	Tol-Pal system protein TolR
Cellular_Pr	Cell Cycle	Cell Cycle/Divisio	EG11008	tolB	-1.936	0.239	Tol-Pal system periplasmic protein TolB
Cellular_Pr	Cell Cycle	Cell Cycle/Divisio	EG11494	mltG	0.025	-0.551	endolytic murein transglycosylase
Cellular_Pr	Cell Cycle	Cell Cycle/Divisio	G6567	nagZ	-0.56	-0.198	CE-N-acetylhexosaminidase
Cellular_Pr	Cell Cycle	Cell Cycle/Divisio	EG10598	minE	-0.963	-1.013	Z-ring positioning protein MinE
Cellular_Pr	Cell Cycle	Cell Cycle/Divisio	EG10597	minD	-1.768	-1.011	Z-ring positioning protein MinD
Cellular_Pr	Cell Cycle	Cell Cycle/Divisio	EG10596	minC	-1.011	-0.28	Z-ring positioning protein MinC
Cellular_Pr	Cell Cycle	Cell Cycle/Divisio	EG11122	yciB	-1.003	-0.178	inner membrane protein
Cellular_Pr	Cell Cycle	Cell Cycle/Divisio	EG12691	lapB	-0.502	-0.143	lipopolysaccharide assembly protein B

Cellular_Pr	Cell Cycle	Cell Cycle/Divisio	G7258	zipA	0.292	-0.348	cell division protein ZipA
Cellular_Pr	Cell Cycle	Cell Cycle/Divisio	EG10208	dapE	1.463	0.274	succinyl-diaminopimelate desuccinylase
Cellular_Pr	Cell Cycle	Cell Cycle/Divisio	EG10015	rodZ	-1.064	-0.309	cytoskeleton protein RodZ
Cellular_Pr	Cell Cycle	Cell Cycle/Divisio	G7424	ftsB	-0.955	-0.98	cell division protein FtsB
Cellular_Pr	Cell Cycle	Cell Cycle/Divisio	EG10686	parC	-1.506	-0.103	DNA topoisomerase IV subunit A
Cellular_Pr	Cell Cycle	Cell Cycle/Divisio	EG10687	parE	-0.81	-0.273	DNA topoisomerase IV subunit B
Cellular_Pr	Cell Cycle	Cell Cycle/Divisio	EG11358	murA	-2.398	-0.867	UDP-N-acetylglucosamine 1-carboxyvinyltransferase
Cellular_Pr	Cell Cycle	Cell Cycle/Divisio	EG11299	rng	-0.09	-0.469	RNase G
Cellular_Pr	Cell Cycle	Cell Cycle/Divisio	EG10608	mreB	-2.414	-0.26	dynamic cytoskeletal protein MreB
Cellular_Pr	Cell Cycle	Cell Cycle/Divisio	EG11191	slmA	-2.165	-0.644	nucleoid occlusion factor SlmA
Cellular_Pr	Cell Cycle	Cell Cycle/Divisio	EG10242	dnaN	-1.232	-0.058	$\text{C}\epsilon\text{S}$ sliding clamp
Cellular_Pr	Cell Cycle	Cell Cycle/Divisio	EG11203	yihA	0.51	0.137	GTP-binding protein YihA
Cellular_Pr	Cell Cycle	Cell Cycle/Divisio	EG11529	ftsN	-1.2	-0.122	cell division protein FtsN
Cellular_Pr	Cell Cycle	Cell Cycle/Divisio	EG11205	murB	-1.449	-1.07	UDP-N-acetylenolpyruvoylglucosamine reductase
Cellular_Pr	Cell Cycle	Cell Cycle/Divisio	EG10600	groS	-2.666	4.238	cochaperonin GroES
Cellular_Pr	Cell Cycle	Cell Cycle/Divisio	EG10599	groL	-2.367	3.304	chaperonin GroEL
Cellular_Pr	Cell Cycle	Cell Cycle/Divisio	EG12440	mpl	-1.659	0.434	UDP-N-acetylmuramate--L-alanyl- $\text{C}\epsilon\text{Z}$ -D-glutamyl-meso-2,6-dia
Cellular_Pr	Proteins I	Genetic Transfer	EG10441	ihfB	0.948	0.144	integration host factor subunit $\text{C}\epsilon\text{S}$
Cellular_Pr	Proteins I	Genetic Transfer	EG10440	ihfA	1.195	0.38	integration host factor subunit $\text{C}\epsilon\pm$
Cellular_Pr	Proteins I	Biofilm Formatio	G6530	pgaB	-0.858	-0.229	poly- $\text{C}\epsilon\text{S}$ -1,6-N-acetyl-D-glucosamine N-deacetylase and $\text{C}\epsilon\text{S}$ -1,6
Cellular_Pr	Proteins I	Biofilm Formatio	G6531	pgaA	0.327	0.158	partially deacetylated poly- $\text{C}\epsilon\text{S}$ -1,6-N-acetyl-D-glucosamine oute
Cellular_Pr	Proteins I	Biofilm Formatio	EG10027	ackA	0.051	-0.046	acetate kinase
Cellular_Pr	Proteins I	Biofilm Formatio	EG12880	dgcN	-1.174	-0.954	diguanylate cyclase DgcN
Cellular_Pr	Proteins I	Biofilm Formatio	EG10357	fumB	1.864	1.605	fumarase B
Cellular_Pr	Proteins I	Biofilm Formatio	EG10308	fimA	-0.087	0.569	type 1 fimbriae major subunit
Cellular_Pr	Proteins I	Adhesion	G7017	znuA	-0.704	-1.053	Zn ²⁺ ABC transporter periplasmic binding protein
Cellular_Pr	Proteins I	Adhesion	G6530	pgaB	-0.858	-0.229	poly- $\text{C}\epsilon\text{S}$ -1,6-N-acetyl-D-glucosamine N-deacetylase and $\text{C}\epsilon\text{S}$ -1,6
Cellular_Pr	Proteins I	Adhesion	EG10308	fimA	-0.087	0.569	type 1 fimbriae major subunit
Cellular_Pr	Proteins I	Adhesion	EG12880	dgcN	-1.174	-0.954	diguanylate cyclase DgcN
Cellular_Pr	Proteins I	Locomotion	G6577	cobB	0.277	0.032	CobB-S

Cellular_Pr Proteins	Locomotion	EG12880	dgcN	-1.174	-0.954	diguanylate cyclase DgcN
Cellular_Pr Proteins	Locomotion	EG10823	recA	0.96	0.456	DNA recombination/repair protein RecA
Cellular_Pr Proteins	Response to Viru	EG10240	dnaJ	0.834	3.71	chaperone protein DnaJ
Cellular_Pr Proteins	Response to Viru	EG10159	clpX	0.221	0.699	ATP-dependent Clp protease ATP-binding subunit ClpX
Cellular_Pr Proteins	Response to Viru	G6577	cobB	0.277	0.032	CobB-S
Cellular_Pr Proteins	Response to Viru	EG10777	pspB	2.455	-0.968	phage shock protein B
Cellular_Pr Proteins	Response to Viru	EG10317	fis	-1.11	-0.32	DNA-binding transcriptional dual regulator Fis
Cellular_Pr Proteins	Response to Viru	EG10600	groS	-2.666	4.238	cochaperonin GroES
Cellular_Pr Proteins	Response to Viru	EG10599	groL	-2.367	3.304	chaperonin GroEL
Cellular_Pr Other Patl	Pathogenesis	EG10735	phoU	-0.423	-0.6	negative regulator of the pho regulon
Cellular_Pr Other Patl	Pathogenesis	EG11259	rnr	0.418	-0.175	RNase R
Regulation Signal tra	Signal transducti	EG11618	baeR	-0.621	-0.351	Phosphorylated DNA-binding transcriptional activator BaeR
Regulation Signal tra	Signal transducti	EG12006	btsR	-1.729	-0.633	Phosphorylated DNA-binding transcriptional dual regulator BtsR
Regulation Signal tra	Signal transducti	G6318	cusS	0.039	-0.296	CusS-N-phospho-L-histidine
Regulation Signal tra	Signal transducti	EG10269	envZ	-0.232	-0.789	sensor histidine kinase EnvZ
Regulation Signal tra	Signal transducti	EG10517	kdpE	-0.11	-0.977	KdpE-Phosphorylated
Regulation Signal tra	Signal transducti	EG10516	kdpD	0.594	-0.207	sensor histidine kinase KdpD
Regulation Signal tra	Signal transducti	EG11602	glnE	-0.956	-1.152	fused glutamine synthetase deadenylase/glutamine synthetase
Regulation Signal tra	Signal transducti	EG11411	glnD	-0.088	-1.547	PII uridylyltransferase / uridylyl removing enzyme
Regulation Signal tra	Signal transducti	EG10387	glnL	0.905	-0.845	sensory histidine kinase NtrB
Regulation Signal tra	Signal transducti	EG12191	glnK	0.174	-0.024	uridylyl-[GlnK]
Regulation Signal tra	Signal transducti	EG10728	phoB	0.981	0.479	Phosphorylated DNA-binding transcriptional dual regulator PhoB
Regulation Signal tra	Signal transducti	EG10733	phoR	-0.729	-0.506	sensor histidine kinase PhoR
Regulation Signal tra	Signal transducti	G6864	rstA	-0.512	0.134	Phosphorylated DNA-binding transcriptional regulator RstA
Regulation Sigma Fac	Sigma Factors (S	EG10897	rpoH	-0.094	1.082	RNA polymerase, sigma 32 (sigma H) factor
Regulation Sigma Fac	Sigma Factors (S	EG10898	rpoN	-0.677	0.137	RNA polymerase, sigma 54 (sigma N) factor
Regulation Sigma Fac	Sigma Factors (S	EG10896	rpoD	0.399	1.815	RNA polymerase, sigma 70 (sigma D) factor
Regulation Sigma Fac	SF Regulons	EG10896	rpoD	0.399	1.815	RNA polymerase, sigma 70 (sigma D) factor
Regulation Sigma Fac	SF Regulons	EG10999	thrB	-1.009	0.011	homoserine kinase
Regulation Sigma Fac	SF Regulons	EG11000	thrC	0.237	-0.236	threonine synthase

Regulation Sigma Fac SF Regulons	EG11079	ribF	-1.418	0.12	bifunctional riboflavin kinase / FMN adenylyltransferase
Regulation Sigma Fac SF Regulons	EG10492	ileS	-2.101	-0.506	isoleucine--tRNA ligase
Regulation Sigma Fac SF Regulons	EG11080	fkpB	0.675	0.045	peptidyl-prolyl cis-trans isomerase FkpB
Regulation Sigma Fac SF Regulons	EG11081	ispH	1.959	0.953	1-hydroxy-2-methyl-2-(E)-butenyl 4-diphosphate reductase
Regulation Sigma Fac SF Regulons	EG10206	dapB	1.053	0.596	4-hydroxy-tetrahydrodipicolinate reductase
Regulation Sigma Fac SF Regulons	EG11561	caiT	-0.636	-0.096	L-carnitine:Æ-butyrobetaine antiporter
Regulation Sigma Fac SF Regulons	EG11569	lptD	0.645	-0.015	lipopolysaccharide assembly protein LptD
Regulation Sigma Fac SF Regulons	EG11576	leuC	-0.084	1.821	3-isopropylmalate dehydratase subunit LeuC
Regulation Sigma Fac SF Regulons	EG11577	leuB	0.548	-0.014	3-isopropylmalate dehydrogenase
Regulation Sigma Fac SF Regulons	EG10531	leuO	-0.344	-0.06	DNA-binding transcriptional dual regulator LeuO
Regulation Sigma Fac SF Regulons	EG10499	ilvH	2.498	-0.422	acetolactate synthase / acetohydroxybutanoate synthase, regulat
Regulation Sigma Fac SF Regulons	EG11085	rsmH	-1.074	-0.3	16S rRNA m4C1402 methyltransferase
Regulation Sigma Fac SF Regulons	EG11086	ftsL	-1	-0.881	cell division protein FtsL
Regulation Sigma Fac SF Regulons	EG10621	murE	-1.931	-0.95	UDP-N-acetylmuramoyl-L-alanyl-D-glutamate--2,6-diaminopimic
Regulation Sigma Fac SF Regulons	EG10622	murF	-3.365	-0.888	D-alanyl-D-alanine-adding enzyme
Regulation Sigma Fac SF Regulons	EG10604	mraY	-2.733	-0.367	phospho-N-acetylmuramoyl-pentapeptide-transferase
Regulation Sigma Fac SF Regulons	EG10620	murD	-1.836	-0.434	UDP-N-acetylmuramoyl-L-alanine--D-glutamate ligase
Regulation Sigma Fac SF Regulons	EG10344	ftsW	-2.063	-0.743	essential cell division protein FtsW
Regulation Sigma Fac SF Regulons	EG10623	murG	-3.656	-0.02	N-acetylglucosaminyl transferase
Regulation Sigma Fac SF Regulons	EG10619	murC	-2.151	-0.568	UDP-N-acetylmuramate--L-alanine ligase
Regulation Sigma Fac SF Regulons	EG10342	ftsQ	-0.409	-0.471	cell division protein FtsQ
Regulation Sigma Fac SF Regulons	EG10347	ftsZ	-1.531	0.206	cell division protein FtsZ
Regulation Sigma Fac SF Regulons	EG10265	lpxC	0.249	-0.258	UDP-3-O-acyl-N-acetylglucosamine deacetylase
Regulation Sigma Fac SF Regulons	EG11088	pdhR	-1.496	-0.29	DNA-binding transcriptional dual regulator PdhR
Regulation Sigma Fac SF Regulons	EG10024	aceE	-1.803	-0.003	pyruvate dehydrogenase E1 component
Regulation Sigma Fac SF Regulons	EG12316	acnB	-0.873	-1.09	AcnB
Regulation Sigma Fac SF Regulons	EG10369	gcd	1.48	-1.72	quinoprotein glucose dehydrogenase
Regulation Sigma Fac SF Regulons	EG20098	hpt	0.019	-0.516	hypoxanthine phosphoribosyltransferase
Regulation Sigma Fac SF Regulons	EG11747	panD	0.418	3.472	PanD Æ≤ cleavage product
Regulation Sigma Fac SF Regulons	EG11746	panC	-0.889	0.715	pantothenate synthetase

Regulation Sigma Fac SF Regulons	EG11675	panB	-0.725	0.652	3-methyl-2-oxobutanoate hydroxymethyltransferase
Regulation Sigma Fac SF Regulons	EG11374	folK	-1.133	0.395	2-amino-4-hydroxy-6-hydroxymethyldihydropteridine diphosphol
Regulation Sigma Fac SF Regulons	EG10690	pcnB	-2.447	0.164	poly(A) polymerase I
Regulation Sigma Fac SF Regulons	EG11362	gluQ	-1.063	0.77	glutamyl-Q tRNAAsp synthetase
Regulation Sigma Fac SF Regulons	EG10230	dksA	1.138	0.95	RNA polymerase-binding transcription factor DksA
Regulation Sigma Fac SF Regulons	EG10207	dapD	-0.767	0.573	tetrahydrodipicolinate succinylase
Regulation Sigma Fac SF Regulons	EG10901	rpsB	-1.039	1.919	30S ribosomal subunit protein S2
Regulation Sigma Fac SF Regulons	EG11033	tsf	-1.036	0.856	protein chain elongation factor EF-Ts
Regulation Sigma Fac SF Regulons	EG11539	pyrH	-3.024	-0.327	UMP kinase
Regulation Sigma Fac SF Regulons	EG10335	frr	-0.829	0.57	ribosome-recycling factor
Regulation Sigma Fac SF Regulons	EG10770	proS	0.626	-0.018	proline--tRNA ligase
Regulation Sigma Fac SF Regulons	G6115	dinB	0.682	0.6	DNA polymerase IV
Regulation Sigma Fac SF Regulons	EG10695	pepD	-2.925	0.275	peptidase D
Regulation Sigma Fac SF Regulons	EG10109	betA	0.13	-0.558	choline dehydrogenase
Regulation Sigma Fac SF Regulons	M012	mhpC	0.297	0.646	2-hydroxy-6-ketono-2,4-dienedioate hydrolase
Regulation Sigma Fac SF Regulons	EG10428	hemB	-3.089	0.592	porphobilinogen synthase
Regulation Sigma Fac SF Regulons	EG10728	phoB	0.981	0.479	Phosphorylated DNA-binding transcriptional dual regulator PhoB
Regulation Sigma Fac SF Regulons	EG10733	phoR	-0.729	-0.506	sensor histidine kinase PhoR
Regulation Sigma Fac SF Regulons	EG11320	nrdR	-0.413	0.531	NrdR transcriptional repressor
Regulation Sigma Fac SF Regulons	EG11321	ribD	0.146	0.562	fused diaminohydroxyphosphoribosylaminopyrimidine deaminas
Regulation Sigma Fac SF Regulons	EG11322	ribE	-0.645	0.727	6,7-dimethyl-8-ribityllumazine synthase
Regulation Sigma Fac SF Regulons	EG10666	nusB	-0.058	-0.27	transcription antitermination protein NusB
Regulation Sigma Fac SF Regulons	G6234	thiL	0.65	-0.881	thiamine monophosphate kinase
Regulation Sigma Fac SF Regulons	EG10704	pgpA	1.116	0.276	phosphatidylglycerophosphatase A
Regulation Sigma Fac SF Regulons	G6237	dxs	-1.417	1.109	1-deoxy-D-xylulose-5-phosphate synthase
Regulation Sigma Fac SF Regulons	EG10508	ispA	-0.868	-0.16	geranyl diphosphate/farnesyl diphosphate synthase
Regulation Sigma Fac SF Regulons	EG10182	cyoE	-0.598	-1.288	heme O synthase
Regulation Sigma Fac SF Regulons	EG10181	cyoD	-1.411	-0.316	cytochrome bo3 ubiquinol oxidase subunit 4
Regulation Sigma Fac SF Regulons	EG10180	cyoC	-1.184	-0.38	cytochrome bo3 ubiquinol oxidase subunit 3
Regulation Sigma Fac SF Regulons	EG10179	cyoB	-1.541	-0.558	cytochrome bo3 ubiquinol oxidase subunit 1

Regulation Sigma Fac SF Regulons	EG10178	cyoA	-2.272	-0.588	cytochrome bo3 ubiquinol oxidase subunit 2
Regulation Sigma Fac SF Regulons	EG12183	ampG	-1.149	-0.168	muropeptide:H ⁺ symporter
Regulation Sigma Fac SF Regulons	EG10125	bolA	1.583	0.948	DNA binding transcriptional dual regulator BolA-phosphate
Regulation Sigma Fac SF Regulons	EG10159	clpX	0.221	0.699	ATP-dependent Clp protease ATP-binding subunit ClpX
Regulation Sigma Fac SF Regulons	EG10467	hupB	-0.906	-1.579	DNA-binding protein HU-CE
Regulation Sigma Fac SF Regulons	G6242	ppiD	-0.294	-0.629	periplasmic folding chaperone
Regulation Sigma Fac SF Regulons	EG11703	acrA	-1.811	-2.56	multidrug efflux pump membrane fusion lipoprotein AcrA
Regulation Sigma Fac SF Regulons	EG10431	hemH	0.33	-0.099	ferrochelataase
Regulation Sigma Fac SF Regulons	EG10796	purK	-1.224	0.745	5-(carboxyamino)imidazole ribonucleotide synthase
Regulation Sigma Fac SF Regulons	EG10793	purE	-2.377	0.876	N5-carboxyaminoimidazole ribonucleotide mutase
Regulation Sigma Fac SF Regulons	G6318	cusS	0.039	-0.296	CusS-N-phospho-L-histidine
Regulation Sigma Fac SF Regulons	EG10708	pheP	-0.138	-0.776	phenylalanine:H ⁺ symporter PheP
Regulation Sigma Fac SF Regulons	EG50005	nfsB	-0.713	-0.053	NAD(P)H nitroreductase NfsB
Regulation Sigma Fac SF Regulons	EG11104	entS	0.344	0.403	enterobactin exporter EntS
Regulation Sigma Fac SF Regulons	EG10261	entC	-0.24	-6.237	isochorismate synthase EntC
Regulation Sigma Fac SF Regulons	EG10263	entE	-1.529	-5.9	2,3-dihydroxybenzoate-AMP ligase
Regulation Sigma Fac SF Regulons	EG10260	entB	-2.806	-6.528	holo EntB
Regulation Sigma Fac SF Regulons	EG10167	cstA	0.373	-0.617	carbon starvation protein A
Regulation Sigma Fac SF Regulons	EG11591	lipB	-1.975	0.059	lipoyl(octanoyl) transferase
Regulation Sigma Fac SF Regulons	EG12662	gltK	0.737	-1.442	glutamate/aspartate ABC transporter membrane subunit GltK
Regulation Sigma Fac SF Regulons	G6359	gltI	1.292	0.048	glutamate/aspartate ABC transporter periplasmic binding prote
Regulation Sigma Fac SF Regulons	EG10390	glnS	-1.557	-0.64	glutamine--tRNA ligase
Regulation Sigma Fac SF Regulons	EG10359	fur	0.268	-0.259	DNA-binding transcriptional dual regulator Fur
Regulation Sigma Fac SF Regulons	EG10515	kdpC	0.615	1.009	K ⁺ transporting P-type ATPase subunit KdpC
Regulation Sigma Fac SF Regulons	EG10514	kdpB	0.18	0.36	K ⁺ transporting P-type ATPase subunit KdpB
Regulation Sigma Fac SF Regulons	EG10513	kdpA	1.508	-0.323	K ⁺ transporting P-type ATPase subunit KdpA
Regulation Sigma Fac SF Regulons	EG10933	sdhC	-0.367	1.083	succinate:quinone oxidoreductase, membrane protein SdhC
Regulation Sigma Fac SF Regulons	EG10934	sdhD	-1.268	1.67	succinate:quinone oxidoreductase, membrane protein SdhD
Regulation Sigma Fac SF Regulons	EG10931	sdhA	-1.15	1.198	succinate:quinone oxidoreductase, FAD binding protein
Regulation Sigma Fac SF Regulons	EG10932	sdhB	-1.309	1.038	succinate:quinone oxidoreductase, iron-sulfur cluster binding prc

Regulation Sigma Fac SF Regulons	EG10979	sucA	-1.352	-0.289	subunit of E1(0) component of 2-oxoglutarate dehydrogenase
Regulation Sigma Fac SF Regulons	EG10980	sucB	-1.441	-0.268	SucB-dihydrolipoate
Regulation Sigma Fac SF Regulons	EG10981	sucC	-2.388	-0.016	succinyl-CoA synthetase subunit $\alpha\leq$
Regulation Sigma Fac SF Regulons	EG10982	sucD	-0.197	0.041	succinyl-CoA synthetase subunit $\alpha\pm$
Regulation Sigma Fac SF Regulons	EG12427	modA	-1.715	1.605	molybdate ABC transporter periplasmic binding protein
Regulation Sigma Fac SF Regulons	EG10002	modB	-1.467	0.096	molybdate ABC transporter membrane subunit
Regulation Sigma Fac SF Regulons	EG10117	bioA	-2.446	-0.277	adenosylmethionine-8-amino-7-oxononanoate aminotransferase
Regulation Sigma Fac SF Regulons	EG10118	bioB	-2.286	0.598	biotin synthase
Regulation Sigma Fac SF Regulons	EG10121	bioF	-1.076	-0.384	8-amino-7-oxononanoate synthase
Regulation Sigma Fac SF Regulons	EG10154	moeB	0.327	0.495	molybdopterin-synthase adenylyltransferase
Regulation Sigma Fac SF Regulons	EG10153	moeA	-0.998	-1.007	molybdopterin molybdotransferase
Regulation Sigma Fac SF Regulons	EG10156	clpA	0.392	-0.303	ATP-dependent Clp protease ATP-binding subunit ClpA
Regulation Sigma Fac SF Regulons	EG10504	infA	-2.268	1.331	translation initiation factor IF-1
Regulation Sigma Fac SF Regulons	G6465	lolA	0.838	1.284	outer membrane lipoprotein carrier protein
Regulation Sigma Fac SF Regulons	EG12690	rarA	0.446	-0.174	replication-associated recombination protein A
Regulation Sigma Fac SF Regulons	EG10946	serC	-0.473	-0.349	phosphoserine/phosphohydroxythreonine aminotransferase
Regulation Sigma Fac SF Regulons	EG10073	aroA	-0.728	-0.927	3-phosphoshikimate 1-carboxyvinyltransferase
Regulation Sigma Fac SF Regulons	EG11265	cmk	0.346	0.562	cytidylate kinase
Regulation Sigma Fac SF Regulons	EG10900	rpsA	-0.386	0.104	30S ribosomal subunit protein S1
Regulation Sigma Fac SF Regulons	EG10441	ihfB	0.948	0.144	integration host factor subunit $\alpha\leq$
Regulation Sigma Fac SF Regulons	EG10519	kdsB	-0.11	0.538	3-deoxy-manno-octulosonate cytidyltransferase
Regulation Sigma Fac SF Regulons	G6477	ssuD	-0.273	-1.791	FMNH ₂ -dependent alkanesulfonate monooxygenase
Regulation Sigma Fac SF Regulons	EG10807	pyrD	-0.102	0.623	dihydroorotate dehydrogenase, type 2
Regulation Sigma Fac SF Regulons	G6491	pqiB	0.021	-1.357	intermembrane transport protein PqiB
Regulation Sigma Fac SF Regulons	EG11380	appC	0.091	1.344	cytochrome bd-II ubiquinol oxidase subunit I
Regulation Sigma Fac SF Regulons	EG11379	appB	1.7	2.186	cytochrome bd-II ubiquinol oxidase subunit II
Regulation Sigma Fac SF Regulons	EG12194	cbpM	0.917	1.59	chaperone modulator CbpM
Regulation Sigma Fac SF Regulons	EG12193	cbpA	0.338	1.02	curved DNA-binding protein
Regulation Sigma Fac SF Regulons	EG12301	rutR	0.034	0.491	DNA-binding transcriptional dual regulator RutR
Regulation Sigma Fac SF Regulons	EG10801	putA	-0.647	-0.46	fused DNA-binding transcriptional repressor / proline dehydroge

Regulation Sigma Fac SF Regulons	EG10802	putP	1.322	0.007	proline:Na ⁺ symporter
Regulation Sigma Fac SF Regulons	EG10806	pyrC	-0.677	-0.487	dihydroorotase
Regulation Sigma Fac SF Regulons	EG10859	rne	-3.562	-0.662	ribonuclease E
Regulation Sigma Fac SF Regulons	EG50003	acpP	0.524	0.277	octanoyl-ACP
Regulation Sigma Fac SF Regulons	EG10649	ndh	-0.631	0.323	NADH:quinone oxidoreductase II
Regulation Sigma Fac SF Regulons	EG11619	mfd	0.305	0.107	transcription-repair coupling factor
Regulation Sigma Fac SF Regulons	EG11314	purB	-3.834	-1.376	adenylosuccinate lyase
Regulation Sigma Fac SF Regulons	EG11345	hflD	0.243	-0.753	lysogenization regulator
Regulation Sigma Fac SF Regulons	EG11408	dadX	-1.042	-2.067	alanine racemase 2
Regulation Sigma Fac SF Regulons	EG11404	ychF	-0.148	1.8	redox-responsive ATPase YchF
Regulation Sigma Fac SF Regulons	EG10785	pth	-1.544	1.147	peptidyl-tRNA hydrolase
Regulation Sigma Fac SF Regulons	EG10774	prs	-2.959	1.676	ribose-phosphate diphosphokinase
Regulation Sigma Fac SF Regulons	EG10427	hemA	-1.609	-0.068	glutamyl-tRNA reductase
Regulation Sigma Fac SF Regulons	EG10761	prfA	-2.256	-0.394	peptide chain release factor RF1
Regulation Sigma Fac SF Regulons	EG12424	prmC	-1.02	-0.329	protein-(glutamine-N5) methyltransferase
Regulation Sigma Fac SF Regulons	EG10518	kdsA	-0.65	-0.99	3-deoxy-D-manno-octulosonate 8-phosphate synthase
Regulation Sigma Fac SF Regulons	EG11122	yciB	-1.003	-0.178	inner membrane protein
Regulation Sigma Fac SF Regulons	EG11024	trpA	-2.399	0.371	tryptophan synthase subunit α
Regulation Sigma Fac SF Regulons	EG11026	trpC	-2.361	0.871	fused indole-3-glycerol phosphate synthase/phosphoribosylanth
Regulation Sigma Fac SF Regulons	EG11028	trpE	-3.801	0.11	anthranilate synthase subunit TrpE
Regulation Sigma Fac SF Regulons	EG11325	acnA	1.373	1.446	aconitate hydratase 1
Regulation Sigma Fac SF Regulons	EG11331	ribA	1.404	-0.477	GTP cyclohydrolase 2
Regulation Sigma Fac SF Regulons	EG12691	lapB	-0.502	-0.143	lipopolysaccharide assembly protein B
Regulation Sigma Fac SF Regulons	EG10809	pyrF	1.959	0.593	orotidine-5'-phosphate decarboxylase
Regulation Sigma Fac SF Regulons	G6706	feaR	0.085	-0.768	DNA-binding transcriptional activator FeaR
Regulation Sigma Fac SF Regulons	G6709	paaA	-5.021	1.126	phenylacetyl-CoA 1,2-epoxidase, monooxygenase subunit
Regulation Sigma Fac SF Regulons	G6710	paaB	-3.909	1.115	phenylacetyl-CoA 1,2-epoxidase subunit B
Regulation Sigma Fac SF Regulons	G6711	paaC	-4.822	1.134	phenylacetyl-CoA 1,2-epoxidase, structural subunit
Regulation Sigma Fac SF Regulons	G6712	paaD	-5.99	1.192	phenylacetate degradation protein
Regulation Sigma Fac SF Regulons	G6713	paaE	-4.088	1.196	phenylacetyl-CoA 1,2-epoxidase, reductase subunit

Regulation Sigma Fac SF Regulons	G6715	paaG	-3.55	0.88	putative ring 1,2-epoxyphenylacetyl-CoA isomerase (oxepin-CoA
Regulation Sigma Fac SF Regulons	G6718	paaJ	-3.848	0.427	CE≤-ketoadipyl-CoA thiolase
Regulation Sigma Fac SF Regulons	G6719	paaK	-2.225	0.205	phenylacetate-CoA ligase
Regulation Sigma Fac SF Regulons	G6720	paaX	0.791	-0.538	DNA-binding transcriptional repressor PaaX
Regulation Sigma Fac SF Regulons	EG10745	pntB	-0.396	2.331	pyridine nucleotide transhydrogenase subunit CE≤
Regulation Sigma Fac SF Regulons	EG10744	pntA	-2.074	2.717	pyridine nucleotide transhydrogenase subunit CE±
Regulation Sigma Fac SF Regulons	EG10358	fumC	0.721	-1.154	fumarase C
Regulation Sigma Fac SF Regulons	EG10030	add	-1.259	-0.114	adenosine deaminase
Regulation Sigma Fac SF Regulons	G6889	nemR	0.676	1.872	DNA-binding transcriptional repressor NemR
Regulation Sigma Fac SF Regulons	G6890	nemaA	1.149	0.75	N-ethylmaleimide reductase
Regulation Sigma Fac SF Regulons	G6891	gloA	-1.408	2.349	glyoxalase I
Regulation Sigma Fac SF Regulons	EG12181	grxD	1.336	0.746	glutaredoxin 4
Regulation Sigma Fac SF Regulons	EG10954	sodB	0.358	1.587	superoxide dismutase (Fe)
Regulation Sigma Fac SF Regulons	G6906	sufS	1.017	-0.397	L-cysteine desulfurase
Regulation Sigma Fac SF Regulons	EG10759	ppsA	-1.103	-0.254	phosphoenolpyruvate synthetase
Regulation Sigma Fac SF Regulons	EG10129	btuE	-0.996	-1.022	thioredoxin/glutathione peroxidase
Regulation Sigma Fac SF Regulons	EG10881	rplT	-1.641	-0.09	50S ribosomal subunit protein L20
Regulation Sigma Fac SF Regulons	EG11231	rpmI	-2.451	0.136	50S ribosomal subunit protein L35
Regulation Sigma Fac SF Regulons	EG10506	infC	-1.165	0.798	translation initiation factor IF-3
Regulation Sigma Fac SF Regulons	EG10663	nadE	-0.718	-0.394	NH3-dependent NAD+ synthetase
Regulation Sigma Fac SF Regulons	EG12394	msrB	0.198	0.18	methionine sulfoxide reductase B
Regulation Sigma Fac SF Regulons	EG11530	fadD	1.067	-1.658	long-chain-fatty-acid--CoA ligase
Regulation Sigma Fac SF Regulons	EG11809	purT	-0.365	-0.318	phosphoribosylglycinamide formyltransferase 2
Regulation Sigma Fac SF Regulons	EG10256	eda	-0.306	-0.472	KHG/KDPG aldolase
Regulation Sigma Fac SF Regulons	EG10257	edd	0.795	-0.31	phosphogluconate dehydratase
Regulation Sigma Fac SF Regulons	G7018	znuC	-0.892	0.026	Zn2+ ABC transporter ATP binding subunit
Regulation Sigma Fac SF Regulons	EG12368	znuB	-2.051	0.342	Zn2+ ABC transporter membrane subunit
Regulation Sigma Fac SF Regulons	EG10925	ruvC	-0.512	-0.508	crossover junction endodeoxyribonuclease RuvC
Regulation Sigma Fac SF Regulons	EG10071	argS	-2.019	-0.646	arginine--tRNA ligase
Regulation Sigma Fac SF Regulons	G7991	cysT	0.693	-3.162	tRNA-Cys(GCA)

Regulation Sigma Fac SF Regulons	EG11063	uvrC	-0.598	1.971	excision nuclease subunit C
Regulation Sigma Fac SF Regulons	EG12150	cobS	-1.564	0.301	cobalamin 5'-phosphate synthase
Regulation Sigma Fac SF Regulons	EG10445	hisB	-2.951	0.393	imidazoleglycerol-phosphate dehydratase / histidinol-phosphatase
Regulation Sigma Fac SF Regulons	EG10450	hisH	-1.627	0.564	imidazole glycerol phosphate synthase subunit HisH
Regulation Sigma Fac SF Regulons	EG10444	hisA	-0.548	0.029	1-(5-phosphoribosyl)-5-[(5-phosphoribosylamino)methylideneamino]imidazole glycerol phosphate synthase subunit HisF
Regulation Sigma Fac SF Regulons	EG10448	hisF	-1.349	0.401	imidazole glycerol phosphate synthase subunit HisF
Regulation Sigma Fac SF Regulons	EG10451	hisI	-1.133	-0.766	putative bifunctional phosphoribosyl-AMP cyclohydrolase/phosphatase
Regulation Sigma Fac SF Regulons	EG12416	gatC	-1.457	0.161	galactitol-specific PTS enzyme IIC component
Regulation Sigma Fac SF Regulons	EG12415	gatB	-0.862	-0.022	galactitol-specific PTS enzyme IIB component
Regulation Sigma Fac SF Regulons	G7137	rcnR	-1.29	0.527	DNA-binding transcriptional repressor RcnR
Regulation Sigma Fac SF Regulons	EG10586	metG	-1.642	-0.168	methionine--tRNA ligase
Regulation Sigma Fac SF Regulons	EG11375	folE	-0.719	0.176	GTP cyclohydrolase 1
Regulation Sigma Fac SF Regulons	EG11337	lysP	-0.898	-0.504	lysine:H ⁺ symporter
Regulation Sigma Fac SF Regulons	EG10885	rplY	-1.984	1.618	50S ribosomal subunit protein L25
Regulation Sigma Fac SF Regulons	EG10037	alkB	-0.524	1.243	DNA oxidative demethylase
Regulation Sigma Fac SF Regulons	EG10423	gyrA	-1.844	-0.652	DNA gyrase subunit A
Regulation Sigma Fac SF Regulons	EG11143	ubiG	-0.471	0.639	bifunctional 3-demethylubiquinone-8 3-O-methyltransferase and ubiquinol dehydrogenase
Regulation Sigma Fac SF Regulons	EG10661	nrdB	-2.608	0.397	ribonucleoside-diphosphate reductase 1 subunit α
Regulation Sigma Fac SF Regulons	EG10399	glpQ	-0.273	0.181	glycerophosphoryl diester phosphodiesterase GlpQ
Regulation Sigma Fac SF Regulons	EG12093	nuoN	-1.763	-0.195	NADH:quinone oxidoreductase subunit N
Regulation Sigma Fac SF Regulons	EG11773	nuoM	-2.108	0.305	NADH:quinone oxidoreductase subunit M
Regulation Sigma Fac SF Regulons	EG12092	nuoL	-2.06	0.479	NADH:quinone oxidoreductase subunit L
Regulation Sigma Fac SF Regulons	EG12091	nuoK	-2.478	1.063	NADH:quinone oxidoreductase subunit K
Regulation Sigma Fac SF Regulons	EG12090	nuoJ	-1.56	1.196	NADH:quinone oxidoreductase subunit J
Regulation Sigma Fac SF Regulons	EG12089	nuoI	-0.888	1.472	NADH:quinone oxidoreductase subunit I
Regulation Sigma Fac SF Regulons	EG12088	nuoH	-1.477	1.386	NADH:quinone oxidoreductase subunit H
Regulation Sigma Fac SF Regulons	EG12087	nuoG	-1.347	1.469	NADH:quinone oxidoreductase subunit G
Regulation Sigma Fac SF Regulons	EG11774	nuoF	-0.226	1.858	NADH:quinone oxidoreductase subunit F
Regulation Sigma Fac SF Regulons	EG12086	nuoE	-0.112	1.772	NADH:quinone oxidoreductase subunit E
Regulation Sigma Fac SF Regulons	EG12084	nuoC	-1.019	1.447	NADH:quinone oxidoreductase subunit CD

Regulation Sigma Fac SF Regulons	EG12083	nuoB	-0.509	2.067	NADH:quinone oxidoreductase subunit B
Regulation Sigma Fac SF Regulons	EG20173	pta	-1.402	-0.828	phosphate acetyltransferase
Regulation Sigma Fac SF Regulons	EG10007	hisM	-1.823	-0.423	lysine/arginine/ornithine ABC transporter / histidine ABC transp
Regulation Sigma Fac SF Regulons	EG10794	purF	-0.892	1.723	amidophosphoribosyltransferase
Regulation Sigma Fac SF Regulons	EG10217	accD	-0.711	0.285	acetyl-CoA carboxyltransferase subunit CEs
Regulation Sigma Fac SF Regulons	EG10274	fabB	0.379	0.23	3-oxoacyl-[acyl carrier protein] synthase 1
Regulation Sigma Fac SF Regulons	G7213	fadI	-0.488	0.196	3-ketoacyl-CoA thiolase FadI
Regulation Sigma Fac SF Regulons	EG10249	dsdA	0.03	0.826	D-serine ammonia-lyase
Regulation Sigma Fac SF Regulons	EG10407	gltX	-0.316	0.544	glutamate--tRNA ligase
Regulation Sigma Fac SF Regulons	EG10193	cysM	-0.615	0.467	cysteine synthase B
Regulation Sigma Fac SF Regulons	EG10198	cysW	-0.283	-0.776	sulfate/thiosulfate ABC transporter inner membrane subunit Cy
Regulation Sigma Fac SF Regulons	EG12189	hemF	-0.006	0.208	coproporphyrinogen III oxidase
Regulation Sigma Fac SF Regulons	EG10208	dapE	1.463	0.274	succinyl-diaminopimelate desuccinylase
Regulation Sigma Fac SF Regulons	EG10791	purC	-0.285	-0.494	phosphoribosylaminoimidazole-succinocarboxamide synthase
Regulation Sigma Fac SF Regulons	EG10108	bcp	0.204	0.571	thiol peroxidase
Regulation Sigma Fac SF Regulons	EG11332	upp	-0.001	0.803	uracil phosphoribosyltransferase
Regulation Sigma Fac SF Regulons	EG10798	purM	-3.537	1.548	phosphoribosylformylglycinamide cyclo-ligase
Regulation Sigma Fac SF Regulons	EG10799	purN	-2.398	0.496	phosphoribosylglycinamide formyltransferase 1
Regulation Sigma Fac SF Regulons	EG10420	guaA	-1.857	0.273	GMP synthetase
Regulation Sigma Fac SF Regulons	EG10421	guaB	-0.735	0.68	inosine 5'-monophosphate dehydrogenase
Regulation Sigma Fac SF Regulons	EG11072	xseA	-0.219	0.056	exodeoxyribonuclease VII subunit XseA
Regulation Sigma Fac SF Regulons	EG10453	hisS	-0.034	-0.571	histidine--tRNA ligase
Regulation Sigma Fac SF Regulons	EG12130	hscA	-1.569	0.685	iron-sulfur cluster biosynthesis chaperone HscA
Regulation Sigma Fac SF Regulons	EG12131	hscB	-3.226	1.032	[Fe-S] cluster biosynthesis co-chaperone HscB
Regulation Sigma Fac SF Regulons	EG12132	iscA	-0.445	1.522	iron-sulfur cluster insertion protein IscA
Regulation Sigma Fac SF Regulons	G7324	iscU	-0.998	1.951	scaffold protein for iron-sulfur cluster assembly
Regulation Sigma Fac SF Regulons	G7325	iscS	-1.254	0.693	cysteine desulfurase IscS
Regulation Sigma Fac SF Regulons	EG10408	glyA	-2.967	0.691	serine hydroxymethyltransferase
Regulation Sigma Fac SF Regulons	EG10797	purL	-2.774	1.427	phosphoribosylformylglycinamide synthetase
Regulation Sigma Fac SF Regulons	EG10693	pdxJ	-2.271	-0.126	pyridoxine 5'-phosphate synthase

Regulation Sigma Fac SF Regulons	EG10832	recO	-0.769	-0.246	DNA repair protein RecO
Regulation Sigma Fac SF Regulons	EG10270	era	-0.458	0.651	30S ribosomal subunit maturation GTPase Era
Regulation Sigma Fac SF Regulons	EG10857	rnc	0.713	0.351	RNase III
Regulation Sigma Fac SF Regulons	EG10631	nadB	-1.72	0.102	L-aspartate oxidase
Regulation Sigma Fac SF Regulons	EG11887	trxC	2.051	0.765	oxidized thioredoxin 2
Regulation Sigma Fac SF Regulons	EG10157	clpB	0.611	1.356	ClpB80
Regulation Sigma Fac SF Regulons	EG10707	pheA	-1.232	0.212	fused chorismate mutase/prephenate dehydratase
Regulation Sigma Fac SF Regulons	EG12880	dgcN	-1.174	-0.954	diguanylate cyclase DgcN
Regulation Sigma Fac SF Regulons	EG10880	rplS	-1.489	0.485	50S ribosomal subunit protein L19
Regulation Sigma Fac SF Regulons	EG11023	trmD	-0.947	0.051	tRNA m1G37 methyltransferase
Regulation Sigma Fac SF Regulons	EG11153	rimM	-1.77	0.772	ribosome maturation factor RimM
Regulation Sigma Fac SF Regulons	EG10915	rpsP	-2.655	1.621	30S ribosomal subunit protein S16
Regulation Sigma Fac SF Regulons	EG10831	recN	0.111	-0.3	DNA repair protein RecN
Regulation Sigma Fac SF Regulons	EG11447	csrA	1.321	-1.204	carbon storage regulator
Regulation Sigma Fac SF Regulons	EG12080	recX	-0.27	1.028	RecA inhibitor RecX
Regulation Sigma Fac SF Regulons	EG10823	recA	0.96	0.456	DNA recombination/repair protein RecA
Regulation Sigma Fac SF Regulons	EG10194	cysN	-0.289	1.25	sulfate adenylyltransferase subunit 1
Regulation Sigma Fac SF Regulons	EG10186	cysD	-2.495	1.049	sulfate adenylyltransferase subunit 2
Regulation Sigma Fac SF Regulons	EG10258	enolase	0.448	-0.774	enolase
Regulation Sigma Fac SF Regulons	EG10835	relA	-0.511	0.982	GDP/GTP pyrophosphokinase
Regulation Sigma Fac SF Regulons	EG10348	fucA	-0.036	0.298	L-fucose-phosphate aldolase
Regulation Sigma Fac SF Regulons	EG10063	argA	-1.559	0.108	N-acetylglutamate synthase
Regulation Sigma Fac SF Regulons	EG10826	recD	-1.861	-0.186	exodeoxyribonuclease V subunit RecD
Regulation Sigma Fac SF Regulons	EG10824	recB	-1.491	0.129	exodeoxyribonuclease V subunit RecB
Regulation Sigma Fac SF Regulons	EG10825	recC	-0.755	-0.461	exodeoxyribonuclease V subunit RecC
Regulation Sigma Fac SF Regulons	EG11002	thyA	-0.966	-0.248	thymidylate synthase
Regulation Sigma Fac SF Regulons	EG12128	lgt	-2.209	1.733	phosphatidylglycerol--prolipoprotein diacylglycerol transferase
Regulation Sigma Fac SF Regulons	EG10549	lysA	1.177	-0.044	diaminopimelate decarboxylase
Regulation Sigma Fac SF Regulons	EG10830	recJ	-1.816	-0.258	ssDNA-specific exonuclease RecJ
Regulation Sigma Fac SF Regulons	EG10371	gcvH	0.207	-0.227	lipoyl-GcvH-protein

Regulation Sigma Fac SF Regulons	EG11333	ubil	0.312	-1.116	2-octaprenylphenol 6-hydroxylase
Regulation Sigma Fac SF Regulons	EG11324	ubiH	-0.578	-0.571	2-octaprenyl-6-methoxyphenol 4-hydroxylase
Regulation Sigma Fac SF Regulons	EG10697	pepP	-0.611	-0.53	Xaa-Pro aminopeptidase
Regulation Sigma Fac SF Regulons	EG11158	fau	-0.996	0.76	putative 5-formyltetrahydrofolate cyclo-ligase
Regulation Sigma Fac SF Regulons	EG10944	serA	0.354	0.313	phosphoglycerate dehydrogenase
Regulation Sigma Fac SF Regulons	EG11159	argO	-0.925	-6.685	L-arginine exporter
Regulation Sigma Fac SF Regulons	EG10703	pgk	0.832	0.751	phosphoglycerate kinase
Regulation Sigma Fac SF Regulons	EG10368	epd	0.878	-0.549	D-erythrose-4-phosphate dehydrogenase
Regulation Sigma Fac SF Regulons	EG11291	loiP	0.149	0.119	metalloprotease LoiP
Regulation Sigma Fac SF Regulons	EG10589	metK	-0.9	-0.553	methionine adenosyltransferase
Regulation Sigma Fac SF Regulons	EG10046	ansB	-0.076	0.21	L-asparaginase 2
Regulation Sigma Fac SF Regulons	EG10920	rpsU	-2.111	1.745	30S ribosomal subunit protein S21
Regulation Sigma Fac SF Regulons	EG10239	dnaG	0.3	-0.241	DNA primase
Regulation Sigma Fac SF Regulons	EG10215	deaD	-2.19	-2.847	ATP-dependent RNA helicase DeaD
Regulation Sigma Fac SF Regulons	EG10743	pnp	-0.553	-1.652	polynucleotide phosphorylase
Regulation Sigma Fac SF Regulons	EG10914	rpsO	-2.11	-0.875	30S ribosomal subunit protein S15
Regulation Sigma Fac SF Regulons	EG11177	truB	0.042	0.069	tRNA pseudouridine55 synthase
Regulation Sigma Fac SF Regulons	EG11178	rbfA	-0.282	0.532	30S ribosome binding factor
Regulation Sigma Fac SF Regulons	EG10505	infB	-0.204	0.659	translation initiation factor IF-2
Regulation Sigma Fac SF Regulons	EG10665	nusA	-0.549	0.59	transcription termination/antitermination protein NusA
Regulation Sigma Fac SF Regulons	EG11179	rimP	0.603	-0.255	ribosome maturation factor RimP
Regulation Sigma Fac SF Regulons	EG10068	argG	-0.453	0.295	argininosuccinate synthetase
Regulation Sigma Fac SF Regulons	EG12095	secG	-1.458	0.553	Sec translocon subunit SecG
Regulation Sigma Fac SF Regulons	EG11506	ftsH	0.675	0.469	ATP-dependent zinc metalloprotease FtsH
Regulation Sigma Fac SF Regulons	EG11507	rlmE	1.076	0.655	23S rRNA 2'-O-ribose U2552 methyltransferase
Regulation Sigma Fac SF Regulons	EG10415	greA	-1.004	-0.046	transcription elongation factor GreA
Regulation Sigma Fac SF Regulons	EG50002	rpmA	-1.371	1.346	50S ribosomal subunit protein L27
Regulation Sigma Fac SF Regulons	EG50001	rplU	-2.149	1.382	50S ribosomal subunit protein L21
Regulation Sigma Fac SF Regulons	G7662	kdsD	-0.507	0.633	D-arabinose 5-phosphate isomerase KdsD
Regulation Sigma Fac SF Regulons	G7663	kdsC	-0.586	-0.059	3-deoxy-D-manno-octulosonate 8-phosphate phosphatase KdsC

Regulation Sigma Fac SF Regulons	G7664	lptC	-0.879	0.663	lipopolysaccharide transport system protein LptC
Regulation Sigma Fac SF Regulons	G7665	lptA	-1.079	0.494	lipopolysaccharide transport system protein LptA
Regulation Sigma Fac SF Regulons	EG10898	rpoN	-0.677	0.137	RNA polymerase, sigma 54 (sigma N) factor
Regulation Sigma Fac SF Regulons	EG11681	hpf	1.151	-1.568	ribosome hibernation-promoting factor
Regulation Sigma Fac SF Regulons	EG12146	rapZ	-1.743	0.627	RNase adaptor protein RapZ
Regulation Sigma Fac SF Regulons	EG12147	npr	0.022	0.374	Npr phosphorylated
Regulation Sigma Fac SF Regulons	EG10403	gltB	-1.41	-0.121	glutamate synthase subunit GltB
Regulation Sigma Fac SF Regulons	EG10404	gltD	-0.677	1.668	glutamate synthase subunit GltD
Regulation Sigma Fac SF Regulons	G7682	degQ	-0.091	-0.064	periplasmic serine endoprotease
Regulation Sigma Fac SF Regulons	EG11652	degS	0.495	0.555	serine endoprotease
Regulation Sigma Fac SF Regulons	EG10609	mreC	-2.1	-0.915	cell shape determining protein MreC
Regulation Sigma Fac SF Regulons	EG10608	mreB	-2.414	-0.26	dynamic cytoskeletal protein MreB
Regulation Sigma Fac SF Regulons	EG10275	accB	-1.479	-1.539	biotin carboxyl carrier protein
Regulation Sigma Fac SF Regulons	EG10276	accC	-0.766	-1.72	biotin carboxylase
Regulation Sigma Fac SF Regulons	EG11497	prmA	0.633	-0.374	ribosomal protein L11 methyltransferase
Regulation Sigma Fac SF Regulons	EG11311	dusB	-2.096	-0.355	tRNA-dihydrouridine synthase B
Regulation Sigma Fac SF Regulons	EG10317	fis	-1.11	-0.32	DNA-binding transcriptional dual regulator Fis
Regulation Sigma Fac SF Regulons	EG11268	fmt	-0.42	0.251	10-formyltetrahydrofolate:L-methionyl-tRNA ^{fMet} N-formyltransf
Regulation Sigma Fac SF Regulons	EG10878	rplQ	-1.649	0.754	50S ribosomal subunit protein L17
Regulation Sigma Fac SF Regulons	EG10893	rpoA	-2.18	0.563	RNA polymerase subunit α
Regulation Sigma Fac SF Regulons	EG10903	rpsD	-2.155	0.66	30S ribosomal subunit protein S4
Regulation Sigma Fac SF Regulons	EG10912	rpsM	-2.616	0.72	30S ribosomal subunit protein S13
Regulation Sigma Fac SF Regulons	EG10916	rpsQ	-1.558	1.906	30S ribosomal subunit protein S17
Regulation Sigma Fac SF Regulons	EG10887	rpmC	-2.174	1.836	50S ribosomal subunit protein L29
Regulation Sigma Fac SF Regulons	EG10877	rplP	-2.62	1.819	50S ribosomal subunit protein L16
Regulation Sigma Fac SF Regulons	EG10902	rpsC	-2.812	1.765	30S ribosomal subunit protein S3
Regulation Sigma Fac SF Regulons	EG10882	rplV	-1.868	1.753	50S ribosomal subunit protein L22
Regulation Sigma Fac SF Regulons	EG10918	rpsS	-2.877	1.849	30S ribosomal subunit protein S19
Regulation Sigma Fac SF Regulons	EG10865	rplB	-1.141	1.812	50S ribosomal subunit protein L2
Regulation Sigma Fac SF Regulons	EG10883	rplW	-1.711	1.921	50S ribosomal subunit protein L23

Regulation Sigma Fac SF Regulons	EG10867	rplD	-2.778	2.173	50S ribosomal subunit protein L4
Regulation Sigma Fac SF Regulons	EG10866	rplC	-3.126	2.123	50S ribosomal subunit protein L3
Regulation Sigma Fac SF Regulons	EG10909	rpsJ	-2.923	2.015	30S ribosomal subunit protein S10
Regulation Sigma Fac SF Regulons	EG11182	yhfA	-0.605	-0.994	OsmC family protein YhfA
Regulation Sigma Fac SF Regulons	EG10066	argD	0.184	0.114	N-acetylornithine aminotransferase / N-succinyldiaminopimelate
Regulation Sigma Fac SF Regulons	EG10757	ppiA	-0.905	-0.928	peptidyl-prolyl cis-trans isomerase A
Regulation Sigma Fac SF Regulons	EG11871	gph	-0.971	-0.101	phosphoglycolate phosphatase
Regulation Sigma Fac SF Regulons	M004	rpe	-0.684	1.758	ribulose-phosphate 3-epimerase
Regulation Sigma Fac SF Regulons	EG10074	aroB	-1.063	-0.829	3-dehydroquinate synthase
Regulation Sigma Fac SF Regulons	EG10081	aroK	-1.714	-0.25	shikimate kinase 1
Regulation Sigma Fac SF Regulons	EG10269	envZ	-0.232	-0.789	sensor histidine kinase EnvZ
Regulation Sigma Fac SF Regulons	EG12102	feoB	-2.241	-1.547	Fe ²⁺ transporter FeoB
Regulation Sigma Fac SF Regulons	G7748	nfuA	-0.202	1.33	iron-sulfur cluster carrier protein NfuA
Regulation Sigma Fac SF Regulons	EG12380	gntT	-0.157	-1.086	high-affinity gluconate transporter
Regulation Sigma Fac SF Regulons	EG10394	glpD	0.381	0.052	aerobic glycerol 3-phosphate dehydrogenase
Regulation Sigma Fac SF Regulons	EG12629	gntK	-0.039	-0.993	D-gluconate kinase, thermostable
Regulation Sigma Fac SF Regulons	EG11050	ugpQ	1.275	-0.56	glycerophosphodiester phosphodiesterase UgpQ
Regulation Sigma Fac SF Regulons	EG10897	rpoH	-0.094	1.082	RNA polymerase, sigma 32 (sigma H) factor
Regulation Sigma Fac SF Regulons	EG10410	glyS	-2.435	-1.428	glycine--tRNA ligase subunit $\alpha_{\leq}$
Regulation Sigma Fac SF Regulons	EG10409	glyQ	-1.526	-1.002	glycine--tRNA ligase subunit $\alpha_{\pm}$
Regulation Sigma Fac SF Regulons	EG10616	mtlD	-0.337	-1.079	mannitol-1-phosphate 5-dehydrogenase
Regulation Sigma Fac SF Regulons	EG11961	lldP	-2.273	0.606	lactate/glycolate:H ⁺ symporter LldP
Regulation Sigma Fac SF Regulons	EG20091	gpsA	0.144	-0.531	glycerol-3-phosphate dehydrogenase
Regulation Sigma Fac SF Regulons	EG10937	secB	-0.431	1.976	protein export chaperone SecB
Regulation Sigma Fac SF Regulons	EG12294	grxC	0.206	2.129	oxidized glutaredoxin 3
Regulation Sigma Fac SF Regulons	EG10520	waaA	-1.834	-0.113	KDO transferase
Regulation Sigma Fac SF Regulons	EG11190	coaD	-0.139	0.254	pantetheine-phosphate adenylyltransferase
Regulation Sigma Fac SF Regulons	EG10251	dut	-1.848	0.839	dUTP diphosphatase
Regulation Sigma Fac SF Regulons	EG11191	slmA	-2.165	-0.644	nucleoid occlusion factor SlmA
Regulation Sigma Fac SF Regulons	EG10965	gmk	-0.246	-0.364	guanylate kinase

Regulation Sigma Fac SF Regulons	EG10899	rpoZ	-1.353	0.111	RNA polymerase subunit σ^{54}
Regulation Sigma Fac SF Regulons	EG10966	spoT	-1.098	-0.172	bifunctional (p)ppGpp synthase/hydrolase SpoT
Regulation Sigma Fac SF Regulons	EG10829	recG	-1.864	-0.102	ATP-dependent DNA helicase RecG
Regulation Sigma Fac SF Regulons	EG10424	gyrB	-0.001	-0.399	DNA gyrase subunit B
Regulation Sigma Fac SF Regulons	EG10242	dnaN	-1.232	-0.058	β' sliding clamp
Regulation Sigma Fac SF Regulons	EG10235	dnaA	-0.446	-0.998	chromosomal replication initiator protein DnaA
Regulation Sigma Fac SF Regulons	EG10735	phoU	-0.423	-0.6	negative regulator of the pho regulon
Regulation Sigma Fac SF Regulons	EG10783	pstB	-0.471	-0.217	phosphate ABC transporter ATP binding subunit
Regulation Sigma Fac SF Regulons	EG11198	glmU	-0.787	-0.277	fused N-acetylglucosamine-1-phosphate uridylyltransferase and g
Regulation Sigma Fac SF Regulons	EG10100	atpC	-0.863	-0.363	ATP synthase F1 complex subunit ϵ_{μ}
Regulation Sigma Fac SF Regulons	EG10104	atpG	-0.713	-0.931	ATP synthase F1 complex subunit $\epsilon_{\geq}$
Regulation Sigma Fac SF Regulons	EG10098	atpA	-2.2	-0.798	ATP synthase F1 complex subunit $\epsilon_{\pm}$
Regulation Sigma Fac SF Regulons	EG10105	atpH	-2.636	-0.803	ATP synthase F1 complex subunit $\epsilon_{\neq}$
Regulation Sigma Fac SF Regulons	EG10103	atpF	-2.285	-0.963	ATP synthase Fo complex subunit b
Regulation Sigma Fac SF Regulons	EG10102	atpE	-2.628	-0.936	ATP synthase Fo complex subunit c
Regulation Sigma Fac SF Regulons	EG10099	atpB	-3.026	-0.605	ATP synthase Fo complex subunit a
Regulation Sigma Fac SF Regulons	EG10376	rsmG	-2.15	-0.341	16S rRNA m7G527 methyltransferase
Regulation Sigma Fac SF Regulons	EG10375	mnmG	-0.824	0.232	5-carboxymethylaminomethyluridine-tRNA synthase subunit Mr
Regulation Sigma Fac SF Regulons	EG10093	asnC	0.026	-0.791	DNA-binding transcriptional dual regulator AsnC
Regulation Sigma Fac SF Regulons	EG10497	ilvE	-1.772	-1.955	branched-chain-amino-acid aminotransferase
Regulation Sigma Fac SF Regulons	EG10496	ilvD	-3.398	0.755	dihydroxy-acid dehydratase
Regulation Sigma Fac SF Regulons	EG10493	ilvA	-1.538	-0.36	threonine deaminase
Regulation Sigma Fac SF Regulons	EG10495	ilvC	0.281	-0.473	ketol-acid reductoisomerase (NADP+)
Regulation Sigma Fac SF Regulons	EG10209	dapF	-0.592	0.528	diaminopimelate epimerase
Regulation Sigma Fac SF Regulons	EG11463	corA	-0.389	0.726	Ni ²⁺ /Co ²⁺ /Mg ²⁺ transporter
Regulation Sigma Fac SF Regulons	G7806	tatA	1.922	0.029	twin arginine protein translocation system - TatA protein
Regulation Sigma Fac SF Regulons	G7808	tatB	0.436	0.558	twin arginine protein translocation system - TatB protein
Regulation Sigma Fac SF Regulons	EG11479	tatC	-0.067	0.791	twin arginine protein translocation system - TatC protein
Regulation Sigma Fac SF Regulons	EG10279	fadB	-0.067	0.034	multifunctional enoyl-CoA hydratase, 3-hydroxyacyl-CoA epimer;
Regulation Sigma Fac SF Regulons	EG11297	dsbA	0.94	1.065	thiol:disulfide oxidoreductase - DsbA-reduced

Regulation Sigma Fac SF Regulons	EG10387	glnL	0.905	-0.845	sensory histidine kinase NtrB
Regulation Sigma Fac SF Regulons	EG11015	tpiA	0.072	1.305	triose-phosphate isomerase
Regulation Sigma Fac SF Regulons	EG10398	glpK	0.274	-0.238	glycerol kinase
Regulation Sigma Fac SF Regulons	EG10585	metF	0.474	-1.001	5,10-methylenetetrahydrofolate reductase
Regulation Sigma Fac SF Regulons	EG10511	katG	0.743	0.489	catalase/hydroperoxidase HPI
Regulation Sigma Fac SF Regulons	EG10065	argC	-3.216	-0.642	N-acetylglutamylphosphate reductase
Regulation Sigma Fac SF Regulons	EG10064	argB	-1.92	0.471	acetylglutamate kinase
Regulation Sigma Fac SF Regulons	EG11223	argH	-1.247	-0.644	argininosuccinate lyase
Regulation Sigma Fac SF Regulons	EG11204	murl	-2.028	0.738	glutamate racemase
Regulation Sigma Fac SF Regulons	EG10792	purD	-0.47	-0.804	phosphoribosylamine--glycine ligase
Regulation Sigma Fac SF Regulons	EG10795	purH	-2.619	-1.683	bifunctional AICAR transformylase/IMP cyclohydrolase
Regulation Sigma Fac SF Regulons	EG10587	metH	-0.146	0.823	cobalamin-dependent methionine synthase
Regulation Sigma Fac SF Regulons	EG10702	pgi	-0.83	0.101	glucose-6-phosphate isomerase
Regulation Sigma Fac SF Regulons	EG11209	psiE	1.457	-0.74	putative phosphate starvation-inducible protein PsiE
Regulation Sigma Fac SF Regulons	EG11369	ubiC	0.163	0.077	chorismate lyase
Regulation Sigma Fac SF Regulons	EG11370	ubiA	1.207	0.337	4-hydroxybenzoate octaprenyltransferase
Regulation Sigma Fac SF Regulons	EG11061	uvrA	-1.562	1.685	excision nuclease subunit A
Regulation Sigma Fac SF Regulons	EG10976	ssb	2.338	1.296	ssDNA-binding protein
Regulation Sigma Fac SF Regulons	EG10957	soxR	1.744	0.712	DNA-binding transcriptional dual regulator SoxR
Regulation Sigma Fac SF Regulons	EG10357	fumB	1.864	1.605	fumarase B
Regulation Sigma Fac SF Regulons	EG10095	aspA	-0.4	0.082	aspartate ammonia-lyase
Regulation Sigma Fac SF Regulons	EG10600	groS	-2.666	4.238	cochaperonin GroES
Regulation Sigma Fac SF Regulons	EG10599	groL	-2.367	3.304	chaperonin GroEL
Regulation Sigma Fac SF Regulons	EG12099	efp	-0.119	1.058	protein chain elongation factor EF-P, Cε-lysyl-Lys34
Regulation Sigma Fac SF Regulons	EG11758	nnr	-1.018	0.137	NAD(P)HX epimerase / NAD(P)HX dehydratase
Regulation Sigma Fac SF Regulons	EG11281	mutL	-1.659	0.053	DNA mismatch repair protein MutL
Regulation Sigma Fac SF Regulons	EG10595	miaA	-0.344	1.252	tRNA dimethylallyltransferase
Regulation Sigma Fac SF Regulons	EG10438	hfq	1.032	0.204	RNA-binding protein Hfq
Regulation Sigma Fac SF Regulons	EG10437	hflX	-0.096	-0.265	ribosome rescue factor HflX
Regulation Sigma Fac SF Regulons	EG10790	purA	-0.652	-1.525	adenylosuccinate synthetase

Regulation Sigma Fac SF Regulons	EG10905	rpsF	-3.975	1.32	30S ribosomal subunit protein S6
Regulation Sigma Fac SF Regulons	EG10917	rpsR	-2.664	1.524	30S ribosomal subunit protein S18
Regulation Sigma Fac SF Regulons	EG10870	rplI	-1.655	1.145	50S ribosomal subunit protein L9
Regulation Sigma Fac SF Regulons	EG12440	mpl	-1.659	0.434	UDP-N-acetylmuramate--L-alanyl- $\rightarrow$ -D-glutamyl-meso-2,6-diaminopimelate
Regulation Sigma Fac SF Regulons	EG12525	mgtA	-0.154	2.412	Mg ²⁺ importing P-type ATPase
Regulation Sigma Fac SF Regulons	EG11067	valS	-0.812	0.402	valine--tRNA ligase
Regulation Sigma Fac SF Regulons	EG10694	pepA	-0.29	-0.865	aminopeptidase A/I
Regulation Sigma Fac SF Regulons	EG10308	fimA	-0.087	0.569	type 1 fimbriae major subunit
Regulation Sigma Fac SF Regulons	EG12191	glnK	0.174	-0.024	uridylyl-[GlnK]
Regulation Sigma Fac SF Regulons	EG10461	htpG	-3.902	2.793	chaperone protein HtpG
Regulation Sigma Fac SF Regulons	G6517	rutG	-0.73	0.35	pyrimidine:H ⁺ symporter
Regulation Sigma Fac SF Regulons	G6518	rutF	0.407	0.155	FMN reductase RutF
Regulation Sigma Fac SF Regulons	G6643	puuP	-0.618	0.221	putrescine:H ⁺ symporter PuuP
Regulation Sigma Fac SF Regulons	EG10777	pspB	2.455	-0.968	phage shock protein B
Regulation Sigma Fac SF Regulons	EG10072	argT	-0.554	-0.254	lysine/arginine/ornithine ABC transporter periplasmic binding protein
Regulation Sigma Fac SF Regulons	EG10432	hemL	0.508	0.208	glutamate-1-semialdehyde 2,1-aminomutase
Regulation Sigma Fac SF Regulons	EG11293	lolB	-0.809	-0.483	outer membrane lipoprotein LolB
Regulation Sigma Fac SF Regulons	G6938	ves	0.502	-0.785	HutD family protein Ves
Regulation Sigma Fac SF Regulons	EG10048	apaH	-1.148	0.322	diadenosine tetraphosphatase
Regulation Sigma Fac SF Regulons	EG10523	rsmA	1.51	-0.022	16S rRNA m62A1518,m62A1519 dimethyltransferase
Regulation Sigma Fac SF Regulons	EG10691	pdxA	-0.002	0.752	4-hydroxythreonine-4-phosphate dehydrogenase
Regulation Sigma Fac SF Regulons	EG10985	surA	-0.337	-0.135	chaperone SurA
Regulation Sigma Fac SF Regulons	EG12436	rseP	-0.733	-0.148	intramembrane zinc metalloprotease RseP
Regulation Sigma Fac SF Regulons	EG11284	fabZ	-1.159	-0.452	3-hydroxy-acyl-[acyl-carrier-protein] dehydratase
Regulation Sigma Fac SF Regulons	EG10545	lpxA	-1.799	-0.737	acyl-[acyl-carrier-protein]--UDP-N-acetylglucosamine O-acyltransferase
Regulation Sigma Fac SF Regulons	EG10546	lpxB	-1.683	-0.69	lipid A disaccharide synthase
Regulation Sigma Fac SF Regulons	EG10861	rnhB	-0.146	-0.281	RNase HII
Regulation Sigma Fac SF Regulons	EG10238	dnaE	-0.288	-0.711	DNA polymerase III subunit α
Regulation Sigma Fac SF Regulons	EG10928	sbmA	-1.261	-0.708	peptide antibiotic/peptide nucleic acid transporter
Regulation Sigma Fac SF Regulons	EG11100	ybaB	0.864	0.453	putative nucleoid-associated protein YbaB

Regulation Sigma Fac SF Regulons	EG10834	recR	-0.47	-0.759	DNA repair protein RecR
Regulation Sigma Fac SF Regulons	G7241	lpxP	-0.555	-1.42	palmitoleoyl acyltransferase
Regulation Sigma Fac SF Regulons	G7319	der	-1.289	0.057	50S ribosomal subunit stability factor
Regulation Sigma Fac SF Regulons	G7320	bamB	-0.674	-0.58	outer membrane protein assembly factor BamB
Regulation Sigma Fac SF Regulons	G7352	bamD	-1.241	0.552	outer membrane protein assembly factor BamD
Regulation Sigma Fac SF Regulons	EG10952	bamE	-0.48	0.678	outer membrane protein assembly factor BamE
Regulation Sigma Fac SF Regulons	EG10762	prfB	-0.766	-0.128	peptide chain release factor RF2
Regulation Sigma Fac SF Regulons	EG10136	cca	0.489	0.563	fused CCA tRNA nucleotidyltransferase/phosphohydrolase
Regulation Sigma Fac SF Regulons	EG11665	bacA	-0.645	-0.074	undecaprenyl pyrophosphate phosphatase
Regulation Sigma Fac SF Regulons	G7716	fkpA	-0.055	0.232	peptidyl-prolyl cis-trans isomerase FkpA
Regulation Sigma Fac SF Regulons	EG10740	plsB	-0.655	-0.114	glycerol-3-phosphate 1-O-acyltransferase
Regulation Sigma Fac SF Regulons	EG10775	psd	-1.783	-0.244	phosphatidylserine decarboxylase proenzyme
Regulation Sigma Fac SF Regulons	EG11648	dkgB	-1.19	0.883	methylglyoxal reductase DkgB
Regulation Sigma Fac SF Regulons	EG10736	phr	1.34	-0.289	deoxyribodipyrimidine photolyase
Regulation Sigma Fac SF Regulons	G6644	puuA	-2.269	0.797	glutamate-putrescine ligase
Regulation Sigma Fac SF Regulons	G6646	puuE	-3.029	3.456	4-aminobutyrate aminotransferase PuuE
Regulation Sigma Fac SF Regulons	G6755	patD	-0.349	2.859	4-aminobutyraldehyde dehydrogenase
Regulation Sigma Fac SF Regulons	G6806	tam	-1.597	0.234	trans-aconitate 2-methyltransferase
Regulation Sigma Fac SF Regulons	EG10440	ihfA	1.195	0.38	integration host factor subunit α
Regulation Sigma Fac SF Regulons	EG10509	katE	-0.414	1.55	catalase HP1
Regulation Sigma Fac SF Regulons	G7017	znuA	-0.704	-1.053	Zn ²⁺ ABC transporter periplasmic binding protein
Regulation Sigma Fac SF Regulons	EG11751	otsA	0.438	1.798	trehalose-6-phosphate synthase
Regulation Sigma Fac SF Regulons	EG11752	otsB	1.361	2.141	trehalose-6-phosphate phosphatase
Regulation Sigma Fac SF Regulons	G7115	mdtC	0.374	-1.041	multidrug efflux pump RND permease subunit MdtC
Regulation Sigma Fac SF Regulons	EG11618	baeR	-0.621	-0.351	Phosphorylated DNA-binding transcriptional activator BaeR
Regulation Sigma Fac SF Regulons	EG11403	ppx	0.41	-0.213	exopolyphosphatase
Regulation Sigma Fac SF Regulons	EG10456	hmp	-0.795	1.432	nitric oxide dioxygenase
Regulation Sigma Fac SF Regulons	EG10625	mutS	-1.27	-1.387	DNA mismatch repair protein MutS
Regulation Sigma Fac SF Regulons	EG11009	tolC	0.015	0.407	outer membrane channel TolC
Regulation Sigma Fac SF Regulons	EG12296	gpmM	0.309	-0.191	2,3-bisphosphoglycerate-independent phosphoglycerate mutase

Regulation Sigma Fac SF Regulons	EG10240	dnaJ	0.834	3.71	chaperone protein DnaJ
Regulation Sigma Fac SF Regulons	G6206	mhpT	0.287	-0.97	3-hydroxyphenylpropionate/3-hydroxycinnamate:H ⁺ symporter
Regulation Sigma Fac SF Regulons	EG10168	Int	-0.456	-0.325	apolipoprotein N-acyltransferase
Regulation Sigma Fac SF Regulons	G6362	ybeY	0.573	-0.711	endoribonuclease YbeY
Regulation Sigma Fac SF Regulons	G6363	ybeZ	0.287	0.153	PhoH-like protein
Regulation Sigma Fac SF Regulons	EG10930	sdaA	0.895	-0.512	L-serine deaminase I
Regulation Sigma Fac SF Regulons	G7184	alaA	-1.27	-0.396	glutamate--pyruvate aminotransferase AlaA
Regulation Sigma Fac SF Regulons	EG10027	ackA	0.051	-0.046	acetate kinase
Regulation Sigma Fac SF Regulons	EG11372	tadA	-0.655	-1.485	tRNA adenosine34 deaminase
Regulation Sigma Fac SF Regulons	EG10416	grpE	-1.164	3.874	nucleotide exchange factor GrpE
Regulation Sigma Fac SF Regulons	EG11969	zntR	0.659	0.855	DNA-binding transcriptional activator ZntR
Regulation Sigma Fac SF Regulons	G7742	yrfG	0.76	0.573	purine nucleotidase
Regulation Sigma Fac SF Regulons	G7743	hslR	-0.385	1.371	heat shock protein Hsp15
Regulation Sigma Fac SF Regulons	G7744	hslO	-0.552	2.225	molecular chaperone Hsp33
Regulation Sigma Fac SF Regulons	EG12233	rsmJ	-1.024	0.917	16S rRNA m2G1516 methyltransferase
Regulation Sigma Fac SF Regulons	EG10329	mutM	-0.431	0.188	DNA-formamidopyrimidine glycosylase
Regulation Sigma Fac SF Regulons	EG10889	rpmE	0.586	2.023	50S ribosomal subunit protein L31
Regulation Sigma Fac SF Regulons	EG11022	trmA	-0.736	-0.816	tRNA m5U54 methyltransferase
Regulation Sigma Fac SF Regulons	EG10950	slt	-0.969	0.428	soluble lytic murein transglycosylase
Regulation Transcript Transcription Fac	EG10531	leuO	-0.344	-0.06	DNA-binding transcriptional dual regulator LeuO
Regulation Transcript Transcription Fac	EG11088	pdhR	-1.496	-0.29	DNA-binding transcriptional dual regulator PdhR
Regulation Transcript Transcription Fac	EG10728	phoB	0.981	0.479	Phosphorylated DNA-binding transcriptional dual regulator PhoB
Regulation Transcript Transcription Fac	EG11320	nrdR	-0.413	0.531	NrdR transcriptional repressor
Regulation Transcript Transcription Fac	EG10125	bolA	1.583	0.948	DNA binding transcriptional dual regulator BolA-phosphate
Regulation Transcript Transcription Fac	EG10467	hupB	-0.906	-1.579	DNA-binding protein HU- $\text{C}\epsilon\leq$
Regulation Transcript Transcription Fac	G6263	cueR	-0.389	-0.506	DNA-binding transcriptional dual regulator CueR
Regulation Transcript Transcription Fac	EG10359	fur	0.268	-0.259	DNA-binding transcriptional dual regulator Fur
Regulation Transcript Transcription Fac	EG10517	kdpE	-0.11	-0.977	KdpE-Phosphorylated
Regulation Transcript Transcription Fac	EG10441	ihfB	0.948	0.144	integration host factor subunit $\text{C}\epsilon\leq$
Regulation Transcript Transcription Fac	EG12301	rutR	0.034	0.491	DNA-binding transcriptional dual regulator RutR

Regulation Transcript Transcription Fac EG10801	putA	-0.647	-0.46	fused DNA-binding transcriptional repressor / proline dehydrogenase
Regulation Transcript Transcription Fac G6569	comR	0.494	1.445	DNA-binding transcriptional repressor ComR
Regulation Transcript Transcription Fac G6706	feaR	0.085	-0.768	DNA-binding transcriptional activator FeaR
Regulation Transcript Transcription Fac G6720	paaX	0.791	-0.538	DNA-binding transcriptional repressor PaaX
Regulation Transcript Transcription Fac G6864	rstA	-0.512	0.134	Phosphorylated DNA-binding transcriptional regulator RstA
Regulation Transcript Transcription Fac G6889	nemR	0.676	1.872	DNA-binding transcriptional repressor NemR
Regulation Transcript Transcription Fac EG10440	ihfA	1.195	0.38	integration host factor subunit α
Regulation Transcript Transcription Fac EG11618	baeR	-0.621	-0.351	Phosphorylated DNA-binding transcriptional activator BaeR
Regulation Transcript Transcription Fac G7137	rcnR	-1.29	0.527	DNA-binding transcriptional repressor RcnR
Regulation Transcript Transcription Fac EG12006	btsR	-1.729	-0.633	Phosphorylated DNA-binding transcriptional dual regulator BtsR
Regulation Transcript Transcription Fac EG12386	glaR	-0.49	0.103	DNA-binding transcriptional repressor GlaR
Regulation Transcript Transcription Fac EG10034	alaS	-1.695	-0.501	alanine--tRNA ligase/DNA-binding transcriptional repressor
Regulation Transcript Transcription Fac EG10275	accB	-1.479	-1.539	biotin carboxyl carrier protein
Regulation Transcript Transcription Fac EG10317	fis	-1.11	-0.32	DNA-binding transcriptional dual regulator Fis
Regulation Transcript Transcription Fac EG11969	zntR	0.659	0.855	DNA-binding transcriptional activator ZntR
Regulation Transcript Transcription Fac EG10235	dnaA	-0.446	-0.998	chromosomal replication initiator protein DnaA
Regulation Transcript Transcription Fac EG10093	asnC	0.026	-0.791	DNA-binding transcriptional dual regulator AsnC
Regulation Transcript Transcription Fac EG10591	metR	-0.36	-0.917	DNA-binding transcriptional dual regulator MetR
Regulation Transcript Transcription Fac EG10123	birA	1.022	-0.972	DNA-binding transcriptional repressor/biotin-[acetyl-CoA-carboxylase]
Regulation Transcript Transcription Fac EG11929	zur	-1.172	0.463	DNA-binding transcriptional repressor Zur
Regulation Transcript Transcription Fac EG10957	soxR	1.744	0.712	DNA-binding transcriptional dual regulator SoxR
Regulation Transcript Transcription Fac EG11212	nsrR	-0.428	1.199	DNA-binding transcriptional repressor NsrR
Regulation Transcript Transcription Fac EG10694	pepA	-0.29	-0.865	aminopeptidase A/I
Regulation Transcript Transcription Fac G7924	hypT	-0.596	-0.257	DNA-binding transcriptional dual regulator HypT
Regulation Transcript TF Regulons	EG10275 accB	-1.479	-1.539	biotin carboxyl carrier protein
Regulation Transcript TF Regulons	EG10276 accC	-0.766	-1.72	biotin carboxylase
Regulation Transcript TF Regulons	EG11561 caiT	-0.636	-0.096	L-carnitine:acetyl-CoA antiporter
Regulation Transcript TF Regulons	EG11088 pdhR	-1.496	-0.29	DNA-binding transcriptional dual regulator PdhR
Regulation Transcript TF Regulons	EG10024 aceE	-1.803	-0.003	pyruvate dehydrogenase E1 component
Regulation Transcript TF Regulons	EG11411 glnD	-0.088	-1.547	PII uridylyltransferase / uridylyl removing enzyme

Regulation Transcript TF Regulons	EG10182	cyoE	-0.598	-1.288	heme O synthase
Regulation Transcript TF Regulons	EG10181	cyoD	-1.411	-0.316	cytochrome bo3 ubiquinol oxidase subunit 4
Regulation Transcript TF Regulons	EG10180	cyoC	-1.184	-0.38	cytochrome bo3 ubiquinol oxidase subunit 3
Regulation Transcript TF Regulons	EG10179	cyoB	-1.541	-0.558	cytochrome bo3 ubiquinol oxidase subunit 1
Regulation Transcript TF Regulons	EG10178	cyoA	-2.272	-0.588	cytochrome bo3 ubiquinol oxidase subunit 2
Regulation Transcript TF Regulons	EG12191	glnK	0.174	-0.024	uridylyl-[GlnK]
Regulation Transcript TF Regulons	EG10933	sdhC	-0.367	1.083	succinate:quinone oxidoreductase, membrane protein SdhC
Regulation Transcript TF Regulons	EG10934	sdhD	-1.268	1.67	succinate:quinone oxidoreductase, membrane protein SdhD
Regulation Transcript TF Regulons	EG10931	sdhA	-1.15	1.198	succinate:quinone oxidoreductase, FAD binding protein
Regulation Transcript TF Regulons	EG10932	sdhB	-1.309	1.038	succinate:quinone oxidoreductase, iron-sulfur cluster binding protein
Regulation Transcript TF Regulons	EG10979	sucA	-1.352	-0.289	subunit of E1(0) component of 2-oxoglutarate dehydrogenase
Regulation Transcript TF Regulons	EG10980	sucB	-1.441	-0.268	SucB-dihydrolipoate
Regulation Transcript TF Regulons	EG10981	sucC	-2.388	-0.016	succinyl-CoA synthetase subunit C _≤
Regulation Transcript TF Regulons	EG10982	sucD	-0.197	0.041	succinyl-CoA synthetase subunit C _±
Regulation Transcript TF Regulons	EG11595	moaA	1.558	0.073	GTP 3',8'-cyclase
Regulation Transcript TF Regulons	EG11666	moaC	0.088	-0.084	cyclic pyranopterin monophosphate synthase
Regulation Transcript TF Regulons	EG10154	moeB	0.327	0.495	molybdopterin-synthase adenylyltransferase
Regulation Transcript TF Regulons	EG10153	moeA	-0.998	-1.007	molybdopterin molybdotransferase
Regulation Transcript TF Regulons	G6477	ssuD	-0.273	-1.791	FMNH ₂ -dependent alkanesulfonate monooxygenase
Regulation Transcript TF Regulons	EG10649	ndh	-0.631	0.323	NADH:quinone oxidoreductase II
Regulation Transcript TF Regulons	EG10427	hemaA	-1.609	-0.068	glutamyl-tRNA reductase
Regulation Transcript TF Regulons	EG10761	prfA	-2.256	-0.394	peptide chain release factor RF1
Regulation Transcript TF Regulons	EG12424	prmC	-1.02	-0.329	protein-(glutamine-N5) methyltransferase
Regulation Transcript TF Regulons	EG11124	ompW	0.706	0.134	outer membrane protein W
Regulation Transcript TF Regulons	EG11325	acnA	1.373	1.446	aconitate hydratase 1
Regulation Transcript TF Regulons	G6643	puuP	-0.618	0.221	putrescine:H ⁺ symporter PuuP
Regulation Transcript TF Regulons	G6644	puuA	-2.269	0.797	glutamate-putrescine ligase
Regulation Transcript TF Regulons	EG10358	fumC	0.721	-1.154	fumarase C
Regulation Transcript TF Regulons	EG10881	rplT	-1.641	-0.09	50S ribosomal subunit protein L20
Regulation Transcript TF Regulons	EG12394	msrB	0.198	0.18	methionine sulfoxide reductase B

Regulation Transcript TF Regulons	EG10399	glpQ	-0.273	0.181	glycerophosphoryl diester phosphodiesterase GlpQ
Regulation Transcript TF Regulons	EG12093	nuoN	-1.763	-0.195	NADH:quinone oxidoreductase subunit N
Regulation Transcript TF Regulons	EG11773	nuoM	-2.108	0.305	NADH:quinone oxidoreductase subunit M
Regulation Transcript TF Regulons	EG12092	nuoL	-2.06	0.479	NADH:quinone oxidoreductase subunit L
Regulation Transcript TF Regulons	EG12091	nuoK	-2.478	1.063	NADH:quinone oxidoreductase subunit K
Regulation Transcript TF Regulons	EG12090	nuoJ	-1.56	1.196	NADH:quinone oxidoreductase subunit J
Regulation Transcript TF Regulons	EG12089	nuoI	-0.888	1.472	NADH:quinone oxidoreductase subunit I
Regulation Transcript TF Regulons	EG12088	nuoH	-1.477	1.386	NADH:quinone oxidoreductase subunit H
Regulation Transcript TF Regulons	EG12087	nuoG	-1.347	1.469	NADH:quinone oxidoreductase subunit G
Regulation Transcript TF Regulons	EG11774	nuoF	-0.226	1.858	NADH:quinone oxidoreductase subunit F
Regulation Transcript TF Regulons	EG12086	nuoE	-0.112	1.772	NADH:quinone oxidoreductase subunit E
Regulation Transcript TF Regulons	EG12084	nuoC	-1.019	1.447	NADH:quinone oxidoreductase subunit CD
Regulation Transcript TF Regulons	EG12083	nuoB	-0.509	2.067	NADH:quinone oxidoreductase subunit B
Regulation Transcript TF Regulons	EG10027	ackA	0.051	-0.046	acetate kinase
Regulation Transcript TF Regulons	EG11332	upp	-0.001	0.803	uracil phosphoribosyltransferase
Regulation Transcript TF Regulons	EG10798	purM	-3.537	1.548	phosphoribosylformylglycinamide cyclo-ligase
Regulation Transcript TF Regulons	EG10799	purN	-2.398	0.496	phosphoribosylglycinamide formyltransferase 1
Regulation Transcript TF Regulons	EG10456	hmp	-0.795	1.432	nitric oxide dioxygenase
Regulation Transcript TF Regulons	EG11058	ung	-1.525	-0.126	uracil-DNA glycosylase
Regulation Transcript TF Regulons	EG10880	rplS	-1.489	0.485	50S ribosomal subunit protein L19
Regulation Transcript TF Regulons	EG11023	trmD	-0.947	0.051	tRNA m1G37 methyltransferase
Regulation Transcript TF Regulons	EG11153	rimM	-1.77	0.772	ribosome maturation factor RimM
Regulation Transcript TF Regulons	EG10915	rpsP	-2.655	1.621	30S ribosomal subunit protein S16
Regulation Transcript TF Regulons	EG10371	gcvH	0.207	-0.227	lipoyl-GcvH-protein
Regulation Transcript TF Regulons	EG10046	ansB	-0.076	0.21	L-asparaginase 2
Regulation Transcript TF Regulons	EG10990	tdcB	0.034	0.312	catabolic threonine dehydratase
Regulation Transcript TF Regulons	EG12522	garD	0.866	-0.44	GarD
Regulation Transcript TF Regulons	EG10403	gltB	-1.41	-0.121	glutamate synthase subunit GltB
Regulation Transcript TF Regulons	EG10404	gltD	-0.677	1.668	glutamate synthase subunit GltD
Regulation Transcript TF Regulons	EG10908	rpsI	-0.92	-0.394	30S ribosomal subunit protein S9

Regulation Transcript TF Regulons	EG10874	rplM	-1.147	-0.133	50S ribosomal subunit protein L13
Regulation Transcript TF Regulons	EG10916	rpsQ	-1.558	1.906	30S ribosomal subunit protein S17
Regulation Transcript TF Regulons	EG10887	rpmC	-2.174	1.836	50S ribosomal subunit protein L29
Regulation Transcript TF Regulons	EG10877	rplP	-2.62	1.819	50S ribosomal subunit protein L16
Regulation Transcript TF Regulons	EG10902	rpsC	-2.812	1.765	30S ribosomal subunit protein S3
Regulation Transcript TF Regulons	EG10882	rplV	-1.868	1.753	50S ribosomal subunit protein L22
Regulation Transcript TF Regulons	EG10918	rpsS	-2.877	1.849	30S ribosomal subunit protein S19
Regulation Transcript TF Regulons	EG10865	rplB	-1.141	1.812	50S ribosomal subunit protein L2
Regulation Transcript TF Regulons	EG10883	rplW	-1.711	1.921	50S ribosomal subunit protein L23
Regulation Transcript TF Regulons	EG10867	rplD	-2.778	2.173	50S ribosomal subunit protein L4
Regulation Transcript TF Regulons	EG10866	rplC	-3.126	2.123	50S ribosomal subunit protein L3
Regulation Transcript TF Regulons	EG10909	rpsJ	-2.923	2.015	30S ribosomal subunit protein S10
Regulation Transcript TF Regulons	EG12102	feoB	-2.241	-1.547	Fe2+ transporter FeoB
Regulation Transcript TF Regulons	EG10735	phoU	-0.423	-0.6	negative regulator of the pho regulon
Regulation Transcript TF Regulons	EG10783	pstB	-0.471	-0.217	phosphate ABC transporter ATP binding subunit
Regulation Transcript TF Regulons	EG10511	katG	0.743	0.489	catalase/hydroperoxidase HPI
Regulation Transcript TF Regulons	EG11369	ubiC	0.163	0.077	chorismate lyase
Regulation Transcript TF Regulons	EG11370	ubiA	1.207	0.337	4-hydroxybenzoate octaprenyltransferase
Regulation Transcript TF Regulons	EG10957	soxR	1.744	0.712	DNA-binding transcriptional dual regulator SoxR
Regulation Transcript TF Regulons	EG10357	fumB	1.864	1.605	fumarase B
Regulation Transcript TF Regulons	EG10095	aspA	-0.4	0.082	aspartate ammonia-lyase
Regulation Transcript TF Regulons	EG10467	hupB	-0.906	-1.579	DNA-binding protein HU- α
Regulation Transcript TF Regulons	EG10423	gyrA	-1.844	-0.652	DNA gyrase subunit A
Regulation Transcript TF Regulons	EG11703	acrA	-1.811	-2.56	multidrug efflux pump membrane fusion lipoprotein AcrA
Regulation Transcript TF Regulons	G6720	paaX	0.791	-0.538	DNA-binding transcriptional repressor PaaX
Regulation Transcript TF Regulons	G6708	paaZ	-3.501	0.382	fused 3-oxo-5,6-dehydrosuberil-CoA semialdehyde dehydrogenase
Regulation Transcript TF Regulons	G6709	paaA	-5.021	1.126	phenylacetyl-CoA 1,2-epoxidase, monooxygenase subunit
Regulation Transcript TF Regulons	G6710	paaB	-3.909	1.115	phenylacetyl-CoA 1,2-epoxidase subunit B
Regulation Transcript TF Regulons	G6711	paaC	-4.822	1.134	phenylacetyl-CoA 1,2-epoxidase, structural subunit
Regulation Transcript TF Regulons	G6712	paaD	-5.99	1.192	phenylacetate degradation protein

Regulation Transcript TF Regulons	G6713	paaE	-4.088	1.196	phenylacetyl-CoA 1,2-epoxidase, reductase subunit
Regulation Transcript TF Regulons	G6715	paaG	-3.55	0.88	putative ring 1,2-epoxyphenylacetyl-CoA isomerase (oxepin-CoA
Regulation Transcript TF Regulons	G6718	paaJ	-3.848	0.427	CoA-ketoadipyl-CoA thiolase
Regulation Transcript TF Regulons	G6719	paaK	-2.225	0.205	phenylacetate-CoA ligase
Regulation Transcript TF Regulons	EG10531	leuO	-0.344	-0.06	DNA-binding transcriptional dual regulator LeuO
Regulation Transcript TF Regulons	EG10347	ftsZ	-1.531	0.206	cell division protein FtsZ
Regulation Transcript TF Regulons	G6465	lolA	0.838	1.284	outer membrane lipoprotein carrier protein
Regulation Transcript TF Regulons	EG12690	rarA	0.446	-0.174	replication-associated recombination protein A
Regulation Transcript TF Regulons	EG50010	frmA	1.617	0.148	S-(hydroxymethyl)glutathione dehydrogenase
Regulation Transcript TF Regulons	EG10125	bolA	1.583	0.948	DNA binding transcriptional dual regulator BolA-phosphate
Regulation Transcript TF Regulons	EG10609	mreC	-2.1	-0.915	cell shape determining protein MreC
Regulation Transcript TF Regulons	EG10608	mreB	-2.414	-0.26	dynamic cytoskeletal protein MreB
Regulation Transcript TF Regulons	G6806	tam	-1.597	0.234	trans-aconitate 2-methyltransferase
Regulation Transcript TF Regulons	EG10109	betA	0.13	-0.558	choline dehydrogenase
Regulation Transcript TF Regulons	EG12301	rutR	0.034	0.491	DNA-binding transcriptional dual regulator RutR
Regulation Transcript TF Regulons	G6517	rutG	-0.73	0.35	pyrimidine:H ⁺ symporter
Regulation Transcript TF Regulons	G6518	rutF	0.407	0.155	FMN reductase RutF
Regulation Transcript TF Regulons	G6889	nemR	0.676	1.872	DNA-binding transcriptional repressor NemR
Regulation Transcript TF Regulons	G6890	nemaA	1.149	0.75	N-ethylmaleimide reductase
Regulation Transcript TF Regulons	G6891	gloA	-1.408	2.349	glyoxalase I
Regulation Transcript TF Regulons	EG10572	mazG	-1.665	0.19	nucleoside triphosphate pyrophosphohydrolase
Regulation Transcript TF Regulons	EG10317	fis	-1.11	-0.32	DNA-binding transcriptional dual regulator Fis
Regulation Transcript TF Regulons	EG10048	apaH	-1.148	0.322	diadenosine tetraphosphatase
Regulation Transcript TF Regulons	EG10523	rsmA	1.51	-0.022	16S rRNA m62A1518,m62A1519 dimethyltransferase
Regulation Transcript TF Regulons	EG10691	pdxA	-0.002	0.752	4-hydroxythreonine-4-phosphate dehydrogenase
Regulation Transcript TF Regulons	EG12316	acnB	-0.873	-1.09	AcnB
Regulation Transcript TF Regulons	EG10812	queA	-2.438	0.39	tRNA preQ134 S-adenosylmethionine ribosyltransferase-isomer
Regulation Transcript TF Regulons	EG10807	pyrD	-0.102	0.623	dihydroorotate dehydrogenase, type 2
Regulation Transcript TF Regulons	EG12194	cbpM	0.917	1.59	chaperone modulator CbpM
Regulation Transcript TF Regulons	EG12193	cbpA	0.338	1.02	curved DNA-binding protein

Regulation Transcript TF Regulons	EG10668	ogt	-0.261	0.181	methyalted-DNA--[protein]-cysteine S-methyltransferase
Regulation Transcript TF Regulons	EG10509	katE	-0.414	1.55	catalase HP11
Regulation Transcript TF Regulons	EG10661	nrdB	-2.608	0.397	ribonucleoside-diphosphate reductase 1 subunit Cε
Regulation Transcript TF Regulons	EG10407	gltX	-0.316	0.544	glutamate--tRNA ligase
Regulation Transcript TF Regulons	EG10420	guaA	-1.857	0.273	GMP synthetase
Regulation Transcript TF Regulons	EG10421	guaB	-0.735	0.68	inosine 5'-monophosphate dehydrogenase
Regulation Transcript TF Regulons	EG11158	fau	-0.996	0.76	putative 5-formyltetrahydrofolate cyclo-ligase
Regulation Transcript TF Regulons	EG10743	pnp	-0.553	-1.652	polynucleotide phosphorylase
Regulation Transcript TF Regulons	EG10914	rpsO	-2.11	-0.875	30S ribosomal subunit protein S15
Regulation Transcript TF Regulons	EG11177	truB	0.042	0.069	tRNA pseudouridine55 synthase
Regulation Transcript TF Regulons	EG11178	rbfA	-0.282	0.532	30S ribosome binding factor
Regulation Transcript TF Regulons	EG10505	infB	-0.204	0.659	translation initiation factor IF-2
Regulation Transcript TF Regulons	EG10665	nusA	-0.549	0.59	transcription termination/antitermination protein NusA
Regulation Transcript TF Regulons	EG11179	rimP	0.603	-0.255	ribosome maturation factor RimP
Regulation Transcript TF Regulons	EG11311	dusB	-2.096	-0.355	tRNA-dihydrouridine synthase B
Regulation Transcript TF Regulons	EG10616	mtlD	-0.337	-1.079	mannitol-1-phosphate 5-dehydrogenase
Regulation Transcript TF Regulons	EG10424	gyrB	-0.001	-0.399	DNA gyrase subunit B
Regulation Transcript TF Regulons	EG10242	dnaN	-1.232	-0.058	Cε sliding clamp
Regulation Transcript TF Regulons	EG10235	dnaA	-0.446	-0.998	chromosomal replication initiator protein DnaA
Regulation Transcript TF Regulons	EG10279	fadB	-0.067	0.034	multifunctional enoyl-CoA hydratase, 3-hydroxyacyl-CoA epimer
Regulation Transcript TF Regulons	EG10387	glnL	0.905	-0.845	sensory histidine kinase NtrB
Regulation Transcript TF Regulons	EG11022	trmA	-0.736	-0.816	tRNA m5U54 methyltransferase
Regulation Transcript TF Regulons	EG11433	msrA	0.515	0.277	methionine sulfoxide reductase A
Regulation Transcript TF Regulons	EG11212	nsrR	-0.428	1.199	DNA-binding transcriptional repressor NsrR
Regulation Transcript TF Regulons	EG11648	dkgB	-1.19	0.883	methylglyoxal reductase DkgB
Regulation Transcript TF Regulons	G6206	mhpT	0.287	-0.97	3-hydroxyphenylpropionate/3-hydroxycinnamate:H ⁺ symporter
Regulation Transcript TF Regulons	G6706	feaR	0.085	-0.768	DNA-binding transcriptional activator FeaR
Regulation Transcript TF Regulons	EG12181	grxD	1.336	0.746	glutaredoxin 4
Regulation Transcript TF Regulons	EG10954	sodB	0.358	1.587	superoxide dismutase (Fe)
Regulation Transcript TF Regulons	G6906	sufS	1.017	-0.397	L-cysteine desulfurase

Regulation Transcript TF Regulons	EG10440	ihfA	1.195	0.38	integration host factor subunit $\text{C}\epsilon\pm$
Regulation Transcript TF Regulons	EG10710	pheT	0.937	-0.471	phenylalanine--tRNA ligase subunit $\text{C}\epsilon\leq$
Regulation Transcript TF Regulons	EG10709	pheS	-2.117	-0.528	phenylalanine--tRNA ligase subunit $\text{C}\epsilon\pm$
Regulation Transcript TF Regulons	EG11231	rpmI	-2.451	0.136	50S ribosomal subunit protein L35
Regulation Transcript TF Regulons	EG10506	infC	-1.165	0.798	translation initiation factor IF-3
Regulation Transcript TF Regulons	EG11001	thrS	-0.405	0.37	threonine--tRNA ligase
Regulation Transcript TF Regulons	EG11372	tadA	-0.655	-1.485	tRNA adenosine34 deaminase
Regulation Transcript TF Regulons	EG10952	bamE	-0.48	0.678	outer membrane protein assembly factor BamE
Regulation Transcript TF Regulons	EG11375	folE	-0.719	0.176	GTP cyclohydrolase 1
Regulation Transcript TF Regulons	EG10589	metK	-0.9	-0.553	methionine adenosyltransferase
Regulation Transcript TF Regulons	EG10591	metR	-0.36	-0.917	DNA-binding transcriptional dual regulator MetR
Regulation Transcript TF Regulons	EG10585	metF	0.474	-1.001	5,10-methylenetetrahydrofolate reductase
Regulation Transcript TF Regulons	EG10441	ihfB	0.948	0.144	integration host factor subunit $\text{C}\epsilon\leq$
Regulation Transcript TF Regulons	EG10369	gcd	1.48	-1.72	quinoprotein glucose dehydrogenase
Regulation Transcript TF Regulons	EG20098	hpt	0.019	-0.516	hypoxanthine phosphoribosyltransferase
Regulation Transcript TF Regulons	EG10777	pspB	2.455	-0.968	phage shock protein B
Regulation Transcript TF Regulons	EG12189	hemF	-0.006	0.208	coproporphyrinogen III oxidase
Regulation Transcript TF Regulons	EG10269	envZ	-0.232	-0.789	sensor histidine kinase EnvZ
Regulation Transcript TF Regulons	EG10897	rpoH	-0.094	1.082	RNA polymerase, sigma 32 (sigma H) factor
Regulation Transcript TF Regulons	EG10497	ilvE	-1.772	-1.955	branched-chain-amino-acid aminotransferase
Regulation Transcript TF Regulons	EG10496	ilvD	-3.398	0.755	dihydroxy-acid dehydratase
Regulation Transcript TF Regulons	EG10493	ilvA	-1.538	-0.36	threonine deaminase
Regulation Transcript TF Regulons	EG10308	fimA	-0.087	0.569	type 1 fimbriae major subunit
Regulation Transcript TF Regulons	EG10759	ppsA	-1.103	-0.254	phosphoenolpyruvate synthetase
Regulation Transcript TF Regulons	EG10256	eda	-0.306	-0.472	KHG/KDPG aldolase
Regulation Transcript TF Regulons	EG10257	edd	0.795	-0.31	phosphogluconate dehydratase
Regulation Transcript TF Regulons	EG10258	enolase	0.448	-0.774	enolase
Regulation Transcript TF Regulons	EG10703	pgk	0.832	0.751	phosphoglycerate kinase
Regulation Transcript TF Regulons	EG10368	epd	0.878	-0.549	D-erythrose-4-phosphate dehydrogenase
Regulation Transcript TF Regulons	EG12296	gpmM	0.309	-0.191	2,3-bisphosphoglycerate-independent phosphoglycerate mutase

Regulation Transcript TF Regulons	EG11015	tpiA	0.072	1.305	triose-phosphate isomerase
Regulation Transcript TF Regulons	EG10756	ppc	-0.142	-0.08	phosphoenolpyruvate carboxylase
Regulation Transcript TF Regulons	EG12440	mpl	-1.659	0.434	UDP-N-acetylmuramate--L-alanyl- ϵ -D-glutamyl-meso-2,6-dia
Regulation Transcript TF Regulons	EG10093	asnC	0.026	-0.791	DNA-binding transcriptional dual regulator AsnC
Regulation Transcript TF Regulons	EG10375	mnM	-0.824	0.232	5-carboxymethylaminomethyluridine-tRNA synthase subunit Mr
Regulation Transcript TF Regulons	EG11085	rsmH	-1.074	-0.3	16S rRNA m4C1402 methyltransferase
Regulation Transcript TF Regulons	EG11086	ftsL	-1	-0.881	cell division protein FtsL
Regulation Transcript TF Regulons	EG10621	murE	-1.931	-0.95	UDP-N-acetylmuramoyl-L-alanyl-D-glutamate--2,6-diaminopime
Regulation Transcript TF Regulons	EG10622	murF	-3.365	-0.888	D-alanyl-D-alanine-adding enzyme
Regulation Transcript TF Regulons	EG10604	mraY	-2.733	-0.367	phospho-N-acetylmuramoyl-pentapeptide-transferase
Regulation Transcript TF Regulons	EG10620	murD	-1.836	-0.434	UDP-N-acetylmuramoyl-L-alanine--D-glutamate ligase
Regulation Transcript TF Regulons	EG10344	ftsW	-2.063	-0.743	essential cell division protein FtsW
Regulation Transcript TF Regulons	EG10623	murG	-3.656	-0.02	N-acetylglucosaminyl transferase
Regulation Transcript TF Regulons	EG10619	murC	-2.151	-0.568	UDP-N-acetylmuramate--L-alanine ligase
Regulation Transcript TF Regulons	EG10342	ftsQ	-0.409	-0.471	cell division protein FtsQ
Regulation Transcript TF Regulons	EG10265	lpxC	0.249	-0.258	UDP-3-O-acyl-N-acetylglucosamine deacetylase
Regulation Transcript TF Regulons	EG10432	hemL	0.508	0.208	glutamate-1-semialdehyde 2,1-aminomutase
Regulation Transcript TF Regulons	EG10796	purK	-1.224	0.745	5-(carboxyamino)imidazole ribonucleotide synthase
Regulation Transcript TF Regulons	EG10793	purE	-2.377	0.876	N5-carboxyaminoimidazole ribonucleotide mutase
Regulation Transcript TF Regulons	EG10806	pyrC	-0.677	-0.487	dihydroorotase
Regulation Transcript TF Regulons	EG11314	purB	-3.834	-1.376	adenylosuccinate lyase
Regulation Transcript TF Regulons	EG11345	hflD	0.243	-0.753	lysogenization regulator
Regulation Transcript TF Regulons	EG10774	prs	-2.959	1.676	ribose-phosphate diphosphokinase
Regulation Transcript TF Regulons	EG11809	purT	-0.365	-0.318	phosphoribosylglycinamide formyltransferase 2
Regulation Transcript TF Regulons	EG10794	purF	-0.892	1.723	amidophosphoribosyltransferase
Regulation Transcript TF Regulons	EG10791	purC	-0.285	-0.494	phosphoribosylaminoimidazole-succinocarboxamide synthase
Regulation Transcript TF Regulons	EG10408	glyA	-2.967	0.691	serine hydroxymethyltransferase
Regulation Transcript TF Regulons	EG10797	purL	-2.774	1.427	phosphoribosylformylglycinamide synthetase
Regulation Transcript TF Regulons	EG10792	purD	-0.47	-0.804	phosphoribosylamine--glycine ligase
Regulation Transcript TF Regulons	EG10795	purH	-2.619	-1.683	bifunctional AICAR transformylase/IMP cyclohydrolase

Regulation Transcript TF Regulons	EG10790	purA	-0.652	-1.525	adenylosuccinate synthetase
Regulation Transcript TF Regulons	M012	mhpC	0.297	0.646	2-hydroxy-6-ketono-2,4-dienedioate hydrolase
Regulation Transcript TF Regulons	G6861	ydgl	0.856	-0.483	putative arginine:ornithine antiporter
Regulation Transcript TF Regulons	EG10007	hisM	-1.823	-0.423	lysine/arginine/ornithine ABC transporter / histidine ABC transp
Regulation Transcript TF Regulons	EG10063	argA	-1.559	0.108	N-acetylglutamate synthase
Regulation Transcript TF Regulons	EG10068	argG	-0.453	0.295	argininosuccinate synthetase
Regulation Transcript TF Regulons	EG10066	argD	0.184	0.114	N-acetylornithine aminotransferase / N-succinyldiaminopimelat
Regulation Transcript TF Regulons	EG10081	aroK	-1.714	-0.25	shikimate kinase 1
Regulation Transcript TF Regulons	EG10520	waaA	-1.834	-0.113	KDO transferase
Regulation Transcript TF Regulons	EG10065	argC	-3.216	-0.642	N-acetylglutamylphosphate reductase
Regulation Transcript TF Regulons	EG10064	argB	-1.92	0.471	acetylglutamate kinase
Regulation Transcript TF Regulons	EG11223	argH	-1.247	-0.644	argininosuccinate lyase
Regulation Transcript TF Regulons	EG10587	metH	-0.146	0.823	cobalamin-dependent methionine synthase
Regulation Transcript TF Regulons	G6530	pgaB	-0.858	-0.229	poly- ϵ -1,6-N-acetyl-D-glucosamine N-deacetylase and ϵ -1,6
Regulation Transcript TF Regulons	G6531	pgaA	0.327	0.158	partially deacetylated poly- ϵ -1,6-N-acetyl-D-glucosamine oute
Regulation Transcript TF Regulons	EG10249	dsdA	0.03	0.826	D-serine ammonia-lyase
Regulation Transcript TF Regulons	EG10348	fucA	-0.036	0.298	L-fuculose-phosphate aldolase
Regulation Transcript TF Regulons	EG11024	trpA	-2.399	0.371	tryptophan synthase subunit ϵ $\pm$
Regulation Transcript TF Regulons	EG11026	trpC	-2.361	0.871	fused indole-3-glycerol phosphate synthase/phosphoribosylanth
Regulation Transcript TF Regulons	EG11028	trpE	-3.801	0.11	anthranilate synthase subunit TrpE
Regulation Transcript TF Regulons	EG10206	dapB	1.053	0.596	4-hydroxy-tetrahydrodipicolinate reductase
Regulation Transcript TF Regulons	EG10207	dapD	-0.767	0.573	tetrahydrodipicolinate succinylase
Regulation Transcript TF Regulons	EG11337	lysP	-0.898	-0.504	lysine:H ⁺ symporter
Regulation Transcript TF Regulons	EG10549	lysA	1.177	-0.044	diaminopimelate decarboxylase
Regulation Transcript TF Regulons	EG11159	argO	-0.925	-6.685	L-arginine exporter
Regulation Transcript TF Regulons	EG11546	nadC	-0.768	0.838	quinolinate phosphoribosyltransferase (decarboxylating)
Regulation Transcript TF Regulons	EG10041	ampD	-3.758	-0.593	1,6-anhydro-N-acetylmuramoyl-L-alanine amidase
Regulation Transcript TF Regulons	EG10230	dksA	1.138	0.95	RNA polymerase-binding transcription factor DksA
Regulation Transcript TF Regulons	EG10261	entC	-0.24	-6.237	isochorismate synthase EntC
Regulation Transcript TF Regulons	EG10263	entE	-1.529	-5.9	2,3-dihydroxybenzoate-AMP ligase

Regulation Transcript TF Regulons	EG10260	entB	-2.806	-6.528	holo EntB
Regulation Transcript TF Regulons	EG10167	cstA	0.373	-0.617	carbon starvation protein A
Regulation Transcript TF Regulons	EG10359	fur	0.268	-0.259	DNA-binding transcriptional dual regulator Fur
Regulation Transcript TF Regulons	EG12427	modA	-1.715	1.605	molybdate ABC transporter periplasmic binding protein
Regulation Transcript TF Regulons	EG10002	modB	-1.467	0.096	molybdate ABC transporter membrane subunit
Regulation Transcript TF Regulons	EG10946	serC	-0.473	-0.349	phosphoserine/phosphohydroxythreonine aminotransferase
Regulation Transcript TF Regulons	EG10073	aroA	-0.728	-0.927	3-phosphoshikimate 1-carboxyvinyltransferase
Regulation Transcript TF Regulons	EG10802	putP	1.322	0.007	proline:Na ⁺ symporter
Regulation Transcript TF Regulons	G6569	comR	0.494	1.445	DNA-binding transcriptional repressor ComR
Regulation Transcript TF Regulons	EG11408	dadX	-1.042	-2.067	alanine racemase 2
Regulation Transcript TF Regulons	G6646	puuE	-3.029	3.456	4-aminobutyrate aminotransferase PuuE
Regulation Transcript TF Regulons	EG12198	chbG	1.838	0.718	chitin disaccharide deacetylase
Regulation Transcript TF Regulons	EG11530	fadD	1.067	-1.658	long-chain-fatty-acid--CoA ligase
Regulation Transcript TF Regulons	EG12416	gatC	-1.457	0.161	galactitol-specific PTS enzyme IIC component
Regulation Transcript TF Regulons	EG12415	gatB	-0.862	-0.022	galactitol-specific PTS enzyme IIB component
Regulation Transcript TF Regulons	EG11143	ubiG	-0.471	0.639	bifunctional 3-demethylubiquinone-8 3-O-methyltransferase and
Regulation Transcript TF Regulons	EG11072	xseA	-0.219	0.056	exodeoxyribonuclease VII subunit XseA
Regulation Transcript TF Regulons	EG10416	grpE	-1.164	3.874	nucleotide exchange factor GrpE
Regulation Transcript TF Regulons	EG10835	relA	-0.511	0.982	GDP/GTP pyrophosphokinase
Regulation Transcript TF Regulons	EG10944	serA	0.354	0.313	phosphoglycerate dehydrogenase
Regulation Transcript TF Regulons	EG11182	yhfA	-0.605	-0.994	OsmC family protein YhfA
Regulation Transcript TF Regulons	EG10757	ppiA	-0.905	-0.928	peptidyl-prolyl cis-trans isomerase A
Regulation Transcript TF Regulons	G7748	nfuA	-0.202	1.33	iron-sulfur cluster carrier protein NfuA
Regulation Transcript TF Regulons	EG12380	gntT	-0.157	-1.086	high-affinity gluconate transporter
Regulation Transcript TF Regulons	EG10397	glpG	-1.12	0.415	rhomboid protease GlpG
Regulation Transcript TF Regulons	EG10394	glpD	0.381	0.052	aerobic glycerol 3-phosphate dehydrogenase
Regulation Transcript TF Regulons	EG12629	gntK	-0.039	-0.993	D-gluconate kinase, thermostable
Regulation Transcript TF Regulons	EG11050	ugpQ	1.275	-0.56	glycerophosphodiester phosphodiesterase UgpQ
Regulation Transcript TF Regulons	EG20091	gpsA	0.144	-0.531	glycerol-3-phosphate dehydrogenase
Regulation Transcript TF Regulons	EG10937	secB	-0.431	1.976	protein export chaperone SecB

Regulation Transcript TF Regulons	EG10398	glpK	0.274	-0.238	glycerol kinase
Regulation Transcript TF Regulons	EG11209	psiE	1.457	-0.74	putative phosphate starvation-inducible protein PsiE
Regulation Transcript TF Regulons	EG10438	hfq	1.032	0.204	RNA-binding protein Hfq
Regulation Transcript TF Regulons	EG10437	hflX	-0.096	-0.265	ribosome rescue factor HflX
Regulation Transcript TF Regulons	EG10905	rpsF	-3.975	1.32	30S ribosomal subunit protein S6
Regulation Transcript TF Regulons	EG10917	rpsR	-2.664	1.524	30S ribosomal subunit protein S18
Regulation Transcript TF Regulons	EG10870	rplI	-1.655	1.145	50S ribosomal subunit protein L9
Regulation Transcript TF Regulons	EG10123	birA	1.022	-0.972	DNA-binding transcriptional repressor/biotin-[acetyl-CoA-carboxylase]
Regulation Transcript TF Regulons	EG10117	bioA	-2.446	-0.277	adenosylmethionine-8-amino-7-oxononanoate aminotransferase
Regulation Transcript TF Regulons	EG10118	bioB	-2.286	0.598	biotin synthase
Regulation Transcript TF Regulons	EG10121	bioF	-1.076	-0.384	8-amino-7-oxononanoate synthase
Regulation Transcript TF Regulons	EG10831	recN	0.111	-0.3	DNA repair protein RecN
Regulation Transcript TF Regulons	EG10746	polA	0.763	-0.118	DNA polymerase I
Regulation Transcript TF Regulons	EG11320	nrdR	-0.413	0.531	NrdR transcriptional repressor
Regulation Transcript TF Regulons	EG10499	ilvH	2.498	-0.422	acetolactate synthase / acetohydroxybutanoate synthase, regulatory
Regulation Transcript TF Regulons	EG10695	pepD	-2.925	0.275	peptidase D
Regulation Transcript TF Regulons	EG12168	brnQ	-1.001	-1.911	branched chain amino acid transporter BrnQ
Regulation Transcript TF Regulons	EG11322	ribE	-0.645	0.727	6,7-dimethyl-8-ribityllumazine synthase
Regulation Transcript TF Regulons	EG10666	nusB	-0.058	-0.27	transcription antitermination protein NusB
Regulation Transcript TF Regulons	G6329	ybdL	-0.625	-0.59	methionine transaminase
Regulation Transcript TF Regulons	G6463	clpS	1.336	-0.027	specificity factor for ClpA-ClpP chaperone-protease complex
Regulation Transcript TF Regulons	EG10947	serS	-1.033	-0.112	serine--tRNA ligase
Regulation Transcript TF Regulons	EG11344	mnmA	-2.793	-0.336	tRNA-specific 2-thiouridylase
Regulation Transcript TF Regulons	EG10744	pntA	-2.074	2.717	pyridine nucleotide transhydrogenase subunit PntA
Regulation Transcript TF Regulons	EG10129	btuE	-0.996	-1.022	thioredoxin/glutathione peroxidase
Regulation Transcript TF Regulons	EG10930	sdaA	0.895	-0.512	L-serine deaminase I
Regulation Transcript TF Regulons	EG10097	aspS	-1.28	-1.541	aspartate--tRNA ligase
Regulation Transcript TF Regulons	EG10071	argS	-2.019	-0.646	arginine--tRNA ligase
Regulation Transcript TF Regulons	G7184	alaA	-1.27	-0.396	glutamate--pyruvate aminotransferase AlaA
Regulation Transcript TF Regulons	EG10072	argT	-0.554	-0.254	lysine/arginine/ornithine ABC transporter periplasmic binding protein

Regulation Transcript TF Regulons	G7213	fadI	-0.488	0.196	3-ketoacyl-CoA thiolase FadI
Regulation Transcript TF Regulons	G7258	zipA	0.292	-0.348	cell division protein ZipA
Regulation Transcript TF Regulons	EG11403	ppx	0.41	-0.213	exopolyphosphatase
Regulation Transcript TF Regulons	EG10034	alaS	-1.695	-0.501	alanine--tRNA ligase/DNA-binding transcriptional repressor
Regulation Transcript TF Regulons	EG11443	rpiA	0.606	1.301	ribose-5-phosphate isomerase A
Regulation Transcript TF Regulons	EG11160	mscS	-0.134	-0.196	small conductance mechanosensitive channel MscS
Regulation Transcript TF Regulons	EG10627	mutY	-0.902	-0.025	adenine DNA glycosylase
Regulation Transcript TF Regulons	EG12732	sstT	-0.381	-0.389	serine/threonine:Na ⁺ symporter
Regulation Transcript TF Regulons	EG10215	deaD	-2.19	-2.847	ATP-dependent RNA helicase DeaD
Regulation Transcript TF Regulons	EG11507	rlmE	1.076	0.655	23S rRNA 2'-O-ribose U2552 methyltransferase
Regulation Transcript TF Regulons	EG10898	rpoN	-0.677	0.137	RNA polymerase, sigma 54 (sigma N) factor
Regulation Transcript TF Regulons	EG11681	hpf	1.151	-1.568	ribosome hibernation-promoting factor
Regulation Transcript TF Regulons	EG11969	zntR	0.659	0.855	DNA-binding transcriptional activator ZntR
Regulation Transcript TF Regulons	EG10879	rplR	-2.04	1.244	50S ribosomal subunit protein L18
Regulation Transcript TF Regulons	EG10869	rplF	-2.061	1.375	50S ribosomal subunit protein L6
Regulation Transcript TF Regulons	EG10907	rpsH	-2.353	1.408	30S ribosomal subunit protein S8
Regulation Transcript TF Regulons	EG11664	slyX	0.689	1.308	protein SlyX
Regulation Transcript TF Regulons	EG10098	atpA	-2.2	-0.798	ATP synthase F1 complex subunit CF_1
Regulation Transcript TF Regulons	EG10105	atpH	-2.636	-0.803	ATP synthase F1 complex subunit CF_0
Regulation Transcript TF Regulons	EG11428	sthA	-0.715	0.024	soluble pyridine nucleotide transhydrogenase
Regulation Transcript TF Regulons	EG11585	thiC	-4.96	-3.898	phosphomethylpyrimidine synthase
Regulation Transcript TF Regulons	EG10600	groS	-2.666	4.238	cochaperonin GroES
Regulation Transcript TF Regulons	EG10599	groL	-2.367	3.304	chaperonin GroEL
Regulation Transcript TF Regulons	EG11259	rnr	0.418	-0.175	RNase R
Regulation Transcript TF Regulons	EG11929	zur	-1.172	0.463	DNA-binding transcriptional repressor Zur
Regulation Transcript TF Regulons	G7017	znuA	-0.704	-1.053	Zn ²⁺ ABC transporter periplasmic binding protein
Regulation Transcript TF Regulons	G7018	znuC	-0.892	0.026	Zn ²⁺ ABC transporter ATP binding subunit
Regulation Transcript TF Regulons	EG12368	znuB	-2.051	0.342	Zn ²⁺ ABC transporter membrane subunit
Regulation Transcript TF Regulons	EG10694	pepA	-0.29	-0.865	aminopeptidase A/I
Regulation Transcript TF Regulons	G6217	tauA	2.153	-2.318	taurine ABC transporter periplasmic binding protein

Regulation Transcript TF Regulons	EG12423	tauD	1.725	-2.071	taurine dioxygenase
Regulation Transcript TF Regulons	EG50005	nfsB	-0.713	-0.053	NAD(P)H nitroreductase NfsB
Regulation Transcript TF Regulons	G6491	pqiB	0.021	-1.357	intermembrane transport protein PqiB
Regulation Transcript TF Regulons	EG11331	ribA	1.404	-0.477	GTP cyclohydrolase 2
Regulation Transcript TF Regulons	EG12656	mdaB	-1.852	1.84	NADPH:quinone oxidoreductase MdaB
Regulation Transcript TF Regulons	EG11009	tolC	0.015	0.407	outer membrane channel TolC
Regulation Transcript TF Regulons	EG10702	pgi	-0.83	0.101	glucose-6-phosphate isomerase
Regulation Transcript TF Regulons	G6977	nimT	0.439	0.249	2-nitroimidazole exporter
Regulation Transcript TF Regulons	EG10187	cysE	-0.596	0.366	serine acetyltransferase
Regulation Transcript TF Regulons	EG12332	erpA	1.272	1.26	iron-sulfur cluster insertion protein ErpA
Regulation Transcript TF Regulons	EG12132	iscA	-0.445	1.522	iron-sulfur cluster insertion protein IscA
Regulation Transcript TF Regulons	G7324	iscU	-0.998	1.951	scaffold protein for iron-sulfur cluster assembly
Regulation Transcript TF Regulons	G7325	iscS	-1.254	0.693	cysteine desulfurase IscS
Regulation Transcript TF Regulons	G6318	cusS	0.039	-0.296	CusS-N-phospho-L-histidine
Regulation Transcript TF Regulons	EG10495	ilvC	0.281	-0.473	ketol-acid reductoisomerase (NADP+)
Regulation Transcript TF Regulons	G7290	eutQ	0.094	0.586	putative ethanolamine utilization acetate kinase EutQ
Regulation Transcript TF Regulons	EG11198	glmU	-0.787	-0.277	fused N-acetylglucosamine-1-phosphate uridyltransferase and g
Regulation Transcript TF Regulons	EG10801	putA	-0.647	-0.46	fused DNA-binding transcriptional repressor / proline dehydroge
Regulation Transcript TF Regulons	G7924	hypT	-0.596	-0.257	DNA-binding transcriptional dual regulator HypT
Regulation Transcript TF Regulons	G6105	fadE	0.82	-0.591	acyl-CoA dehydrogenase
Regulation Transcript TF Regulons	EG10513	kdpA	1.508	-0.323	K ⁺ transporting P-type ATPase subunit KdpA
Regulation Transcript TF Regulons	EG11380	appC	0.091	1.344	cytochrome bd-II ubiquinol oxidase subunit I
Regulation Transcript TF Regulons	EG11379	appB	1.7	2.186	cytochrome bd-II ubiquinol oxidase subunit II
Regulation Transcript TF Regulons	EG50003	acpP	0.524	0.277	octanoyl-ACP
Regulation Transcript TF Regulons	EG11393	dsbB	-2.303	0.749	protein thiol:quinone oxidoreductase DsbBReduced
Regulation Transcript TF Regulons	G6864	rstA	-0.512	0.134	Phosphorylated DNA-binding transcriptional regulator RstA
Regulation Transcript TF Regulons	EG10650	ndk	-2.887	0.526	nucleoside diphosphate kinase
Regulation Transcript TF Regulons	EG11961	lldP	-2.273	0.606	lactate/glycolate:H ⁺ symporter LldP
Regulation Transcript TF Regulons	EG10845	rho	-2.507	-1.357	transcription termination factor Rho
Regulation Transcript TF Regulons	EG11061	uvrA	-1.562	1.685	excision nuclease subunit A

Regulation Transcript TF Regulons	EG10976	ssb	2.338	1.296	ssDNA-binding protein
Regulation Transcript TF Regulons	G6439	ybjG	0.847	0.701	undecaprenyl pyrophosphate phosphatase
Regulation Transcript TF Regulons	G7443	queE	0.346	-1.428	putative 7-carboxy-7-deazaguanine synthase QueE
Regulation Transcript TF Regulons	EG12525	mgtA	-0.154	2.412	Mg2+ importing P-type ATPase
Regulation Transcript TF Regulons	EG11618	baeR	-0.621	-0.351	Phosphorylated DNA-binding transcriptional activator BaeR
Regulation Transcript TF Regulons	G7115	mdtC	0.374	-1.041	multidrug efflux pump RND permease subunit MdtC
Regulation Transcript TF Regulons	G7167	arnC	0.529	-0.966	undecaprenyl-phosphate 4-deoxy-4-formamido-L-arabinose tran
Regulation Transcript TF Regulons	G7170	arnT	-0.793	-0.084	lipid IVA 4-amino-4-deoxy-L-arabinosyltransferase
Regulation Transcript TF Regulons	EG10224	dgkA	-3.379	-0.259	diacylglycerol kinase
Regulation Transcript TF Regulons	EG11613	eptA	-0.706	0.055	phosphoethanolamine transferase EptA
Regulation Transcript TF Regulons	EG20173	pta	-1.402	-0.828	phosphate acetyltransferase
Regulation Transcript TF Regulons	EG10687	parE	-0.81	-0.273	DNA topoisomerase IV subunit B
Regulation Transcript TF Regulons	EG12633	nudF	-1.223	-0.671	ADP-sugar pyrophosphatase
Regulation Transcript TF Regulons	EG10829	recG	-1.864	-0.102	ATP-dependent DNA helicase RecG
Regulation Transcript TF Regulons	EG10728	phoB	0.981	0.479	Phosphorylated DNA-binding transcriptional dual regulator PhoB
Regulation Transcript TF Regulons	EG10733	phoR	-0.729	-0.506	sensor histidine kinase PhoR
Regulation Transcript TF Regulons	G7698	tsaC	0.46	0.353	L-threonylcarbamoyladenylate synthase
Regulation Transcript TF Regulons	EG11284	fabZ	-1.159	-0.452	3-hydroxy-acyl-[acyl-carrier-protein] dehydratase
Regulation Transcript TF Regulons	EG10545	lpxA	-1.799	-0.737	acyl-[acyl-carrier-protein]--UDP-N-acetylglucosamine O-acyltrar
Regulation Transcript TF Regulons	EG10928	sbmA	-1.261	-0.708	peptide antibiotic/peptide nucleic acid transporter
Regulation Transcript TF Regulons	G6242	ppiD	-0.294	-0.629	periplasmic folding chaperone
Regulation Transcript TF Regulons	EG11665	bacA	-0.645	-0.074	undecaprenyl pyrophosphate phosphatase
Regulation Transcript TF Regulons	EG11297	dsbA	0.94	1.065	thiol:disulfide oxidoreductase - DsbA reduced
Regulation Transcript TF Regulons	EG10775	psd	-1.783	-0.244	phosphatidylserine decarboxylase proenzyme
Regulation Transcript TF Regulons	EG10950	slt	-0.969	0.428	soluble lytic murein transglycosylase
Regulation Transcript TF Regulons	EG11166	ygiD	0.511	0.767	4,5-DOPA dioxygenase extradiol
Regulation Transcript TF Regulons	G7615	yqjF	-0.196	-0.131	DoxX family protein
Regulation Transcript TF Regulons	EG10030	add	-1.259	-0.114	adenosine deaminase
Regulation Transcript TF Regulons	EG11418	dcd	-1.016	0.373	dCTP deaminase
Regulation Transcript TF Regulons	EG10428	hemB	-3.089	0.592	porphobilinogen synthase

Regulation Transcript TF Regulons	G6234	thiL	0.65	-0.881	thiamine monophosphate kinase
Regulation Transcript TF Regulons	EG10461	htpG	-3.902	2.793	chaperone protein HtpG
Regulation Transcript TF Regulons	EG10431	hemH	0.33	-0.099	ferrochelata
Regulation Transcript TF Regulons	EG12623	ybaL	-0.978	-0.23	putative transporter YbaL
Regulation Transcript TF Regulons	EG12666	lpxH	-0.67	-1.62	UDP-2,3-diacetylglucosamine diphosphatase
Regulation Transcript TF Regulons	EG10196	cysS	-1.29	-0.876	cysteine--tRNA ligase
Regulation Transcript TF Regulons	EG11110	ybgC	-1.376	0.593	esterase/thioesterase
Regulation Transcript TF Regulons	EG11008	tolB	-1.936	0.239	Tol-Pal system periplasmic protein TolB
Regulation Transcript TF Regulons	G6461	macA	-0.357	0.344	ABC-type tripartite efflux pump membrane fusion protein
Regulation Transcript TF Regulons	EG11493	pabC	-1.179	0.586	aminodeoxychorismate lyase
Regulation Transcript TF Regulons	EG10518	kdsA	-0.65	-0.99	3-deoxy-D-manno-octulosonate 8-phosphate synthase
Regulation Transcript TF Regulons	G6755	patD	-0.349	2.859	α-aminobutyraldehyde dehydrogenase
Regulation Transcript TF Regulons	G7014	yobA	-0.39	0.548	CopC domain-containing protein
Regulation Transcript TF Regulons	G7038	dcyD	1.114	-0.313	D-cysteine desulfhydrase
Regulation Transcript TF Regulons	EG10231	dld	-1.435	0.167	quinone-dependent D-lactate dehydrogenase
Regulation Transcript TF Regulons	EG12038	yejB	-1.107	-0.323	putative oligopeptide ABC transporter membrane subunit YejB
Regulation Transcript TF Regulons	EG12449	prmB	-1.534	-0.361	50S ribosomal subunit protein L3 N5-glutamine methyltransferase
Regulation Transcript TF Regulons	EG10530	lepB	0.02	-0.907	signal peptidase I
Regulation Transcript TF Regulons	EG10529	lepA	-0.673	0.031	30S ribosomal subunit biogenesis factor LepA
Regulation Transcript TF Regulons	G7423	ispD	-0.939	-1.472	2-C-methyl-D-erythritol 4-phosphate cytidyltransferase
Regulation Transcript TF Regulons	G7452	queF	-0.849	-0.663	7-cyano-7-deazaguanine reductase
Regulation Transcript TF Regulons	EG12095	secG	-1.458	0.553	Sec translocon subunit SecG
Regulation Transcript TF Regulons	EG50001	rplU	-2.149	1.382	50S ribosomal subunit protein L21
Regulation Transcript TF Regulons	EG11180	mscL	1.216	-0.212	large conductance mechanosensitive channel
Regulation Transcript TF Regulons	EG11181	bfd	-0.459	0.574	bacterioferritin-associated ferredoxin
Regulation Transcript TF Regulons	EG11578	greB	-0.353	0.166	transcription elongation factor GreB
Regulation Transcript TF Regulons	EG10965	gmK	-0.246	-0.364	guanylate kinase
Regulation Transcript TF Regulons	EG10899	rpoZ	-1.353	0.111	RNA polymerase subunit α
Regulation Transcript TF Regulons	EG11829	mobA	0.538	-0.523	molybdenum cofactor guanylyltransferase
Regulation Transcript TF Regulons	EG11859	fdhD	0.569	-1.622	sulfurtransferase for molybdenum cofactor sulfuration

Regulation Transcript TF Regulons	EG10043	cysQ	0.979	-0.124	3'(2'),5'-bisphosphate nucleotidase
Regulation Transcript TF Regulons	EG10805	pyrB	-0.876	1.419	aspartate carbamoyltransferase catalytic subunit
Regulation Transcript TF Regulons	EG12114	prfC	-1.037	0.158	peptide chain release factor RF3
Regulation Transcript TF Regulons	G7137	rcnR	-1.29	0.527	DNA-binding transcriptional repressor RcnR
Regulation Transcript TF Regulons	G7445	gudD	1.446	-0.694	D-glucarate dehydratase
Regulation Transcript TF Regulons	EG11404	ychF	-0.148	1.8	redox-responsive ATPase YchF
Regulation Transcript TF Regulons	EG11887	trxC	2.051	0.765	oxidized thioredoxin 2
Regulation Transcript TF Regulons	EG11104	entS	0.344	0.403	enterobactin exporter EntS
Regulation Transcript TF Regulons	G7659	mlaC	-1.437	0.429	intermembrane phospholipid transport system - periplasmic bin
Regulation Transcript TF Regulons	EG12799	mlaD	-1.43	0.249	intermembrane phospholipid transport system, substrate bindin
Regulation Transcript TF Regulons	EG12800	mlaE	-0.022	-0.412	intermembrane phospholipid transport system, integral membr
Regulation Transcript TF Regulons	EG12801	mlaF	-0.511	0.137	intermembrane phospholipid transport system, ATP binding sub
Regulation Transcript TF Regulons	EG10193	cysM	-0.615	0.467	cysteine synthase B
Regulation Transcript TF Regulons	EG10198	cysW	-0.283	-0.776	sulfate/thiosulfate ABC transporter inner membrane subunit Cy
Regulation Transcript TF Regulons	EG11528	fabI	-0.122	0.666	enoyl-[acyl-carrier-protein] reductase
Regulation Transcript TF Regulons	EG10217	accD	-0.711	0.285	acetyl-CoA carboxyltransferase subunit Cε
Regulation Transcript TF Regulons	EG10274	fabB	0.379	0.23	3-oxoacyl-[acyl carrier protein] synthase 1
Regulation Transcript TF Regulons	EG12880	dgcN	-1.174	-0.954	diguanylate cyclase DgcN
Regulation Transcript TF Regulons	EG50002	rpmA	-1.371	1.346	50S ribosomal subunit protein L27
Regulation Transcript TF Regulons	EG12386	glaR	-0.49	0.103	DNA-binding transcriptional repressor GlaR
Regulation Transcript TF Regulons	G7217	yfdC	1.018	0.777	inner membrane protein YfdC
Regulation Transcript TF Regulons	EG10194	cysN	-0.289	1.25	sulfate adenylyltransferase subunit 1
Regulation Transcript TF Regulons	EG10074	aroB	-1.063	-0.829	3-dehydroquinate synthase
Regulation Transcript TF Regulons	G7841	rsgA	0.638	-0.12	ribosome small subunit-dependent GTPase A
Regulation Transcript TF Regulons	G7842	orn	-1.098	-0.538	oligoribonuclease
Regulation Transcript TF Regulons	EG10517	kdpE	-0.11	-0.977	KdpE-Phosphorylated
Regulation Transcript TF Regulons	EG10515	kdpC	0.615	1.009	K ⁺ transporting P-type ATPase subunit KdpC
Regulation Transcript TF Regulons	EG10514	kdpB	0.18	0.36	K ⁺ transporting P-type ATPase subunit KdpB
Regulation Transcript TF Regulons	EG11204	murI	-2.028	0.738	glutamate racemase
Regulation Transcript TF Regulons	G6115	dinB	0.682	0.6	DNA polymerase IV

Regulation Transcript TF Regulons	EG10736	phr	1.34	-0.289	deoxyribodipyrimidine photolyase
Regulation Transcript TF Regulons	RUVA	ruvA	-0.836	0.414	Holliday junction branch migration complex subunit RuvA
Regulation Transcript TF Regulons	EG11063	uvrC	-0.598	1.971	excision nuclease subunit C
Regulation Transcript TF Regulons	EG12080	recX	-0.27	1.028	RecA inhibitor RecX
Regulation Transcript TF Regulons	EG10823	recA	0.96	0.456	DNA recombination/repair protein RecA
Regulation Transcript TF Regulons	EG10826	recD	-1.861	-0.186	exodeoxyribonuclease V subunit RecD
Regulation Transcript TF Regulons	EG10824	recB	-1.491	0.129	exodeoxyribonuclease V subunit RecB
Regulation Transcript TF Regulons	EG10920	rpsU	-2.111	1.745	30S ribosomal subunit protein S21
Regulation Transcript TF Regulons	EG10239	dnaG	0.3	-0.241	DNA primase
Regulation Transcript TF Regulons	EG10896	rpoD	0.399	1.815	RNA polymerase, sigma 70 (sigma D) factor
Regulation Transcript TF Regulons	EG12662	gltK	0.737	-1.442	glutamate/aspartate ABC transporter membrane subunit GltK
Regulation Transcript TF Regulons	G6359	gltI	1.292	0.048	glutamate/aspartate ABC transporter periplasmic binding prote
Regulation Transcript TF Regulons	EG10825	recC	-0.755	-0.461	exodeoxyribonuclease V subunit RecC
Regulation Transcript TF Regulons	G6263	cueR	-0.389	-0.506	DNA-binding transcriptional dual regulator CueR
Regulation Transcript TF Regulons	G6934	tcyP	-0.73	0.721	cystine/sulfocysteine:cation symporter
Regulation Transcript TF Regulons	EG10186	cysD	-2.495	1.049	sulfate adenylyltransferase subunit 2
Regulation Transcript TF Regulons	EG11576	leuC	-0.084	1.821	3-isopropylmalate dehydratase subunit LeuC
Regulation Transcript TF Regulons	EG11577	leuB	0.548	-0.014	3-isopropylmalate dehydrogenase
Regulation Transcript TF Regulons	EG12006	btsR	-1.729	-0.633	Phosphorylated DNA-binding transcriptional dual regulator BtsR
Regulation Transcript TF Regulons	EG10630	nadA	-2.85	0.575	quinolinate synthase
Regulation Transcript TF Regulons	EG11700	pnuC	1.702	0.91	nicotinamide riboside transporter
Regulation Transcript TF Regulons	EG10631	nadB	-1.72	0.102	L-aspartate oxidase
Regulation Transcript TF Regulons	EG10037	alkB	-0.524	1.243	DNA oxidative demethylase
Central_Dc Transcript Transcription	EG11969	zntR	0.659	0.855	DNA-binding transcriptional activator ZntR
Central_Dc Transcript Transcription	EG10423	gyrA	-1.844	-0.652	DNA gyrase subunit A
Central_Dc Transcript Transcription	EG10893	rpoA	-2.18	0.563	RNA polymerase subunit $\sigma^{\pm}$
Central_Dc Transcript Transcription	EG10424	gyrB	-0.001	-0.399	DNA gyrase subunit B
Central_Dc Transcript Transcription	EG10899	rpoZ	-1.353	0.111	RNA polymerase subunit $\sigma^{\hat{a}}$
Central_Dc Transcript Transcription	EG10894	rpoB	-1.791	-0.953	RNA polymerase subunit $\sigma^{\leq}$
Central_Dc Transcript Transcription	EG10895	rpoC	-0.146	-0.827	RNA polymerase subunit $\sigma^{\leq'}$

Central_Dc Transcript Transcription	EG11618	baeR	-0.621	-0.351	Phosphorylated DNA-binding transcriptional activator BaeR
Central_Dc Transcript Transcription	EG10694	pepA	-0.29	-0.865	aminopeptidase A/I
Central_Dc Transcript Transcription	EG11929	zur	-1.172	0.463	DNA-binding transcriptional repressor Zur
Central_Dc Transcript Transcription	G6263	cueR	-0.389	-0.506	DNA-binding transcriptional dual regulator CueR
Central_Dc Transcript Transcription	G7924	hypT	-0.596	-0.257	DNA-binding transcriptional dual regulator HypT
Central_Dc Transcript Transcription	EG10125	bolA	1.583	0.948	DNA binding transcriptional dual regulator BolA-phosphate
Central_Dc Transcript Transcription	EG10440	ihfA	1.195	0.38	integration host factor subunit α
Central_Dc Transcript Transcription	EG10441	ihfB	0.948	0.144	integration host factor subunit β
Central_Dc Transcript Transcription	G6720	paaX	0.791	-0.538	DNA-binding transcriptional repressor PaaX
Central_Dc Transcript Transcription	EG10467	hupB	-0.906	-1.579	DNA-binding protein HU- α
Central_Dc Transcript Transcription	EG10317	fis	-1.11	-0.32	DNA-binding transcriptional dual regulator Fis
Central_Dc Transcript Transcription	EG10415	greA	-1.004	-0.046	transcription elongation factor GreA
Central_Dc Transcript Transcription	EG10898	rpoN	-0.677	0.137	RNA polymerase, sigma 54 (sigma N) factor
Central_Dc Transcript Transcription	EG11578	greB	-0.353	0.166	transcription elongation factor GreB
Central_Dc Transcript Transcription	EG10896	rpoD	0.399	1.815	RNA polymerase, sigma 70 (sigma D) factor
Central_Dc Transcript Transcription	EG10897	rpoH	-0.094	1.082	RNA polymerase, sigma 32 (sigma H) factor
Central_Dc Transcript Transcription	EG10666	nusB	-0.058	-0.27	transcription antitermination protein NusB
Central_Dc Transcript Transcription	EG10867	rplD	-2.778	2.173	50S ribosomal subunit protein L4
Central_Dc Transcript Transcription	EG10903	rpsD	-2.155	0.66	30S ribosomal subunit protein S4
Central_Dc Transcript Transcription	EG10845	rho	-2.507	-1.357	transcription termination factor Rho
Central_Dc Transcript Transcription	EG10667	nusG	0.661	1.657	transcription termination factor NusG
Central_Dc Transcript Transcription	EG10665	nusA	-0.549	0.59	transcription termination/antitermination protein NusA
Central_Dc Translatio Translation	EG10917	rpsR	-2.664	1.524	30S ribosomal subunit protein S18
Central_Dc Translatio Translation	EG10901	rpsB	-1.039	1.919	30S ribosomal subunit protein S2
Central_Dc Translatio Translation	EG10880	rplS	-1.489	0.485	50S ribosomal subunit protein L19
Central_Dc Translatio Translation	G7746	yhgF	-0.142	-0.592	putative RNA-binding protein YhgF
Central_Dc Translatio Translation	EG12343	ettA	-1.151	0.017	energy-dependent translational throttle protein EttA
Central_Dc Translatio Translation	EG10876	rplO	1.654	0.525	50S ribosomal subunit protein L15
Central_Dc Translatio Translation	EG10890	rpmF	-2.098	0.87	50S ribosomal subunit protein L32
Central_Dc Translatio Translation	EG10873	rplL	-0.351	1.527	50S ribosomal subunit protein L7

Central_Dc Translatio Translation	EG10908	rpsI	-0.92	-0.394	30S ribosomal subunit protein S9
Central_Dc Translatio Translation	EG10887	rpmC	-2.174	1.836	50S ribosomal subunit protein L29
Central_Dc Translatio Translation	EG12454	ybaK	0.287	0.552	Cys-tRNA ^{Pro} and Cys-tRNA ^{Cys} deacylase
Central_Dc Translatio Translation	EG10905	rpsF	-3.975	1.32	30S ribosomal subunit protein S6
Central_Dc Translatio Translation	EG10884	rplX	-2.656	0.982	50S ribosomal subunit protein L24
Central_Dc Translatio Translation	EG10866	rplC	-3.126	2.123	50S ribosomal subunit protein L3
Central_Dc Translatio Translation	EG50001	rplU	-2.149	1.382	50S ribosomal subunit protein L21
Central_Dc Translatio Translation	EG10918	rpsS	-2.877	1.849	30S ribosomal subunit protein S19
Central_Dc Translatio Translation	EG10902	rpsC	-2.812	1.765	30S ribosomal subunit protein S3
Central_Dc Translatio Translation	EG10881	rplT	-1.641	-0.09	50S ribosomal subunit protein L20
Central_Dc Translatio Translation	EG10915	rpsP	-2.655	1.621	30S ribosomal subunit protein S16
Central_Dc Translatio Translation	EG10878	rplQ	-1.649	0.754	50S ribosomal subunit protein L17
Central_Dc Translatio Translation	EG10912	rpsM	-2.616	0.72	30S ribosomal subunit protein S13
Central_Dc Translatio Translation	EG10891	rpmG	-2.074	2.118	50S ribosomal subunit protein L33
Central_Dc Translatio Translation	EG10874	rplM	-1.147	-0.133	50S ribosomal subunit protein L13
Central_Dc Translatio Translation	EG10909	rpsJ	-2.923	2.015	30S ribosomal subunit protein S10
Central_Dc Translatio Translation	EG10888	rpmD	-0.82	1.301	50S ribosomal subunit protein L30
Central_Dc Translatio Translation	EG10870	rplI	-1.655	1.145	50S ribosomal subunit protein L9
Central_Dc Translatio Translation	EG10906	rpsG	-0.76	2.531	30S ribosomal subunit protein S7
Central_Dc Translatio Translation	EG10867	rplD	-2.778	2.173	50S ribosomal subunit protein L4
Central_Dc Translatio Translation	EG10785	pth	-1.544	1.147	peptidyl-tRNA hydrolase
Central_Dc Translatio Translation	EG50002	rpmA	-1.371	1.346	50S ribosomal subunit protein L27
Central_Dc Translatio Translation	EG10864	rplA	-2.482	2.275	50S ribosomal subunit protein L1
Central_Dc Translatio Translation	EG10916	rpsQ	-1.558	1.906	30S ribosomal subunit protein S17
Central_Dc Translatio Translation	EG10879	rplR	-2.04	1.244	50S ribosomal subunit protein L18
Central_Dc Translatio Translation	EG10913	rpsN	-1.991	1.133	30S ribosomal subunit protein S14
Central_Dc Translatio Translation	EG10875	rplN	-2.153	1.064	50S ribosomal subunit protein L14
Central_Dc Translatio Translation	EG11231	rpmI	-2.451	0.136	50S ribosomal subunit protein L35
Central_Dc Translatio Translation	EG11179	rimP	0.603	-0.255	ribosome maturation factor RimP
Central_Dc Translatio Translation	EG10871	rplJ	-2.382	1.646	50S ribosomal subunit protein L10

Central_Dc Translatio Translation	EG10907	rpsH	-2.353	1.408	30S ribosomal subunit protein S8
Central_Dc Translatio Translation	EG10886	rpmB	-2.249	1.777	50S ribosomal subunit protein L28
Central_Dc Translatio Translation	EG10868	rplE	-2.16	0.987	50S ribosomal subunit protein L5
Central_Dc Translatio Translation	EG10877	rplP	-2.62	1.819	50S ribosomal subunit protein L16
Central_Dc Translatio Translation	EG10920	rpsU	-2.111	1.745	30S ribosomal subunit protein S21
Central_Dc Translatio Translation	EG10883	rplW	-1.711	1.921	50S ribosomal subunit protein L23
Central_Dc Translatio Translation	EG10885	rplY	-1.984	1.618	50S ribosomal subunit protein L25
Central_Dc Translatio Translation	EG10882	rplV	-1.868	1.753	50S ribosomal subunit protein L22
Central_Dc Translatio Translation	EG10914	rpsO	-2.11	-0.875	30S ribosomal subunit protein S15
Central_Dc Translatio Translation	G6362	ybeY	0.573	-0.711	endoribonuclease YbeY
Central_Dc Translatio Translation	EG11837	bipA	-0.475	1.467	50S ribosomal subunit assembly factor BipA
Central_Dc Translatio Translation	EG10900	rpsA	-0.386	0.104	30S ribosomal subunit protein S1
Central_Dc Translatio Translation	EG10869	rplF	-2.061	1.375	50S ribosomal subunit protein L6
Central_Dc Translatio Translation	EG10865	rplB	-1.141	1.812	50S ribosomal subunit protein L2
Central_Dc Translatio Translation	EG10506	infC	-1.165	0.798	translation initiation factor IF-3
Central_Dc Translatio Translation	EG11268	fmt	-0.42	0.251	10-formyltetrahydrofolate:L-methionyl-tRNA ^{fMet} N-formyltrans
Central_Dc Translatio Translation	EG10504	infA	-2.268	1.331	translation initiation factor IF-1
Central_Dc Translatio Translation	EG10889	rpmE	0.586	2.023	50S ribosomal subunit protein L31
Central_Dc Translatio Translation	EG10505	infB	-0.204	0.659	translation initiation factor IF-2
Central_Dc Translatio Translation	EG11033	tsf	-1.036	0.856	protein chain elongation factor EF-Ts
Central_Dc Translatio Translation	EG10529	lepA	-0.673	0.031	30S ribosomal subunit biogenesis factor LepA
Central_Dc Translatio Translation	EG10437	hflX	-0.096	-0.265	ribosome rescue factor HflX
Central_Dc Translatio Translation	EG12099	efp	-0.119	1.058	protein chain elongation factor EF-P, Cε ^S -lysyl-Lys34
Central_Dc Translatio Translation	EG11782	smpB	-1.008	0.074	SsrA-binding protein
Central_Dc Translatio Translation	EG12424	prmC	-1.02	-0.329	protein-(glutamine-N5) methyltransferase
Central_Dc Translatio Translation	EG10872	rplK	-3.399	2.273	50S ribosomal subunit protein L11
Central_Dc Translatio Translation	EG12114	prfC	-1.037	0.158	peptide chain release factor RF3
Central_Dc Translatio Translation	EG10761	prfA	-2.256	-0.394	peptide chain release factor RF1
Central_Dc Translatio Translation	EG10762	prfB	-0.766	-0.128	peptide chain release factor RF2
Central_Dc Translatio Translation	EG10335	frr	-0.829	0.57	ribosome-recycling factor

Central_Dc Translatio Translation	EG11067	valS	-0.812	0.402	valine--tRNA ligase
Central_Dc Translatio Translation	EG10097	aspS	-1.28	-1.541	aspartate--tRNA ligase
Central_Dc Translatio Translation	EG11001	thrS	-0.405	0.37	threonine--tRNA ligase
Central_Dc Translatio Translation	EG10034	alaS	-1.695	-0.501	alanine--tRNA ligase/DNA-binding transcriptional repressor
Central_Dc Translatio Translation	EG10709	pheS	-2.117	-0.528	phenylalanine--tRNA ligase subunit C $\pm$
Central_Dc Translatio Translation	EG10710	pheT	0.937	-0.471	phenylalanine--tRNA ligase subunit C $\leq$
Central_Dc Translatio Translation	EG10532	leuS	-1.762	-0.689	leucine--tRNA ligase
Central_Dc Translatio Translation	EG10409	glyQ	-1.526	-1.002	glycine--tRNA ligase subunit C $\pm$
Central_Dc Translatio Translation	EG10196	cysS	-1.29	-0.876	cysteine--tRNA ligase
Central_Dc Translatio Translation	EG10410	glyS	-2.435	-1.428	glycine--tRNA ligase subunit C $\leq$
Central_Dc Translatio Translation	EG10071	argS	-2.019	-0.646	arginine--tRNA ligase
Central_Dc Translatio Translation	EG10770	proS	0.626	-0.018	proline--tRNA ligase
Central_Dc Translatio Translation	EG10552	lysS	-1.739	-0.265	lysine--tRNA ligase, constitutive
Central_Dc Translatio Translation	EG11211	epmA	0.395	0.053	EF-P-lysine lysyltransferase
Central_Dc Translatio Translation	EG10453	hisS	-0.034	-0.571	histidine--tRNA ligase
Central_Dc Translatio Translation	EG11362	gluQ	-1.063	0.77	glutamyl-Q tRNAAsp synthetase
Central_Dc Translatio Translation	EG10390	glnS	-1.557	-0.64	glutamine--tRNA ligase
Central_Dc Translatio Translation	EG10407	gltX	-0.316	0.544	glutamate--tRNA ligase
Central_Dc Translatio Translation	EG11043	tyrS	-1.379	0.1	tyrosine--tRNA ligase
Central_Dc Translatio Translation	EG10947	serS	-1.033	-0.112	serine--tRNA ligase
Central_Dc Translatio Translation	EG10586	metG	-1.642	-0.168	methionine--tRNA ligase
Central_Dc Translatio Translation	EG10492	ileS	-2.101	-0.506	isoleucine--tRNA ligase
Central_Dc Translatio Translation	EG10911	rpsL	-0.447	2.627	30S ribosomal subunit protein S12
Central_Dc Translatio Translation	EG10903	rpsD	-2.155	0.66	30S ribosomal subunit protein S4
Central_Dc Translatio Translation	EG10904	rpsE	-1.721	1.148	30S ribosomal subunit protein S5
Central_Dc DNA Met& DNA Metabolism	EG10976	ssb	2.338	1.296	ssDNA-binding protein
Central_Dc DNA Met& DNA Metabolism	EG10661	nrdB	-2.608	0.397	ribonucleoside-diphosphate reductase 1 subunit C $\leq$
Central_Dc DNA Met& DNA Metabolism	EG10240	dnaJ	0.834	3.71	chaperone protein DnaJ
Central_Dc DNA Met& DNA Metabolism	EG10534	ligA	-1.559	-0.32	DNA ligase
Central_Dc DNA Met& DNA Metabolism	EG10238	dnaE	-0.288	-0.711	DNA polymerase III subunit C $\pm$

Central_Dc DNA Metabolism	EG10423	gyrA	-1.844	-0.652	DNA gyrase subunit A
Central_Dc DNA Metabolism	EG10424	gyrB	-0.001	-0.399	DNA gyrase subunit B
Central_Dc DNA Metabolism	G6115	dinB	0.682	0.6	DNA polymerase IV
Central_Dc DNA Metabolism	EG10746	polA	0.763	-0.118	DNA polymerase I
Central_Dc DNA Metabolism	EG12690	rarA	0.446	-0.174	replication-associated recombination protein A
Central_Dc DNA Metabolism	EG11412	holA	-1.276	-1.411	DNA polymerase III subunit ϵ
Central_Dc DNA Metabolism	EG10242	dnaN	-1.232	-0.058	ϵ sliding clamp
Central_Dc DNA Metabolism	EG10239	dnaG	0.3	-0.241	DNA primase
Central_Dc DNA Metabolism	G7016	exoX	-1.739	0.797	exonuclease X
Central_Dc DNA Metabolism	EG11547	rnt	-1.276	-1.165	RNase T
Central_Dc DNA Metabolism	EG10925	ruvC	-0.512	-0.508	crossover junction endodeoxyribonuclease RuvC
Central_Dc DNA Metabolism	RUVA	ruvA	-0.836	0.414	Holliday junction branch migration complex subunit RuvA
Central_Dc DNA Metabolism	EG10861	rnhB	-0.146	-0.281	RNase HII
Central_Dc DNA Metabolism	EG10235	dnaA	-0.446	-0.998	chromosomal replication initiator protein DnaA
Central_Dc DNA Metabolism	G7313	hda	-1.214	-0.84	inhibitor of reinitiation of DNA replication
Central_Dc DNA Metabolism	EG10763	priA	-0.874	-0.533	primosomal protein N'
Central_Dc DNA Metabolism	EG10834	recR	-0.47	-0.759	DNA repair protein RecR
Central_Dc DNA Metabolism	EG10897	rpoH	-0.094	1.082	RNA polymerase, sigma 32 (sigma H) factor
Central_Dc DNA Metabolism	EG10832	recO	-0.769	-0.246	DNA repair protein RecO
Central_Dc DNA Metabolism	EG10829	recG	-1.864	-0.102	ATP-dependent DNA helicase RecG
Central_Dc DNA Metabolism	EG10830	recJ	-1.816	-0.258	ssDNA-specific exonuclease RecJ
Central_Dc DNA Metabolism	EG10694	pepA	-0.29	-0.865	aminopeptidase A/I
Central_Dc DNA Metabolism	EG10440	ihfA	1.195	0.38	integration host factor subunit ϵ
Central_Dc DNA Metabolism	EG10441	ihfB	0.948	0.144	integration host factor subunit ϵ
Central_Dc DNA Metabolism	EG11296	radA	-2.417	0.217	DNA recombination protein
Central_Dc DNA Metabolism	EG10826	recD	-1.861	-0.186	exodeoxyribonuclease V subunit RecD
Central_Dc DNA Metabolism	EG10825	recC	-0.755	-0.461	exodeoxyribonuclease V subunit RecC
Central_Dc DNA Metabolism	EG10824	recB	-1.491	0.129	exodeoxyribonuclease V subunit RecB
Central_Dc DNA Metabolism	EG10831	recN	0.111	-0.3	DNA repair protein RecN
Central_Dc DNA Metabolism	EG10823	recA	0.96	0.456	DNA recombination/repair protein RecA

Central_Dc DNA Metabolism	EG10686	parC	-1.506	-0.103	DNA topoisomerase IV subunit A
Central_Dc DNA Metabolism	EG10687	parE	-0.81	-0.273	DNA topoisomerase IV subunit B
Central_Dc DNA Metabolism	EG12080	recX	-0.27	1.028	RecA inhibitor RecX
Central_Dc DNA Metabolism	G7742	yrfG	0.76	0.573	purine nucleotidase
Central_Dc DNA Metabolism	G7647	yhbO	-0.602	0.194	protein/nucleic acid deglycase 2
Central_Dc DNA Metabolism	EG11871	gph	-0.971	-0.101	phosphoglycolate phosphatase
Central_Dc DNA Metabolism	EG10625	mutS	-1.27	-1.387	DNA mismatch repair protein MutS
Central_Dc DNA Metabolism	EG11281	mutL	-1.659	0.053	DNA mismatch repair protein MutL
Central_Dc DNA Metabolism	EG10627	mutY	-0.902	-0.025	adenine DNA glycosylase
Central_Dc DNA Metabolism	EG11058	ung	-1.525	-0.126	uracil-DNA glycosylase
Central_Dc DNA Metabolism	EG10662	nth	-0.162	0.537	endonuclease III
Central_Dc DNA Metabolism	G6489	uup	0.195	1.196	ATP-binding protein Uup
Central_Dc DNA Metabolism	EG11063	uvrC	-0.598	1.971	excision nuclease subunit C
Central_Dc DNA Metabolism	EG10329	mutM	-0.431	0.188	DNA-formamidopyrimidine glycosylase
Central_Dc DNA Metabolism	EG11061	uvrA	-1.562	1.685	excision nuclease subunit A
Central_Dc DNA Metabolism	EG11619	mfd	0.305	0.107	transcription-repair coupling factor
Central_Dc DNA Metabolism	EG10230	dksA	1.138	0.95	RNA polymerase-binding transcription factor DksA
Central_Dc DNA Metabolism	EG10736	phr	1.34	-0.289	deoxyribodipyrimidine photolyase
Central_Dc DNA Metabolism	EG10668	ogt	-0.261	0.181	methylated-DNA--[protein]-cysteine S-methyltransferase
Central_Dc DNA Metabolism	EG10986	tag	-0.699	-0.289	3-methyl-adenine DNA glycosylase I, constitutive
Central_Dc DNA Metabolism	EG10037	alkB	-0.524	1.243	DNA oxidative demethylase
Central_Dc DNA Metabolism	EG12449	prmB	-1.534	-0.361	50S ribosomal subunit protein L3 N5-glutamine methyltransferase
Central_Dc DNA Metabolism	EG11072	xseA	-0.219	0.056	exodeoxyribonuclease VII subunit XseA
Central_Dc DNA Metabolism	EG10860	rnhA	-0.099	-0.23	ribonuclease HI
Central_Dc DNA Metabolism	G6634	yciV	1.546	-0.305	RNA/ssDNA 5',3' exonuclease
Central_Dc DNA Metabolism	EG10915	rpsP	-2.655	1.621	30S ribosomal subunit protein S16
Central_Dc DNA Metabolism	G7525	yqgF	1.245	-0.145	ribonuclease H-like domain containing nuclease
Central_Dc DNA Metabolism	G7842	orn	-1.098	-0.538	oligoribonuclease
Central_Dc DNA Metabolism	G7952	yjjV	-1.611	-1.065	putative DNase YjjV
Central_Dc RNA Metabolism	EG10857	rnc	0.713	0.351	RNase III

Central_Dc RNA Metabolism	EG10690	pcnB	-2.447	0.164	poly(A) polymerase I
Central_Dc RNA Metabolism	EG11299	rng	-0.09	-0.469	RNase G
Central_Dc RNA Metabolism	G7698	tsaC	0.46	0.353	L-threonylcarbamoyladenylyl synthase
Central_Dc RNA Metabolism	G7525	yqgF	1.245	-0.145	ribonuclease H-like domain containing nuclease
Central_Dc RNA Metabolism	EG10859	rne	-3.562	-0.662	ribonuclease E
Central_Dc RNA Metabolism	EG11153	rimM	-1.77	0.772	ribosome maturation factor RimM
Central_Dc RNA Metabolism	EG11178	rbfA	-0.282	0.532	30S ribosome binding factor
Central_Dc RNA Metabolism	EG10864	rplA	-2.482	2.275	50S ribosomal subunit protein L1
Central_Dc RNA Metabolism	EG12098	rluD	-0.369	0.687	23S rRNA pseudouridine1911/1915/1917 synthase
Central_Dc RNA Metabolism	EG11118	rluC	1.347	-1.007	23S rRNA pseudouridine955/2504/2580 synthase
Central_Dc RNA Metabolism	EG12433	rluB	0.924	0.183	23S rRNA pseudouridine2605 synthase
Central_Dc RNA Metabolism	EG12044	rsuA	-2.31	-0.61	16S rRNA pseudouridine516 synthase
Central_Dc RNA Metabolism	G7641	rsml	-1.432	0.329	16S rRNA 2'-O-ribose C1402 methyltransferase
Central_Dc RNA Metabolism	EG11507	rlmE	1.076	0.655	23S rRNA 2'-O-ribose U2552 methyltransferase
Central_Dc RNA Metabolism	EG12234	rlmJ	-0.622	-0.04	23S rRNA m6A2030 methyltransferase
Central_Dc RNA Metabolism	EG12233	rsmJ	-1.024	0.917	16S rRNA m2G1516 methyltransferase
Central_Dc RNA Metabolism	G7950	rsmC	-1.283	-0.609	16S rRNA m2G1207 methyltransferase
Central_Dc RNA Metabolism	EG10343	rsmD	1.086	0.187	16S rRNA m2G966 methyltransferase
Central_Dc RNA Metabolism	EG12401	rlmN	-0.233	0.183	23S rRNA m2A2503 methyltransferase/tRNA m2A37 methyltransferase
Central_Dc RNA Metabolism	EG11254	rlmH	-2.51	-0.43	23S rRNA m3C ¹⁹¹⁵ methyltransferase
Central_Dc RNA Metabolism	EG12207	rlmA	-0.442	-0.65	23S rRNA m1G745 methyltransferase
Central_Dc RNA Metabolism	EG11247	rlmD	-0.976	2.425	23S rRNA m5U1939 methyltransferase
Central_Dc RNA Metabolism	EG10523	rsmA	1.51	-0.022	16S rRNA m62A1518,m62A1519 dimethyltransferase
Central_Dc RNA Metabolism	EG12163	rsmB	-1.635	-0.435	16S rRNA m5C967 methyltransferase
Central_Dc RNA Metabolism	EG11085	rsmH	-1.074	-0.3	16S rRNA m4C1402 methyltransferase
Central_Dc RNA Metabolism	EG10376	rsmG	-2.15	-0.341	16S rRNA m7G527 methyltransferase
Central_Dc RNA Metabolism	G6488	rlmL	0.17	-0.021	fused 23S rRNA m2G2445 methyltransferase and 23S rRNA m7G2445 methyltransferase
Central_Dc RNA Metabolism	G6362	ybeY	0.573	-0.711	endoribonuclease YbeY
Central_Dc RNA Metabolism	G7511	ygfZ	-0.627	0.789	folate-binding protein
Central_Dc RNA Metabolism	G7843	queG	-2.26	0.57	epoxyqueuosine reductase

Central_Dc RNA Metabolism	EG10034	alaS	-1.695	-0.501	alanine--tRNA ligase/DNA-binding transcriptional repressor
Central_Dc RNA Metabolism	G6435	rimO	-0.767	0.596	ribosomal protein S12 methylthiotransferase RimO
Central_Dc RNA Metabolism	EG10595	miaA	-0.344	1.252	tRNA dimethylallyltransferase
Central_Dc RNA Metabolism	EG11177	truB	0.042	0.069	tRNA pseudouridine55 synthase
Central_Dc RNA Metabolism	EG10454	truA	-1.379	0.887	tRNA pseudouridine38-40 synthase
Central_Dc RNA Metabolism	EG11171	tsaD	0.374	1.255	N6-L-threonylcarbamoyladenine synthase, TsaD subunit
Central_Dc RNA Metabolism	G6991	tsaB	-1.528	0.552	N6-L-threonylcarbamoyladenine synthase, TsaB subunit
Central_Dc RNA Metabolism	G7456	tcdA	-1.675	0.87	tRNA threonylcarbamoyladenosine dehydratase
Central_Dc RNA Metabolism	G6675	ttcA	-2.051	0.156	tRNA cytosine32 2-sulfurtransferase TtcA
Central_Dc RNA Metabolism	G7325	iscS	-1.254	0.693	cysteine desulfurase IscS
Central_Dc RNA Metabolism	EG11362	gluQ	-1.063	0.77	glutamyl-Q tRNAAsp synthetase
Central_Dc RNA Metabolism	EG10812	queA	-2.438	0.39	tRNA preQ134 S-adenosylmethionine ribosyltransferase-isomer
Central_Dc RNA Metabolism	EG11372	tadA	-0.655	-1.485	tRNA adenosine34 deaminase
Central_Dc RNA Metabolism	G6096	tilS	-1.851	-0.559	tRNAIle-lysine synthetase
Central_Dc RNA Metabolism	G7020	cmoA	-0.098	-3.964	carboxy-S-adenosyl-L-methionine synthase
Central_Dc RNA Metabolism	G7714	tusD	-2.498	-0.176	sulfurtransferase complex subunit TusD
Central_Dc RNA Metabolism	EG12876	tusE	-1.135	0.067	sulfur transfer protein TusE
Central_Dc RNA Metabolism	EG11344	mnmA	-2.793	-0.336	tRNA-specific 2-thiouridylase
Central_Dc RNA Metabolism	EG12022	dusC	-1.022	1.376	tRNA-dihydrouridine16 synthase
Central_Dc RNA Metabolism	EG11932	dusA	1.003	-0.429	tRNA-dihydrouridine synthase A
Central_Dc RNA Metabolism	EG11311	dusB	-2.096	-0.355	tRNA-dihydrouridine synthase B
Central_Dc RNA Metabolism	EG10996	tgt	-1.011	-1.184	tRNA-guanine transglycosylase
Central_Dc RNA Metabolism	EG11503	trmO	-2.79	-0.36	tRNA m6t6A37 methyltransferase
Central_Dc RNA Metabolism	EG10997	mnmE	-1.361	0.871	5-carboxymethylaminomethyluridine-tRNA synthase GTPase sul
Central_Dc RNA Metabolism	EG10375	mnmG	-0.824	0.232	5-carboxymethylaminomethyluridine-tRNA synthase subunit Mr
Central_Dc RNA Metabolism	EG11022	trmA	-0.736	-0.816	tRNA m5U54 methyltransferase
Central_Dc RNA Metabolism	G7199	mnmC	0.054	-0.903	fused 5-methylaminomethyl-2-thiouridine-forming methyltransf
Central_Dc RNA Metabolism	G6364	miaB	-1.879	-1.064	isopentenyl-adenosine A37 tRNA methylthiolase
Central_Dc RNA Metabolism	EG11023	trmD	-0.947	0.051	tRNA m1G37 methyltransferase
Central_Dc RNA Metabolism	G7327	trmJ	-2.075	-0.343	tRNA Cm32/Um32 methyltransferase

Central_Dc RNA Metabolism EG11268	fmt	-0.42	0.251	10-formyltetrahydrofolate:L-methionyl-tRNA ^{fMet} N-formyltransf
Central_Dc RNA Metabolism EG11547	rnt	-1.276	-1.165	RNase T
Central_Dc RNA Metabolism EG10136	cca	0.489	0.563	fused CCA tRNA nucleotidyltransferase/phosphohydrolase
Central_Dc RNA Metabolism EG10862	rnpA	-3.14	1.013	RNase P protein component
Central_Dc RNA Metabolism EG10844	rhIB	-1.567	0.352	ATP-dependent RNA helicase RhIB
Central_Dc RNA Metabolism EG10215	deaD	-2.19	-2.847	ATP-dependent RNA helicase DeaD
Central_Dc RNA Metabolism G7842	orn	-1.098	-0.538	oligoribonuclease
Central_Dc RNA Metabolism EG10743	pnp	-0.553	-1.652	polynucleotide phosphorylase
Central_Dc RNA Metabolism EG11447	csrA	1.321	-1.204	carbon storage regulator
Central_Dc RNA Metabolism EG11259	rnr	0.418	-0.175	RNase R
Central_Dc RNA Metabolism EG10861	rnhB	-0.146	-0.281	RNase HII
Central_Dc RNA Metabolism EG10860	rnhA	-0.099	-0.23	ribonuclease HI
Central_Dc RNA Metabolism EG10665	nusA	-0.549	0.59	transcription termination/antitermination protein NusA
Central_Dc RNA Metabolism EG10977	sspA	-0.926	-0.467	stringent starvation protein A
Central_Dc RNA Metabolism G6889	nemR	0.676	1.872	DNA-binding transcriptional repressor NemR
Central_Dc RNA Metabolism EG12301	rutR	0.034	0.491	DNA-binding transcriptional dual regulator RutR
Central_Dc RNA Metabolism G7137	rcnR	-1.29	0.527	DNA-binding transcriptional repressor RcnR
Central_Dc RNA Metabolism EG10733	phoR	-0.729	-0.506	sensor histidine kinase PhoR
Central_Dc RNA Metabolism EG11337	lysP	-0.898	-0.504	lysine:H ⁺ symporter
Central_Dc RNA Metabolism EG10591	metR	-0.36	-0.917	DNA-binding transcriptional dual regulator MetR
Central_Dc RNA Metabolism EG12006	btsR	-1.729	-0.633	Phosphorylated DNA-binding transcriptional dual regulator BtsR
Central_Dc RNA Metabolism EG11212	nsrR	-0.428	1.199	DNA-binding transcriptional repressor NsrR
Central_Dc RNA Metabolism EG10907	rpsH	-2.353	1.408	30S ribosomal subunit protein S8
Central_Dc RNA Metabolism EG10438	hfq	1.032	0.204	RNA-binding protein Hfq
Central_Dc RNA Metabolism G6720	paaX	0.791	-0.538	DNA-binding transcriptional repressor PaaX
Central_Dc RNA Metabolism EG10897	rpoH	-0.094	1.082	RNA polymerase, sigma 32 (sigma H) factor
Central_Dc RNA Metabolism EG11320	nrdR	-0.413	0.531	NrdR transcriptional repressor
Central_Dc RNA Metabolism EG11619	mfd	0.305	0.107	transcription-repair coupling factor
Central_Dc RNA Metabolism EG10777	pspB	2.455	-0.968	phage shock protein B
Central_Dc RNA Metabolism EG10387	glnL	0.905	-0.845	sensory histidine kinase NtrB

Central_Dc RNA Metabolism G6569	comR	0.494	1.445	DNA-binding transcriptional repressor ComR
Central_Dc RNA Metabolism EG10666	nusB	-0.058	-0.27	transcription antitermination protein NusB
Central_Dc RNA Metabolism EG11578	greB	-0.353	0.166	transcription elongation factor GreB
Central_Dc RNA Metabolism G6706	feaR	0.085	-0.768	DNA-binding transcriptional activator FeaR
Central_Dc RNA Metabolism EG10317	fis	-1.11	-0.32	DNA-binding transcriptional dual regulator Fis
Central_Dc RNA Metabolism EG11969	zntR	0.659	0.855	DNA-binding transcriptional activator ZntR
Central_Dc RNA Metabolism EG10898	rpoN	-0.677	0.137	RNA polymerase, sigma 54 (sigma N) factor
Central_Dc RNA Metabolism EG10359	fur	0.268	-0.259	DNA-binding transcriptional dual regulator Fur
Central_Dc RNA Metabolism EG10240	dnaJ	0.834	3.71	chaperone protein DnaJ
Central_Dc RNA Metabolism EG11191	slmA	-2.165	-0.644	nucleoid occlusion factor SlmA
Central_Dc RNA Metabolism EG10694	pepA	-0.29	-0.865	aminopeptidase A/I
Central_Dc RNA Metabolism EG11618	baeR	-0.621	-0.351	Phosphorylated DNA-binding transcriptional activator BaeR
Central_Dc RNA Metabolism EG10903	rpsD	-2.155	0.66	30S ribosomal subunit protein S4
Central_Dc RNA Metabolism EG10801	putA	-0.647	-0.46	fused DNA-binding transcriptional repressor / proline dehydrogenase
Central_Dc RNA Metabolism EG12314	yacG	0.69	1.283	DNA gyrase inhibitor YacG
Central_Dc RNA Metabolism EG10440	ihfA	1.195	0.38	integration host factor subunit α
Central_Dc RNA Metabolism EG10667	nusG	0.661	1.657	transcription termination factor NusG
Central_Dc RNA Metabolism EG10957	soxR	1.744	0.712	DNA-binding transcriptional dual regulator SoxR
Central_Dc RNA Metabolism EG11929	zur	-1.172	0.463	DNA-binding transcriptional repressor Zur
Central_Dc RNA Metabolism EG10123	birA	1.022	-0.972	DNA-binding transcriptional repressor/biotin-[acetyl-CoA-carboxylase]
Central_Dc RNA Metabolism EG10531	leuO	-0.344	-0.06	DNA-binding transcriptional dual regulator LeuO
Central_Dc RNA Metabolism G6263	cueR	-0.389	-0.506	DNA-binding transcriptional dual regulator CueR
Central_Dc RNA Metabolism EG12436	rseP	-0.733	-0.148	intramembrane zinc metalloprotease RseP
Central_Dc RNA Metabolism EG10517	kdpE	-0.11	-0.977	KdpE-Phosphorylated
Central_Dc RNA Metabolism EG10867	rplD	-2.778	2.173	50S ribosomal subunit protein L4
Central_Dc RNA Metabolism EG10728	phoB	0.981	0.479	Phosphorylated DNA-binding transcriptional dual regulator PhoB
Central_Dc RNA Metabolism EG12146	rapZ	-1.743	0.627	RNase adaptor protein RapZ
Central_Dc RNA Metabolism EG10896	rpoD	0.399	1.815	RNA polymerase, sigma 70 (sigma D) factor
Central_Dc RNA Metabolism G7924	hypT	-0.596	-0.257	DNA-binding transcriptional dual regulator HypT
Central_Dc RNA Metabolism EG10093	asnC	0.026	-0.791	DNA-binding transcriptional dual regulator AsnC

Central_Dc RNA Metabolism G6864	rstA	-0.512	0.134	Phosphorylated DNA-binding transcriptional regulator RstA
Central_Dc RNA Metabolism EG10911	rpsL	-0.447	2.627	30S ribosomal subunit protein S12
Central_Dc RNA Metabolism EG10441	ihfB	0.948	0.144	integration host factor subunit α
Central_Dc RNA Metabolism EG10415	greA	-1.004	-0.046	transcription elongation factor GreA
Central_Dc RNA Metabolism EG12386	glaR	-0.49	0.103	DNA-binding transcriptional repressor GlaR
Central_Dc RNA Metabolism EG10909	rpsJ	-2.923	2.015	30S ribosomal subunit protein S10
Central_Dc RNA Metabolism EG11088	pdhR	-1.496	-0.29	DNA-binding transcriptional dual regulator PdhR
Central_Dc RNA Metabolism EG10492	ileS	-2.101	-0.506	isoleucine--tRNA ligase
Central_Dc RNA Metabolism EG10048	apaH	-1.148	0.322	diadenosine tetraphosphatase
Central_Dc RNA Metabolism EG10770	proS	0.626	-0.018	proline--tRNA ligase
Central_Dc RNA Metabolism EG10125	bolA	1.583	0.948	DNA binding transcriptional dual regulator BolA-phosphate
Central_Dc RNA Metabolism EG10467	hupB	-0.906	-1.579	DNA-binding protein HU- α
Central_Dc RNA Metabolism EG12454	ybaK	0.287	0.552	Cys-tRNA ^{Pro} and Cys-tRNA ^{Cys} deacylase
Central_Dc RNA Metabolism EG10196	cysS	-1.29	-0.876	cysteine--tRNA ligase
Central_Dc RNA Metabolism EG10532	leuS	-1.762	-0.689	leucine--tRNA ligase
Central_Dc RNA Metabolism EG10390	glnS	-1.557	-0.64	glutamine--tRNA ligase
Central_Dc RNA Metabolism EG10947	serS	-1.033	-0.112	serine--tRNA ligase
Central_Dc RNA Metabolism G6634	yciV	1.546	-0.305	RNA/ssDNA 5',3' exonuclease
Central_Dc RNA Metabolism EG11043	tyrS	-1.379	0.1	tyrosine--tRNA ligase
Central_Dc RNA Metabolism EG10710	pheT	0.937	-0.471	phenylalanine--tRNA ligase subunit α
Central_Dc RNA Metabolism EG10709	pheS	-2.117	-0.528	phenylalanine--tRNA ligase subunit β
Central_Dc RNA Metabolism EG11001	thrS	-0.405	0.37	threonine--tRNA ligase
Central_Dc RNA Metabolism EG10097	aspS	-1.28	-1.541	aspartate--tRNA ligase
Central_Dc RNA Metabolism EG10071	argS	-2.019	-0.646	arginine--tRNA ligase
Central_Dc RNA Metabolism EG10586	metG	-1.642	-0.168	methionine--tRNA ligase
Central_Dc RNA Metabolism EG10037	alkB	-0.524	1.243	DNA oxidative demethylase
Central_Dc RNA Metabolism EG10423	gyrA	-1.844	-0.652	DNA gyrase subunit A
Central_Dc RNA Metabolism EG10407	gltX	-0.316	0.544	glutamate--tRNA ligase
Central_Dc RNA Metabolism EG10453	hisS	-0.034	-0.571	histidine--tRNA ligase
Central_Dc RNA Metabolism EG10552	lysS	-1.739	-0.265	lysine--tRNA ligase, constitutive

Central_Dc RNA Metabolism EG10239	dnaG	0.3	-0.241	DNA primase
Central_Dc RNA Metabolism EG10893	rpoA	-2.18	0.563	RNA polymerase subunit α
Central_Dc RNA Metabolism EG10410	glyS	-2.435	-1.428	glycine--tRNA ligase subunit α
Central_Dc RNA Metabolism EG10409	glyQ	-1.526	-1.002	glycine--tRNA ligase subunit α
Central_Dc RNA Metabolism EG10899	rpoZ	-1.353	0.111	RNA polymerase subunit σ
Central_Dc RNA Metabolism EG10424	gyrB	-0.001	-0.399	DNA gyrase subunit B
Central_Dc RNA Metabolism EG10845	rho	-2.507	-1.357	transcription termination factor Rho
Central_Dc RNA Metabolism EG11852	dtd	-1.017	1.039	D-aminoacyl-tRNA deacylase
Central_Dc RNA Metabolism EG10763	priA	-0.874	-0.533	primosomal protein N'
Central_Dc RNA Metabolism EG10894	rpoB	-1.791	-0.953	RNA polymerase subunit β
Central_Dc RNA Metabolism EG10895	rpoC	-0.146	-0.827	RNA polymerase subunit β'
Central_Dc RNA Metabolism EG11211	epmA	0.395	0.053	EF-P-lysine lysyltransferase
Central_Dc RNA Metabolism EG11067	valS	-0.812	0.402	valine--tRNA ligase
Central_Dc Protein Metabolism: G7647	yhbO	-0.602	0.194	protein/nucleic acid deglycase 2
Central_Dc Protein Metabolism: EG11080	fkpB	0.675	0.045	peptidyl-prolyl cis-trans isomerase FkpB
Central_Dc Protein Metabolism: EG11782	smpB	-1.008	0.074	SsrA-binding protein
Central_Dc Protein Metabolism: EG11591	lipB	-1.975	0.059	lipoyl(octanoyl) transferase
Central_Dc Protein Metabolism: EG10736	phr	1.34	-0.289	deoxyribodipyrimidine photolyase
Central_Dc Protein Metabolism: EG11003	tig	-2.353	0.398	trigger factor
Central_Dc Protein Metabolism: EG10733	phoR	-0.729	-0.506	sensor histidine kinase PhoR
Central_Dc Protein Metabolism: G6435	rimO	-0.767	0.596	ribosomal protein S12 methylthiotransferase RimO
Central_Dc Protein Metabolism: EG12449	prnB	-1.534	-0.361	50S ribosomal subunit protein L3 N5-glutamine methyltransferase
Central_Dc Protein Metabolism: EG12188	ptsP	-1.02	-0.025	PtsP-phosphorylated
Central_Dc Protein Metabolism: G7170	arnT	-0.793	-0.084	lipid IVA 4-amino-4-deoxy-L-arabinosyltransferase
Central_Dc Protein Metabolism: EG10387	glnL	0.905	-0.845	sensory histidine kinase NtrB
Central_Dc Protein Metabolism: G7836	epmB	-0.452	-0.834	lysine 2,3-aminomutase
Central_Dc Protein Metabolism: EG10757	ppiA	-0.905	-0.928	peptidyl-prolyl cis-trans isomerase A
Central_Dc Protein Metabolism: EG10270	era	-0.458	0.651	30S ribosomal subunit maturation GTPase Era
Central_Dc Protein Metabolism: G6577	cobB	0.277	0.032	CobB-S
Central_Dc Protein Metabolism: EG10850	rimI	-1.499	1.11	protein N-acetyltransferase RimI

Central_Dc Protein M Protein Metaboli: EG10985	surA	-0.337	-0.135	chaperone SurA
Central_Dc Protein M Protein Metaboli: G6906	sufS	1.017	-0.397	L-cysteine desulfurase
Central_Dc Protein M Protein Metaboli: EG11268	fmt	-0.42	0.251	10-formyltetrahydrofolate:L-methionyl-tRNA ^{Met} N-formyltrans
Central_Dc Protein M Protein Metaboli: EG10437	hflX	-0.096	-0.265	ribosome rescue factor HflX
Central_Dc Protein M Protein Metaboli: G6318	cusS	0.039	-0.296	CusS-N-phospho-L-histidine
Central_Dc Protein M Protein Metaboli: EG11132	ppsR	-1.485	0.084	phosphoenolpyruvate synthetase regulatory protein
Central_Dc Protein M Protein Metaboli: EG10275	accB	-1.479	-1.539	biotin carboxyl carrier protein
Central_Dc Protein M Protein Metaboli: EG12424	prmC	-1.02	-0.329	protein-(glutamine-N5) methyltransferase
Central_Dc Protein M Protein Metaboli: EG10123	birA	1.022	-0.972	DNA-binding transcriptional repressor/biotin-[acetyl-CoA-carbox
Central_Dc Protein M Protein Metaboli: EG10153	moeA	-0.998	-1.007	molybdopterin molybdotransferase
Central_Dc Protein M Protein Metaboli: EG11411	glnD	-0.088	-1.547	PII uridylyltransferase / uridylyl removing enzyme
Central_Dc Protein M Protein Metaboli: EG12147	npr	0.022	0.374	Npr phosphorylated
Central_Dc Protein M Protein Metaboli: EG11497	prmA	0.633	-0.374	ribosomal protein L11 methyltransferase
Central_Dc Protein M Protein Metaboli: EG10429	hemC	-0.452	0.623	hydroxymethylbilane synthase
Central_Dc Protein M Protein Metaboli: EG11433	msrA	0.515	0.277	methionine sulfoxide reductase A
Central_Dc Protein M Protein Metaboli: G7716	fkpA	-0.055	0.232	peptidyl-prolyl cis-trans isomerase FkpA
Central_Dc Protein M Protein Metaboli: G6242	ppiD	-0.294	-0.629	periplasmic folding chaperone
Central_Dc Protein M Protein Metaboli: EG11553	glmM	-1.071	-0.191	phosphoglucosamine mutase
Central_Dc Protein M Protein Metaboli: EG10982	sucD	-0.197	0.041	succinyl-CoA synthetase subunit C ϵ
Central_Dc Protein M Protein Metaboli: EG10516	kdpD	0.594	-0.207	sensor histidine kinase KdpD
Central_Dc Protein M Protein Metaboli: EG10269	envZ	-0.232	-0.789	sensor histidine kinase EnvZ
Central_Dc Protein M Protein Metaboli: EG11211	epmA	0.395	0.053	EF-P-lysine lysyltransferase
Central_Dc Protein M Protein Metaboli: EG12132	iscA	-0.445	1.522	iron-sulfur cluster insertion protein IscA
Central_Dc Protein M Protein Metaboli: EG12130	hscA	-1.569	0.685	iron-sulfur cluster biosynthesis chaperone HscA
Central_Dc Protein M Protein Metaboli: EG12131	hscB	-3.226	1.032	[Fe-S] cluster biosynthesis co-chaperone HscB
Central_Dc Protein M Protein Metaboli: EG12332	erpA	1.272	1.26	iron-sulfur cluster insertion protein ErpA
Central_Dc Protein M Protein Metaboli: G7748	nfuA	-0.202	1.33	iron-sulfur cluster carrier protein NfuA
Central_Dc Protein M Protein Metaboli: EG10530	lepB	0.02	-0.907	signal peptidase I
Central_Dc Protein M Protein Metaboli: EG11747	panD	0.418	3.472	PanD C ϵ cleavage product
Central_Dc Protein M Protein Metaboli: EG10775	psd	-1.783	-0.244	phosphatidylserine decarboxylase proenzyme

Central_Dc Protein M Protein Metaboli: EG12394	msrB	0.198	0.18	methionine sulfoxide reductase B
Central_Dc Protein M Protein Metaboli: EG12436	rseP	-0.733	-0.148	intramembrane zinc metalloprotease RseP
Central_Dc Protein M Protein Metaboli: EG10159	clpX	0.221	0.699	ATP-dependent Clp protease ATP-binding subunit ClpX
Central_Dc Protein M Protein Metaboli: EG11542	tesA	-1.684	0.281	multifunctional acyl-CoA thioesterase I and protease I and lysop
Central_Dc Protein M Protein Metaboli: EG10201	dacA	-2.586	-0.494	D-alanyl-D-alanine carboxypeptidase DacA
Central_Dc Protein M Protein Metaboli: EG11893	dacD	-0.102	0.976	D-alanyl-D-alanine carboxypeptidase DacD
Central_Dc Protein M Protein Metaboli: EG10605	mrcB	-0.486	-0.255	PBP1BCE≥
Central_Dc Protein M Protein Metaboli: EG10748	mrcA	0.098	-0.227	peptidoglycan glycosyltransferase / peptidoglycan DD-transpept
Central_Dc Protein M Protein Metaboli: EG11652	degS	0.495	0.555	serine endoprotease
Central_Dc Protein M Protein Metaboli: EG10697	pepP	-0.611	-0.53	Xaa-Pro aminopeptidase
Central_Dc Protein M Protein Metaboli: G6991	tsaB	-1.528	0.552	N6-L-threonylcarbamoyladenine synthase, TsaB subunit
Central_Dc Protein M Protein Metaboli: G6362	ybeY	0.573	-0.711	endoribonuclease YbeY
Central_Dc Protein M Protein Metaboli: EG10694	pepA	-0.29	-0.865	aminopeptidase A/I
Central_Dc Protein M Protein Metaboli: EG11744	pqqL	-0.315	-0.882	periplasmic metalloprotease
Central_Dc Protein M Protein Metaboli: EG11291	loiP	0.149	0.119	metalloprotease LoiP
Central_Dc Protein M Protein Metaboli: EG10580	mepA	-2.092	-0.477	peptidoglycan DD-endopeptidase/peptidoglycan LD-endopeptida
Central_Dc Protein M Protein Metaboli: G6463	clpS	1.336	-0.027	specificity factor for ClpA-ClpP chaperone-protease complex
Central_Dc Protein M Protein Metaboli: EG10695	pepD	-2.925	0.275	peptidase D
Central_Dc Protein M Protein Metaboli: EG10397	glpG	-1.12	0.415	rhomboid protease GlpG
Central_Dc Protein M Protein Metaboli: EG11506	ftsH	0.675	0.469	ATP-dependent zinc metalloprotease FtsH
Central_Dc Protein M Protein Metaboli: EG10760	prc	0.012	-0.244	tail-specific protease
Central_Dc Protein M Protein Metaboli: EG10156	clpA	0.392	-0.303	ATP-dependent Clp protease ATP-binding subunit ClpA
Central_Dc Protein M Protein Metaboli: EG10374	ggt	-0.378	-1.098	glutathione hydrolase, small subunit
Central_Dc Protein M Protein Metaboli: G7682	degQ	-0.091	-0.064	periplasmic serine endoprotease
Central_Dc Protein M Protein Metaboli: EG10785	pth	-1.544	1.147	peptidyl-tRNA hydrolase
Central_Dc Protein M Protein Metaboli: EG10914	rpsO	-2.11	-0.875	30S ribosomal subunit protein S15
Central_Dc Protein M Protein Metaboli: EG10440	ihfA	1.195	0.38	integration host factor subunit CE±
Central_Dc Protein M Protein Metaboli: EG10441	ihfB	0.948	0.144	integration host factor subunit CE≤
Central_Dc Protein M Protein Metaboli: EG10907	rpsH	-2.353	1.408	30S ribosomal subunit protein S8
Central_Dc Protein M Protein Metaboli: EG11002	thyA	-0.966	-0.248	thymidylate synthase

Central_Dc Protein M Protein Metaboli: EG12316	acnB	-0.873	-1.09	AcnB
Central_Dc Protein M Protein Metaboli: EG12114	prfC	-1.037	0.158	peptide chain release factor RF3
Central_Dc Protein M Protein Metaboli: EG10881	rplT	-1.641	-0.09	50S ribosomal subunit protein L20
Central_Dc Protein M Protein Metaboli: EG11255	rsfS	-1.728	1.202	ribosomal silencing factor RsfS
Central_Dc Protein M Protein Metaboli: EG10871	rplJ	-2.382	1.646	50S ribosomal subunit protein L10
Central_Dc Protein M Protein Metaboli: EG10874	rplM	-1.147	-0.133	50S ribosomal subunit protein L13
Central_Dc Protein M Protein Metaboli: EG10885	rplY	-1.984	1.618	50S ribosomal subunit protein L25
Central_Dc Protein M Protein Metaboli: EG10906	rpsG	-0.76	2.531	30S ribosomal subunit protein S7
Central_Dc Protein M Protein Metaboli: EG10217	accD	-0.711	0.285	acetyl-CoA carboxyltransferase subunit Cε
Central_Dc Protein M Protein Metaboli: EG10867	rplD	-2.778	2.173	50S ribosomal subunit protein L4
Central_Dc Protein M Protein Metaboli: EG10900	rpsA	-0.386	0.104	30S ribosomal subunit protein S1
Central_Dc Protein M Protein Metaboli: EG11681	hpf	1.151	-1.568	ribosome hibernation-promoting factor
Central_Dc Protein M Protein Metaboli: EG12343	ettA	-1.151	0.017	energy-dependent translational throttle protein EttA
Central_Dc Protein M Protein Metaboli: EG10917	rpsR	-2.664	1.524	30S ribosomal subunit protein S18
Central_Dc Protein M Protein Metaboli: EG10905	rpsF	-3.975	1.32	30S ribosomal subunit protein S6
Central_Dc Protein M Protein Metaboli: EG11001	thrS	-0.405	0.37	threonine--tRNA ligase
Central_Dc Protein M Protein Metaboli: EG10864	rplA	-2.482	2.275	50S ribosomal subunit protein L1
Central_Dc Protein M Protein Metaboli: EG10889	rpmE	0.586	2.023	50S ribosomal subunit protein L31
Central_Dc Protein M Protein Metaboli: EG10595	miaA	-0.344	1.252	tRNA dimethylallyltransferase
Central_Dc Protein M Protein Metaboli: EG12099	efp	-0.119	1.058	protein chain elongation factor EF-P, Cε-lysyl-Lys34
Central_Dc Protein M Protein Metaboli: EG10529	lepA	-0.673	0.031	30S ribosomal subunit biogenesis factor LepA
Central_Dc Protein M Protein Metaboli: EG10215	deaD	-2.19	-2.847	ATP-dependent RNA helicase DeaD
Central_Dc Protein M Protein Metaboli: EG10903	rpsD	-2.155	0.66	30S ribosomal subunit protein S4
Central_Dc Protein M Protein Metaboli: EG11067	valS	-0.812	0.402	valine--tRNA ligase
Central_Dc Protein M Protein Metaboli: EG10438	hfq	1.032	0.204	RNA-binding protein Hfq
Central_Dc Protein M Protein Metaboli: EG11447	csrA	1.321	-1.204	carbon storage regulator
Central_Dc Protein M Protein Metaboli: EG10492	ileS	-2.101	-0.506	isoleucine--tRNA ligase
Central_Dc Protein M Protein Metaboli: EG11362	gluQ	-1.063	0.77	glutamyl-Q tRNA ^{Asp} synthetase
Central_Dc Protein M Protein Metaboli: EG10901	rpsB	-1.039	1.919	30S ribosomal subunit protein S2
Central_Dc Protein M Protein Metaboli: EG11033	tsf	-1.036	0.856	protein chain elongation factor EF-Ts

Central_Dc Protein M Protein Metaboli: EG10335	frr	-0.829	0.57	ribosome-recycling factor
Central_Dc Protein M Protein Metaboli: EG10770	proS	0.626	-0.018	proline--tRNA ligase
Central_Dc Protein M Protein Metaboli: EG12454	ybaK	0.287	0.552	Cys-tRNA ^{Pro} and Cys-tRNA ^{Cys} deacylase
Central_Dc Protein M Protein Metaboli: EG10196	cysS	-1.29	-0.876	cysteine--tRNA ligase
Central_Dc Protein M Protein Metaboli: EG10532	leuS	-1.762	-0.689	leucine--tRNA ligase
Central_Dc Protein M Protein Metaboli: EG10168	Int	-0.456	-0.325	apolipoprotein N-acyltransferase
Central_Dc Protein M Protein Metaboli: EG10390	glnS	-1.557	-0.64	glutamine--tRNA ligase
Central_Dc Protein M Protein Metaboli: EG11595	moaA	1.558	0.073	GTP 3',8'-cyclase
Central_Dc Protein M Protein Metaboli: EG11666	moaC	0.088	-0.084	cyclic pyranopterin monophosphate synthase
Central_Dc Protein M Protein Metaboli: EG10154	moeB	0.327	0.495	molybdopterin-synthase adenylyltransferase
Central_Dc Protein M Protein Metaboli: EG10504	infA	-2.268	1.331	translation initiation factor IF-1
Central_Dc Protein M Protein Metaboli: EG11112	aat	0.326	-0.603	leucyl/phenylalanyl-tRNA--protein transferase
Central_Dc Protein M Protein Metaboli: EG10947	serS	-1.033	-0.112	serine--tRNA ligase
Central_Dc Protein M Protein Metaboli: EG10890	rpmF	-2.098	0.87	50S ribosomal subunit protein L32
Central_Dc Protein M Protein Metaboli: EG11293	lolB	-0.809	-0.483	outer membrane lipoprotein LolB
Central_Dc Protein M Protein Metaboli: EG10761	prfA	-2.256	-0.394	peptide chain release factor RF1
Central_Dc Protein M Protein Metaboli: EG11043	tyrS	-1.379	0.1	tyrosine--tRNA ligase
Central_Dc Protein M Protein Metaboli: EG10710	pheT	0.937	-0.471	phenylalanine--tRNA ligase subunit $\alpha_{\pm}$
Central_Dc Protein M Protein Metaboli: EG10709	pheS	-2.117	-0.528	phenylalanine--tRNA ligase subunit $\alpha_{\pm}$
Central_Dc Protein M Protein Metaboli: EG11231	rpmI	-2.451	0.136	50S ribosomal subunit protein L35
Central_Dc Protein M Protein Metaboli: EG10506	infC	-1.165	0.798	translation initiation factor IF-3
Central_Dc Protein M Protein Metaboli: EG10097	aspS	-1.28	-1.541	aspartate--tRNA ligase
Central_Dc Protein M Protein Metaboli: EG10071	argS	-2.019	-0.646	arginine--tRNA ligase
Central_Dc Protein M Protein Metaboli: EG10586	metG	-1.642	-0.168	methionine--tRNA ligase
Central_Dc Protein M Protein Metaboli: EG10407	gltX	-0.316	0.544	glutamate--tRNA ligase
Central_Dc Protein M Protein Metaboli: EG10453	hisS	-0.034	-0.571	histidine--tRNA ligase
Central_Dc Protein M Protein Metaboli: EG10880	rplS	-1.489	0.485	50S ribosomal subunit protein L19
Central_Dc Protein M Protein Metaboli: EG10915	rpsP	-2.655	1.621	30S ribosomal subunit protein S16
Central_Dc Protein M Protein Metaboli: EG10034	alaS	-1.695	-0.501	alanine--tRNA ligase/DNA-binding transcriptional repressor
Central_Dc Protein M Protein Metaboli: EG12128	lgt	-2.209	1.733	phosphatidylglycerol--phospholipoprotein diacylglycerol transferase

Central_Dc Protein M Protein Metaboli: EG10552	lysS	-1.739	-0.265	lysine--tRNA ligase, constitutive
Central_Dc Protein M Protein Metaboli: EG10762	prfB	-0.766	-0.128	peptide chain release factor RF2
Central_Dc Protein M Protein Metaboli: EG10920	rpsU	-2.111	1.745	30S ribosomal subunit protein S21
Central_Dc Protein M Protein Metaboli: EG10505	infB	-0.204	0.659	translation initiation factor IF-2
Central_Dc Protein M Protein Metaboli: EG11179	rimP	0.603	-0.255	ribosome maturation factor RimP
Central_Dc Protein M Protein Metaboli: EG50002	rpmA	-1.371	1.346	50S ribosomal subunit protein L27
Central_Dc Protein M Protein Metaboli: EG50001	rplU	-2.149	1.382	50S ribosomal subunit protein L21
Central_Dc Protein M Protein Metaboli: EG10908	rpsI	-0.92	-0.394	30S ribosomal subunit protein S9
Central_Dc Protein M Protein Metaboli: EG10878	rplQ	-1.649	0.754	50S ribosomal subunit protein L17
Central_Dc Protein M Protein Metaboli: EG10912	rpsM	-2.616	0.72	30S ribosomal subunit protein S13
Central_Dc Protein M Protein Metaboli: EG10876	rplO	1.654	0.525	50S ribosomal subunit protein L15
Central_Dc Protein M Protein Metaboli: EG10888	rpmD	-0.82	1.301	50S ribosomal subunit protein L30
Central_Dc Protein M Protein Metaboli: EG10904	rpsE	-1.721	1.148	30S ribosomal subunit protein S5
Central_Dc Protein M Protein Metaboli: EG10879	rplR	-2.04	1.244	50S ribosomal subunit protein L18
Central_Dc Protein M Protein Metaboli: EG10869	rplF	-2.061	1.375	50S ribosomal subunit protein L6
Central_Dc Protein M Protein Metaboli: EG10913	rpsN	-1.991	1.133	30S ribosomal subunit protein S14
Central_Dc Protein M Protein Metaboli: EG10868	rplE	-2.16	0.987	50S ribosomal subunit protein L5
Central_Dc Protein M Protein Metaboli: EG10884	rplX	-2.656	0.982	50S ribosomal subunit protein L24
Central_Dc Protein M Protein Metaboli: EG10875	rplN	-2.153	1.064	50S ribosomal subunit protein L14
Central_Dc Protein M Protein Metaboli: EG10916	rpsQ	-1.558	1.906	30S ribosomal subunit protein S17
Central_Dc Protein M Protein Metaboli: EG10887	rpmC	-2.174	1.836	50S ribosomal subunit protein L29
Central_Dc Protein M Protein Metaboli: EG10877	rplP	-2.62	1.819	50S ribosomal subunit protein L16
Central_Dc Protein M Protein Metaboli: EG10902	rpsC	-2.812	1.765	30S ribosomal subunit protein S3
Central_Dc Protein M Protein Metaboli: EG10882	rplV	-1.868	1.753	50S ribosomal subunit protein L22
Central_Dc Protein M Protein Metaboli: EG10918	rpsS	-2.877	1.849	30S ribosomal subunit protein S19
Central_Dc Protein M Protein Metaboli: EG10865	rplB	-1.141	1.812	50S ribosomal subunit protein L2
Central_Dc Protein M Protein Metaboli: EG10883	rplW	-1.711	1.921	50S ribosomal subunit protein L23
Central_Dc Protein M Protein Metaboli: EG10866	rplC	-3.126	2.123	50S ribosomal subunit protein L3
Central_Dc Protein M Protein Metaboli: EG10909	rpsJ	-2.923	2.015	30S ribosomal subunit protein S10
Central_Dc Protein M Protein Metaboli: EG10911	rpsL	-0.447	2.627	30S ribosomal subunit protein S12

Central_Dc Protein M Protein Metaboli: G7746	yhgF	-0.142	-0.592	putative RNA-binding protein YhgF
Central_Dc Protein M Protein Metaboli: EG10410	glyS	-2.435	-1.428	glycine--tRNA ligase subunit Cε≤
Central_Dc Protein M Protein Metaboli: EG10409	glyQ	-1.526	-1.002	glycine--tRNA ligase subunit Cε±
Central_Dc Protein M Protein Metaboli: EG10891	rpmG	-2.074	2.118	50S ribosomal subunit protein L33
Central_Dc Protein M Protein Metaboli: EG10886	rpmB	-2.249	1.777	50S ribosomal subunit protein L28
Central_Dc Protein M Protein Metaboli: EG11829	mobA	0.538	-0.523	molybdenum cofactor guanylyltransferase
Central_Dc Protein M Protein Metaboli: EG11837	bipA	-0.475	1.467	50S ribosomal subunit assembly factor BipA
Central_Dc Protein M Protein Metaboli: EG11859	fdhD	0.569	-1.622	sulfurtransferase for molybdenum cofactor sulfuration
Central_Dc Protein M Protein Metaboli: EG10872	rplK	-3.399	2.273	50S ribosomal subunit protein L11
Central_Dc Protein M Protein Metaboli: EG10873	rplL	-0.351	1.527	50S ribosomal subunit protein L7
Central_Dc Protein M Protein Metaboli: EG10870	rplI	-1.655	1.145	50S ribosomal subunit protein L9
Central_Dc Protein Fc Folding/Secretior EG10757	ppiA	-0.905	-0.928	peptidyl-prolyl cis-trans isomerase A
Central_Dc Protein Fc Folding/Secretior EG12131	hscB	-3.226	1.032	[Fe-S] cluster biosynthesis co-chaperone HscB
Central_Dc Protein Fc Folding/Secretior EG12130	hscA	-1.569	0.685	iron-sulfur cluster biosynthesis chaperone HscA
Central_Dc Protein Fc Folding/Secretior EG11197	yidC	-3.025	-0.122	membrane protein insertase YidC
Central_Dc Protein Fc Folding/Secretior EG10159	clpX	0.221	0.699	ATP-dependent Clp protease ATP-binding subunit ClpX
Central_Dc Protein Fc Folding/Secretior EG11393	dsbB	-2.303	0.749	protein thiol:quinone oxidoreductase DsbBReduced
Central_Dc Protein Fc Folding/Secretior G7716	fkpA	-0.055	0.232	peptidyl-prolyl cis-trans isomerase FkpA
Central_Dc Protein Fc Folding/Secretior EG10157	clpB	0.611	1.356	ClpB80
Central_Dc Protein Fc Folding/Secretior G7744	hslO	-0.552	2.225	molecular chaperone Hsp33
Central_Dc Protein Fc Folding/Secretior EG10985	surA	-0.337	-0.135	chaperone SurA
Central_Dc Protein Fc Folding/Secretior EG10937	secB	-0.431	1.976	protein export chaperone SecB
Central_Dc Protein Fc Folding/Secretior G6242	ppiD	-0.294	-0.629	periplasmic folding chaperone
Central_Dc Protein Fc Folding/Secretior EG10936	secA	-1.291	1.148	protein translocation ATPase
Central_Dc Protein Fc Folding/Secretior EG11080	fkpB	0.675	0.045	peptidyl-prolyl cis-trans isomerase FkpB
Central_Dc Protein Fc Folding/Secretior EG10997	mnmE	-1.361	0.871	5-carboxymethylaminomethyluridine-tRNA synthase GTPase sul
Central_Dc Protein Fc Folding/Secretior EG10461	htpG	-3.902	2.793	chaperone protein HtpG
Central_Dc Protein Fc Folding/Secretior EG11003	tig	-2.353	0.398	trigger factor
Central_Dc Protein Fc Folding/Secretior EG12193	cbpA	0.338	1.02	curved DNA-binding protein
Central_Dc Protein Fc Folding/Secretior EG10416	grpE	-1.164	3.874	nucleotide exchange factor GrpE

Central_Dc Protein Fc Folding/Secretion	EG10240	dnaJ	0.834	3.71	chaperone protein DnaJ
Central_Dc Protein Fc Folding/Secretion	EG10599	groL	-2.367	3.304	chaperonin GroEL
Central_Dc Protein Fc Folding/Secretion	EG10600	groS	-2.666	4.238	cochaperonin GroES
Central_Dc Protein Fc Folding/Secretion	EG10156	clpA	0.392	-0.303	ATP-dependent Clp protease ATP-binding subunit ClpA
Central_Dc Protein Fc Folding/Secretion	EG12095	secG	-1.458	0.553	Sec translocon subunit SecG
Central_Dc Protein Fc Folding/Secretion	EG10939	secE	0.521	1.014	Sec translocon subunit SecE
Other_Patl C1 Compo C1 Compounds	EG50010	frmA	1.617	0.148	S-(hydroxymethyl)glutathione dehydrogenase
Other_Patl Inorganic Nutrient	EG10403	gltB	-1.41	-0.121	glutamate synthase subunit GltB
Other_Patl Inorganic Nutrient	EG10404	gltD	-0.677	1.668	glutamate synthase subunit GltD
Other_Patl Inorganic Nutrient	EG10649	ndh	-0.631	0.323	NADH:quinone oxidoreductase II
Other_Patl Inorganic Nutrient	EG10394	glpD	0.381	0.052	aerobic glycerol 3-phosphate dehydrogenase
Other_Patl Inorganic Nutrient	EG12088	nuoH	-1.477	1.386	NADH:quinone oxidoreductase subunit H
Other_Patl Inorganic Nutrient	EG12090	nuoJ	-1.56	1.196	NADH:quinone oxidoreductase subunit J
Other_Patl Inorganic Nutrient	EG12091	nuoK	-2.478	1.063	NADH:quinone oxidoreductase subunit K
Other_Patl Inorganic Nutrient	EG12092	nuoL	-2.06	0.479	NADH:quinone oxidoreductase subunit L
Other_Patl Inorganic Nutrient	EG11773	nuoM	-2.108	0.305	NADH:quinone oxidoreductase subunit M
Other_Patl Inorganic Nutrient	EG12093	nuoN	-1.763	-0.195	NADH:quinone oxidoreductase subunit N
Other_Patl Inorganic Nutrient	EG12089	nuoI	-0.888	1.472	NADH:quinone oxidoreductase subunit I
Other_Patl Inorganic Nutrient	EG12087	nuoG	-1.347	1.469	NADH:quinone oxidoreductase subunit G
Other_Patl Inorganic Nutrient	EG11774	nuoF	-0.226	1.858	NADH:quinone oxidoreductase subunit F
Other_Patl Inorganic Nutrient	EG12086	nuoE	-0.112	1.772	NADH:quinone oxidoreductase subunit E
Other_Patl Inorganic Nutrient	EG12084	nuoC	-1.019	1.447	NADH:quinone oxidoreductase subunit CD
Other_Patl Inorganic Nutrient	EG12083	nuoB	-0.509	2.067	NADH:quinone oxidoreductase subunit B
Other_Patl Inorganic Nutrient	EG12423	tauD	1.725	-2.071	taurine dioxygenase
Other_Patl Inorganic Nutrient	EG10186	cysD	-2.495	1.049	sulfate adenylyltransferase subunit 2
Other_Patl Inorganic Nutrient	EG10194	cysN	-0.289	1.25	sulfate adenylyltransferase subunit 1
Other_Patl Inorganic Nutrient	EG11887	trxC	2.051	0.765	oxidized thioredoxin 2
Other_Patl Inorganic Nutrient	G6477	ssuD	-0.273	-1.791	FMN/2-dependent alkanesulfonate monooxygenase
Other_Patl Detoxification	G7167	arnC	0.529	-0.966	undecaprenyl-phosphate 4-deoxy-4-formamido-L-arabinose transferase
Other_Patl Detoxification	G7170	arnT	-0.793	-0.084	lipid IVA 4-amino-4-deoxy-L-arabinosyltransferase

Other_Patl Detoxifica Detoxification	EG12294	grxC	0.206	2.129	oxidized glutaredoxin 3
Other_Patl Detoxifica Detoxification	G6891	gloA	-1.408	2.349	glyoxalase I
Other_Patl Detoxifica Detoxification	G6475	gloC	1.386	0.925	hydroxyacylglutathione hydrolase GloC
Other_Patl Detoxifica Detoxification	EG10231	dld	-1.435	0.167	quinone-dependent D-lactate dehydrogenase
Other_Patl Detoxifica Detoxification	EG11648	dkgB	-1.19	0.883	methylglyoxal reductase DkgB
Other_Patl Detoxifica Detoxification	EG10954	sodB	0.358	1.587	superoxide dismutase (Fe)
Other_Patl Detoxifica Detoxification	EG10509	katE	-0.414	1.55	catalase HP11
Other_Patl Detoxifica Detoxification	EG10511	katG	0.743	0.489	catalase/hydroperoxidase HPI
Other_Patl Macromol Macromolecule	EG7452	queF	-0.849	-0.663	7-cyano-7-deazaguanine reductase
Other_Patl Macromol Macromolecule	EG10996	tgt	-1.011	-1.184	tRNA-guanine transglycosylase
Other_Patl Macromol Macromolecule	EG10812	queA	-2.438	0.39	tRNA preQ134 S-adenosylmethionine ribosyltransferase-isomer
Other_Patl Macromol Macromolecule	EG7843	queG	-2.26	0.57	epoxyqueuosine reductase
Other_Patl Macromol Macromolecule	EG7020	cmoA	-0.098	-3.964	carboxy-S-adenosyl-L-methionine synthase
Other_Patl Macromol Macromolecule	EG11171	tsaD	0.374	1.255	N6-L-threonylcarbamoyladenine synthase, TsaD subunit
Other_Patl Macromol Macromolecule	EG6991	tsaB	-1.528	0.552	N6-L-threonylcarbamoyladenine synthase, TsaB subunit
Other_Patl Macromol Macromolecule	EG7698	tsaC	0.46	0.353	L-threonylcarbamoyladenylate synthase
Other_Patl Macromol Macromolecule	EG7199	mnmc	0.054	-0.903	fused 5-methylaminomethyl-2-thiouridine-forming methyltransf
Other_Patl Macromol Macromolecule	EG11344	mnmA	-2.793	-0.336	tRNA-specific 2-thiouridyase
Other_Patl Macromol Macromolecule	EG7325	iscS	-1.254	0.693	cysteine desulfurase IscS
Other_Patl Macromol Macromolecule	EG6906	sufS	1.017	-0.397	L-cysteine desulfurase
Other_Patl Macromol Macromolecule	EG12876	tusE	-1.135	0.067	sulfur transfer protein TusE
Other_Patl Macromol Macromolecule	EG7714	tusD	-2.498	-0.176	sulfurtransferase complex subunit TusD
Other_Patl Macromol Macromolecule	EG10997	mnmc	-1.361	0.871	5-carboxymethylaminomethyluridine-tRNA synthase GTPase sul
Other_Patl Macromol Macromolecule	EG10375	mnmc	-0.824	0.232	5-carboxymethylaminomethyluridine-tRNA synthase subunit Mr
Other_Patl Macromol Macromolecule	EG10743	pnp	-0.553	-1.652	polynucleotide phosphorylase
Other_Patl Macromol Macromolecule	EG10862	rnpA	-3.14	1.013	RNase P protein component
Other_Patl Macromol Macromolecule	EG11547	rnt	-1.276	-1.165	RNase T
Other_Patl Macromol Macromolecule	EG10859	rne	-3.562	-0.662	ribonuclease E
Other_Patl Macromol Macromolecule	EG11393	dsbB	-2.303	0.749	protein thiol:quinone oxidoreductase DsbBReduced
Other_Patl Macromol Macromolecule	EG11112	aat	0.326	-0.603	leucyl/phenylalanyl-tRNA--protein transferase

Other_Patl	Macromo	Macromolecule	MEG12128	lgt	-2.209	1.733	phosphatidylglycerol--prolipoprotein diacylglyceryl transferase
Other_Patl	Macromo	Macromolecule	MEG10168	Int	-0.456	-0.325	apolipoprotein N-acyltransferase
Other_Patl	Macromo	Macromolecule	MEG12436	rseP	-0.733	-0.148	intramembrane zinc metalloprotease RseP
Other_Patl	Macromo	Macromolecule	MEG11096	yajC	-1.271	-0.86	Sec translocon accessory complex subunit YajC
Other_Patl	Macromo	Macromolecule	MEG10940	secF	-0.852	-0.815	Sec translocon accessory complex subunit SecF
Other_Patl	Macromo	Macromolecule	MEG10938	secD	-1.865	-1.123	Sec translocon accessory complex subunit SecD
Other_Patl	Macromo	Macromolecule	MEG10766	secY	-1.205	0.529	Sec translocon subunit SecY
Other_Patl	Macromo	Macromolecule	MEG12095	secG	-1.458	0.553	Sec translocon subunit SecG
Other_Patl	Macromo	Macromolecule	MEG10939	secE	0.521	1.014	Sec translocon subunit SecE
Other_Patl	Macromo	Macromolecule	MEG11197	yidC	-3.025	-0.122	membrane protein insertase YidC
Other_Patl	Macromo	Macromolecule	MEG11887	trxC	2.051	0.765	oxidized thioredoxin 2
Other_Patl	Macromo	Macromolecule	MEG11297	dsbA	0.94	1.065	thiol:disulfide oxidoreductase - DsbA reduced
Other_Patl	Activation	Activation/Inactivation	EG50003	acpP	0.524	0.277	octanoyl-ACP
Other_Patl	Activation	Activation/Inactivation	EG10260	entB	-2.806	-6.528	holo EntB
Other_Patl	Activation	Activation/Inactivation	EG10186	cysD	-2.495	1.049	sulfate adenylyltransferase subunit 2
Other_Patl	Activation	Activation/Inactivation	EG10194	cysN	-0.289	1.25	sulfate adenylyltransferase subunit 1
Other_Patl	Enzymes	Enzymes not in P	G7193	yfcF	-1.17	0.308	glutathione S-transferase YfcF
Other_Patl	Enzymes	Enzymes not in P	EG11281	mutL	-1.659	0.053	DNA mismatch repair protein MutL
Other_Patl	Enzymes	Enzymes not in P	EG10625	mutS	-1.27	-1.387	DNA mismatch repair protein MutS
Other_Patl	Enzymes	Enzymes not in P	G7456	tcdA	-1.675	0.87	tRNA threonylcarbamoyladenosine dehydratase
Other_Patl	Enzymes	Enzymes not in P	EG12401	rlmN	-0.233	0.183	23S rRNA m2A2503 methyltransferase/tRNA m2A37 methyltransferase
Other_Patl	Enzymes	Enzymes not in P	EG10159	clpX	0.221	0.699	ATP-dependent Clp protease ATP-binding subunit ClpX
Other_Patl	Enzymes	Enzymes not in P	EG10826	recD	-1.861	-0.186	exodeoxyribonuclease V subunit RecD
Other_Patl	Enzymes	Enzymes not in P	EG10825	recC	-0.755	-0.461	exodeoxyribonuclease V subunit RecC
Other_Patl	Enzymes	Enzymes not in P	EG10824	recB	-1.491	0.129	exodeoxyribonuclease V subunit RecB
Other_Patl	Enzymes	Enzymes not in P	G7641	rsml	-1.432	0.329	16S rRNA 2'-O-ribose C1402 methyltransferase
Other_Patl	Enzymes	Enzymes not in P	G6530	pgaB	-0.858	-0.229	poly- ϵ -1,6-N-acetyl-D-glucosamine N-deacetylase and ϵ -1,6
Other_Patl	Enzymes	Enzymes not in P	EG10690	pcnB	-2.447	0.164	poly(A) polymerase I
Other_Patl	Enzymes	Enzymes not in P	G7553	yghU	0.684	0.026	disulfide reductase / organic hydroperoxide reductase
Other_Patl	Enzymes	Enzymes not in P	G7682	degQ	-0.091	-0.064	periplasmic serine endoprotease

Other_Patl Enzymes Enzymes not in P	EG10830	recJ	-1.816	-0.258	ssDNA-specific exonuclease RecJ
Other_Patl Enzymes Enzymes not in P	EG10850	rimI	-1.499	1.11	protein N-acetyltransferase RimI
Other_Patl Enzymes Enzymes not in P	EG11507	rlmE	1.076	0.655	23S rRNA 2'-O-ribose U2552 methyltransferase
Other_Patl Enzymes Enzymes not in P	EG10225	dgt	0.955	0.573	dGTP triphosphohydrolase
Other_Patl Enzymes Enzymes not in P	EG10374	ggt	-0.378	-1.098	glutathione hydrolase, small subunit
Other_Patl Enzymes Enzymes not in P	EG10580	mepA	-2.092	-0.477	peptidoglycan DD-endopeptidase/peptidoglycan LD-endopeptidase
Other_Patl Enzymes Enzymes not in P	EG10215	deaD	-2.19	-2.847	ATP-dependent RNA helicase DeaD
Other_Patl Enzymes Enzymes not in P	EG11058	ung	-1.525	-0.126	uracil-DNA glycosylase
Other_Patl Enzymes Enzymes not in P	EG11211	epmA	0.395	0.053	EF-P-lysine lysyltransferase
Other_Patl Enzymes Enzymes not in P	EG11085	rsmH	-1.074	-0.3	16S rRNA m4C1402 methyltransferase
Other_Patl Enzymes Enzymes not in P	EG10423	gyrA	-1.844	-0.652	DNA gyrase subunit A
Other_Patl Enzymes Enzymes not in P	EG10424	gyrB	-0.001	-0.399	DNA gyrase subunit B
Other_Patl Enzymes Enzymes not in P	EG11298	yhdE	-3.027	-0.444	nucleoside triphosphate pyrophosphatase YhdE
Other_Patl Enzymes Enzymes not in P	EG10925	ruvC	-0.512	-0.508	crossover junction endodeoxyribonuclease RuvC
Other_Patl Enzymes Enzymes not in P	RUVA	ruvA	-0.836	0.414	Holliday junction branch migration complex subunit RuvA
Other_Patl Enzymes Enzymes not in P	G6329	ybdL	-0.625	-0.59	methionine transaminase
Other_Patl Enzymes Enzymes not in P	EG10697	pepP	-0.611	-0.53	Xaa-Pro aminopeptidase
Other_Patl Enzymes Enzymes not in P	EG11072	xseA	-0.219	0.056	exodeoxyribonuclease VII subunit XseA
Other_Patl Enzymes Enzymes not in P	EG11299	rng	-0.09	-0.469	RNase G
Other_Patl Enzymes Enzymes not in P	EG10156	clpA	0.392	-0.303	ATP-dependent Clp protease ATP-binding subunit ClpA
Other_Patl Enzymes Enzymes not in P	EG10182	cyoE	-0.598	-1.288	heme O synthase
Other_Patl Enzymes Enzymes not in P	G6634	yciV	1.546	-0.305	RNA/ssDNA 5',3' exonuclease
Other_Patl Enzymes Enzymes not in P	EG11436	ahr	-0.79	-0.205	NADPH-dependent aldehyde reductase Ahr
Other_Patl Enzymes Enzymes not in P	EG10454	truA	-1.379	0.887	tRNA pseudouridine38-40 synthase
Other_Patl Enzymes Enzymes not in P	EG11403	ppx	0.41	-0.213	exopolyphosphatase
Other_Patl Enzymes Enzymes not in P	EG11652	degS	0.495	0.555	serine endoprotease
Other_Patl Enzymes Enzymes not in P	EG10599	groL	-2.367	3.304	chaperonin GroEL
Other_Patl Enzymes Enzymes not in P	EG10600	groS	-2.666	4.238	cochaperonin GroES
Other_Patl Enzymes Enzymes not in P	EG10037	alkB	-0.524	1.243	DNA oxidative demethylase
Other_Patl Enzymes Enzymes not in P	G7842	orn	-1.098	-0.538	oligoribonuclease

Other_Patl Enzymes Enzymes not in P	G7319	der	-1.289	0.057	50S ribosomal subunit stability factor
Other_Patl Enzymes Enzymes not in P	EG12656	mdaB	-1.852	1.84	NADPH:quinone oxidoreductase MdaB
Other_Patl Enzymes Enzymes not in P	EG10844	rhIB	-1.567	0.352	ATP-dependent RNA helicase RhIB
Other_Patl Enzymes Enzymes not in P	G6435	rimO	-0.767	0.596	ribosomal protein S12 methylthiotransferase RimO
Other_Patl Enzymes Enzymes not in P	EG10662	nth	-0.162	0.537	endonuclease III
Other_Patl Enzymes Enzymes not in P	EG11362	gluQ	-1.063	0.77	glutamyl-Q tRNAAsp synthetase
Other_Patl Enzymes Enzymes not in P	EG11497	prmA	0.633	-0.374	ribosomal protein L11 methyltransferase
Other_Patl Enzymes Enzymes not in P	EG12207	rlmA	-0.442	-0.65	23S rRNA m1G745 methyltransferase
Other_Patl Enzymes Enzymes not in P	EG11758	nnr	-1.018	0.137	NAD(P)HX epimerase / NAD(P)HX dehydratase
Other_Patl Enzymes Enzymes not in P	EG10239	dnaG	0.3	-0.241	DNA primase
Other_Patl Enzymes Enzymes not in P	EG12449	prmB	-1.534	-0.361	50S ribosomal subunit protein L3 N5-glutamine methyltransferase
Other_Patl Enzymes Enzymes not in P	EG11177	truB	0.042	0.069	tRNA pseudouridine55 synthase
Other_Patl Enzymes Enzymes not in P	EG11166	ygiD	0.511	0.767	4,5-DOPA dioxygenase extradiol
Other_Patl Enzymes Enzymes not in P	EG10529	lepA	-0.673	0.031	30S ribosomal subunit biogenesis factor LepA
Other_Patl Enzymes Enzymes not in P	EG10595	miaA	-0.344	1.252	tRNA dimethylallyltransferase
Other_Patl Enzymes Enzymes not in P	EG11247	rlmD	-0.976	2.425	23S rRNA m5U1939 methyltransferase
Other_Patl Enzymes Enzymes not in P	EG11268	fmt	-0.42	0.251	10-formyltetrahydrofolate:L-methionyl-tRNA ^{fMet} N-formyltransferase
Other_Patl Enzymes Enzymes not in P	EG10757	ppiA	-0.905	-0.928	peptidyl-prolyl cis-trans isomerase A
Other_Patl Enzymes Enzymes not in P	EG11613	eptA	-0.706	0.055	phosphoethanolamine transferase EptA
Other_Patl Enzymes Enzymes not in P	EG10986	tag	-0.699	-0.289	3-methyl-adenine DNA glycosylase I, constitutive
Other_Patl Enzymes Enzymes not in P	EG10136	cca	0.489	0.563	fused CCA tRNA nucleotidyltransferase/phosphohydrolase
Other_Patl Enzymes Enzymes not in P	EG10785	pth	-1.544	1.147	peptidyl-tRNA hydrolase
Other_Patl Enzymes Enzymes not in P	EG12394	msrB	0.198	0.18	methionine sulfoxide reductase B
Other_Patl Enzymes Enzymes not in P	EG11118	rluC	1.347	-1.007	23S rRNA pseudouridine955/2504/2580 synthase
Other_Patl Enzymes Enzymes not in P	EG11494	mltG	0.025	-0.551	endolytic murein transglycosylase
Other_Patl Enzymes Enzymes not in P	EG10376	rsmG	-2.15	-0.341	16S rRNA m7G527 methyltransferase
Other_Patl Enzymes Enzymes not in P	EG10456	hmp	-0.795	1.432	nitric oxide dioxygenase
Other_Patl Enzymes Enzymes not in P	EG12233	rsmJ	-1.024	0.917	16S rRNA m2G1516 methyltransferase
Other_Patl Enzymes Enzymes not in P	EG11404	ychF	-0.148	1.8	redox-responsive ATPase YchF
Other_Patl Enzymes Enzymes not in P	G6096	tilS	-1.851	-0.559	tRNA ^{Ala} -lysine synthetase

Other_Patl Enzymes Enzymes not in P	EG10826	recD	-1.861	-0.186	exodeoxyribonuclease V subunit RecD
Other_Patl Enzymes Enzymes not in P	EG12130	hscA	-1.569	0.685	iron-sulfur cluster biosynthesis chaperone HscA
Other_Patl Enzymes Enzymes not in P	G7647	yhbO	-0.602	0.194	protein/nucleic acid deglycase 2
Other_Patl Enzymes Enzymes not in P	EG11003	tig	-2.353	0.398	trigger factor
Other_Patl Enzymes Enzymes not in P	EG12433	rluB	0.924	0.183	23S rRNA pseudouridine2605 synthase
Other_Patl Enzymes Enzymes not in P	G6890	nemaA	1.149	0.75	N-ethylmaleimide reductase
Other_Patl Enzymes Enzymes not in P	EG10397	glpG	-1.12	0.415	rhomboid protease GlpG
Other_Patl Enzymes Enzymes not in P	EG12880	dgcN	-1.174	-0.954	diguanylate cyclase DgcN
Other_Patl Enzymes Enzymes not in P	G6488	rlmL	0.17	-0.021	fused 23S rRNA m2G2445 methyltransferase and 23S rRNA m7G2445 methyltransferase
Other_Patl Enzymes Enzymes not in P	EG10523	rsmA	1.51	-0.022	16S rRNA m62A1518,m62A1519 dimethyltransferase
Other_Patl Enzymes Enzymes not in P	EG12022	dusC	-1.022	1.376	tRNA-dihydrouridine16 synthase
Other_Patl Enzymes Enzymes not in P	G6518	rutF	0.407	0.155	FMN reductase RutF
Other_Patl Enzymes Enzymes not in P	EG10829	recG	-1.864	-0.102	ATP-dependent DNA helicase RecG
Other_Patl Enzymes Enzymes not in P	G6806	tam	-1.597	0.234	trans-aconitate 2-methyltransferase
Other_Patl Enzymes Enzymes not in P	EG10746	polA	0.763	-0.118	DNA polymerase I
Other_Patl Enzymes Enzymes not in P	EG12097	pgeF	0.58	1.171	polyphenol oxidase YfiH
Other_Patl Enzymes Enzymes not in P	EG10343	rsmD	1.086	0.187	16S rRNA m2G966 methyltransferase
Other_Patl Enzymes Enzymes not in P	EG10736	phr	1.34	-0.289	deoxyribodipyrimidine photolyase
Other_Patl Enzymes Enzymes not in P	EG11022	trmA	-0.736	-0.816	tRNA m5U54 methyltransferase
Other_Patl Enzymes Enzymes not in P	EG10043	cysQ	0.979	-0.124	3'(2'),5'-bisphosphate nucleotidase
Other_Patl Enzymes Enzymes not in P	G7841	rsgA	0.638	-0.12	ribosome small subunit-dependent GTPase A
Other_Patl Enzymes Enzymes not in P	G7324	iscU	-0.998	1.951	scaffold protein for iron-sulfur cluster assembly
Other_Patl Enzymes Enzymes not in P	G7836	epmB	-0.452	-0.834	lysine 2,3-aminomutase
Other_Patl Enzymes Enzymes not in P	EG10270	era	-0.458	0.651	30S ribosomal subunit maturation GTPase Era
Other_Patl Enzymes Enzymes not in P	G7410	mltB	-1.328	-0.087	membrane-bound lytic murein transglycosylase B
Other_Patl Enzymes Enzymes not in P	EG10224	dgkA	-3.379	-0.259	diacylglycerol kinase
Other_Patl Enzymes Enzymes not in P	EG10437	hflX	-0.096	-0.265	ribosome rescue factor HflX
Other_Patl Enzymes Enzymes not in P	EG10668	ogt	-0.261	0.181	methylated-DNA--[protein]-cysteine S-methyltransferase
Other_Patl Enzymes Enzymes not in P	G6675	ttcA	-2.051	0.156	tRNA cytosine32 2-sulfurtransferase TtcA
Other_Patl Enzymes Enzymes not in P	EG10530	lepB	0.02	-0.907	signal peptidase I

Other_Patl Enzymes Enzymes not in P	EG11932	dusA	1.003	-0.429	tRNA-dihydrouridine synthase A
Other_Patl Enzymes Enzymes not in P	EG11063	uvrC	-0.598	1.971	excision nuclease subunit C
Other_Patl Enzymes Enzymes not in P	EG11061	uvrA	-1.562	1.685	excision nuclease subunit A
Other_Patl Enzymes Enzymes not in P	EG12234	rlmJ	-0.622	-0.04	23S rRNA m6A2030 methyltransferase
Other_Patl Enzymes Enzymes not in P	G7716	fkpA	-0.055	0.232	peptidyl-prolyl cis-trans isomerase FkpA
Other_Patl Enzymes Enzymes not in P	EG10129	btuE	-0.996	-1.022	thioredoxin/glutathione peroxidase
Other_Patl Enzymes Enzymes not in P	EG10694	pepA	-0.29	-0.865	aminopeptidase A/I
Other_Patl Enzymes Enzymes not in P	EG10857	rnc	0.713	0.351	RNase III
Other_Patl Enzymes Enzymes not in P	EG10824	recB	-1.491	0.129	exodeoxyribonuclease V subunit RecB
Other_Patl Enzymes Enzymes not in P	G6115	dinB	0.682	0.6	DNA polymerase IV
Other_Patl Enzymes Enzymes not in P	EG10238	dnaE	-0.288	-0.711	DNA polymerase III subunit ϵ
Other_Patl Enzymes Enzymes not in P	EG11023	trmD	-0.947	0.051	tRNA m1G37 methyltransferase
Other_Patl Enzymes Enzymes not in P	EG10860	rnhA	-0.099	-0.23	ribonuclease HI
Other_Patl Enzymes Enzymes not in P	G6437	ylil	0.451	0.014	aldose sugar dehydrogenase Ylil
Other_Patl Enzymes Enzymes not in P	EG10950	slt	-0.969	0.428	soluble lytic murein transglycosylase
Other_Patl Enzymes Enzymes not in P	EG12098	rluD	-0.369	0.687	23S rRNA pseudouridine1911/1915/1917 synthase
Other_Patl Enzymes Enzymes not in P	EG11372	tadA	-0.655	-1.485	tRNA adenosine34 deaminase
Other_Patl Enzymes Enzymes not in P	EG10048	apaH	-1.148	0.322	diadenosine tetraphosphatase
Other_Patl Enzymes Enzymes not in P	EG10985	surA	-0.337	-0.135	chaperone SurA
Other_Patl Enzymes Enzymes not in P	EG10156	clpA	0.392	-0.303	ATP-dependent Clp protease ATP-binding subunit ClpA
Other_Patl Enzymes Enzymes not in P	EG10159	clpX	0.221	0.699	ATP-dependent Clp protease ATP-binding subunit ClpX
Other_Patl Enzymes Enzymes not in P	EG10834	recR	-0.47	-0.759	DNA repair protein RecR
Other_Patl Enzymes Enzymes not in P	EG10832	recO	-0.769	-0.246	DNA repair protein RecO
Other_Patl Enzymes Enzymes not in P	EG12424	prmC	-1.02	-0.329	protein-(glutamine-N5) methyltransferase
Other_Patl Enzymes Enzymes not in P	EG11428	sthA	-0.715	0.024	soluble pyridine nucleotide transhydrogenase
Other_Patl Enzymes Enzymes not in P	G6988	yeaW	-1.108	1.766	carnitine monooxygenase subunit YeaW
Other_Patl Enzymes Enzymes not in P	G7327	trmJ	-2.075	-0.343	tRNA Cm32/Um32 methyltransferase
Other_Patl Enzymes Enzymes not in P	EG11819	purU	0.397	-0.257	formyltetrahydrofolate deformylase
Other_Patl Enzymes Enzymes not in P	G7950	rsmC	-1.283	-0.609	16S rRNA m2G1207 methyltransferase
Other_Patl Enzymes Enzymes not in P	EG11291	loiP	0.149	0.119	metalloprotease LoiP

Other_Patl Enzymes Enzymes not in P	EG11311	dusB	-2.096	-0.355	tRNA-dihydrouridine synthase B
Other_Patl Enzymes Enzymes not in P	EG10627	mutY	-0.902	-0.025	adenine DNA glycosylase
Other_Patl Enzymes Enzymes not in P	EG11506	ftsH	0.675	0.469	ATP-dependent zinc metalloprotease FtsH
Other_Patl Enzymes Enzymes not in P	EG10760	prc	0.012	-0.244	tail-specific protease
Other_Patl Enzymes Enzymes not in P	EG11433	msrA	0.515	0.277	methionine sulfoxide reductase A
Other_Patl Enzymes Enzymes not in P	EG11254	rlmH	-2.51	-0.43	23S rRNA m3C ¹⁹¹⁵ methyltransferase
Other_Patl Enzymes Enzymes not in P	EG12163	rsmB	-1.635	-0.435	16S rRNA m5C967 methyltransferase
Other_Patl Enzymes Enzymes not in P	EG10861	rnhB	-0.146	-0.281	RNase HII
Other_Patl Enzymes Enzymes not in P	G7525	yqgF	1.245	-0.145	ribonuclease H-like domain containing nuclease
Other_Patl Enzymes Enzymes not in P	EG12044	rsuA	-2.31	-0.61	16S rRNA pseudouridine516 synthase
Other_Patl Enzymes Enzymes not in P	EG11871	gph	-0.971	-0.101	phosphoglycolate phosphatase
Other_Patl Enzymes Enzymes not in P	G6136	mmuM	0.225	-1.181	CP4-6 prophage; homocysteine S-methyltransferase
Other_Patl Enzymes Enzymes not in P	EG11080	fkpB	0.675	0.045	peptidyl-prolyl cis-trans isomerase FkpB
Other_Patl Enzymes Enzymes not in P	EG11852	dtd	-1.017	1.039	D-aminoacyl-tRNA deacylase
Other_Patl Enzymes Enzymes not in P	EG10240	dnaJ	0.834	3.71	chaperone protein DnaJ
Other_Patl Enzymes Enzymes not in P	EG11503	trmO	-2.79	-0.36	tRNA m6t6A37 methyltransferase
Other_Patl Enzymes Enzymes not in P	EG10329	mutM	-0.431	0.188	DNA-formamidopyrimidine glycosylase
Other_Patl Enzymes Enzymes not in P	EG10893	rpoA	-2.18	0.563	RNA polymerase subunit α
Other_Patl Enzymes Enzymes not in P	EG10895	rpoC	-0.146	-0.827	RNA polymerase subunit α'
Other_Patl Enzymes Enzymes not in P	EG10894	rpoB	-1.791	-0.953	RNA polymerase subunit α
Other_Patl Enzymes Enzymes not in P	EG11259	rnr	0.418	-0.175	RNase R
Other_Patl Enzymes Enzymes not in P	EG10995	tesB	0.901	0.693	acyl-CoA thioesterase II
Other_Patl Enzymes Enzymes not in P	EG50005	nfsB	-0.713	-0.053	NAD(P)H nitroreductase NfsB
Degradatic Amino Acid	EG11408	dadX	-1.042	-2.067	alanine racemase 2
Degradatic Amino Acid	G6755	patD	-0.349	2.859	α -aminobutyraldehyde dehydrogenase
Degradatic Amino Acid	G6644	puuA	-2.269	0.797	glutamate-putrescine ligase
Degradatic Amino Acid	EG10046	ansB	-0.076	0.21	L-asparaginase 2
Degradatic Amino Acid	EG10045	ansA	-3.497	0.269	L-asparaginase 1
Degradatic Amino Acid	EG10193	cysM	-0.615	0.467	cysteine synthase B
Degradatic Amino Acid	EG11887	trxC	2.051	0.765	oxidized thioredoxin 2

Degradatic Amino Acid	Amino Acid	EG10403	gltB	-1.41	-0.121	glutamate synthase subunit GltB
Degradatic Amino Acid	Amino Acid	EG10404	gltD	-0.677	1.668	glutamate synthase subunit GltD
Degradatic Amino Acid	Amino Acid	EG10420	guaA	-1.857	0.273	GMP synthetase
Degradatic Amino Acid	Amino Acid	EG10450	hisH	-1.627	0.564	imidazole glycerol phosphate synthase subunit HisH
Degradatic Amino Acid	Amino Acid	EG10448	hisF	-1.349	0.401	imidazole glycerol phosphate synthase subunit HisF
Degradatic Amino Acid	Amino Acid	EG10095	aspA	-0.4	0.082	aspartate ammonia-lyase
Degradatic Amino Acid	Amino Acid	EG10371	gcvH	0.207	-0.227	lipoyl-GcvH-protein
Degradatic Amino Acid	Amino Acid	G6646	puuE	-3.029	3.456	4-aminobutyrate aminotransferase PuuE
Degradatic Amino Acid	Amino Acid	EG10801	putA	-0.647	-0.46	fused DNA-binding transcriptional repressor / proline dehydrogenase
Degradatic Amino Acid	Amino Acid	EG10990	tdcB	0.034	0.312	catabolic threonine dehydratase
Degradatic Amino Acid	Amino Acid	EG10930	sdaA	0.895	-0.512	L-serine deaminase I
Degradatic Amino Acid	Amino Acid	EG20173	pta	-1.402	-0.828	phosphate acetyltransferase
Degradatic Amino Acid	Amino Acid	EG10027	ackA	0.051	-0.046	acetate kinase
Degradatic Amino Acid	Amino Acid	EG10496	ilvD	-3.398	0.755	dihydroxy-acid dehydratase
Degradatic Amino Acid	Amino Acid	EG10497	ilvE	-1.772	-1.955	branched-chain-amino-acid aminotransferase
Degradatic Amino Acid	Amino Acid	EG10495	ilvC	0.281	-0.473	ketol-acid reductoisomerase (NADP+)
Degradatic Amino Acid	Amino Acid	EG10499	ilvH	2.498	-0.422	acetolactate synthase / acetohydroxybutanoate synthase, regulatory
Degradatic Nucleoside	Nucleoside and Nucleotide	EG7742	yrfG	0.76	0.573	purine nucleotidase
Degradatic Nucleoside	Nucleoside and Nucleotide	EG12159	ppnP	-0.031	0.369	nucleoside phosphorylase PpnP
Degradatic Nucleoside	Nucleoside and Nucleotide	EG10030	add	-1.259	-0.114	adenosine deaminase
Degradatic Nucleoside	Nucleoside and Nucleotide	EG12345	ydfG	-0.241	0.421	3-hydroxy acid dehydrogenase YdfG
Degradatic Nucleoside	Nucleoside and Nucleotide	EG10572	mazG	-1.665	0.19	nucleoside triphosphate pyrophosphohydrolase
Degradatic Nucleoside	Nucleoside and Nucleotide	EG10251	dut	-1.848	0.839	dUTP diphosphatase
Degradatic Fatty Acid	Fatty Acid and Lipid	EG11530	fadD	1.067	-1.658	long-chain-fatty-acid--CoA ligase
Degradatic Fatty Acid	Fatty Acid and Lipid	G7213	fadI	-0.488	0.196	3-ketoacyl-CoA thiolase FadI
Degradatic Fatty Acid	Fatty Acid and Lipid	G6105	fadE	0.82	-0.591	acyl-CoA dehydrogenase
Degradatic Fatty Acid	Fatty Acid and Lipid	EG10279	fadB	-0.067	0.034	multifunctional enoyl-CoA hydratase, 3-hydroxyacyl-CoA epimerase
Degradatic Fatty Acid	Fatty Acid and Lipid	EG10398	glpK	0.274	-0.238	glycerol kinase
Degradatic Fatty Acid	Fatty Acid and Lipid	EG10394	glpD	0.381	0.052	aerobic glycerol 3-phosphate dehydrogenase
Degradatic Amine and Polyamine	Amine and Polyamine	G6646	puuE	-3.029	3.456	4-aminobutyrate aminotransferase PuuE

Degradatic Amine an	Amine and Polya	EG20173	pta	-1.402	-0.828	phosphate acetyltransferase
Degradatic Amine an	Amine and Polya	EG10027	ackA	0.051	-0.046	acetate kinase
Degradatic Amine an	Amine and Polya	EG11809	purT	-0.365	-0.318	phosphoribosylglycinamide formyltransferase 2
Degradatic Amine an	Amine and Polya	G6755	patD	-0.349	2.859	CE≥-aminobutyraldehyde dehydrogenase
Degradatic Amine an	Amine and Polya	G6644	puuA	-2.269	0.797	glutamate-putrescine ligase
Degradatic Carbohydr	Carbohydrates/C	EG12198	chbG	1.838	0.718	chitin disaccharide deacetylase
Degradatic Carbohydr	Carbohydrates/C	EG10348	fucA	-0.036	0.298	L-fuculose-phosphate aldolase
Degradatic Carbohydr	Carbohydrates/C	EG10256	eda	-0.306	-0.472	KHG/KDPG aldolase
Degradatic Carbohydr	Carbohydrates/C	EG10257	edd	0.795	-0.31	phosphogluconate dehydratase
Degradatic Carbohydr	Carbohydrates/C	EG11319	galU	-1.393	0.37	UTP--glucose-1-phosphate uridylyltransferase
Degradatic Carbohydr	Carbohydrates/C	G6425	ybiV	-0.548	-0.937	sugar phosphatase YbiV
Degradatic Carbohydr	Carbohydrates/C	EG10369	gcd	1.48	-1.72	quinoprotein glucose dehydrogenase
Degradatic Carbohydr	Carbohydrates/C	EG12629	gntK	-0.039	-0.993	D-gluconate kinase, thermostable
Degradatic Carbohydr	Carbohydrates/C	G6986	dmlA	0.049	-0.239	D-malate/3-isopropylmalate dehydrogenase (decarboxylating)
Degradatic Carbohydr	Carbohydrates/C	EG10027	ackA	0.051	-0.046	acetate kinase
Degradatic Carbohydr	Carbohydrates/C	EG20173	pta	-1.402	-0.828	phosphate acetyltransferase
Degradatic Carbohydr	Carbohydrates/C	EG11530	fadD	1.067	-1.658	long-chain-fatty-acid--CoA ligase
Degradatic Carbohydr	Carbohydrates/C	EG12316	acnB	-0.873	-1.09	AcnB
Degradatic Carbohydr	Carbohydrates/C	EG10024	aceE	-1.803	-0.003	pyruvate dehydrogenase E1 component
Degradatic Carbohydr	Carbohydrates/C	EG12522	garD	0.866	-0.44	GarD
Degradatic Carbohydr	Carbohydrates/C	G7445	gudD	1.446	-0.694	D-glucarate dehydratase
Degradatic Carbohydr	Carbohydrates/C	EG11648	dkgB	-1.19	0.883	methylglyoxal reductase DkgB
Degradatic Carbohydr	Carbohydrates/C	EG12272	ghrB	0.916	-0.416	glyoxylate reductase
Degradatic Secondary	Secondary Meta	G6880	anmK	-1.086	-0.543	anhydro-N-acetylmuramic acid kinase
Degradatic Secondary	Secondary Meta	G6567	nagZ	-0.56	-0.198	CE≤-N-acetylhexosaminidase
Degradatic Secondary	Secondary Meta	EG10041	ampD	-3.758	-0.593	1,6-anhydro-N-acetylmuramoyl-L-alanine amidase
Degradatic Secondary	Secondary Meta	EG11553	glmM	-1.071	-0.191	phosphoglucosamine mutase
Degradatic Secondary	Secondary Meta	EG11198	glmU	-0.787	-0.277	fused N-acetylglucosamine-1-phosphate uridyltransferase and g
Degradatic Secondary	Secondary Meta	EG12440	mpl	-1.659	0.434	UDP-N-acetylmuramate--L-alanyl-CE≥-D-glutamyl-meso-2,6-dia
Degradatic Secondary	Secondary Meta	EG11358	murA	-2.398	-0.867	UDP-N-acetylglucosamine 1-carboxyvinyltransferase

Degradatic Secondary Secondary Metabolite	EG11205	murB	-1.449	-1.07	UDP-N-acetylenolpyruvoylglucosamine reductase
Degradatic Secondary Secondary Metabolite	EG12416	gatC	-1.457	0.161	galactitol-specific PTS enzyme IIC component
Degradatic Secondary Secondary Metabolite	EG12415	gatB	-0.862	-0.022	galactitol-specific PTS enzyme IIB component
Degradatic Secondary Secondary Metabolite	EG10616	mtlD	-0.337	-1.079	mannitol-1-phosphate 5-dehydrogenase
Degradatic Alcohol Degradation	EG10398	glpK	0.274	-0.238	glycerol kinase
Degradatic Alcohol Degradation	EG10399	glpQ	-0.273	0.181	glycerophosphoryl diester phosphodiesterase GlpQ
Degradatic Alcohol Degradation	EG11050	ugpQ	1.275	-0.56	glycerophosphodiester phosphodiesterase UgpQ
Degradatic Alcohol Degradation	EG10394	glpD	0.381	0.052	aerobic glycerol 3-phosphate dehydrogenase
Degradatic Aromatic Aromatic Compound	M012	mhpC	0.297	0.646	2-hydroxy-6-ketono-2,4-dienedioate hydrolase
Degradatic Aromatic Aromatic Compound	G6713	paaE	-4.088	1.196	phenylacetyl-CoA 1,2-epoxidase, reductase subunit
Degradatic Aromatic Aromatic Compound	G6709	paaA	-5.021	1.126	phenylacetyl-CoA 1,2-epoxidase, monooxygenase subunit
Degradatic Aromatic Aromatic Compound	G6711	paaC	-4.822	1.134	phenylacetyl-CoA 1,2-epoxidase, structural subunit
Degradatic Aromatic Aromatic Compound	G6710	paaB	-3.909	1.115	phenylacetyl-CoA 1,2-epoxidase subunit B
Degradatic Aromatic Aromatic Compound	G6718	paaJ	-3.848	0.427	CoA-ketoadipyl-CoA thiolase
Degradatic Aromatic Aromatic Compound	G6715	paaG	-3.55	0.88	putative ring 1,2-epoxyphenylacetyl-CoA isomerase (oxepin-CoA
Degradatic Aromatic Aromatic Compound	G6708	paaZ	-3.501	0.382	fused 3-oxo-5,6-dehydrosuberil-CoA semialdehyde dehydrogenase
Degradatic Aromatic Aromatic Compound	G6719	paaK	-2.225	0.205	phenylacetate-CoA ligase
Degradatic Polymeric Polymeric Compound	EG10695	pepD	-2.925	0.275	peptidase D
Degradatic Other Degradation	EG10249	dsdA	0.03	0.826	D-serine ammonia-lyase
Biosynthesis Amino Acid Amino Acid	G7325	iscS	-1.254	0.693	cysteine desulfurase IscS
Biosynthesis Amino Acid Amino Acid	G6906	sufS	1.017	-0.397	L-cysteine desulfurase
Biosynthesis Amino Acid Amino Acid	G7184	alaA	-1.27	-0.396	glutamate--pyruvate aminotransferase AlaA
Biosynthesis Amino Acid Amino Acid	EG10497	ilvE	-1.772	-1.955	branched-chain-amino-acid aminotransferase
Biosynthesis Amino Acid Amino Acid	EG10068	argG	-0.453	0.295	argininosuccinate synthetase
Biosynthesis Amino Acid Amino Acid	EG11223	argH	-1.247	-0.644	argininosuccinate lyase
Biosynthesis Amino Acid Amino Acid	EG10063	argA	-1.559	0.108	N-acetylglutamate synthase
Biosynthesis Amino Acid Amino Acid	EG10064	argB	-1.92	0.471	acetylglutamate kinase
Biosynthesis Amino Acid Amino Acid	EG10065	argC	-3.216	-0.642	N-acetylglutamylphosphate reductase
Biosynthesis Amino Acid Amino Acid	EG10066	argD	0.184	0.114	N-acetylornithine aminotransferase / N-succinyldiaminopimelate
Biosynthesis Amino Acid Amino Acid	EG10193	cysM	-0.615	0.467	cysteine synthase B

Biosynthes Amino Ac	Amino Acid	EG10187	cysE	-0.596	0.366	serine acetyltransferase
Biosynthes Amino Ac	Amino Acid	EG12294	grxC	0.206	2.129	oxidized glutaredoxin 3
Biosynthes Amino Ac	Amino Acid	EG10403	gltB	-1.41	-0.121	glutamate synthase subunit GltB
Biosynthes Amino Ac	Amino Acid	EG10404	gltD	-0.677	1.668	glutamate synthase subunit GltD
Biosynthes Amino Ac	Amino Acid	EG10408	glyA	-2.967	0.691	serine hydroxymethyltransferase
Biosynthes Amino Ac	Amino Acid	EG10447	hisD	-1.215	-1.022	histidinal/histidinol dehydrogenase
Biosynthes Amino Ac	Amino Acid	EG10445	hisB	-2.951	0.393	imidazoleglycerol-phosphate dehydratase / histidinol-phosphatase
Biosynthes Amino Ac	Amino Acid	EG10450	hisH	-1.627	0.564	imidazole glycerol phosphate synthase subunit HisH
Biosynthes Amino Ac	Amino Acid	EG10448	hisF	-1.349	0.401	imidazole glycerol phosphate synthase subunit HisF
Biosynthes Amino Ac	Amino Acid	EG10444	hisA	-0.548	0.029	1-(5-phosphoribosyl)-5-[(5-phosphoribosylamino)methylideneamino]imidazole ribotide synthase
Biosynthes Amino Ac	Amino Acid	EG10451	hisI	-1.133	-0.766	putative bifunctional phosphoribosyl-AMP cyclohydrolase/phosphoribosyltransferase
Biosynthes Amino Ac	Amino Acid	EG10449	hisG	-1.931	-0.738	ATP phosphoribosyltransferase
Biosynthes Amino Ac	Amino Acid	EG10496	ilvD	-3.398	0.755	dihydroxy-acid dehydratase
Biosynthes Amino Ac	Amino Acid	EG10495	ilvC	0.281	-0.473	ketol-acid reductoisomerase (NADP+) (ilvC)
Biosynthes Amino Ac	Amino Acid	EG10499	ilvH	2.498	-0.422	acetolactate synthase / acetohydroxybutanoate synthase, regulated
Biosynthes Amino Ac	Amino Acid	EG10493	ilvA	-1.538	-0.36	threonine deaminase
Biosynthes Amino Ac	Amino Acid	EG11577	leuB	0.548	-0.014	3-isopropylmalate dehydrogenase
Biosynthes Amino Ac	Amino Acid	G6986	dmlA	0.049	-0.239	D-malate/3-isopropylmalate dehydrogenase (decarboxylating)
Biosynthes Amino Ac	Amino Acid	EG11576	leuC	-0.084	1.821	3-isopropylmalate dehydratase subunit LeuC
Biosynthes Amino Ac	Amino Acid	EG10209	dapF	-0.592	0.528	diaminopimelate epimerase
Biosynthes Amino Ac	Amino Acid	EG10549	lysA	1.177	-0.044	diaminopimelate decarboxylase
Biosynthes Amino Ac	Amino Acid	EG10208	dapE	1.463	0.274	succinyl-diaminopimelate desuccinylase
Biosynthes Amino Ac	Amino Acid	EG10946	serC	-0.473	-0.349	phosphoserine/phosphohydroxythreonine aminotransferase
Biosynthes Amino Ac	Amino Acid	EG10207	dapD	-0.767	0.573	tetrahydrodipicolinate succinylase
Biosynthes Amino Ac	Amino Acid	EG10206	dapB	1.053	0.596	4-hydroxy-tetrahydrodipicolinate reductase
Biosynthes Amino Ac	Amino Acid	EG10587	metH	-0.146	0.823	cobalamin-dependent methionine synthase
Biosynthes Amino Ac	Amino Acid	EG10707	pheA	-1.232	0.212	fused chorismate mutase/prephenate dehydratase
Biosynthes Amino Ac	Amino Acid	EG10768	proB	-2.066	-0.743	glutamate 5-kinase
Biosynthes Amino Ac	Amino Acid	EG10947	serS	-1.033	-0.112	serine--tRNA ligase
Biosynthes Amino Ac	Amino Acid	EG10944	serA	0.354	0.313	phosphoglycerate dehydrogenase

Biosynthes Amino Ac	Amino Acid	EG10999	thrB	-1.009	0.011	homoserine kinase
Biosynthes Amino Ac	Amino Acid	EG11000	thrC	0.237	-0.236	threonine synthase
Biosynthes Amino Ac	Amino Acid	EG11026	trpC	-2.361	0.871	fused indole-3-glycerol phosphate synthase/phosphoribosylanth
Biosynthes Amino Ac	Amino Acid	EG11028	trpE	-3.801	0.11	anthranilate synthase subunit TrpE
Biosynthes Amino Ac	Amino Acid	EG11024	trpA	-2.399	0.371	tryptophan synthase subunit α
Biosynthes Nucleosid	Nucleoside/Nucle	EG11809	purT	-0.365	-0.318	phosphoribosylglycinamide formyltransferase 2
Biosynthes Nucleosid	Nucleoside/Nucle	EG10794	purF	-0.892	1.723	amidophosphoribosyltransferase
Biosynthes Nucleosid	Nucleoside/Nucle	EG10792	purD	-0.47	-0.804	phosphoribosylamine--glycine ligase
Biosynthes Nucleosid	Nucleoside/Nucle	EG10799	purN	-2.398	0.496	phosphoribosylglycinamide formyltransferase 1
Biosynthes Nucleosid	Nucleoside/Nucle	EG10797	purL	-2.774	1.427	phosphoribosylformylglycinamide synthetase
Biosynthes Nucleosid	Nucleoside/Nucle	EG10798	purM	-3.537	1.548	phosphoribosylformylglycinamide cyclo-ligase
Biosynthes Nucleosid	Nucleoside/Nucle	EG10421	guaB	-0.735	0.68	inosine 5'-monophosphate dehydrogenase
Biosynthes Nucleosid	Nucleoside/Nucle	EG10420	guaA	-1.857	0.273	GMP synthetase
Biosynthes Nucleosid	Nucleoside/Nucle	EG10965	gmK	-0.246	-0.364	guanylate kinase
Biosynthes Nucleosid	Nucleoside/Nucle	EG10661	nrdB	-2.608	0.397	ribonucleoside-diphosphate reductase 1 subunit α
Biosynthes Nucleosid	Nucleoside/Nucle	EG10650	ndk	-2.887	0.526	nucleoside diphosphate kinase
Biosynthes Nucleosid	Nucleoside/Nucle	EG11887	trxC	2.051	0.765	oxidized thioredoxin 2
Biosynthes Nucleosid	Nucleoside/Nucle	EG10030	add	-1.259	-0.114	adenosine deaminase
Biosynthes Nucleosid	Nucleoside/Nucle	EG10791	purC	-0.285	-0.494	phosphoribosylaminoimidazole-succinocarboxamide synthase
Biosynthes Nucleosid	Nucleoside/Nucle	EG10795	purH	-2.619	-1.683	bifunctional AICAR transformylase/IMP cyclohydrolase
Biosynthes Nucleosid	Nucleoside/Nucle	EG10793	purE	-2.377	0.876	N5-carboxyaminoimidazole ribonucleotide mutase
Biosynthes Nucleosid	Nucleoside/Nucle	EG10796	purK	-1.224	0.745	5-(carboxyamino)imidazole ribonucleotide synthase
Biosynthes Nucleosid	Nucleoside/Nucle	EG20098	hpt	0.019	-0.516	hypoxanthine phosphoribosyltransferase
Biosynthes Nucleosid	Nucleoside/Nucle	EG12159	ppnP	-0.031	0.369	nucleoside phosphorylase PpnP
Biosynthes Nucleosid	Nucleoside/Nucle	EG10790	purA	-0.652	-1.525	adenylosuccinate synthetase
Biosynthes Nucleosid	Nucleoside/Nucle	EG11314	purB	-3.834	-1.376	adenylosuccinate lyase
Biosynthes Nucleosid	Nucleoside/Nucle	EG10032	adk	-3.243	-0.148	adenylate kinase
Biosynthes Nucleosid	Nucleoside/Nucle	EG11418	dcd	-1.016	0.373	dCTP deaminase
Biosynthes Nucleosid	Nucleoside/Nucle	EG10572	mazG	-1.665	0.19	nucleoside triphosphate pyrophosphohydrolase
Biosynthes Nucleosid	Nucleoside/Nucle	EG10251	dut	-1.848	0.839	dUTP diphosphatase

Biosynthes Nucleosid Nucleoside/Nucleotide	EG11002	thyA	-0.966	-0.248	thymidylate synthase
Biosynthes Nucleosid Nucleoside/Nucleotide	EG12302	tmk	0.7	-0.258	Tmk
Biosynthes Nucleosid Nucleoside/Nucleotide	EG10805	pyrB	-0.876	1.419	aspartate carbamoyltransferase catalytic subunit
Biosynthes Nucleosid Nucleoside/Nucleotide	EG10806	pyrC	-0.677	-0.487	dihydroorotase
Biosynthes Nucleosid Nucleoside/Nucleotide	EG10808	pyrE	-1.335	0.321	orotate phosphoribosyltransferase
Biosynthes Nucleosid Nucleoside/Nucleotide	EG10809	pyrF	1.959	0.593	orotidine-5'-phosphate decarboxylase
Biosynthes Nucleosid Nucleoside/Nucleotide	EG10807	pyrD	-0.102	0.623	dihydroorotate dehydrogenase, type 2
Biosynthes Nucleosid Nucleoside/Nucleotide	EG11539	pyrH	-3.024	-0.327	UMP kinase
Biosynthes Nucleosid Nucleoside/Nucleotide	EG11265	cmk	0.346	0.562	cytidylate kinase
Biosynthes Nucleosid Nucleoside/Nucleotide	EG11332	upp	-0.001	0.803	uracil phosphoribosyltransferase
Biosynthes Fatty Acid Fatty Acid/Lipid	EG50003	acpP	0.524	0.277	octanoyl-ACP
Biosynthes Fatty Acid Fatty Acid/Lipid	EG10123	birA	1.022	-0.972	DNA-binding transcriptional repressor/biotin-[acetyl-CoA-carboxylase]
Biosynthes Fatty Acid Fatty Acid/Lipid	EG10276	accC	-0.766	-1.72	biotin carboxylase
Biosynthes Fatty Acid Fatty Acid/Lipid	EG10217	accD	-0.711	0.285	acetyl-CoA carboxyltransferase subunit CEs
Biosynthes Fatty Acid Fatty Acid/Lipid	EG10274	fabB	0.379	0.23	3-oxoacyl-[acyl carrier protein] synthase 1
Biosynthes Fatty Acid Fatty Acid/Lipid	EG11284	fabZ	-1.159	-0.452	3-hydroxy-acyl-[acyl-carrier-protein] dehydratase
Biosynthes Fatty Acid Fatty Acid/Lipid	EG11528	fabI	-0.122	0.666	enoyl-[acyl-carrier-protein] reductase
Biosynthes Fatty Acid Fatty Acid/Lipid	EG11542	tesA	-1.684	0.281	multifunctional acyl-CoA thioesterase I and protease I and lysophosphatidyltransferase
Biosynthes Fatty Acid Fatty Acid/Lipid	EG10545	lpxA	-1.799	-0.737	acyl-[acyl-carrier-protein]--UDP-N-acetylglucosamine O-acyltransferase
Biosynthes Fatty Acid Fatty Acid/Lipid	EG10265	lpxC	0.249	-0.258	UDP-3-O-acyl-N-acetylglucosamine deacetylase
Biosynthes Fatty Acid Fatty Acid/Lipid	EG12666	lpxH	-0.67	-1.62	UDP-2,3-diacylglucosamine diphosphatase
Biosynthes Fatty Acid Fatty Acid/Lipid	EG10546	lpxB	-1.683	-0.69	lipid A disaccharide synthase
Biosynthes Fatty Acid Fatty Acid/Lipid	EG11409	lpxK	-1.452	0.473	tetraacyldisaccharide 4'-kinase
Biosynthes Fatty Acid Fatty Acid/Lipid	EG11608	clsA	0.636	0.215	cardiolipin synthase A
Biosynthes Fatty Acid Fatty Acid/Lipid	EG10706	pgsA	-0.381	-0.271	CDP-diacylglycerol--glycerol-3-phosphate 3-phosphatidyltransferase
Biosynthes Fatty Acid Fatty Acid/Lipid	EG10704	pgpA	1.116	0.276	phosphatidylglycerophosphatase A
Biosynthes Fatty Acid Fatty Acid/Lipid	EG20091	gpsA	0.144	-0.531	glycerol-3-phosphate dehydrogenase
Biosynthes Fatty Acid Fatty Acid/Lipid	EG10740	plsB	-0.655	-0.114	glycerol-3-phosphate 1-O-acyltransferase
Biosynthes Fatty Acid Fatty Acid/Lipid	EG10775	psd	-1.783	-0.244	phosphatidylserine decarboxylase proenzyme
Biosynthes Amine and Amine/Polyamine	EG10109	betA	0.13	-0.558	choline dehydrogenase

Biosynthes Carbohydr Carbohydrate	EG10702	pgi	-0.83	0.101	glucose-6-phosphate isomerase
Biosynthes Carbohydr Carbohydrate	EG10703	pgk	0.832	0.751	phosphoglycerate kinase
Biosynthes Carbohydr Carbohydrate	EG12296	gpmM	0.309	-0.191	2,3-bisphosphoglycerate-independent phosphoglycerate mutase
Biosynthes Carbohydr Carbohydrate	EG10258	enolase	0.448	-0.774	enolase
Biosynthes Carbohydr Carbohydrate	EG10759	ppsA	-1.103	-0.254	phosphoenolpyruvate synthetase
Biosynthes Carbohydr Carbohydrate	EG10948	maeA	-3.205	-0.891	NAD+-dependent malate dehydrogenase
Biosynthes Carbohydr Carbohydrate	G7293	maeB	-0.532	-0.418	NADP+-dependent malate dehydrogenase
Biosynthes Carbohydr Carbohydrate	EG11015	tpiA	0.072	1.305	triose-phosphate isomerase
Biosynthes Carbohydr Carbohydrate	EG10774	prs	-2.959	1.676	ribose-phosphate diphosphokinase
Biosynthes Carbohydr Carbohydrate	EG10519	kdsB	-0.11	0.538	3-deoxy-manno-octulosonate cytidyltransferase
Biosynthes Carbohydr Carbohydrate	G7663	kdsC	-0.586	-0.059	3-deoxy-D-manno-octulosonate 8-phosphate phosphatase KdsC
Biosynthes Carbohydr Carbohydrate	EG10518	kdsA	-0.65	-0.99	3-deoxy-D-manno-octulosonate 8-phosphate synthase
Biosynthes Carbohydr Carbohydrate	G7662	kdsD	-0.507	0.633	D-arabinose 5-phosphate isomerase KdsD
Biosynthes Carbohydr Carbohydrate	EG11198	glmU	-0.787	-0.277	fused N-acetylglucosamine-1-phosphate uridyltransferase and g
Biosynthes Carbohydr Carbohydrate	EG11553	glmM	-1.071	-0.191	phosphoglucosamine mutase
Biosynthes Carbohydr Carbohydrate	EG11319	galU	-1.393	0.37	UTP--glucose-1-phosphate uridylyltransferase
Biosynthes Carbohydr Carbohydrate	EG11751	otsA	0.438	1.798	trehalose-6-phosphate synthase
Biosynthes Carbohydr Carbohydrate	EG11752	otsB	1.361	2.141	trehalose-6-phosphate phosphatase
Biosynthes Secondary Secondary Metab	EG11375	folE	-0.719	0.176	GTP cyclohydrolase 1
Biosynthes Secondary Secondary Metab	G7443	queE	0.346	-1.428	putative 7-carboxy-7-deazaguanine synthase QueE
Biosynthes Secondary Secondary Metab	EG10261	entC	-0.24	-6.237	isochorismate synthase EntC
Biosynthes Secondary Secondary Metab	EG10263	entE	-1.529	-5.9	2,3-dihydroxybenzoate-AMP ligase
Biosynthes Secondary Secondary Metab	EG10260	entB	-2.806	-6.528	holo EntB
Biosynthes Secondary Secondary Metab	G6237	dxs	-1.417	1.109	1-deoxy-D-xylulose-5-phosphate synthase
Biosynthes Secondary Secondary Metab	EG12715	dxr	-1.405	-0.536	1-deoxy-D-xylulose 5-phosphate reductoisomerase
Biosynthes Secondary Secondary Metab	EG11081	ispH	1.959	0.953	1-hydroxy-2-methyl-2-(E)-butenyl 4-diphosphate reductase
Biosynthes Secondary Secondary Metab	G7423	ispD	-0.939	-1.472	2-C-methyl-D-erythritol 4-phosphate cytidyltransferase
Biosynthes Secondary Secondary Metab	EG11816	ispF	-0.889	-0.131	2-C-methyl-D-erythritol 2,4-cyclodiphosphate synthase
Biosynthes Secondary Secondary Metab	EG10370	ispG	-0.712	-0.389	(E)-4-hydroxy-3-methylbut-2-enyl-diphosphate synthase (flavod
Biosynthes Cofactor, Cofactor/Carrier/	EG50003	acpP	0.524	0.277	octanoyl-ACP

Biosynthes Cofactor, Cofactor/Carrier/	EG10260	entB	-2.806	-6.528	holo EntB
Biosynthes Cofactor, Cofactor/Carrier/	EG11746	panC	-0.889	0.715	pantothenate synthetase
Biosynthes Cofactor, Cofactor/Carrier/	EG10495	ilvC	0.281	-0.473	ketol-acid reductoisomerase (NADP+)
Biosynthes Cofactor, Cofactor/Carrier/	EG11675	panB	-0.725	0.652	3-methyl-2-oxobutanoate hydroxymethyltransferase
Biosynthes Cofactor, Cofactor/Carrier/	EG11747	panD	0.418	3.472	PanD C $\leq$ cleavage product
Biosynthes Cofactor, Cofactor/Carrier/	EG11190	coaD	-0.139	0.254	pantetheine-phosphate adenylyltransferase
Biosynthes Cofactor, Cofactor/Carrier/	EG12312	coaE	0.74	-1.522	dephospho-CoA kinase
Biosynthes Cofactor, Cofactor/Carrier/	EG10004	dfp	-2.205	0.207	fused 4'-phosphopantothenoylcysteine decarboxylase and phospho
Biosynthes Cofactor, Cofactor/Carrier/	EG11369	ubiC	0.163	0.077	chorismate lyase
Biosynthes Cofactor, Cofactor/Carrier/	EG11324	ubiH	-0.578	-0.571	2-octaprenyl-6-methoxyphenol 4-hydroxylase
Biosynthes Cofactor, Cofactor/Carrier/	EG11143	ubiG	-0.471	0.639	bifunctional 3-demethylubiquinone-8 3-O-methyltransferase and
Biosynthes Cofactor, Cofactor/Carrier/	EG11333	ubil	0.312	-1.116	2-octaprenylphenol 6-hydroxylase
Biosynthes Cofactor, Cofactor/Carrier/	EG11370	ubiA	1.207	0.337	4-hydroxybenzoate octaprenyltransferase
Biosynthes Cofactor, Cofactor/Carrier/	EG10508	ispA	-0.868	-0.16	geranyl diphosphate/farnesyl diphosphate synthase
Biosynthes Cofactor, Cofactor/Carrier/	EG12437	menE	-1.712	-0.96	o-succinylbenzoate--CoA ligase
Biosynthes Cofactor, Cofactor/Carrier/	EG12362	menF	0.133	1.405	isochorismate synthase MenF
Biosynthes Cofactor, Cofactor/Carrier/	EG11887	trxC	2.051	0.765	oxidized thioredoxin 2
Biosynthes Cofactor, Cofactor/Carrier/	EG11297	dsbA	0.94	1.065	thiol:disulfide oxidoreductase - DsbA reduced
Biosynthes Cofactor, Cofactor/Carrier/	EG12294	grxC	0.206	2.129	oxidized glutaredoxin 3
Biosynthes Cofactor, Cofactor/Carrier/	EG12633	nudF	-1.223	-0.671	ADP-sugar pyrophosphatase
Biosynthes Cofactor, Cofactor/Carrier/	G6580	nudJ	-0.768	-0.445	phosphatase NudJ
Biosynthes Cofactor, Cofactor/Carrier/	M007	thiM	-0.845	0.002	hydroxyethylthiazole kinase
Biosynthes Cofactor, Cofactor/Carrier/	EG11135	pncA	0.784	-0.12	nicotinamidase
Biosynthes Cofactor, Cofactor/Carrier/	EG11079	ribF	-1.418	0.12	bifunctional riboflavin kinase / FMN adenylyltransferase
Biosynthes Cofactor, Cofactor/Carrier/	EG11322	ribE	-0.645	0.727	6,7-dimethyl-8-ribityllumazine synthase
Biosynthes Cofactor, Cofactor/Carrier/	EG10465	ribB	-0.737	2.272	3,4-dihydroxy-2-butanone-4-phosphate synthase
Biosynthes Cofactor, Cofactor/Carrier/	EG11321	ribD	0.146	0.562	fused diaminoxyphosphoribosylaminopyrimidine deaminase
Biosynthes Cofactor, Cofactor/Carrier/	EG11331	ribA	1.404	-0.477	GTP cyclohydrolase 2
Biosynthes Cofactor, Cofactor/Carrier/	EG11546	nadC	-0.768	0.838	quinolinate phosphoribosyltransferase (decarboxylating)
Biosynthes Cofactor, Cofactor/Carrier/	EG10630	nadA	-2.85	0.575	quinolinate synthase

Biosynthes Cofactor, Cofactor/Carrier/	EG10631	nadB	-1.72	0.102	L-aspartate oxidase
Biosynthes Cofactor, Cofactor/Carrier/	EG12192	nadK	-0.647	0.388	NAD kinase
Biosynthes Cofactor, Cofactor/Carrier/	EG10745	pntB	-0.396	2.331	pyridine nucleotide transhydrogenase subunit C $\leq$
Biosynthes Cofactor, Cofactor/Carrier/	EG10744	pntA	-2.074	2.717	pyridine nucleotide transhydrogenase subunit C $\pm$
Biosynthes Cofactor, Cofactor/Carrier/	EG10663	nadE	-0.718	-0.394	NH ₃ -dependent NAD ⁺ synthetase
Biosynthes Cofactor, Cofactor/Carrier/	EG10418	gshA	0.525	-0.038	glutamate--cysteine ligase
Biosynthes Cofactor, Cofactor/Carrier/	EG10419	gshB	-0.949	0.071	glutathione synthetase
Biosynthes Cofactor, Cofactor/Carrier/	G6092	uppS	-0.759	-1.223	ditrans, polycis-undecaprenyl-diphosphate synthase [(2E,6E)-farr
Biosynthes Cofactor, Cofactor/Carrier/	EG11665	bacA	-0.645	-0.074	undecaprenyl pyrophosphate phosphatase
Biosynthes Cofactor, Cofactor/Carrier/	G6439	ybjG	0.847	0.701	undecaprenyl pyrophosphate phosphatase
Biosynthes Cofactor, Cofactor/Carrier/	EG11493	pabC	-1.179	0.586	aminodeoxychorismate lyase
Biosynthes Cofactor, Cofactor/Carrier/	EG11374	folK	-1.133	0.395	2-amino-4-hydroxy-6-hydroxymethyldihydropteridine diphosphol
Biosynthes Cofactor, Cofactor/Carrier/	EG11673	folB	-0.65	-0.704	dihydroneopterin aldolase
Biosynthes Cofactor, Cofactor/Carrier/	EG11375	folE	-0.719	0.176	GTP cyclohydrolase 1
Biosynthes Cofactor, Cofactor/Carrier/	EG10589	metK	-0.9	-0.553	methionine adenosyltransferase
Biosynthes Cofactor, Cofactor/Carrier/	EG11158	fau	-0.996	0.76	putative 5-formyltetrahydrofolate cyclo-ligase
Biosynthes Cofactor, Cofactor/Carrier/	EG10585	metF	0.474	-1.001	5,10-methylenetetrahydrofolate reductase
Biosynthes Cofactor, Cofactor/Carrier/	EG10587	metH	-0.146	0.823	cobalamin-dependent methionine synthase
Biosynthes Cofactor, Cofactor/Carrier/	EG10371	gcvH	0.207	-0.227	lipoyl-GcvH-protein
Biosynthes Cofactor, Cofactor/Carrier/	EG10328	folD	-0.217	-0.144	bifunctional methylenetetrahydrofolate dehydrogenase / meth
Biosynthes Cofactor, Cofactor/Carrier/	EG11002	thyA	-0.966	-0.248	thymidylate synthase
Biosynthes Cofactor, Cofactor/Carrier/	EG10408	glyA	-2.967	0.691	serine hydroxymethyltransferase
Biosynthes Cofactor, Cofactor/Carrier/	EG10327	folC	-0.523	0.214	bifunctional folylpolyglutamate synthetase / dihydrofolate synth
Biosynthes Cofactor, Cofactor/Carrier/	EG10122	bioH	1.306	-0.803	pimeloyl-acyl carrier protein methyl ester esterase
Biosynthes Cofactor, Cofactor/Carrier/	EG10274	fabB	0.379	0.23	3-oxoacyl-[acyl carrier protein] synthase 1
Biosynthes Cofactor, Cofactor/Carrier/	EG11528	fabI	-0.122	0.666	enoyl-[acyl-carrier-protein] reductase
Biosynthes Cofactor, Cofactor/Carrier/	EG11284	fabZ	-1.159	-0.452	3-hydroxy-acyl-[acyl-carrier-protein] dehydratase
Biosynthes Cofactor, Cofactor/Carrier/	EG10121	bioF	-1.076	-0.384	8-amino-7-oxononanoate synthase
Biosynthes Cofactor, Cofactor/Carrier/	EG10117	bioA	-2.446	-0.277	adenosylmethionine-8-amino-7-oxononanoate aminotransferase
Biosynthes Cofactor, Cofactor/Carrier/	EG10118	bioB	-2.286	0.598	biotin synthase

Biosynthes Cofactor, † Cofactor/Carrier/ EG12150	cobS	-1.564	0.301	cobalamin 5'-phosphate synthase
Biosynthes Cofactor, † Cofactor/Carrier/ EG11096	yajC	-1.271	-0.86	Sec translocon accessory complex subunit YajC
Biosynthes Cofactor, † Cofactor/Carrier/ EG10940	secF	-0.852	-0.815	Sec translocon accessory complex subunit SecF
Biosynthes Cofactor, † Cofactor/Carrier/ EG10938	secD	-1.865	-1.123	Sec translocon accessory complex subunit SecD
Biosynthes Cofactor, † Cofactor/Carrier/ EG10766	secY	-1.205	0.529	Sec translocon subunit SecY
Biosynthes Cofactor, † Cofactor/Carrier/ EG12095	secG	-1.458	0.553	Sec translocon subunit SecG
Biosynthes Cofactor, † Cofactor/Carrier/ EG10939	secE	0.521	1.014	Sec translocon subunit SecE
Biosynthes Cofactor, † Cofactor/Carrier/ EG11197	yidC	-3.025	-0.122	membrane protein insertase YidC
Biosynthes Cofactor, † Cofactor/Carrier/ EG12189	hemF	-0.006	0.208	coproporphyrinogen III oxidase
Biosynthes Cofactor, † Cofactor/Carrier/ EG10431	hemH	0.33	-0.099	ferrochelataase
Biosynthes Cofactor, † Cofactor/Carrier/ EG11543	hemE	0.811	0.955	uroporphyrinogen decarboxylase
Biosynthes Cofactor, † Cofactor/Carrier/ EG11591	lipB	-1.975	0.059	lipoyl(octanoyl) transferase
Biosynthes Cofactor, † Cofactor/Carrier/ EG11595	moaA	1.558	0.073	GTP 3',8'-cyclase
Biosynthes Cofactor, † Cofactor/Carrier/ EG10154	moeB	0.327	0.495	molybdopterin-synthase adenyltransferase
Biosynthes Cofactor, † Cofactor/Carrier/ EG11666	moaC	0.088	-0.084	cyclic pyranopterin monophosphate synthase
Biosynthes Cofactor, † Cofactor/Carrier/ EG11829	mobA	0.538	-0.523	molybdenum cofactor guanylyltransferase
Biosynthes Cofactor, † Cofactor/Carrier/ EG11859	fdhD	0.569	-1.622	sulfurtransferase for molybdenum cofactor sulfuration
Biosynthes Cofactor, † Cofactor/Carrier/ G7325	iscS	-1.254	0.693	cysteine desulfurase IscS
Biosynthes Cofactor, † Cofactor/Carrier/ G6906	sufS	1.017	-0.397	L-cysteine desulfurase
Biosynthes Cofactor, † Cofactor/Carrier/ EG10153	moeA	-0.998	-1.007	molybdopterin molybdotransferase
Biosynthes Cofactor, † Cofactor/Carrier/ EG10002	modB	-1.467	0.096	molybdate ABC transporter membrane subunit
Biosynthes Cofactor, † Cofactor/Carrier/ EG12427	modA	-1.715	1.605	molybdate ABC transporter periplasmic binding protein
Biosynthes Cofactor, † Cofactor/Carrier/ EG10198	cysW	-0.283	-0.776	sulfate/thiosulfate ABC transporter inner membrane subunit Cy
Biosynthes Cofactor, † Cofactor/Carrier/ G7135	thiD	-3.478	0.488	bifunctional hydroxymethylpyrimidine kinase/phosphomethylpyr
Biosynthes Cofactor, † Cofactor/Carrier/ EG11585	thiC	-4.96	-3.898	phosphomethylpyrimidine synthase
Biosynthes Cofactor, † Cofactor/Carrier/ G6234	thiL	0.65	-0.881	thiamine monophosphate kinase
Biosynthes Cofactor, † Cofactor/Carrier/ EG11589	thiG	-3.54	-1.055	1-deoxy-D-xylulose 5-phosphate:thiol sulfurtransferase
Biosynthes Cofactor, † Cofactor/Carrier/ G6237	dxs	-1.417	1.109	1-deoxy-D-xylulose-5-phosphate synthase
Biosynthes Cofactor, † Cofactor/Carrier/ EG10368	epd	0.878	-0.549	D-erythrose-4-phosphate dehydrogenase
Biosynthes Cofactor, † Cofactor/Carrier/ EG10693	pdxJ	-2.271	-0.126	pyridoxine 5'-phosphate synthase

Biosynthes Cofactor, Cofactor/Carrier/	G0-9461	pdxB	-1.26	0.082	erythronate-4-phosphate dehydrogenase
Biosynthes Cofactor, Cofactor/Carrier/	EG10946	serC	-0.473	-0.349	phosphoserine/phosphohydroxythreonine aminotransferase
Biosynthes Cofactor, Cofactor/Carrier/	EG10691	pdxA	-0.002	0.752	4-hydroxythreonine-4-phosphate dehydrogenase
Biosynthes Cofactor, Cofactor/Carrier/	EG11487	pdxH	-0.967	-0.009	pyridoxine/pyridoxamine 5'-phosphate oxidase
Biosynthes Cell Struct Cell Structure	EG10520	waaA	-1.834	-0.113	KDO transferase
Biosynthes Cell Struct Cell Structure	EG10545	lpxA	-1.799	-0.737	acyl-[acyl-carrier-protein]--UDP-N-acetylglucosamine O-acyltransferase
Biosynthes Cell Struct Cell Structure	EG10265	lpxC	0.249	-0.258	UDP-3-O-acyl-N-acetylglucosamine deacetylase
Biosynthes Cell Struct Cell Structure	EG12666	lpxH	-0.67	-1.62	UDP-2,3-diacetylglucosamine diphosphatase
Biosynthes Cell Struct Cell Structure	EG10546	lpxB	-1.683	-0.69	lipid A disaccharide synthase
Biosynthes Cell Struct Cell Structure	EG11409	lpxK	-1.452	0.473	tetraacyldisaccharide 4'-kinase
Biosynthes Cell Struct Cell Structure	EG50003	acpP	0.524	0.277	octanoyl-ACP
Biosynthes Cell Struct Cell Structure	EG10623	murG	-3.656	-0.02	N-acetylglucosaminyl transferase
Biosynthes Cell Struct Cell Structure	EG10604	mraY	-2.733	-0.367	phospho-N-acetylmuramoyl-pentapeptide-transferase
Biosynthes Cell Struct Cell Structure	EG11358	murA	-2.398	-0.867	UDP-N-acetylglucosamine 1-carboxyvinyltransferase
Biosynthes Cell Struct Cell Structure	EG11205	murB	-1.449	-1.07	UDP-N-acetylenolpyruvoylglucosamine reductase
Biosynthes Cell Struct Cell Structure	EG10622	murF	-3.365	-0.888	D-alanyl-D-alanine-adding enzyme
Biosynthes Cell Struct Cell Structure	EG10619	murC	-2.151	-0.568	UDP-N-acetylmuramate--L-alanine ligase
Biosynthes Cell Struct Cell Structure	EG10620	murD	-1.836	-0.434	UDP-N-acetylmuramoyl-L-alanine--D-glutamate ligase
Biosynthes Cell Struct Cell Structure	EG11204	murI	-2.028	0.738	glutamate racemase
Biosynthes Cell Struct Cell Structure	EG10621	murE	-1.931	-0.95	UDP-N-acetylmuramoyl-L-alanyl-D-glutamate--2,6-diaminopimelate ligase
Biosynthes Cell Struct Cell Structure	G7668	mtgA	-1.745	0.142	peptidoglycan glycosyltransferase MtgA
Biosynthes Cell Struct Cell Structure	EG11893	dacD	-0.102	0.976	D-alanyl-D-alanine carboxypeptidase DacD
Biosynthes Cell Struct Cell Structure	EG10201	dacA	-2.586	-0.494	D-alanyl-D-alanine carboxypeptidase DacA
Biosynthes Cell Struct Cell Structure	EG10605	mrcB	-0.486	-0.255	PBP1BCE
Biosynthes Cell Struct Cell Structure	EG10748	mrcA	0.098	-0.227	peptidoglycan glycosyltransferase / peptidoglycan DD-transpeptidase
Biosynthes Cell Struct Cell Structure	G7167	arnC	0.529	-0.966	undecaprenyl-phosphate 4-deoxy-4-formamido-L-arabinose transferase
Biosynthes Cell Struct Cell Structure	G7170	arnT	-0.793	-0.084	lipid IVA 4-amino-4-deoxy-L-arabinosyltransferase
Biosynthes Metabolic Metabolic Regulat	EG10109	betA	0.13	-0.558	choline dehydrogenase
Biosynthes Metabolic Metabolic Regulat	EG10650	ndk	-2.887	0.526	nucleoside diphosphate kinase
Biosynthes Metabolic Metabolic Regulat	EG10032	adk	-3.243	-0.148	adenylate kinase

Biosynthes Metabolic Metabolic Regul	EG10966	spoT	-1.098	-0.172	bifunctional (p)ppGpp synthase/hydrolase SpoT
Biosynthes Metabolic Metabolic Regul	EG10835	relA	-0.511	0.982	GDP/GTP pyrophosphokinase
Biosynthes Metabolic Metabolic Regul	EG11751	otsA	0.438	1.798	trehalose-6-phosphate synthase
Biosynthes Metabolic Metabolic Regul	EG11752	otsB	1.361	2.141	trehalose-6-phosphate phosphatase
Biosynthes Other Bio: Other	EG10261	entC	-0.24	-6.237	isochorismate synthase EntC
Biosynthes Other Bio: Other	EG10260	entB	-2.806	-6.528	holo EntB
Biosynthes Other Bio: Other	EG10074	aroB	-1.063	-0.829	3-dehydroquinate synthase
Biosynthes Other Bio: Other	EG11369	ubiC	0.163	0.077	chorismate lyase
Biosynthes Other Bio: Other	EG10122	bioH	1.306	-0.803	pimeloyl-acyl carrier protein methyl ester esterase
Biosynthes Other Bio: Other	EG10274	fabB	0.379	0.23	3-oxoacyl-[acyl carrier protein] synthase 1
Biosynthes Other Bio: Other	EG11528	fabI	-0.122	0.666	enoyl-[acyl-carrier-protein] reductase
Biosynthes Other Bio: Other	EG11284	fabZ	-1.159	-0.452	3-hydroxy-acyl-[acyl-carrier-protein] dehydratase
Biosynthes Other Bio: Other	EG10121	bioF	-1.076	-0.384	8-amino-7-oxononanoate synthase
Biosynthes Other Bio: Other	EG50003	acpP	0.524	0.277	octanoyl-ACP
Biosynthes Other Bio: Other	EG11408	dadX	-1.042	-2.067	alanine racemase 2
Biosynthes Other Bio: Other	EG11747	panD	0.418	3.472	PanD $\text{C}\epsilon$ cleavage product
Biosynthes Other Bio: Other	EG10075	aroC	-1.913	-0.29	chorismate synthase
Biosynthes Other Bio: Other	EG10073	aroA	-0.728	-0.927	3-phosphoshikimate 1-carboxyvinyltransferase
Biosynthes Other Bio: Other	EG10081	aroK	-1.714	-0.25	shikimate kinase 1
Biosynthes Other Bio: Other	EG10063	argA	-1.559	0.108	N-acetylglutamate synthase
Biosynthes Other Bio: Other	EG10064	argB	-1.92	0.471	acetylglutamate kinase
Biosynthes Other Bio: Other	EG10065	argC	-3.216	-0.642	N-acetylglutamylphosphate reductase
Biosynthes Other Bio: Other	EG10066	argD	0.184	0.114	N-acetylornithine aminotransferase / N-succinyldiaminopimelat
Biosynthes Other Bio: Other	EG10407	gltX	-0.316	0.544	glutamate--tRNA ligase
Biosynthes Other Bio: Other	EG10427	hemA	-1.609	-0.068	glutamyl-tRNA reductase
Biosynthes Other Bio: Other	EG10432	hemL	0.508	0.208	glutamate-1-semialdehyde 2,1-aminomutase
Biosynthes Other Bio: Other	EG10428	hemB	-3.089	0.592	porphobilinogen synthase
Biosynthes Other Bio: Other	EG10429	hemC	-0.452	0.623	hydroxymethylbilane synthase
Biosynthes Other Bio: Other	EG10508	ispA	-0.868	-0.16	geranyl diphosphate/farnesyl diphosphate synthase
Biosynthes Other Bio: Other	EG10410	glyS	-2.435	-1.428	glycine--tRNA ligase subunit $\text{C}\epsilon$

Biosynthes Other Bio: Other	EG10409	glyQ	-1.526	-1.002	glycine--tRNA ligase subunit $\text{CE}\pm$
Biosynthes Other Bio: Other	EG10453	hisS	-0.034	-0.571	histidine--tRNA ligase
Biosynthes Other Bio: Other	EG10552	lysS	-1.739	-0.265	lysine--tRNA ligase, constitutive
Biosynthes Other Bio: Other	EG10586	metG	-1.642	-0.168	methionine--tRNA ligase
Biosynthes Other Bio: Other	EG10709	pheS	-2.117	-0.528	phenylalanine--tRNA ligase subunit $\text{CE}\pm$
Biosynthes Other Bio: Other	EG10710	pheT	0.937	-0.471	phenylalanine--tRNA ligase subunit $\text{CE}\leq$
Biosynthes Other Bio: Other	EG10770	proS	0.626	-0.018	proline--tRNA ligase
Biosynthes Other Bio: Other	EG10947	serS	-1.033	-0.112	serine--tRNA ligase
Biosynthes Other Bio: Other	EG11001	thrS	-0.405	0.37	threonine--tRNA ligase
Biosynthes Other Bio: Other	EG11043	tyrS	-1.379	0.1	tyrosine--tRNA ligase
Biosynthes Other Bio: Other	EG10097	aspS	-1.28	-1.541	aspartate--tRNA ligase
Biosynthes Other Bio: Other	EG10034	alaS	-1.695	-0.501	alanine--tRNA ligase/DNA-binding transcriptional repressor
Biosynthes Other Bio: Other	EG11067	valS	-0.812	0.402	valine--tRNA ligase
Biosynthes Other Bio: Other	EG10532	leuS	-1.762	-0.689	leucine--tRNA ligase
Biosynthes Other Bio: Other	EG10492	ileS	-2.101	-0.506	isoleucine--tRNA ligase
Biosynthes Other Bio: Other	EG10390	glnS	-1.557	-0.64	glutamine--tRNA ligase
Biosynthes Other Bio: Other	EG10196	cysS	-1.29	-0.876	cysteine--tRNA ligase
Biosynthes Other Bio: Other	EG10071	argS	-2.019	-0.646	arginine--tRNA ligase
Biosynthes Other Bio: Other	G7991	cysT	0.693	-3.162	tRNA-Cys(GCA) (cysT)
Energy_Mε Glycolysis Glycolysis	EG10702	pgi	-0.83	0.101	glucose-6-phosphate isomerase
Energy_Mε Glycolysis Glycolysis	EG10258	enolase	0.448	-0.774	enolase
Energy_Mε Glycolysis Glycolysis	EG12296	gpmM	0.309	-0.191	2,3-bisphosphoglycerate-independent phosphoglycerate mutase
Energy_Mε Glycolysis Glycolysis	EG10703	pgk	0.832	0.751	phosphoglycerate kinase
Energy_Mε Glycolysis Glycolysis	EG11015	tpiA	0.072	1.305	triose-phosphate isomerase
Energy_Mε Glycolysis Glycolysis	EG10759	ppsA	-1.103	-0.254	phosphoenolpyruvate synthetase
Energy_Mε TCA cycle TCA cycle	EG10948	maeA	-3.205	-0.891	NAD ⁺ -dependent malate dehydrogenase
Energy_Mε TCA cycle TCA cycle	EG10358	fumC	0.721	-1.154	fumarase C
Energy_Mε TCA cycle TCA cycle	EG10357	fumB	1.864	1.605	fumarase B
Energy_Mε TCA cycle TCA cycle	EG10982	sucD	-0.197	0.041	succinyl-CoA synthetase subunit $\text{CE}\pm$
Energy_Mε TCA cycle TCA cycle	EG10981	sucC	-2.388	-0.016	succinyl-CoA synthetase subunit $\text{CE}\leq$

Energy_Mε TCA cycle TCA cycle	EG10979	sucA	-1.352	-0.289	subunit of E1(0) component of 2-oxoglutarate dehydrogenase
Energy_Mε TCA cycle TCA cycle	EG10980	sucB	-1.441	-0.268	SucB-dihydrolipoate
Energy_Mε TCA cycle TCA cycle	EG11325	acnA	1.373	1.446	aconitate hydratase 1
Energy_Mε TCA cycle TCA cycle	EG12316	acnB	-0.873	-1.09	AcnB
Energy_Mε TCA cycle TCA cycle	EG10934	sdhD	-1.268	1.67	succinate:quinone oxidoreductase, membrane protein SdhD
Energy_Mε TCA cycle TCA cycle	EG10933	sdhC	-0.367	1.083	succinate:quinone oxidoreductase, membrane protein SdhC
Energy_Mε TCA cycle TCA cycle	EG10932	sdhB	-1.309	1.038	succinate:quinone oxidoreductase, iron-sulfur cluster binding protein
Energy_Mε TCA cycle TCA cycle	EG10931	sdhA	-1.15	1.198	succinate:quinone oxidoreductase, FAD binding protein
Energy_Mε Pentose P PPP	M004	rpe	-0.684	1.758	ribulose-phosphate 3-epimerase
Energy_Mε Pentose P PPP	EG11443	rpiA	0.606	1.301	ribose-5-phosphate isomerase A
Energy_Mε Fermenta Fermentation	EG20173	pta	-1.402	-0.828	phosphate acetyltransferase
Energy_Mε Fermenta Fermentation	EG10027	ackA	0.051	-0.046	acetate kinase
Energy_Mε Fermenta Fermentation	EG10358	fumC	0.721	-1.154	fumarase C
Energy_Mε Fermenta Fermentation	EG10357	fumB	1.864	1.605	fumarase B
Energy_Mε Fermenta Fermentation	EG10948	maeA	-3.205	-0.891	NAD ⁺ -dependent malate dehydrogenase
Energy_Mε Fermenta Fermentation	EG10756	ppc	-0.142	-0.08	phosphoenolpyruvate carboxylase
Energy_Mε Fermenta Fermentation	EG12316	acnB	-0.873	-1.09	AcnB
Energy_Mε Aerobic R _l Respiration	EG10231	dld	-1.435	0.167	quinone-dependent D-lactate dehydrogenase
Energy_Mε Aerobic R _l Respiration	EG10181	cyoD	-1.411	-0.316	cytochrome bo3 ubiquinol oxidase subunit 4
Energy_Mε Aerobic R _l Respiration	EG10178	cyoA	-2.272	-0.588	cytochrome bo3 ubiquinol oxidase subunit 2
Energy_Mε Aerobic R _l Respiration	EG10179	cyoB	-1.541	-0.558	cytochrome bo3 ubiquinol oxidase subunit 1
Energy_Mε Aerobic R _l Respiration	EG10180	cyoC	-1.184	-0.38	cytochrome bo3 ubiquinol oxidase subunit 3
Energy_Mε Aerobic R _l Respiration	EG10394	glpD	0.381	0.052	aerobic glycerol 3-phosphate dehydrogenase
Energy_Mε Aerobic R _l Respiration	EG12088	nuoH	-1.477	1.386	NADH:quinone oxidoreductase subunit H
Energy_Mε Aerobic R _l Respiration	EG12090	nuoJ	-1.56	1.196	NADH:quinone oxidoreductase subunit J
Energy_Mε Aerobic R _l Respiration	EG12091	nuoK	-2.478	1.063	NADH:quinone oxidoreductase subunit K
Energy_Mε Aerobic R _l Respiration	EG12092	nuoL	-2.06	0.479	NADH:quinone oxidoreductase subunit L
Energy_Mε Aerobic R _l Respiration	EG11773	nuoM	-2.108	0.305	NADH:quinone oxidoreductase subunit M
Energy_Mε Aerobic R _l Respiration	EG12093	nuoN	-1.763	-0.195	NADH:quinone oxidoreductase subunit N
Energy_Mε Aerobic R _l Respiration	EG12089	nuoI	-0.888	1.472	NADH:quinone oxidoreductase subunit I

Energy_M€ Aerobic R€ Respiration	EG12087	nuoG	-1.347	1.469	NADH:quinone oxidoreductase subunit G
Energy_M€ Aerobic R€ Respiration	EG11774	nuoF	-0.226	1.858	NADH:quinone oxidoreductase subunit F
Energy_M€ Aerobic R€ Respiration	EG12086	nuoE	-0.112	1.772	NADH:quinone oxidoreductase subunit E
Energy_M€ Aerobic R€ Respiration	EG12084	nuoC	-1.019	1.447	NADH:quinone oxidoreductase subunit CD
Energy_M€ Aerobic R€ Respiration	EG12083	nuoB	-0.509	2.067	NADH:quinone oxidoreductase subunit B
Energy_M€ Aerobic R€ Respiration	EG10649	ndh	-0.631	0.323	NADH:quinone oxidoreductase II
Energy_M€ Aerobic R€ Respiration	EG10801	putA	-0.647	-0.46	fused DNA-binding transcriptional repressor / proline dehydroge
Energy_M€ Aerobic R€ Respiration	EG10934	sdhD	-1.268	1.67	succinate:quinone oxidoreductase, membrane protein SdhD
Energy_M€ Aerobic R€ Respiration	EG10933	sdhC	-0.367	1.083	succinate:quinone oxidoreductase, membrane protein SdhC
Energy_M€ Aerobic R€ Respiration	EG10932	sdhB	-1.309	1.038	succinate:quinone oxidoreductase, iron-sulfur cluster binding pr
Energy_M€ Aerobic R€ Respiration	EG10931	sdhA	-1.15	1.198	succinate:quinone oxidoreductase, FAD binding protein
Energy_M€ Anaerobic Anaerobic Respir	EG12088	nuoH	-1.477	1.386	NADH:quinone oxidoreductase subunit H
Energy_M€ Anaerobic Anaerobic Respir	EG12090	nuoJ	-1.56	1.196	NADH:quinone oxidoreductase subunit J
Energy_M€ Anaerobic Anaerobic Respir	EG12091	nuoK	-2.478	1.063	NADH:quinone oxidoreductase subunit K
Energy_M€ Anaerobic Anaerobic Respir	EG12092	nuoL	-2.06	0.479	NADH:quinone oxidoreductase subunit L
Energy_M€ Anaerobic Anaerobic Respir	EG11773	nuoM	-2.108	0.305	NADH:quinone oxidoreductase subunit M
Energy_M€ Anaerobic Anaerobic Respir	EG12093	nuoN	-1.763	-0.195	NADH:quinone oxidoreductase subunit N
Energy_M€ Anaerobic Anaerobic Respir	EG12089	nuoI	-0.888	1.472	NADH:quinone oxidoreductase subunit I
Energy_M€ Anaerobic Anaerobic Respir	EG12087	nuoG	-1.347	1.469	NADH:quinone oxidoreductase subunit G
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Energy_M€ Anaerobic Anaerobic Respir	EG12083	nuoB	-0.509	2.067	NADH:quinone oxidoreductase subunit B
Energy_M€ Anaerobic Anaerobic Respir	EG10649	ndh	-0.631	0.323	NADH:quinone oxidoreductase II
Energy_M€ Anaerobic Anaerobic Respir	EG10394	glpD	0.381	0.052	aerobic glycerol 3-phosphate dehydrogenase
Energy_M€ ATP biosyn ATP biosynthesis	EG10099	atpB	-3.026	-0.605	ATP synthase Fo complex subunit a
Energy_M€ ATP biosyn ATP biosynthesis	EG10103	atpF	-2.285	-0.963	ATP synthase Fo complex subunit b
Energy_M€ ATP biosyn ATP biosynthesis	EG10102	atpE	-2.628	-0.936	ATP synthase Fo complex subunit c
Energy_M€ ATP biosyn ATP biosynthesis	EG10104	atpG	-0.713	-0.931	ATP synthase F1 complex subunit C€±
Energy_M€ ATP biosyn ATP biosynthesis	EG10098	atpA	-2.2	-0.798	ATP synthase F1 complex subunit C€±

Energy_M€ ATP biosyn	ATP biosynthesis	EG10105	atpH	-2.636	-0.803	ATP synthase F1 complex subunit C€¥
Energy_M€ ATP biosyn	ATP biosynthesis	EG10100	atpC	-0.863	-0.363	ATP synthase F1 complex subunit C€µ
Energy_M€ Other Ene	Other Energy	EG10979	sucA	-1.352	-0.289	subunit of E1(0) component of 2-oxoglutarate dehydrogenase (s
Energy_M€ Other Ene	Other Energy	EG10980	sucB	-1.441	-0.268	SucB-dihydrolipoate
Energy_M€ Other Ene	Other Energy	EG10948	maeA	-3.205	-0.891	NAD ⁺ -dependent malate dehydrogenase
Energy_M€ Other Ene	Other Energy	EG11325	acnA	1.373	1.446	aconitate hydratase 1
Energy_M€ Other Ene	Other Energy	EG12316	acnB	-0.873	-1.09	AcnB
Energy_M€ Other Ene	Other Energy	EG12088	nuoH	-1.477	1.386	NADH:quinone oxidoreductase subunit H
Energy_M€ Other Ene	Other Energy	EG12090	nuoJ	-1.56	1.196	NADH:quinone oxidoreductase subunit J
Energy_M€ Other Ene	Other Energy	EG12091	nuoK	-2.478	1.063	NADH:quinone oxidoreductase subunit K
Energy_M€ Other Ene	Other Energy	EG12092	nuoL	-2.06	0.479	NADH:quinone oxidoreductase subunit L
Energy_M€ Other Ene	Other Energy	EG11773	nuoM	-2.108	0.305	NADH:quinone oxidoreductase subunit M
Energy_M€ Other Ene	Other Energy	EG12093	nuoN	-1.763	-0.195	NADH:quinone oxidoreductase subunit N
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Energy_M€ Other Ene	Other Energy	EG12084	nuoC	-1.019	1.447	NADH:quinone oxidoreductase subunit CD
Energy_M€ Other Ene	Other Energy	EG12083	nuoB	-0.509	2.067	NADH:quinone oxidoreductase subunit B

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