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Comparing the mechanisms of metal action in bacteria: insight into novel genes involved in silver, gallium and copper resistance and toxicity in *Escherichia coli*

Gugala, Natalie

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ID	Uniprot	Name	Function	Score	P-value
JW3516	P37662	yhjX	putative MFS antiporter, pyr	-0.0094227	0.75832636
JW5353	P0AD14	yehU	sensory kinase regulating bt	0.03349198	0.31687252
JW0482	P0AFP4	ybbO	short-chain dehydrogenases	0.05511688	0.03562276
JW2755	P0AG20	relA	(p)ppGpp synthetase I/GTP	0.0977304	0.00153611
JW2509	P0A9R4	fdx	[2Fe-2S] ferredoxin	-0.047874	0.28996995
JW1389	P77467	paaG	1,2-epoxyphenylacetyl-CoA i	0.01941066	0.62523151
JW3395	P07762	glgB	1,4-alpha-glucan branching	-0.0730086	0.27820955
JW3901	P32166	menA	1,4-dihydroxy-2-naphthoate	0.14625731	0.03829739
JW1676	P77781	ydil	1,4-dihydroxy-2-naphthoyl-C	-0.0083402	0.77540207
JW0106	P13016	ampD	1,6-anhydro-N-acetylmurarr	-0.0928795	0.07518533
JW0851	P75820	ybjR	1,6-anhydro-N-acetylmurarr	0.07006163	0.12070984
JW4333	P39406	rsmC	16S rRNA m(2)G1207 meth	-0.1422955	0.00190736
JW5672	P68567	yhiQ	16S rRNA m(2)G1516 meth	0.07636778	0.01289805
JW2913	P0AGL7	yggJ	16S rRNA m(3)U1498 meth	-0.24971	3.06E-06
JW0080	P60390	mraW	16S rRNA m(4)C1402 methy	0.01180704	0.56585641
JW5301	P76273	yebU	16S rRNA m(5)C1407 methy	-0.0546588	0.32412244
JW3250	P36929	rsmB	16S rRNA m(5)C967 methyl	0.05413032	0.06354124
JW0050	P06992	ksgA	16S rRNA m(6)A1518, m(6)	0.06483977	0.01279738
JW3718	P0A6U5	gidB	16S rRNA m(7)G527 methyl	0.0660759	0.00121537
JW2171	P0AA43	rsuA	16S rRNA pseudouridine(51	-0.0010139	0.97207634
JW0605	P77231	citG	2-(5''-triphosphoribosyl)-3''-	0.05361818	0.0384471
JW0409	P77735	yajO	2-carboxybenzaldehyde red	-0.0599285	0.08603609
JW2810	P37769	kduD	2-dehydro-3-deoxy-D-glucor	0.00380025	0.93586291
JW5668	P37647	kdgK	2-dehydro-3-deoxygluconoki	0.06302534	0.03436847
JW0415	P0A9J4	panE	2-dehydropantoate reductas	-0.0214515	0.60878549
JW4344	P0A6L0	deoC	2-deoxyribose-5-phosphate	-0.0256729	0.65350026
JW0340	P77044	mhpC	2-hydroxy-6-ke-tonona-2,4-di	-0.1638682	0.00304433
JW0073	P09151	leuA	2-isopropylmalate synthase	-0.0198658	0.5889044
JW0261	P75682	yagE	2-keto-3-deoxy gluconate (K	0.08031097	0.06616296
JW5560	P0A712	kdgT	2-keto-3-deoxy-D-gluconate	0.05374753	0.06215274
JW2239	P76469	yfaU	2-keto-3-deoxy-L-rhamnona	0.16916832	0.00827785
JW0341	P77608	mhpD	2-keto-4-pentenoate hydrat	0.0628282	0.50745792
JW0325	P77243	prpD	2-methylcitrate dehydratas	-0.0238842	0.45677542
JW0324	P31660	prpC	2-methylcitrate synthase	-0.069348	0.00169246
JW0323	P77541	prpB	2-methylisocitrate lyase	-0.0165989	0.84760387
JW0659	P75728	ubiF	2-octaprenyl-3-methyl-6-m	0.04710153	0.29752563
JW2875	P25534	ubiH	2-octaprenyl-6-methoxyphe	-0.0838042	0.17938238
JW2874	P25535	visC	2-octaprenylphenol hydroxyl	-0.0584181	0.22430842
JW5628	Q6BF16	dgoA	2-oxo-3-deoxygalactonate 6	0.00309534	0.89220201
JW3670	P31459	dgoK	2-oxo-3-deoxygalactonate ki	0.02091408	0.49535842
JW0715	P0AFG3	sucA	2-oxoglutarate decarboxylas	-0.0290205	0.76992274
JW5374	P17109	menD	2-succinyl-5-enolpyruvyl-6-h	0.05665752	0.00015432
JW2258	P37355	yfbB	2-succinyl-6-hydroxy-2,4-cyc	0.01645596	0.3780676
JW1388	P76082	paaF	2,3-dehydroadipyl-CoA hydr	0.08921026	0.14419544

JW2839	P66899	ygeX	2,3-diaminopropionate amn	-0.1030357	0.02484087
JW0588	P15047	entA	2,3-dihydro-2,3-dihydroxybe	-0.0259133	0.30351095
JW2525	POCI31	hcaB	2,3-dihydroxy-2,3-dihydroph	-0.0221137	0.82245276
JW0586	P10378	entE	2,3-dihydroxybenzoate-AMP	0.08628843	0.17071503
JW0339	POABR9	mhpB	2,3-dihydroxyphenylpropiona	-0.0497744	0.18513662
JW3547	P37672	yiaK	2,3-diketo-L-gulonate reduci	0.0199267	0.26429538
JW5651	P37675	yiaN	2,3-diketo-L-gulonate TRAP	-0.5407217	0.00073835
JW3549	P37674	yiaM	2,3-diketo-L-gulonate TRAP	-0.0371124	0.23309424
JW3551	P37676	yiaO	2,3-diketo-L-gulonate-bindir	0.14482861	0.08708849
JW3052	P42593	fadH	2,4-dienoyl-CoA reductase, I	0.01755443	0.6414153
JW5499	Q46857	dkgA	2,5-diketo-D-gluconate redu	-0.0267406	0.36801906
JW0197	P30863	dkgB	2,5-diketo-D-gluconate redu	0.02551518	0.3855537
JW5011	P37025	ligT	2'-5' RNA ligase	0.06875453	0.02535416
JW4171	P08331	cpdB	2':3'-cyclic-nucleotide 2'-ph	0.00879063	0.76778308
JW2777	POADR6	ygdE	23S rRNA C2498 2'-O-ribose	0.14688828	0.01828809
JW1811	P36999	rrmA	23S rRNA m(1)G745 methyl	-0.0590032	0.01296014
JW5513	P42596	ygjO	23S rRNA m(2)G1835 meth	0.00950064	0.61725626
JW0931	P75864	ycbY	23S rRNA m(2)G2445 and m	-0.1018162	0.00077605
JW0631	POA818	ybeA	23S rRNA m(3)Psi1915 pseu	0.05586709	0.02044358
JW5898	P75876	yccW	23S rRNA m(5)C1962 methy	-0.0067345	0.65579551
JW2756	P55135	rumA	23S rRNA m(5)U1939 meth	0.02129046	0.32521459
JW5107	P75782	ybiN	23S rRNA m(6)A1618 methy	-0.0067662	0.76653513
JW3466	P37634	yhiR	23S rRNA m(6)A2030 methy	0.02258741	0.36232519
JW2576	P33643	rluD	23S rRNA pseudouridine(19	-0.0269674	0.12046455
JW1121	P75966	ymfC	23S rRNA pseudouridine(24	-0.1131625	0.02870614
JW3982	P32684	yjbC	23S rRNA pseudouridine(26	0.21569337	0.00578486
JW1261	P37765	rluB	23S rRNA pseudouridine(26	0.00744416	0.77914534
JW1072	POAA39	rluC	23S rRNA pseudouridine(95	0.06195164	0.01371294
JW3146	POCOR7	rrmJ	23S rRNA U2552 2'-O-ribose	0.09631105	0.03975397
JW0338	P77397	mhpA	3-(3-hydroxyphenyl)propiona	-0.0050174	0.77085009
JW1683	P05194	aroD	3-dehydroquinate dehydrata	0.19334468	0.0543661
JW3352	P07639	aroB	3-dehydroquinate synthase	-0.0079749	0.81926602
JW0737	POAB91	aroG	3-deoxy-D-arabino-heptulos	0.04528195	0.09965631
JW1694	P00887	aroH	3-deoxy-D-arabino-heptulos	0.04538398	0.31020443
JW3165	POABZ4	kdsC	3-deoxy-D-manno-octulosor	-0.0221716	0.6081186
JW1390	P76083	paaH	3-hydroxyadipyl-CoA dehydr	-0.1077619	0.004191
JW5046	P77589	mhpT	3-hydroxyphenylpropionic tr	0.00223677	0.91066445
JW0071	POA6A6	leuC	3-isopropylmalate dehydrat	0.1345512	0.00240557
JW0070	P30126	leuD	3-isopropylmalate dehydrat	0.01290592	0.83618217
JW5807	P30125	leuB	3-isopropylmalate dehydrog	0.26619334	0.13465379
JW3553	P37678	sgbH	3-keto-L-gulonate 6-phosph	-0.0041485	0.8959562
JW4154	P39304	ulaD	3-keto-L-gulonate 6-phosph	0.13503125	0.00137601
JW5578	P21151	fadA	3-ketoacyl-CoA thiolase (thi	-0.0823507	0.29748236
JW2505	P31142	sseA	3-mercaptopyruvate sulfurtr	0.06120503	0.03051086
JW0130	P31057	panB	3-methyl-2-oxobutanoate hy	0.05832602	0.39302823

JW3518	P05100	tag	3-methyl-adenine DNA glyco	0.11028256	0.00971054
JW2053	P04395	alkA	3-methyl-adenine DNA glyco	-0.0433042	0.11305472
JW2308	P0AG03	ubiX	3-octaprenyl-4-hydroxybenz	0.00754816	0.97291603
JW1081	P0AAI5	fabF	3-oxoacyl-[acyl-carrier-prote	-0.1611774	0.00386397
JW1077	P0A6R0	fabH	3-oxoacyl-[acyl-carrier-prote	0.08871444	0.01708626
JW1392	P0C7L2	paaJ	3-oxoadipyl-CoA/3-oxo-5,6- ϵ	0.08273519	0.00561353
JW2524	P0ABW0	hcaC	3-phenylpropionate dioxyge	0.04565247	0.00225601
JW2522	P0ABR5	hcaE	3-phenylpropionate dioxyge	-0.0157746	0.4729639
JW2523	Q47140	hcaF	3-phenylpropionate dioxyge	-0.1065538	5.06E-07
JW4351	P0AGB0	serB	3-phosphoserine phosphata	0.1340982	0.00813573
JW0890	P23721	serC	3-phosphoserine/phosphohy	0.19420527	0.00337718
JW3853	P0A9V8	yihU	3-sulpholactaldehyde (SLA)	-0.1101724	0.39134139
JW3000	P0AEW4	cpdA	3',5' cAMP phosphodiestera	0.0032107	0.92157593
JW4172	P22255	cysQ	3'(2'),5'-bisphosphate nucle	0.19045952	0.00794534
JW3134	P0ADZ4	rpsO	30S ribosomal subunit prote	-0.0177786	0.37549242
JW0022	P0A7U7	rpsT	30S ribosomal subunit prote	-0.0187924	0.56750569
JW3037	P68679	rpsU	30S ribosomal subunit prote	0.02893477	0.33136569
JW4158	P02358	rpsF	30S ribosomal subunit prote	-0.1205043	0.10959556
JW3136	P0A7G2	rbfA	30s ribosome binding factor	-0.2261172	0.08845111
JW3379	P15977	malQ	4-alpha-glucanotransferase	-0.0138058	0.28412037
JW2251	P76473	arnT	4-amino-4-deoxy-L-arabinos	-0.0474651	0.05884056
JW1082	P28305	pabC	4-amino-4-deoxychorismate	-0.0195167	0.55479191
JW2637	P22256	gabT	4-aminobutyrate aminotran	-0.0086114	0.66534423
JW1295	P50457	puuE	4-aminobutyrate aminotran	0.00543999	0.90461566
JW0051	P19624	pdxA	4-hydroxy-L-threonine phosp	0.2949379	0.05567603
JW0343	P51020	mhpE	4-hydroxy-2-oxovalerate/4-hy	-0.0150789	0.4418481
JW1456	P31992	ydcE	4-oxalocrotonate tautomera	-0.0020014	0.94634989
JW3007	P24197	zupT	4,5- DOPA-extradiol-dioxyge	-0.0697492	0.04378331
JW3440	P37623	acpT	4'-phosphopantetheinyl trar	0.06482067	0.01797077
JW5588	P0ADP2	yigI	4HBT thioesterase family pr	0.03124612	0.34359907
JW5113	P75809	ybjI	5-amino-6-(5-phospho-D-rik	0.07170007	0.35969707
JW0891	P0A6D3	aroA	5-enolpyruvylshikimate-3-ph	0.10665751	0.02396147
JW2879	P0AC28	ygfA	5-formyltetrahydrofolate cy	0.02176892	0.29526624
JW4223	P0A9P9	idnO	5-keto-D-gluconate-5-reduc	0.06870862	0.02134568
JW3719	P0A6U3	gidA	5-methylaminomethyl-2-thi	0.0487053	0.08657798
JW5871	P15005	mcrB	5-methylcytosine-specific re	0.01065833	0.74551335
JW5789	P15006	mcrC	5-methylcytosine-specific re	-0.031176	0.06166256
JW3805	P25665	metE	5-methyltetrahydropteroyltr	-0.1560491	0.04383048
JW4053	P16692	phnP	5-phospho-alpha-D-ribosyl 1	-0.0206718	0.40108464
JW3913	P0AEZ1	metF	5,10-methylenetetrahydrofc	0.12437997	0.09893863
JW3835	P00582	polA	5' to 3' DNA polymerase an	-0.1283145	0.16084709
JW0155	P0AF12	pfs	5'-methylthioadenosine/S-a	-0.1135322	0.07075335
JW2288	P76491	yfbR	5'-nucleotidase	-0.0769633	0.03608079
JW1114	P27431	ycfD	50S ribosomal protein L16 a	-0.0882631	0.001663
JW5035	P0A7N1	ykgM	50S ribosomal protein L31 t'	-0.0549348	0.00269341

JW3947	P0A7L0	rplA	50S ribosomal subunit prote	0.04296979	0.09669343
JW3946	P0A7J7	rplK	50S ribosomal subunit prote	-0.1409869	0.00054421
JW2173	P68919	rplY	50S ribosomal subunit prote	0.0178315	0.72121853
JW3907	P0A7M9	rpmE	50S ribosomal subunit prote	-0.0299574	0.39273059
JW1075	P0A7N4	rpmF	50S ribosomal subunit prote	-0.079673	0.01742777
JW3611	P0A7N9	rpmG	50S ribosomal subunit prote	-0.0690273	0.11706207
JW3261	P0A7Q6	rpmJ	50S ribosomal subunit prote	0.02878205	0.26038367
JW4161	P0A7R1	rplI	50S ribosomal subunit prote	-0.2102288	0.00018583
JW5568	P32143	yihV	6-deoxy-6-sulphofructose ki	0.01675856	0.4206572
JW3852	P32141	yihT	6-deoxy-6-sulphofructose-1-	-0.0213678	0.44962833
JW5126	P75863	ycbX	6-N-hydroxylaminopurine de	-0.0609008	0.12456825
JW5559	P32157	yiiM	6-N-hydroxylaminopurine re	-0.0227019	0.33410933
JW2869	Q46829	bgIA	6-phospho-beta-glucosidase	0.03946348	0.14753799
JW3887	P0A796	pfkA	6-phosphofructokinase I	-0.0066103	0.92588189
JW5280	P06999	pfkB	6-phosphofructokinase II	0.1006803	0.03312209
JW1840	P0ADF6	edd	6-phosphogluconate dehydr	0.01577556	0.54025132
JW2011	P00350	gnd	6-phosphogluconate dehydr	-0.0161463	0.64540635
JW0750	P52697	ybhE	6-phosphogluconolactonase	-0.0628185	0.04080902
JW2735	P65870	ygcM	6-pyruvoyl tetrahydrobiopte	0.03504246	0.02453856
JW1611	P0AET8	hdhA	7-alpha-hydroxysteroid dehy	0.11522798	0.23008793
JW2748	P64554	ygcF	7-carboxy-7-deazaguanine s	-0.0337064	0.49360022
JW0434	P77756	ybaX	7-cyano-7-deazaguanine (pr	-0.080165	0.00402749
JW2765	Q46920	yqcD	7-cyano-7-deazaguanine rec	-0.0252565	0.77671258
JW0757	P12995	bioA	7,8-diaminopelargonic acid	0.12482282	0.00193939
JW3144	P0AC13	folP	7,8-dihydropteroate synthas	0.19403855	0.05940984
JW0759	P12998	bioF	8-amino-7-oxononanoate sy	0.18904023	0.00102789
JW4272	P39370	yjHS	9-O-acetyl N-acetylneurami	-0.0242719	0.1039236
JW1903	P0AFT2	yecS	ABC family putative inner m	0.01826114	0.4429515
JW3162	P63386	yrbF	ABC transporter maintaining	-0.0069836	0.81325064
JW3161	P64606	yrbE	ABC transporter maintaining	-0.0270542	0.22381158
JW2343	P76506	vacJ	ABC transporter maintaining	-0.038107	0.11627134
JW3159	P0ADV7	yrbC	ABC transporter maintaining	-0.084174	0.04495221
JW3315	P63389	yheS	ABC-F family protein predic	0.03091353	0.2322607
JW0804	P0A9U3	ybiT	ABC-F family putative regul	-0.2324945	0.05658251
JW5505	Q46868	yqiC	accessory factor for ubiquin	-0.0690734	0.17518517
JW0342	P77580	mhpF	acetaldehyde-CoA dehydrog	-0.033594	0.36307078
JW2293	P0A6A3	ackA	acetate kinase A and propio	-0.0356601	0.21690816
JW4028	P32705	actP	acetate transporter	-0.0060734	0.64179685
JW3645	P0ADF8	ilvN	acetolactate synthase 1 sma	-0.0173141	0.75377569
JW3646	P08142	ilvB	acetolactate synthase 2 larg	-0.1983709	0.14690397
JW3646	P08142	ilvB	acetolactate synthase 2 larg	0.08521448	0.29607556
JW3742	P0ADG1	ilvM	acetolactate synthase 2 sma	-0.0098606	0.71332261
JW0076	P00893	ilvI	acetolactate synthase 3 larg	-0.0103294	0.68056332
JW0077	P00894	ilvH	acetolactate synthase 3, sm	-0.0073246	0.78926004
JW0465	P23872	aes	acetyl esterase	0.11309401	0.0501982

JW2218	P76461	atoB	acetyl-CoA acetyltransferase	-0.0541181	0.09468623
JW4030	P27550	acs	acetyl-CoA synthetase	-0.0422548	0.5786219
JW2215	P76458	atoD	acetyl-CoA:acetoacetyl-CoA	-0.11699	0.01633947
JW2216	P76459	atoA	acetyl-CoA:acetoacetyl-CoA	-0.0444807	0.06360255
JW2368	P76518	yfdE	acetyl-CoA:oxalate CoA-tran	0.01511646	0.66531126
JW5553	P0A6C8	argB	acetylglutamate kinase	-0.0046815	0.90249769
JW3929	P23908	argE	acetylornithine deacetylase	0.15142753	0.01821486
JW3929	P23908	argE	acetylornithine deacetylase	0.200931	0.09785792
JW4015	P0AE22	aphA	acid phosphatase/phosphot	-0.0096358	0.73296724
JW5944	P37630	yhiM	acid resistance protein, inne	-0.0245373	0.35211672
JW3484	P37639	gadX	acid resistance regulon tran	0.00352366	0.88217563
JW5826	P36560	asr	acid shock-inducible peripla:	0.0171691	0.57461109
JW3157	P0A9W6	yrbA	acid stress protein; putative	-0.0527476	0.29000778
JW2231	P27294	inaA	acid-inducible Kdo/WaaP fa	-0.1541473	0.30193096
JW1711	P76206	ydiY	acid-inducible putative oute	-0.0150821	0.58885913
JW3479	P0AET5	hdeD	acid-resistance membrane p	0.01595281	0.35888948
JW5669	P0AET2	hdeB	acid-resistance protein	-0.0340513	0.42627181
JW5103	P75764	ybhJ	aconitase family protein	-0.0103694	0.51607201
JW1268	P25516	acnA	aconitate hydratase 1; aconi	-0.0317578	0.13845288
JW0114	P36683	acnB	aconitate hydratase 2; aconi	0.03614104	0.07670133
JW3232	P0ACT2	envR	acrAB operon transcriptiona	-0.0444983	0.07622095
JW5102	P0AAW9	ybhT	AcrAB-TolC efflux pump acc	-0.1644939	0.04241593
JW5646	P37690	envC	activator of AmiB,C murein	0.07999688	0.00465598
JW2712	P0ADA3	nlpD	activator of AmiC murein hy	0.01332426	0.88666937
JW3837	P0A8H6	yihI	activator of Der GTPase	0.0348728	0.09227934
JW0394	P21515	yajB	acyl carrier protein (ACP) ph	0.02278219	0.00249959
JW2999	P0A8Z7	yqiA	acyl CoA esterase	-0.1919794	0.09828046
JW4148	P39298	yjFP	acyl CoA esterase	-0.1374926	0.02698598
JW5020	Q47146	fadE	acyl coenzyme A dehydroge	0.05162579	0.09024026
JW1245	P0A8Z0	yciA	acyl-CoA esterase	-0.0816655	0.00227863
JW0673	P75736	ybfF	acyl-CoA esterase	0.01724136	0.27574977
JW1794	P69451	fadD	acyl-CoA synthetase (long-cl	0.03152273	0.16251004
JW0726	P0A8Z3	ybgC	acyl-CoA thioester hydrolase	-0.1117744	0.03421768
JW0483	P0ADA1	tesA	acyl-CoA thioesterase 1 and	-0.0862472	0.06031318
JW0442	P0AGG2	tesB	acyl-CoA thioesterase 2	-0.0543877	0.49010214
JW0755	P46130	ybhC	acyl-CoA thioesterase, lipop	0.14518802	0.02114408
JW3172	P0A894	yhbJ	adaptor protein for GlnZ/G	0.0287263	0.5445224
JW2928	P17802	mutY	adenine DNA glycosylase	0.06845713	0.01483333
JW3692	P31466	yieG	adenine permease, high affi	0.00871708	0.86976418
JW5636	P31440	yicO	adenine permease, high affi	0.00938457	0.73850613
JW0458	P69503	apt	adenine phosphoribosyltran:	-0.0455085	0.18074713
JW2720	P0A6J1	cysC	adenosine 5'-phosphosulfat	0.15292806	0.00030396
JW1615	P22333	add	adenosine deaminase	-0.2905506	0.01652023
JW3360	P45799	nudE	adenosine nucleotide hydrol	-0.0253374	0.30595075
JW3778	P00936	cyaA	adenylate cyclase	0.03035575	0.1221368

JW4135	P0A7D4	purA	adenylosuccinate synthetase	0.03756264	0.14331582
JW3956	P30138	thiF	adenylyltransferase, modified	0.12047887	0.01586683
JW2227	P45508	yfaL	adhesin	0.05732309	0.01589447
JW5422	P52143	ypjA	adhesin-like autotransporter	-0.0321225	0.12305301
JW4077	P33234	adiY	adi system transcriptional a	0.01072552	0.68576081
JW3596	P24173	rfaC	ADP-heptose:LPS heptosyl tr	-0.1843885	0.145709
JW3594	P67910	rfaD	ADP-L-glycero-D-mannohepi	-0.4486635	5.74E-05
JW3002	Q93K97	nudF	ADP-ribose pyrophosphatas	-0.1752508	0.00892662
JW2086	P76418	yegU	ADP-ribosylglycohydrolase f	0.08481694	0.05980497
JW5536	P0AEC3	arcB	aerobic respiration control s	-0.1866409	0.00215716
JW2904	P60651	speB	agmatinase	0.01348899	0.66757769
JW2645	P64550	ygaW	alanine exporter, alanine-in	-0.0164583	0.48849476
JW4013	P0A6B4	alr	alanine racemase, biosynth	-0.1504454	0.28186516
JW1179	P29012	dadX	alanine racemase, catabolic	0.01253384	0.77707765
JW2667	P00957	alaS	alanyl-tRNA synthetase	0.1678295	0.00690934
JW0347	P25437	frmA	alcohol dehydrogenase clas	0.00053712	0.98408311
JW1412	P25553	aldA	aldehyde dehydrogenase A,	0.05709582	0.00356313
JW3561	P37685	aldB	aldehyde dehydrogenase B	0.06635784	0.08421511
JW2439	P77445	eutE	aldehyde oxidoreductase, et	0.08720215	0.03009369
JW2978	Q46856	yqhD	aldehyde reductase, NADPH	-0.0016504	0.94854098
JW1770	P76234	yeaE	aldo-keto reductase, methyl	-0.0183266	0.50869873
JW0739	P0A9C3	galM	aldose 1-epimerase; type-1	0.15771456	1.49E-05
JW0916	P0AAI1	ssuB	aliphatic sulfonate ABC tran	-0.0691234	0.06608713
JW0919	P75853	ssuA	aliphatic sulfonate ABC tran	-0.0111998	0.80077464
JW5121	P75851	ssuC	aliphatic sulfonate ABC tran	0.01997151	0.29696329
JW1017	P75914	ycdX	alkaline phosphatase	0.04447736	0.01758729
JW0918	P80645	ssuD	alkanesulfonate monooxyge	-0.0514347	0.07074785
JW0598	P0AE08	ahpC	alkyl hydroperoxide reducta	0.01599289	0.59502639
JW0599	P35340	ahpF	alkyl hydroperoxide reducta	0.46323428	0.00780736
JW0504	P77425	allC	allantoate amidohydrolase	-0.0556361	0.01262074
JW0500	P77671	allB	allantoinase	-0.1141839	1.11E-05
JW0492	P0ACR0	ybbS	allD operon transcriptional a	-0.0514854	0.00180091
JW4046	P32719	alsE	allulose-6-phosphate 3-epin	-0.0256807	0.31934731
JW1302	P76041	ycjM	alpha amylase catalytic don	-0.0318928	0.35287327
JW3543	P25718	malS	alpha-amylase	-0.0835442	0.00619929
JW5566	P0A8Y3	yihX	alpha-D-glucose-1-phosphat	0.01749666	0.69714071
JW3095	P23522	garL	alpha-dehydro-beta-deoxy-L	-0.0743939	0.10668656
JW4080	P06720	melA	alpha-galactosidase, NAD(P	0.06145692	0.18312629
JW3051	P42592	ygjK	alpha-glucosidase	0.03389228	0.56043287
JW2571	P0AEX3	kgtP	alpha-ketoglutarate transpo	-0.020462	0.42811415
JW0721	P54746	mngB	alpha-mannosidase	-0.0134283	0.43230002
JW3253	P36675	yhdL	alternate ribosome-rescue f	-0.2504453	0.02338683
JW0187	P40711	yaeJ	alternative stalled-ribosom	0.05627572	0.06719786
JW3062	P42604	uxaA	altronate hydrolase	-0.0899638	0.0009161
JW1514	P0A6L7	uxaB	altronate oxidoreductase, N	-0.0813993	0.00802675

JW2309	P0AG16	purF	amidophosphoribosyltransfe	0.1567499	0.04010051
JW1942	P0AA70	yedA	amino acid exporter for phe	0.05136761	0.07435452
JW0320	P75693	yahN	amino acid exporter for prol	0.05329506	0.19286567
JW2786	P0A6C5	argA	amino acid N-acetyltransfer	-0.0447355	0.69903245
JW0227	P15288	pepD	aminoacyl-histidine dipeptic	0.04304494	0.20606127
JW1776	P64483	yeaK	aminoacyl-tRNA editing dor	-0.042761	0.42781782
JW4054	P16691	phnO	aminoalkylphosphonate N-a	-0.0207087	0.45352249
JW1801	P05041	pabB	aminodeoxychorismate synt	0.02476765	0.60402376
JW3323	P00903	pabA	aminodeoxychorismate synt	-0.0818244	0.00011344
JW2454	P24177	acrD	aminoglycoside/multidrug e	-0.013525	0.77164706
JW2873	P27248	gcvT	aminomethyltransferase, te	-0.0314004	0.29211188
JW2381	P77585	ypdE	aminopeptidase	0.06789239	0.04021173
JW2507	P37095	pepB	aminopeptidase B	0.18996835	0.00979996
JW2723	P10423	iap	aminopeptidase in alkaline	-0.0682956	0.24551224
JW0915	P04825	pepN	aminopeptidase N	-0.0112681	0.68998689
JW0441	P69681	amtB	ammonium transporter	0.00165156	0.95345476
JW1963	P0AE12	amn	AMP nucleosidase	-0.0945379	0.08919435
JW0107	P0AE14	ampE	ampicillin resistance inner r	0.14362336	0.01370944
JW0040	P60566	fixA	anaerobic carnitine reductio	0.04582435	0.00285925
JW4083	P14407	fumB	anaerobic class I fumarate f	-0.08272	0.00013295
JW4115	P00363	frdA	anaerobic fumarate reducta	-0.0388826	0.38839824
JW3481	P37636	mdtE	anaerobic multidrug efflux t	0.07892251	0.01750611
JW3482	P37637	mdtF	anaerobic multidrug efflux t	0.08093613	0.00018258
JW5843	P37013	norR	anaerobic nitric oxide reduc	0.02499317	0.17591553
JW2680	Q46877	norV	anaerobic nitric oxide reduc	-0.0220192	0.53259989
JW4197	P28903	nrdD	anaerobic ribonucleoside-tri	-0.0578261	0.0812188
JW4196	P0A9N8	nrdG	anaerobic ribonucleotide rec	-0.0067469	0.71740269
JW2236	P13033	glpB	anaerobic sn-glycerol-3-pho	0.15109892	0.04524429
JW2237	P0A996	glpC	anaerobic sn-glycerol-3-pho	-0.0068516	0.66709133
JW2235	P0A9C0	glpA	anaerobic sn-glycerol-3-pho	-0.039841	0.12591743
JW2497	P76576	yfgM	ancillary SecYEG translocon	0.00942899	0.5548835
JW1632	P77570	ydhH	anhydro-N-acetylmuramic a	0.03018922	0.36795959
JW0310	P77736	yahD	ankyrin repeat protein	-0.0003154	0.99268706
JW3977	P23325	arpA	ankyrin repeat protein	0.00045648	0.98978311
JW3905	P0ACN7	cytR	Anti-activator for CytR-CRP	-0.0329731	0.37922831
JW1697	P76204	ydiV	anti-FlhD4C2 factor, inactive	0.01419516	0.76087351
JW1958	P76346	yeel	anti-repressor for DgsA(Mlc	0.05571955	0.22341336
JW1150	P75990	ycgF	anti-repressor for YcgE, blue	0.03918287	0.1744242
JW0373	P0AAN9	yaiB	anti-RssB factor, RpoS stabi	-0.048668	0.00623965
JW2555	P0AFX9	rseB	anti-sigma E factor, binds R	-0.1031647	0.12438625
JW4252	P23485	fecR	anti-sigma transmembrane	0.02375104	0.39850674
JW1283	P0AAH8	sapF	antimicrobial peptide ABC ti	-0.0369507	0.12249577
JW1284	P0AAH4	sapD	antimicrobial peptide ABC ti	0.03547837	0.49755507
JW1287	Q47622	sapA	antimicrobial peptide transp	-0.0816642	0.07514746
JW1286	P0AGH3	sapB	antimicrobial peptide transp	-0.0054044	0.80012677

JW1285	P0AGH5	sapC	antimicrobial peptide transp	0.06727139	0.04155095
JW2100	P0AF08	mrp	antiporter inner membrane	0.18670529	0.03445013
JW1433	P67697	ydcQ	antitoxin for the HicAB toxir	0.00518178	0.81840612
JW4089	P0AF61	yjdK	antitoxin of GhoTS toxin-ant	-0.0226982	0.44296871
JW1501	P23873	hipB	antitoxin of HipAB toxin-ant	0.11434902	6.17E-05
JW1556	P0C079	relB	antitoxin of the RelE-RelB t	0.05836035	0.13827762
JW3098	P15373	sohA	antitoxin of the SohA(PrIF)-	0.09635977	0.12119241
JW0222	Q47156	yafN	antitoxin of the YafO-YafN t	0.02629782	0.20771284
JW0216	Q47150	dinJ	antitoxin of YafQ-DinJ toxin-	-0.057028	0.10642848
JW3053	P67701	ygjM	antitoxinof the HigB-HigA tc	-0.0528765	0.13554427
JW0606	P0A6G5	citX	apo-citrate lyase phosphorik	-0.0157764	0.65824859
JW0859	P60844	aqpZ	aquaporin Z	0.09190564	0.0384853
JW0063	P0A9E0	araC	ara regulon transcriptional a	-0.1093504	0.00556655
JW1521	P31122	ydeA	arabinose efflux transporter	0.01229344	0.64026252
JW2809	P0AE24	araE	arabinose transporter	0.03684588	0.34482043
JW3926	P32677	yijO	AraC family putative transcr	0.07472013	0.00738306
JW3656	P31449	yidL	AraC family putative transcr	0.02829101	0.76028091
JW0848	P0AAF6	artP	arginine ABC transporter AT	0.00941393	0.69159267
JW0844	P30860	artJ	arginine ABC transporter pe	0.05453448	0.4118117
JW0846	P0AE34	artQ	arginine ABC transporter pe	-0.0120879	0.68263839
JW0845	P0AE30	artM	arginine ABC transporter pe	-0.0106074	0.72531675
JW5731	P28629	adiA	arginine decarboxylase	0.00266524	0.93161991
JW1736	P0AE37	astA	arginine succinyltransferase	0.15018769	0.00115483
JW2890	P11667	argO	arginine transporter	0.02273311	0.60349112
JW0847	P30859	artI	arginine transporter subunit	0.00109021	0.9631588
JW4076	P60061	adiC	arginine:agmatine antiporte	0.02859424	0.3353012
JW3932	P11447	argH	argininosuccinate lyase	0.2251399	0.07384751
JW3140	P0A6E4	argG	argininosuccinate synthetas	0.10904057	0.00635867
JW0381	P0AE28	aroM	AroM family protein	-0.2023949	0.28638218
JW1316	P07604	tyrR	aromatic amino acid biosyn:	-0.0110216	0.57557129
JW1469	P46136	yddG	aromatic amino acid export:	0.07128093	0.01386286
JW0108	P15993	aroP	aromatic amino acid transp:	-0.3680474	0.04911561
JW3470	P0AB96	arsC	arsenate reductase	-0.218128	0.14557385
JW3468	P37309	arsR	arsenical resistance operon	-0.0105003	0.8502481
JW3469	P0AB93	arsB	arsenite/antimonite transpc	0.08403655	0.00519073
JW5434	P24242	ascG	asc operon transcriptional re	-0.0725189	0.09698242
JW2808	P03813	ygeA	Asp/Glu_racemase family p	0.00726837	0.67026828
JW3722	P00963	asnA	asparagine synthetase A	-0.0072811	0.77504928
JW0660	P22106	asnB	asparagine synthetase B	0.06391076	0.01355134
JW0127	P0A790	panD	aspartate 1-decarboxylase	-0.0100833	0.65676341
JW0911	P00509	aspC	aspartate aminotransferase	-0.0803372	0.25174843
JW4099	P0AC38	aspA	aspartate ammonia-lyase	0.02190074	0.27866629
JW4204	P0A786	pyrB	aspartate carbamoyltransfe	0.02749225	0.47604291
JW4203	P0A7F3	pyrI	aspartate carbamoyltransfe	0.04901468	0.00287669
JW1059	P75933	flgA	assembly protein for flagelli	0.11451059	0.0108662

JW2195	P0A9I5	napD	assembly protein for peripla	0.04725101	0.03714938
JW0102	P36646	hofC	assembly protein in type IV	-0.0394912	0.15988177
JW2001	P60757	hisG	ATP phosphoribosyltransfer	0.09491168	0.1703615
JW5611	P0ABC0	atpI	ATP synthase, membrane-bi	0.03371467	0.38834652
JW1447	P76116	yncE	ATP-binding protein, peripla	0.00108421	0.95817537
JW1005	P0A9K1	phoH	ATP-binding protein; putativ	-0.0297227	0.40781035
JW3627	P24230	recG	ATP-dependent DNA helicase	-0.1451249	0.00938473
JW0784	P27296	dinG	ATP-dependent DNA helicase	0.00199923	0.9425215
JW5855	P15043	recQ	ATP-dependent DNA helicase	0.03069433	0.32499933
JW1849	P0A812	ruvB	ATP-dependent DNA helicase	-0.0368537	0.39751011
JW5531	P0A9P6	deaD	ATP-dependent RNA helicase	-0.1239666	0.04626991
JW2560	P21507	srmB	ATP-dependent RNA helicase	-0.0439451	0.20809917
JW3753	P0A8J8	rhIB	ATP-dependent RNA helicase	-0.0271104	0.55877073
JW0781	P25888	rhIE	ATP-dependent RNA helicase	0.03769356	0.47122714
JW1337	P21693	dbpA	ATP-dependent RNA helicase	-0.1538434	0.21647031
JW3006	P0ADT5	ygiC	ATP-Grasp family ATPase	0.00940721	0.78713149
JW4144	P33222	yjfC	ATP-Grasp family ATPase	0.10500096	0.01286467
JW4019	P0A698	uvrA	ATPase and DNA damage re	0.05908046	0.1647509
JW0866	P0ABH9	clpA	ATPase and specificity subu	-0.0009146	0.97611989
JW0428	P0A6H1	clpX	ATPase and specificity subu	0.03638439	0.21359688
JW5397	P69931	hda	ATPase regulatory factor in	0.04309359	0.05752679
JW1506	P77257	ego	autoinducer 2 import ATP-bi	0.07555505	0.17851691
JW1507	P77672	lsrC	autoinducer 2 import system	-0.0387132	0.20657463
JW1508	P0AFS1	lsrD	autoinducer 2 import system	0.01572622	0.48880325
JW1509	P76142	lsrB	autoinducer 2-binding prote	-0.1057328	0.02681435
JW1511	P64461	lsrG	autoinducer-2 (AI-2) degrad	-0.0236486	0.13668946
JW1504	P77432	ydeV	autoinducer-2 (AI-2) kinase	0.09604303	0.00047364
JW2563	P68066	yfiD	autonomous glycyl radical c	-0.0159574	0.43993184
JW1656	P77552	ydhQ	autotransporter adhesin-rel	0.03688487	0.10334067
JW5659	P37663	yhjY	autotransporter beta-domai	-0.0455992	0.06670233
JW2553	P60785	lepA	back-translocating elongatic	0.04245532	0.00808138
JW0374	P00634	phoA	bacterial alkaline phosphata	-0.0604189	0.17398261
JW2504	P76578	yfhM	bacterial alpha2-macroglobi	0.03175107	0.19211222
JW5710	P0A9W9	yrdA	bacterial transferase hexape	-0.1903675	0.00763912
JW3299	P0AE56	bfd	bacterioferritin-associated f	-0.3629918	0.01337645
JW3298	P0ABD3	bfr	bacterioferritin, iron storage	-0.0737151	0.09180713
JW0558	P0AFA5	nfrB	bacteriophage N4 receptor,	0.06595502	0.06177571
JW0557	P31600	nfrA	bacteriophage N4 receptor,	0.06601604	0.00635674
JW2462	P0A903	nlpB	BamABCDE complex OM bic	0.01760535	0.54002935
JW2496	P77774	yfgL	BamABCDE complex OM bic	0.10931011	0.01713857
JW5655	P0ADK0	yiaF	barrier effect co-colonizatio	-0.0349313	0.18311592
JW0770	P75769	ybhM	BAX Inhibitor-1 family inner	0.00265571	0.88980146
JW5229	P76103	ydcO	BenE family inner membrar	-0.0463514	0.36545651
JW5245	P76146	yneE	bestrophin family putative i	-0.0868561	0.00910373
JW1093	P75949	nagZ	beta N-acetyl-glucosaminid	0.0145063	0.62688211

JW2120	P33363	bgIX	beta-D-glucoside glucohydrc	-0.0990943	0.00443735
JW1609	P05804	uidA	beta-D-glucuronidase	0.0392066	0.16229706
JW2339	P76503	yfcY	beta-ketoacyl-CoA thiolase,	0.00695029	0.80136717
JW5963	P56976	blr	beta-lactam resistance mer	-0.0269219	0.29114658
JW1310	P77366	ycjU	beta-phosphoglucomutase	-0.1092102	0.39323352
JW5955	P39404	bgIJ	bgl operon transcriptional a	-0.0649092	0.00148416
JW5363	P28246	bcr	bicyclomycin/cysteine/sulfo	0.08648779	0.00694377
JW5581	P0A887	ubiE	bifunctional 2-octaprenyl-6-	-0.4015735	0.00327641
JW2226	P17993	ubiG	bifunctional 3-demethylubic	0.09194726	0.15661232
JW3322	P18335	argD	bifunctional acetylornithine	-0.0206611	0.52365063
JW0001	P00561	thrA	Bifunctional aspartokinase/	-0.0534402	0.25685433
JW3911	P00562	metL	Bifunctional aspartokinase/	0.28346001	5.56E-05
JW1573	P38104	rspA	bifunctional D-altronate/D-r	-0.017213	0.68323573
JW1068	P75942	flgJ	bifunctional flagellar rod as	0.13023709	0.00896228
JW2037	P32055	fcl	bifunctional GDP-fucose syn	0.01999809	0.78357784
JW2002	P06988	hisD	bifunctional histidinal dehyd	0.00409044	0.96900877
JW4125	P31806	yjeF	bifunctional NAD(P)H-hydra	-0.0618724	0.02273735
JW2939	Q46836	pppA	bifunctional prepilin leader	0.07837892	0.01862117
JW3297	P25960	gspO	bifunctional prepilin leader	0.23645558	0.02827035
JW1120	P0AEI6	ymfB	bifunctional thiamine pyrim	0.06739201	0.11634264
JW0469	P07024	ushA	bifunctional UDP-sugar hydr	-0.0553524	0.00883361
JW1010	P69434	ycdS	biofilm adhesin polysacchar	0.08864099	0.01143603
JW5756	P0AF96	yjgK	biofilm modulator regulatec	-0.1294941	0.25633846
JW1007	P75905	ycdQ	biofilm PGA synthase PgaCC	0.05882744	0.02324437
JW1006	P69432	ycdP	biofilm PGA synthase PgaCC	0.0426745	0.07147724
JW5152	P0AB33	yceP	biofilm regulator	-0.2637743	0.03066273
JW5239	P76127	bdm	biofilm-dependent modulati	-0.0469311	0.02279551
JW1098	P0AB40	ycfR	biofilm, cell surface and sig	0.04354825	0.04786849
JW5743	P39297	yjfO	bioflm peroxide resistance p	-0.0180492	0.57824048
JW2905	P21170	speA	biosynthetic arginine decarb	0.00340976	0.91064993
JW3175	P46022	mtgA	biosynthetic peptidoglycan t	0.06876259	0.22446494
JW5940	P20099	bisC	biotin sulfoxide reductase	0.02717855	0.12742339
JW0758	P12996	bioB	biotin synthase	0.19071043	0.08539162
JW1154	P75994	ymgC	blue light, low temperature	-0.0162204	0.55409463
JW3419	P22731	livF	branched-chain amino acid	-0.1603277	0.12599748
JW3420	P0A9S7	livG	branched-chain amino acid	-0.0277501	0.30415812
JW3425	P0AD96	livJ	branched-chain amino acid	-0.0347101	0.13444205
JW3422	P0AEX7	livH	branched-chain amino acid	0.00023094	0.99489407
JW3421	P22729	livM	branched-chain amino acid	0.04623905	0.10238815
JW5606	P0AB80	ilvE	branched-chain amino acid	0.0395626	0.5012844
JW0391	P0AD99	brnQ	branched-chain amino acid	-0.0001304	0.99540447
JW3857	P0A8K8	rbn	BrkB family putative transp	0.03669859	0.19016478
JW2714	P0A840	surE	broad specificity 5'(3')-nucl	0.01136884	0.57353795
JW0317	P75691	yahK	broad specificity NADPH-dep	-0.0650155	0.01137794
JW5761	P27250	yjgB	broad specificity NADPH-dep	-0.0643375	0.0975374

JW0069	P31675	setA	broad specificity sugar efflu	-0.109421	0.36195286
JW4207	P39333	yjgI	c-di-GMP-binding biofilm di	-0.1706692	0.14059962
JW0307	P21514	yahA	c-di-GMP-specific phosphod	-0.0858086	0.00176748
JW1832	P76280	yobB	C-N hydrolase family protei	-0.1898644	5.36E-06
JW5735	P0ABN5	dcuA	C4-dicarboxylate antiporter	-0.0154195	0.7295852
JW4084	P0ABN9	dcuB	C4-dicarboxylate transporte	-0.0881472	0.01673643
JW5189	P0AFR2	ychM	C4-dicarboxylic acid transpo	0.0627364	0.00832666
JW3496	P0A830	dctA	C4-dicarboxylic acid, orotate	0.09498216	0.00077919
JW4094	P23890	cadC	cadBA operon transcriptiona	-0.0314558	0.32593045
JW5540	P64614	yhcN	cadmium and peroxide resis	-0.0098919	0.75088728
JW0033	P0AE58	caiF	cai operon transcriptional ac	0.05524865	0.29744166
JW1207	P31801	chaA	calcium/sodium:proton anti	-0.04008	0.72265267
JW5702	P0ACJ8	crp	cAMP-activated global trans	0.38453215	2.25E-05
JW0315	P77624	yahI	carbamate kinase-like prote	-0.0434926	0.10407093
JW2700	P24193	hypE	carbamoyl dehydratase, hyd	0.02633326	0.20178998
JW5433	P30131	hypF	carbamoyl phosphate phosp	0.22524533	0.0304334
JW0030	P0A6F1	carA	carbamoyl phosphate synth	-0.0749478	0.06148268
JW0031	P00968	carB	carbamoyl-phosphate synth	0.0024422	0.96488637
JW5013	P37047	cdaR	carbohydrate diacid regulon	-0.2759362	0.08030217
JW3698	P26218	bglH	carbohydrate-specific outer	-0.0034732	0.86808555
JW5427	P76621	ygaT	carbon starvation protein	0.07508402	0.0851679
JW0590	P15078	cstA	carbon starvation protein in	-0.1689504	5.79E-06
JW5727	P16678	phnK	carbon-phosphorus lyase co	0.0134634	0.7383853
JW4059	P16688	phnJ	carbon-phosphorus lyase, S/	-0.1328841	0.00657173
JW0330	P0ABE9	cynT	carbonic anhydrase	-0.0940391	0.03683649
JW1859	P76290	yecO	carboxy-SAM synthase	-0.0461326	0.00034044
JW1819	P23865	prc	carboxy-terminal protease f	0.2087637	1.68E-05
JW1742	P76222	ynjA	carboxymuconolactone deca	-0.0155225	0.48570848
JW1241	P0A6H8	cls	cardiolipin synthase 1	-0.0674337	0.0021514
JW0772	P0AA84	ybhO	cardiolipin synthase 2	-0.2683355	0.00056678
JW0035	P31551	caiD	carnitiny-CoA dehydratase	0.03197082	0.12898425
JW2731	P38036	ygcB	Cascade complex anti-viral I	0.0378933	0.08532127
JW1721	P21179	katE	catalase HPII, heme d-conta	0.09682627	0.06184709
JW1194	P0ABU2	ychF	catalase inhibitor protein; A	-0.0115674	0.50482348
JW3914	P13029	katG	catalase-peroxidase HPI, he	0.17400456	0.04408164
JW0790	P75780	fiu	catecholate siderophore rec	0.01061188	0.73703338
JW1208	P0AE63	chaB	cation transport regulator	-0.0632543	0.5162686
JW1209	P39163	chaC	cation transport regulator	-0.0134294	0.75989037
JW1747	P76226	ynjF	CDP-alcohol phosphatidyltra	0.07407183	0.12528983
JW3889	P06282	cdh	CDP-diacylglycerol phosphot	0.04644658	0.21000118
JW1720	P0AE60	cedA	cell division modulator	-0.013765	0.52791815
JW3351	P11557	damX	cell division protein that bin	0.17844919	4.51E-06
JW5435	P24241	ascF	cellobiose/arbutin/salicin-s	0.07183151	0.0156919
JW3504	P37657	bcsE	cellulose production protein	-0.0367927	0.19295434
JW5942	P37650	bcsC	cellulose synthase subunit	0.00058749	0.98023669

JW5665	P37653	bcsA	cellulose synthase, catalytic	-0.0448725	0.09705707
JW0014	P08622	dnaJ	chaperone Hsp40, DnaK co-c	-0.11713	0.00370344
JW0013	P0A6Y8	dnaK	chaperone Hsp70, with co-cl	0.09895525	0.00284787
JW1871	P0AE67	cheY	chemotaxis regulator transr	0.00766794	0.80215291
JW1870	P0A9H9	cheZ	chemotaxis regulator, prote	0.0388467	0.42036613
JW1873	P07364	cheR	chemotaxis regulator, prote	-0.0537757	0.17441123
JW1722	P37794	chbG	chito-oligosaccharide deace	-0.090676	0.03273385
JW0667	P75733	ybfM	chitoporin, uptake of chitosu	0.01835571	0.628449
JW0668	P75734	ybfN	chitosugar-induced verified	0.02720769	0.48002321
JW0303	P17444	betA	choline dehydrogenase, a fla	-0.0592829	0.27268593
JW0306	P0ABC9	betT	choline transporter of high a	-0.0693944	0.0508499
JW0305	P17446	betI	choline-inducible betIBA-bei	0.06939013	0.0719745
JW2580	P0A9J8	pheA	chorismate mutase and prepe	-0.0155675	0.71170209
JW2326	P12008	aroC	chorismate synthase	0.27331817	0.01412859
JW5713	P26602	ubiC	chorismate--pyruvate lyase	-0.0412464	0.18193604
JW3691	P0AGE6	yieF	chromate reductase, Class I,	0.02314103	0.41320116
JW1642	P77258	nemA	chromate reductase, quinon	-0.0066913	0.81474411
JW0610	P77390	citC	citrate lyase ligase; [citrate	-0.0413984	0.20160257
JW0609	P69330	citD	citrate lyase, acyl carrier (ga	0.02138941	0.17208284
JW5087	P75726	citF	citrate lyase, citrate-ACP tra	-0.0347386	0.16752802
JW0608	P0A9I1	citE	citrate lyase, citryl-ACP lyas	0.00093133	0.96370003
JW0710	P0ABH7	gltA	citrate synthase	0.12771053	0.08848629
JW0604	P0AE74	citT	citrate/succinate antiporter,	-0.0126736	0.62053691
JW4070	P0DM85	yjdA	clamp-binding sister replica	0.25617273	0.00166223
JW3197	P0AFZ3	sspB	ClpXP protease specificity ei	0.02606043	0.37162252
JW1262	P0A9H5	btuR	cob(I)yrinic acid a,c-diamide	0.039803	0.12064435
JW2443	P65643	eutT	cobalamin adenosyltransfer	0.06753511	0.1331054
JW1970	P36561	cobS	cobalamin synthase	-0.0868349	0.2185634
JW1971	P0AE76	cobU	cobinamide kinase and cobi	0.01811506	0.54513396
JW2664	P0ADR0	yqaA	COG1238 family inner mem	0.03608264	0.25734853
JW1445	P76114	yncC	colanic acid and biofilm gen	-0.0843747	0.04343072
JW2030	P71242	wcaK	colanic acid biosynthesis pro	-0.1009997	0.04045784
JW2028	P71244	wcaM	colanic acid biosynthesis pro	0.04927652	0.09462327
JW2047	P0A930	wza	colanic acid export protein; c	-0.0092884	0.70777735
JW5106	P0AAX6	ybiM	colanic acid mucoidy stimuli	0.00879827	0.76851255
JW2046	P0AAB2	wzb	colanic acid production prot	-0.0094345	0.79935588
JW2045	P76387	wzc	colanic acid production tyros	-0.0008899	0.92554869
JW2032	P71241	wcaJ	colanic biosynthesis UDP-glu	0.04135906	0.09917414
JW0975	P0AAA5	ymcE	cold shock gene	0.06854073	0.08349389
JW2578	P0AD49	yfiA	cold shock protein associate	0.06505271	0.00651594
JW0974	P0A978	cspG	cold shock protein homolog,	-0.1133164	0.40601048
JW1537	P76154	ydfK	cold shock protein, function	0.04191597	0.24122622
JW1369	P76073	ynaE	cold shock protein, Rac prop	-0.0019993	0.87348212
JW1731	P76214	ydjR	cold- and stress-inducible pr	-0.0693847	0.01070125
JW2142	P17315	cirA	colicin IA outer membrane r	-0.0309202	0.3061878

JW5631	P31456	cbrA	colicin M resistance protein	0.03207164	0.45392782
JW2310	P08550	cvpA	colicin V production protein	-0.0912793	0.16170485
JW5120	P37443	ycal	ComEC family inner membr	0.00767075	0.78682309
JW1256	P00895	trpE	component I of anthranilate	-0.0849123	0.05212599
JW1852	P0A814	ruvC	component of RuvABC resol	0.16386355	0.40896425
JW1850	P0A809	ruvA	component of RuvABC resol	-0.4220662	0.00327083
JW5273	P77522	sufB	component of SufBCD Fe-S c	0.013806	0.69605381
JW1671	P77689	sufD	component of SufBCD Fe-S c	0.11137399	0.00145232
JW1346	P38394	ydaE	conserved protein, Rac prop	0.08657905	1.27E-05
JW0618	P0A972	cspE	constitutive cold shock fami	-0.0278459	0.2150426
JW1830	P0AA57	yobA	CopC family protein	0.07843588	0.06324851
JW5929	P0ADQ5	yiiE	CopG family putative transc	0.02809565	0.24856942
JW0473	Q59385	copA	copper transporter	0.05706226	0.39648195
JW0476	P0A9G4	cueR	copper-responsive regulon t	0.05625879	0.06087485
JW5082	P77485	cusS	copper-sensing histidine kin	-0.0240816	0.06346288
JW0564	P38054	cusA	copper/silver efflux system,	0.02800861	0.29911066
JW0563	P77239	cusB	copper/silver efflux system,	-0.4172217	0.0001351
JW0561	P77211	cusC	copper/silver efflux system,	0.0121369	0.52904626
JW3838	P32131	hemN	coproporphyrinogen III oxida	-0.0986968	0.04814321
JW1982	P39180	flu	CP4-44 prophage; antigen 4	0.03928914	0.13205051
JW1986	P76364	yeeU	CP4-44 prophage; cytoskelet	-0.0787628	0.11422476
JW5326	NA	yoeA	CP4-44 prophage; putative c	0.09968069	0.00743713
JW1984	P76362	yeeS	CP4-44 prophage; putative C	0.04148519	0.05522631
JW1983	P76361	yeeR	CP4-44 prophage; putative r	-0.0130675	0.5730361
JW1987	P64524	yeeV	CP4-44 prophage; toxin of th	0.02145832	0.43934897
JW1985	P64521	yeeT	CP4-44 prophage; uncharact	0.01201003	0.53731299
JW1988	P64526	yeeW	CP4-44 prophage; uncharact	0.03131505	0.07881217
JW5419	P52131	yfjP	CP4-57 prophage; 50S ribosc	-0.3228824	0.00285927
JW2626	P52141	yfjZ	CP4-57 prophage; antitoxin c	0.00967874	0.62673293
JW2619	NA	yfjU	CP4-57 prophage; conservec	0.08355548	0.00039489
JW2604	P33997	alpA	CP4-57 prophage; DNA-bind	-0.0440727	0.23809721
JW2602	P32053	intA	CP4-57 prophage; integrase	-0.0842765	0.03178696
JW2624	P52139	yfjX	CP4-57 prophage; putative a	0.10640925	0.17250818
JW2625	P52140	yfjY	CP4-57 prophage; putative C	-0.0428063	0.1744143
JW2615	P52133	yfjR	CP4-57 prophage; putative C	-0.2140017	0.00394268
JW2623	P52138	yfjW	CP4-57 prophage; putative i	-0.0091984	0.81874894
JW2618	P52135	yfjT	CP4-57 prophage; putative p	-0.0209437	0.652713
JW2611	P52129	yfjN	CP4-57 prophage; RNase LS	0.01547103	0.68181743
JW2627	Q46953	ypjF	CP4-57 prophage; toxin of th	0.02468796	0.22600439
JW2605	P52124	yfjI	CP4-57 prophage; uncharact	-0.0801229	0.0012743
JW5921	O52982	yfjS	CP4-57 prophage; uncharact	-0.0656374	0.00130527
JW2614	P52132	yfjQ	CP4-57 prophage; uncharact	-0.0593842	0.19102305
JW2610	P52128	yfjM	CP4-57 prophage; uncharact	-0.0210767	0.28350226
JW5418	P52130	yfjO	CP4-57 prophage; uncharact	-0.0116525	0.50919646
JW2603	P52123	yfjH	CP4-57 prophage; uncharact	0.00891607	0.42487782

JW2607	P52125	yfjJ	CP4-57 prophage; uncharact	0.05247007	0.02917318
JW2609	P52127	yfjL	CP4-57 putative defective p	-0.0326783	0.02051153
JW0235	Q47684	yafW	CP4-6 prophage; antitoxin o	0.01946329	0.59687994
JW0271	P77657	yagK	CP4-6 prophage; conserved	0.02724032	0.21895338
JW0242	P77206	yafZ	CP4-6 prophage; conserved	0.02861591	0.39407816
JW5813	Q47688	ykfC	CP4-6 prophage; conserved	0.05294892	0.04485485
JW0272	P77607	yagL	CP4-6 prophage; DNA-bindir	-0.0265844	0.29167213
JW0244	Q57083	perR	CP4-6 prophage; putative Df	-0.1394524	0.03648569
JW0260	P37007	yagA	CP4-6 prophage; putative Df	-0.0561587	0.11468892
JW0265	P77300	yagl	CP4-6 prophage; putative Df	-0.0266512	0.18484746
JW0254	P37009	afuC	CP4-6 prophage; putative fe	-0.0625323	0.00377089
JW0243	P75678	ykfA	CP4-6 prophage; putative G ⁻	0.00135341	0.97596792
JW0275	P71298	intF	CP4-6 prophage; putative pF	-0.0275862	0.60622848
JW5027	Q47689	mmuP	CP4-6 prophage; putative S-	0.03520626	0.01555251
JW0264	P77713	yagH	CP4-6 prophage; putative xy	0.0204626	0.31255667
JW0236	Q47685	ykfG	CP4-6 prophage; RadC-like J	-0.0027886	0.9443652
JW0253	Q47690	mmuM	CP4-6 prophage; S-methylm	0.01232934	0.85976451
JW0234	P77692	ykfl	CP4-6 prophage; toxin of the	0.01488646	0.23317265
JW0273	P71296	yagM	CP4-6 prophage; uncharacte	-0.010294	0.75240184
JW0270	P77169	yagJ	CP4-6 prophage; uncharacte	0.00732044	0.7908834
JW5023	P75677	ykfF	CP4-6 prophage; uncharacte	0.01220058	0.69331121
JW5022	P75676	yafX	CP4-6 prophage; uncharacte	0.02225871	0.58181397
JW0239	P77162	ykfb	CP4-6 prophage; uncharacte	0.0306094	0.31865397
JW4103	P0A6F5	groL	Cpn60 chaperonin GroEL, la	-0.0812334	0.04905686
JW2347	P77293	yfdH	CPS-53 (KpLE1) prophage; b	-0.0140042	0.30238035
JW2346	P77682	yfdG	CPS-53 (KpLE1) prophage; b	0.02704746	0.43797308
JW2358	P76514	yfdR	CPS-53 (KpLE1) prophage; c	-0.0066972	0.83197276
JW2350	P77656	yfdK	CPS-53 (KpLE1) prophage; c	0.10763803	4.11E-05
JW2352	P76509	yfdM	CPS-53 (KpLE1) prophage; p	0.12351132	0.0130945
JW2345	P37326	intS	CPS-53 (KpLE1) prophage; p	0.03770282	0.19428709
JW2359	P76515	yfdS	CPS-53 (KpLE1) prophage; u	-0.3320213	0.01053655
JW2356	P76512	yfdP	CPS-53 (KpLE1) prophage; u	-0.0334173	0.09409649
JW2357	P76513	yfdQ	CPS-53 (KpLE1) prophage; u	0.02736574	0.52986623
JW5385	P76510	yfdN	CPS-53 (KpLE1) prophage; u	0.04612159	0.07107546
JW3831	P0C0K3	yihE	Cpx stress response Thr/Ser	0.00404672	0.85455264
JW5844	Q46898	ygcl	CRISP RNA (crRNA) containi	-0.0456309	0.02635069
JW2730	Q46901	ygcl	CRISP RNA (crRNA) containi	-0.0131502	0.60587389
JW2729	P76632	ygck	CRISP RNA (crRNA) containi	0.0139504	0.72620117
JW2728	Q46899	ygcl	CRISP RNA (crRNA) containi	0.02913557	0.5751606
JW5438	P45956	ygbF	CRISPR adaptation ssRNA ei	0.04671602	0.28229087
JW2726	Q46897	ygcH	CRISPR RNA precursor cleav	-0.0350105	0.05476006
JW0038	P60584	caiA	crotonobetaine reductase st	-0.0578602	0.19345896
JW0037	P31572	caiB	crotonobetainyl CoA:carnitir	-0.0479771	0.16435718
JW0942	P75869	yccR	CRP-S-dependent promoter	-0.0778145	0.11439738
JW2686	P24240	ascB	cryptic 6-phospho-beta-gluc	0.08289097	0.01836899

JW3640	P31441	ade	cryptic adenine deaminase	-0.0366849	0.4538949
JW3699	P11988	bgIB	cryptic phospho-beta-glucos	0.2994782	0.00301068
JW2782	P0AGF2	ygdK	CsdA-binding activator; Fe-S	-0.0466513	0.04646824
JW1023	P52106	csgD	csgBAC operon transcriptior	-0.0486814	0.14331501
JW1748	P77788	nudG	CTP pyrophosphohydrolase;	-0.016886	0.57776058
JW2845	Q46810	ygfJ	CTP:molybdopterin cytidylylt	-0.0133036	0.50667534
JW5907	P76113	yncB	curcumin/dihydrocurcumin i	0.04486506	0.44437934
JW1026	P52107	csgC	curli assembly protein	-0.0224365	0.43781846
JW1021	P0AE98	csgF	curli nucleation outer memk	0.17882493	0.00058773
JW1020	P0AEA2	csgG	curli production assembly/tr	-0.1015934	0.00027584
JW1024	P0ABK7	csgB	curlin nucleator protein, mir	-0.0026352	0.94539648
JW1022	P0AE95	csgE	curlin secretion specificity fa	-0.0185412	0.60239873
JW1025	P28307	csgA	curlin subunit, amyloid curli	0.03289409	0.51620134
JW0331	P00816	cynS	cyanate aminohydrolase	0.01081059	0.70287778
JW5943	P37649	yhjK	cyclic-di-GMP phosphodiester	0.01620316	0.56653652
JW2488	P77172	yfgF	cyclic-di-GMP phosphodiester	-0.0288798	0.12816815
JW3493	P37646	yhjH	cyclic-di-GMP phosphodiester	-0.0607093	0.04657022
JW1278	P77334	gmr	cyclic-di-GMP phosphodiester	-0.0145795	0.69256356
JW1653	P0A9H7	cfa	cyclopropane fatty acyl phos	0.08182456	0.1248959
JW0470	P0AAR3	ybaK	Cys-tRNA(Pro)/Cys-tRNA(Cy	0.08134693	0.00057881
JW2975	P06721	metC	cystathionine beta-lyase, PL	-0.0642767	0.57632351
JW3910	P00935	metB	cystathionine gamma-synth	0.14535373	0.03354679
JW5250	P31125	eamA	cysteine and O-acetyl-L-seri	-0.035485	0.47694677
JW2562	P38101	yfiK	cysteine and O-acetylserine	0.01544138	0.43306565
JW2514	P0A6B7	iscS	cysteine desulfurase (tRNA	0.01158518	0.55147086
JW1670	P77444	sufS	cysteine desulfurase, stimul	0.00047615	0.97863179
JW2781	Q46925	csdA	cysteine sulfinat desulfina	-0.0371062	0.10882773
JW2407	P0ABK5	cysK	cysteine synthase A, O-acet	0.29261939	0.00027766
JW2414	P16703	cysM	cysteine synthase B (O-acet	-0.0437194	0.11195949
JW5041	P77252	ykgE	cysteine-rich LutA family pro	-0.0679155	0.00012173
JW1905	P0AEM9	fliY	cystine transporter subunit	0.0545592	0.59772074
JW2131	P0ABF6	cdd	cytidine/deoxycytidine deam	0.04690235	0.3172752
JW0893	P0A6I0	cmk	cytidylate kinase	-0.2030663	0.10694053
JW5224	P0ABE5	cybB	cytochrome b561	0.07059315	0.01172783
JW5323	P76345	yodB	cytochrome b561 homolog	-0.0202253	0.61193129
JW0960	P26459	appC	cytochrome bd-II oxidase, st	0.03530217	0.3251169
JW0961	P26458	appB	cytochrome bd-II oxidase, st	0.04348632	0.41327431
JW2592	P64432	ypjD	cytochrome c assembly prot	-0.0889092	0.00139318
JW3486	P37197	yhjA	cytochrome c peroxidase	-0.0779583	0.2853467
JW0724	P56100	ybgT	cytochrome d (bd-I) ubiquin	0.06760054	0.01257204
JW0723	P0ABK2	cydB	cytochrome d terminal oxid	0.00720745	0.66528729
JW0421	P0ABI8	cyoB	cytochrome o ubiquinol oxid	-0.1840347	0.12367447
JW0422	P0ABJ1	cyoA	cytochrome o ubiquinol oxid	-0.0479909	0.29199265
JW0420	P0ABJ3	cyoC	cytochrome o ubiquinol oxid	0.1647478	2.68E-05
JW0419	P0ABJ6	cyoD	cytochrome o ubiquinol oxid	-0.0606542	0.00531133

JW1756	P0A962	ansA	cytoplasmic L-asparaginase	0.08349607	0.04470611
JW3233	P24180	acrE	cytoplasmic membrane lipo	-0.0264989	0.06045041
JW3635	P04846	nlpA	cytoplasmic membrane lipo	-0.1042762	3.23E-07
JW3487	P62601	treF	cytoplasmic trehalase	0.02987259	0.18089424
JW0327	P0AA82	codB	cytosine transporter	-0.0054209	0.97328964
JW0328	P25524	codA	cytosine/isoguanine deaminase	0.07260043	0.01232461
JW2880	P0A9T0	serA	D-3-phosphoglycerate dehydrogenase	0.27267254	0.0123834
JW2880	P0A9T0	serA	D-3-phosphoglycerate dehydrogenase	0.47923592	0.00084558
JW1483	P77790	ddpX	D-ala-D-ala dipeptidase, Zn-dependent	-0.0656389	0.04064271
JW0372	P0A6J8	ddlA	D-alanine-D-alanine ligase / D-alanine:D-alanine ligase	0.06965434	0.07915705
JW0090	P07862	ddlB	D-alanine:D-alanine ligase	0.13855051	0.00019681
JW4166	P0AAE0	cycA	D-alanine/D-serine/glycine D-alanine:D-serine/glycine cyclase	-0.0519755	0.13732652
JW3149	P24228	dacB	D-alanyl-D-alanine carboxypeptidase	-0.0920699	0.06466699
JW0823	P08506	dacC	D-alanyl-D-alanine carboxypeptidase	-0.0097744	0.80996828
JW5329	P33013	dacD	D-alanyl-D-alanine carboxypeptidase	-0.000667	0.32842864
JW5355	P0AFI5	pbpG	D-alanyl-D-alanine endopeptidase	0.03493396	0.26054084
JW5052	P0AD70	ampH	D-alanyl-D-alanine-carboxypeptidase	0.02440196	0.05078618
JW4048	P32721	alsA	D-allose ABC transporter ATP-binding subunit	-0.0296826	0.17392551
JW4049	P39265	alsB	D-allose ABC transporter permease	0.01977037	0.48835208
JW4047	P32720	alsC	D-allose ABC transporter permease	-0.0934227	0.00538922
JW4050	P0ACS7	rpiR	D-allose-inducible als operon regulatory protein	-0.0239955	0.62152443
JW1178	P0A6J5	dadA	D-amino acid dehydrogenase	0.02478751	0.52896718
JW3164	P45395	kdsD	D-arabinose 5-phosphate isomerase	-0.1796968	0.00867109
JW5431	P17115	gutQ	D-arabinose 5-phosphate isomerase	0.00096019	0.97955055
JW5313	P76316	yedO	D-cysteine desulfhydrase, PI-dependent	-0.0372559	0.16510959
JW2300	P0AC19	folX	D-erythro-7,8-dihydroneopterinase	0.0596827	0.07834787
JW2894	P0A9B6	epd	D-erythrose 4-phosphate dehydrogenase	0.02409895	0.444673
JW3097	P39829	garD	D-galactarate dehydrogenase	-0.2433085	0.03034707
JW5627	P31460	dgoR	D-galactonate catabolism operon regulatory protein	-0.0144595	0.56608925
JW5629	Q6BF17	dgoD	D-galactonate dehydratase	-0.0483663	0.21204481
JW5859	P0AA76	dgoT	D-galactonate transporter	0.03852718	0.18731073
JW2910	P0AEP1	galP	D-galactose transporter	-0.0023572	0.96440051
JW2019	P37749	wbbl	D-Galf:alpha-D-Glc beta-1,6-galactosyltransferase	-0.1341026	0.00075928
JW2758	P0AES2	gudD	D-gluconate dehydratase 1	0.00126081	0.95464389
JW5946	P0ACP5	gntR	D-gluconate inducible gluconate dehydratase	0.02925653	0.39122245
JW4225	P39208	idnK	D-gluconate kinase, thermophilic	0.05190573	0.21797577
JW1769	P39173	yeaD	D-hexose-6-phosphate epimerase	0.00077662	0.9652174
JW2121	P06149	dld	D-lactate dehydrogenase, FAD-dependent	0.01574289	0.54903802
JW1789	P76251	yeaU	D-malate oxidase, NAD-dependent	-0.1026822	0.08755299
JW4286	P39160	uxuB	D-mannonate oxidoreductase	-0.0113499	0.42244144
JW3728	P04983	rbsA	D-ribose ABC transporter ATP-binding subunit	-0.039965	0.07434347
JW3730	P02925	rbsB	D-ribose ABC transporter permease	-0.0082135	0.67295422
JW3729	P0AGI1	rbsC	D-ribose ABC transporter permease	0.03439478	0.40196701
JW5857	P04982	rbsD	D-ribose pyranase	0.04515279	0.01112866
JW3349	P0AG07	rpe	D-ribulose-5-phosphate 3-epimerase	-0.0382186	0.59007449

JW0212	P63224	lpcA	D-sedoheptulose 7-phospha	-0.294232	0.07242836
JW2363	P00926	dsdA	D-serine dehydratase	-0.0596916	0.04513197
JW2362	P08555	dsdX	D-serine transporter	0.00658771	0.8713376
JW2841	Q46806	hyuA	D-stereospecific phenylhyda	0.00419064	0.92042335
JW5343	POC8J6	gatY	D-tagatose 1,6-bisphosphat	0.03691817	0.28342548
JW2082	POC8J8	gatZ	D-tagatose 1,6-bisphosphat	-0.1107157	0.00024089
JW3858	POA6M4	dtd	D-tyr-tRNA(Tyr) deacylase	0.02172632	0.42513169
JW3539	P37388	xylG	D-xylose ABC transporter du	-0.0511986	0.07998744
JW3540	POAGI4	xylH	D-xylose ABC transporter pe	-0.0647331	0.00808986
JW3537	P00944	xylA	D-xylose isomerase	0.01216349	0.71120493
JW3991	POAGF4	xylE	D-xylose transporter	0.03304615	0.46977946
JW3538	P37387	xylF	D-xylose transporter subunit	0.07110146	0.09911001
JW1479	P77268	ddpD	D,D-dipeptide ABC transport	0.11495813	0.15724126
JW1478	P77622	ddpF	D,D-dipeptide ABC transport	0.12998161	0.00038472
JW5240	P76128	ddpA	D,D-dipeptide ABC transport	-0.065423	0.18581461
JW1481	P77308	ddpB	D,D-dipeptide ABC transport	-0.0468152	0.28769719
JW1480	P77463	ddpC	D,D-dipeptide ABC transport	0.11752213	0.43462053
JW0196	P63228	gmhB	D,D-heptose 1,7-bisphospha	-0.0253717	0.2336226
JW1106	P75960	cobB	deacetylase of acs and cheY	-0.0473228	0.05421545
JW2124	P33366	yohD	DedA family inner membrar	-0.0610347	0.03167738
JW2314	POABP6	dedA	DedA family inner membrar	0.0535045	0.0124488
JW4064	NA	phnE	defective phosphonate ABC	-0.0266276	0.08330174
JW1004	P31545	ycdB	deferrochelataase, periplasr	-0.0377981	0.14237256
JW3242	P15770	aroE	dehydroshikimate reductase	0.00492216	0.91814001
JW4129	P16384	miaA	delta(2)-isopentenylpyrophc	0.02136462	0.48458167
JW2705	P52598	ygbI	DeoR family putative transc	-0.1130243	0.00046899
JW2050	P28248	dcd	deoxycytidine triphosphate (0.22400943	0.0078174
JW0156	P15723	dgt	deoxyguanosine triphosphat	0.05199309	0.25785461
JW0698	P00914	phr	deoxyribodipyrimidine photc	-0.1874319	0.11712809
JW0824	POACK5	deoR	deoxyribose-5-phosphate-in	-0.0029701	0.80561314
JW0100	POA6I9	coaE	dephospho-CoA kinase	-0.0408851	0.08173194
JW0761	P13000	bioD	dethiobiotin synthetase	0.03682954	0.43112786
JW0097	P08337	mutT	dGTP-preferring nucleoside	-0.1217828	0.37309256
JW4002	POABN1	dgkA	diacylglycerol kinase	-0.0104924	0.78887507
JW0048	P05637	apaH	diadenosine tetraphosphata	-0.1555828	0.24813315
JW2806	P00861	lysA	diaminopimelate decarboxy	0.05162366	0.07750218
JW5592	POA6K1	dapF	diaminopimelate epimerase	0.0801326	0.66598435
JW5292	P76245	yeaP	diguanylate cyclase	-0.1216467	0.20609746
JW0376	POAAP1	yaiC	diguanylate cyclase, cellulose	-0.0073007	0.80526246
JW5241	POAA89	yddV	diguanylate cyclase, cold- ai	0.06378756	0.07880923
JW5206	P77302	ydaM	diguanylate cyclase, csgD re	-0.0377968	0.1017722
JW5143	P75908	ycdT	diguanylate cyclase, membr	0.31622319	0.06024674
JW1528	P31129	ydeH	diguanylate cyclase, zinc-se	0.01905584	0.64596762
JW1049	P05020	pyrC	dihydro-orotase	0.04471952	0.23337917
JW0928	POA7E1	pyrD	dihydro-orotate oxidase, FM	-0.0379507	0.47235967

JW0112	P0A9P0	lpd	dihydrolipoyl dehydrogenase	0.01029571	0.58470532
JW0716	P0AFG6	sucB	dihydrolipoyl succinyltransferase	0.11705641	0.00039891
JW1598	P0AFS3	folM	dihydromonapterin reductase	0.06854966	0.01489305
JW3030	P0AC16	folB	dihydroneopterin aldolase a	0.01442216	0.71009692
JW1854	P0AFC0	nudB	dihydroneopterin triphosphatase	0.24391545	0.00028895
JW0567	P38489	nfnB	dihydropteridine reductase, NADPH-dependent	-0.1839227	0.00582461
JW2134	P25889	yeiA	dihydropyrimidine dehydrogenase	0.09183772	0.01119597
JW2133	P76440	yeiT	dihydropyrimidine dehydrogenase	-0.0712993	0.04906754
JW5186	P76014	dhaL	dihydroxyacetone kinase, C-terminal	-0.082519	0.07740747
JW5187	P76015	dhaK	dihydroxyacetone kinase, P-loop	0.07821189	0.01330969
JW5605	P05791	ilvD	dihydroxyacid dehydratase	-0.0505676	0.16002643
JW2257	P0ABU0	menB	dihydroxynaphthoic acid synthase	0.00922094	0.83646943
JW5118	P18775	dmsA	dimethyl sulfoxide reductase, NADPH-dependent	-0.0115852	0.50523122
JW0878	P18776	dmsB	dimethyl sulfoxide reductase, NADPH-dependent	0.08829168	0.00798962
JW0879	P18777	dmsC	dimethyl sulfoxide reductase, NADPH-dependent	0.09258649	0.00797495
JW3077	P42624	yhaK	dinitrotoluene degradation protein	-0.0353433	0.10583457
JW4091	P39276	yjDL	dipeptide and tripeptide peroxidase	0.03514194	0.32454701
JW1626	P77304	ydgR	dipeptide and tripeptide peroxidase	-0.0031361	0.90053667
JW3463	P36837	yhiP	dipeptide and tripeptide peroxidase	-0.3839132	0.01369557
JW0699	P75742	ybgH	dipeptide and tripeptide peroxidase	0.02909049	0.22224192
JW3510	P0AAG0	dppD	dipeptide/heme ABC transporter	0.07851443	0.06558372
JW3509	P37313	dppF	dipeptide/heme ABC transporter	0.16888873	0.00402469
JW3513	P23847	dppA	dipeptide/heme ABC transporter	-0.03091	0.3577407
JW3512	P0AEF8	dppB	dipeptide/heme ABC transporter	-0.0198702	0.50277009
JW1531	P24171	dcp	dipeptidyl carboxypeptidase	-0.0134517	0.73323483
JW2921	P52061	yggV	dITP/XTP pyrophosphatase	0.15658085	0.10904465
JW4097	P69488	cutA	divalent-cation tolerance protein	0.14322334	0.14809571
JW3201	P64612	yhcM	divisome ATPase	0.05799125	0.17274322
JW0788	P41039	ybil	DksA-type zinc finger protein	-0.0693394	0.00151336
JW0195	P30750	metN	DL-methionine transporter	-0.025226	0.14737759
JW0193	P28635	metQ	DL-methionine transporter	-0.018161	0.45026305
JW0194	P31547	metI	DL-methionine transporter	0.07944096	0.05496757
JW0536	Q47270	ninE	DLP12 prophage; conserved	-0.0225322	0.26339802
JW0549	P31062	nohB	DLP12 prophage; DNA packaging	-0.0737878	0.13838835
JW0537	P68661	ybcO	DLP12 prophage; DUF1364 family	-0.005557	0.75314021
JW5081	P77598	ybcV	DLP12 prophage; DUF1398 family	-0.0639926	0.01815014
JW0538	P0AG74	rusA	DLP12 prophage; endonuclease	0.04725157	0.01827001
JW0533	P77368	ybcL	DLP12 prophage; inactive protein	0.04631128	0.02513606
JW0531	P23895	emrE	DLP12 prophage; multidrug resistance	-0.0773696	0.01795005
JW0554	P09169	ompT	DLP12 prophage; outer membrane	-0.0186964	0.66593845
JW0539	Q47274	ybcQ	DLP12 prophage; putative attachment	0.08513694	0.08461901
JW0534	P77634	ybcM	DLP12 prophage; putative DNA	0.13927677	0.00537741
JW0546	P77330	borD	DLP12 prophage; putative lysis	-0.0588835	0.01413591
JW5080	P58041	rzoD	DLP12 prophage; putative lysis	0.09870887	0.01348327
JW0544	P78285	ybcS	DLP12 prophage; putative lysis	-0.0100655	0.73549762

JW5079	P75719	rzpD	DLP12 prophage; putative m	0.19781164	0.00135671
JW0525	P24218	intD	DLP12 prophage; putative pl	0.00208872	0.87365868
JW0543	P0A9R2	essD	DLP12 prophage; putative pl	-0.0080594	0.74895874
JW0532	P77698	ybcK	DLP12 prophage; putative pl	-0.0136407	0.76904847
JW0535	Q47269	ybcN	DLP12 prophage; SSB and ss	0.02548825	0.16520243
JW0548	P64435	ybcW	DLP12 prophage; uncharacte	0.15601313	0.09246228
JW4168	P39314	ytfF	DMT transporter family inne	-0.0011884	0.96292578
JW3350	P0AEE8	dam	DNA adenine methyltransfe	0.23773697	9.12E-06
JW5543	P28638	yhdJ	DNA adenine methyltransfe	0.05324097	0.00668458
JW5867	P33224	aidB	DNA alkylation damage repa	-0.0345293	0.32178807
JW2644	P0ACG1	stpA	DNA binding protein, nucleo	-0.0277822	0.53895925
JW4326	P0A8J2	dnaT	DNA biosynthesis protein (p	0.12344908	0.00260868
JW5691	P46846	gntX	DNA catabolic protein	-0.1109707	0.00062158
JW5694	P45750	yrfA	DNA catabolic protein	-0.1083349	0.0235801
JW3356	P45751	yrfB	DNA catabolic protein	0.00664966	0.83951586
JW3357	P64634	yrfC	DNA catabolic putative fimk	0.02434519	0.29804932
JW3354	P34749	hofQ	DNA catabolic putative fimk	-0.029749	0.19096482
JW5693	P45753	yrfD	DNA catabolic putative pilus	-0.1613213	0.0106407
JW1944	P0AED9	dcm	DNA cytosine methyltransfe	0.09575962	0.00664352
JW3620	P23840	dinD	DNA damage-inducible prot	-0.038914	0.17163877
JW1048	P0ABR1	dinI	DNA damage-inducible prot	-0.0669964	0.71875651
JW1837	P0ACY9	yebG	DNA damage-inducible prot	0.09342257	0.00147759
JW1334	P76053	ydaL	DNA endonuclease	-0.0682416	0.01586558
JW1625	P0AB83	nth	DNA glycosylase and apyrim	0.00125344	0.94089312
JW5008	P0A8H8	yacG	DNA gyrase inhibitor	0.05579007	0.0148074
JW1991	P33012	sbmC	DNA gyrase inhibitor	0.09762183	0.02898725
JW5604	P09980	rep	DNA helicase and single-str	-0.1013016	0.01346004
JW0945	P15038	helD	DNA helicase IV	0.08568731	8.99E-05
JW3622	P25772	ligB	DNA ligase, NAD(+)-depend	-0.0191275	0.30643992
JW4312	P08957	hsdM	DNA methyltransferase M	-0.0949736	0.0897281
JW1943	P09184	vsr	DNA mismatch endonucleas	0.14699267	0.02221537
JW0059	P21189	polB	DNA polymerase II	0.00692295	0.82116556
JW0205	P03007	dnaQ	DNA polymerase III epsilon :	0.03114637	0.45719061
JW4216	P28905	holC	DNA polymerase III, chi sub	0.04835971	0.10663571
JW4334	P28632	holD	DNA polymerase III, psi sub	0.09729914	0.21522602
JW1831	P0ABS8	holE	DNA polymerase III, theta s	-0.1075738	0.00395108
JW0221	Q47155	dinB	DNA polymerase IV	-0.0101008	0.66854267
JW3038	P0ABS5	dnaG	DNA primase	0.09392622	7.89E-05
JW2669	P0A7G6	recA	DNA recombination and rep	-0.0880848	0.29774718
JW3809	P0AG71	rmuC	DNA recombination protein	-0.1448424	0.14694736
JW5708	P30852	smf	DNA recombination-mediat	0.08249106	0.02235243
JW4352	P24554	radA	DNA repair protein	0.00423966	0.96284741
JW1752	P14294	topB	DNA topoisomerase III	0.02289795	0.09799739
JW2987	P0AF12	parC	DNA topoisomerase IV, sub	-0.0009207	0.98533332
JW0460	P0A8B5	ybaB	DNA-binding protein, putati	-0.0570203	0.09129882

JW3786	P03018	uvrD	DNA-dependent ATPase I ar	0.0137279	0.63640755
JW2912	P25736	endA	DNA-specific endonuclease	-0.0587125	0.11268814
JW3118	P66817	yraO	DnaA initiator-associating f	-0.0503933	0.23009713
JW5067	P77395	ybbN	DnaK co-chaperone, thioered	-0.0353367	0.30529794
JW0985	P36659	cbpA	DnaK co-chaperone; curved	0.02676118	0.52770943
JW2510	P0A6Z1	hscA	DnaK-like molecular chaper	0.10126342	0.01929904
JW2527	P0AD47	yphA	DoxX family inner membran	-0.0148453	0.55734165
JW2361	P46068	dsdC	dsd operon activator; autore	-0.0212164	0.33637861
JW2023	P37745	rfbC	dTDP-4-deoxyrhamnose-3,5	0.07282009	0.00193465
JW2026	P37759	rfbB	dTDP-glucose 4,6 dehydrata	-0.0116005	0.52431613
JW5598	P27830	rffG	dTDP-glucose 4,6-dehydrata	-0.0876057	0.04713423
JW2025	P37760	rfbD	dTDP-L-rhamnose synthase,	0.08615783	0.15747315
JW3217	P25536	yhdE	dTTP/UTP pyrophosphatase,	-0.0657507	0.00337152
JW5409	Q47319	yfiP	DTW domain protein	-0.0186879	0.5942282
JW3579	P0ACL7	lldR	dual role activator/represso	0.00560748	0.76010203
JW2501	P36979	yfgB	dual specificity 23S rRNA m	0.01706931	0.64022751
JW0057	P0AA37	rluA	dual specificity 23S rRNA ps	-0.0156004	0.5631659
JW0899	P75843	ycaQ	DUF1006 family protein wit	-0.0707962	0.00192158
JW3189	P45423	yhcG	DUF1016 family protein in t	-0.0319399	0.27485681
JW3830	P0ADP9	yihD	DUF1040 protein YihD	0.12983368	0.00053919
JW5539	P0ADW3	yhcB	DUF1043 family inner mem	0.03521565	0.4569883
JW1271	P0ACV4	yciS	DUF1049 family inner mem	-0.050801	0.0878582
JW5516	P42616	yqjC	DUF1090 family putative pe	0.01130364	0.5496367
JW5147	P75916	ycdZ	DUF1097 family inner mem	-0.0182844	0.71287593
JW5749	P0ADE2	ytfK	DUF1107 family protein	0.00839103	0.66459113
JW0313	P77221	yahG	DUF1116 family protein	0.00875647	0.56587829
JW4304	P39390	yjiS	DUF1127 family protein	-0.2021883	0.31568022
JW5683	P37614	yhhL	DUF1145 family protein	-0.0244361	0.13661648
JW0569	P77506	ybdJ	DUF1158 family putative in	-0.001341	0.9596292
JW5259	P76172	ynfD	DUF1161 family periplasmic	-0.076013	0.0081858
JW2223	P76466	yfaT	DUF1175 family protein, pu	0.04007969	0.37228314
JW2450	P76559	yphG	DUF1176 family protein	0.10758869	0.01875675
JW1341	P33230	ydaC	DUF1187 family protein, Ra	-0.0511873	0.08544209
JW4143	P39295	yjfM	DUF1190 family protein	-0.0606626	0.0003309
JW5927	P0ADT2	ygiB	DUF1190 family protein	0.05615963	0.11697942
JW5637	P0ADL3	yciN	DUF1198 family protein	-0.0912375	0.03420362
JW2923	P46142	yggM	DUF1202 family putative se	0.00835908	0.73845188
JW5796	P0ADD5	yjjP	DUF1212 family inner mem	-0.0568756	0.00400528
JW4295	P39381	yjiJ	DUF1228 family putative in	0.06281891	0.00175454
JW3001	P0ADU7	yqiB	DUF1249 protein YqiB	0.07375317	0.30120802
JW0640	P77627	ybeR	DUF1266 family protein	-0.1019118	0.00011167
JW0643	P77427	ybeU	DUF1266 family protein	-0.0377541	0.1455082
JW3916	P32668	yijF	DUF1287 family protein	0.10077331	0.0604705
JW5827	P64474	ydhL	DUF1289 family protein	0.03644059	0.24960403
JW1766	P76231	yeaC	DUF1315 family protein	-0.0530247	0.31808962

JW5216	P76076	ydbL	DUF1318 family protein	0.00394833	0.9300856
JW2393	P0AD37	yfeC	DUF1323 family putative DN	-0.0322183	0.16627478
JW2394	P27238	yfeD	DUF1323 family putative DN	0.0265314	0.15822392
JW5633	P0ADM4	ydQ	DUF1375 family outer mem	0.0315182	0.46842206
JW1148	P75988	ycgX	DUF1398 family protein	0.00533026	0.83750529
JW5402	P76575	yfgJ	DUF1407 family protein	0.02762871	0.46870819
JW0834	P46119	ybjC	DUF1418 family protein	-0.0248106	0.42002786
JW3936	P0AF40	yijD	DUF1422 family inner mem	0.06226974	0.03033397
JW0445	P0AAQ6	ybaA	DUF1428 family protein	0.05932011	0.19069663
JW0281	P0AAA1	yagU	DUF1440 family inner mem	-0.0113197	0.54262097
JW3022	P76657	yqiJ	DUF1449 family inner mem	-0.1502321	0.01181127
JW5063	P0AAS0	ylaC	DUF1449 family inner mem	-0.0570997	0.023521
JW0638	P0AAT9	ybeL	DUF1451 family protein	-0.0384606	0.09074863
JW3891	P32160	yiiQ	DUF1454 family putative pe	-0.0510528	0.24458274
JW2112	P33355	yehS	DUF1456 family protein	0.01581623	0.51562467
JW3070	P64585	yqjE	DUF1469 family inner mem	-0.0306784	0.33915622
JW1596	P76177	ydgH	DUF1471 family periplasmic	-0.1507767	0.00265843
JW5742	P0AF82	yjfN	DUF1471 family periplasmic	0.04135035	0.11170151
JW0787	P0AAX3	ybiJ	DUF1471 family periplasmic	-0.0337416	0.16258569
JW0805	P75791	ybiU	DUF1479 family protein	-0.0064906	0.76222721
JW3965	P32681	yjaH	DUF1481 family putative lip	-0.1814562	0.17889996
JW3241	P45795	yrdB	DUF1488 family protein	-0.0394996	0.05595437
JW1749	P76227	ynjH	DUF1496 family protein	-0.0713242	0.00629729
JW1916	P76318	yedK	DUF159 family protein	0.00091468	0.96772792
JW5541	P46478	aaeX	DUF1656 family putative in	-0.0175407	0.53989738
JW1635	P64471	ydhI	DUF1656 family putative in	0.04527014	0.02475536
JW0697	P24252	ybgA	DUF1722 family protein	0.00417949	0.87104674
JW0783	P30176	ybiA	DUF1768 family protein	-0.0281448	0.08169452
JW1074	P0AB28	yceD	DUF177 family protein	-0.001645	0.91477428
JW2267	P76483	yfbM	DUF1877 family protein	0.05299393	0.01526892
JW5296	P64490	yoaC	DUF1889 family protein	0.07345044	0.09962541
JW0780	P0ACU0	ybiH	DUF1956 domain-containing	-0.0021697	0.94183115
JW1786	P64488	yeaR	DUF1971 family protein, nit	0.00885962	0.58973884
JW3255	P36677	yhdN	DUF1992 family protein	-0.0140939	0.75188506
JW3652	P0ADM0	ydH	DUF202 family inner memb	0.00420247	0.72412972
JW0345	P51024	yaiL	DUF2058 family protein	0.0103272	0.78987282
JW4134	P0AF73	yjeT	DUF2065 family protein	0.09370533	0.0126304
JW2219	P76462	yfaP	DUF2135 family protein, pu	-0.0076918	0.08307609
JW2224	P17994	yfaA	DUF2138 family protein, pu	0.16037558	8.82E-05
JW4139	P0AF76	yjfl	DUF2170 family protein	0.00392451	0.86547797
JW3057	P42598	ygjQ	DUF218 superfamily proteir	-0.0711082	0.49944831
JW1411	P34209	ydcF	DUF218 superfamily proteir	-0.0111002	0.65809597
JW2132	P0AFY2	sanA	DUF218 superfamily vancon	-0.3201232	0.00426329
JW5591	P27840	yigE	DUF2233 family protein	0.07675906	0.09957117
JW4082	P39270	yjdf	DUF2238 family inner mem	-0.0720804	0.01418821

JW2056	P76394	yegJ	DUF2314 family protein	0.04072483	0.13766388
JW3312	P0ADW8	yheV	DUF2387 family putative m	-0.1310872	0.01959509
JW5747	P0ACN2	ytfH	DUF24 family HxlR-type put	-0.0180772	0.37240081
JW4141	P39293	yjfK	DUF2491 family protein	0.0021636	0.97683226
JW1894	P46887	yecH	DUF2492 family protein	-0.0565642	0.06083739
JW0455	P45807	ybaM	DUF2496 family protein	0.15873303	6.56E-05
JW1265	P0AB61	yciN	DUF2498 protein YciN	-0.01528	0.39234473
JW3432	P37615	yhhM	DUF2500 family protein	-0.0192792	0.54769902
JW0004	P75616	yaaX	DUF2502 family putative pe	0.00011732	0.99408779
JW2387	P64542	ypeC	DUF2502 family putative pe	0.03771638	0.2592174
JW5450	P08370	ygdB	DUF2509 family protein	0.09722577	0.14689399
JW1828	P64506	yebY	DUF2511 family protein	-0.0712979	0.09159587
JW0688	P0AAU2	ybfA	DUF2517 family protein	-0.0628476	0.08447113
JW1441	P64455	ydcY	DUF2526 family protein	0.00593331	0.76352715
JW1813	P64508	yobF	DUF2527 family heat-induct	-0.1873316	0.00670995
JW1326	P64445	ynaJ	DUF2534 family putative in	-0.0857997	0.03310131
JW5359	P64536	yeiS	DUF2542 family protein	0.01702247	0.46532607
JW1288	P0ACV8	ymjA	DUF2543 family protein	0.01732876	0.16332632
JW2329	P76498	yfcO	DUF2544 family putative ou	-0.0735608	0.2227649
JW2374	P76521	yfdY	DUF2545 family putative in	-0.0677173	0.01739574
JW5232	P64453	ydcX	DUF2566 family protein	-0.0029044	0.88150712
JW2099	P33344	yehE	DUF2574 family protein	-0.1350385	0.12200758
JW1196	P0AB49	yehH	DUF2583 family putative in	-0.0008565	0.95784412
JW0842	P0AAZ0	ybjO	DUF2593 family inner mem	0.05207385	0.07663704
JW1900	P0AD07	yecF	DUF2594 family protein	-0.013319	0.49600044
JW5697	P64631	yhfU	DUF2620 family protein	0.09507373	0.00675636
JW2966	P64574	yghW	DUF2623 family protein	0.06407996	0.26969704
JW3503	P0ADJ3	yhjR	DUF2629 family protein	0.00266954	0.92997336
JW5663	P0ADJ5	bcsF	DUF2636 family cellulose pi	-0.320832	0.00516383
JW5053	P0AAQ0	yaiZ	DUF2754 family putative in	0.06598656	0.03651662
JW0370	P0AAP7	yaiY	DUF2755 family inner mem	0.05150599	0.27438085
JW3413	P0ADX7	yhhA	DUF2756 family protein	-0.3401544	0.05683022
JW1891	P0AD10	yecJ	DUF2766 family protein	0.01606744	0.62139852
JW5221	P25907	ydbD	DUF2773 family methylglyo	-0.1215869	0.15582359
JW0311	P77297	yahE	DUF2877 family protein	-0.0451093	0.10408314
JW2925	P0ADS9	yggN	DUF2884 family putative pe	-0.0251191	0.28208289
JW2643	P55734	ygaP	DUF2892 family inner mem	-0.0181645	0.63252038
JW4343	P37342	yjjI	DUF3029 family protein, pu	0.26952437	8.87E-06
JW0944	P0AB12	yccF	DUF307 family inner memb	0.15144145	0.0021609
JW3506	P37659	bcsG	DUF3260 family cellulose pi	0.03059675	0.10585309
JW0113	P36682	yacH	DUF3300 family protein	-0.0650496	0.00102777
JW3572	P32108	yibl	DUF3302 family inner mem	-0.0422118	0.3336822
JW3559	P0ADK4	yiaW	DUF3302 family inner mem	0.0360343	0.26931255
JW1782	P64493	yoaF	DUF333 family outer memb	0.04926631	0.09508156
JW5215	P0ACW2	ydbJ	DUF333 family putative lipo	0.08729169	0.01068795

JW2944	P0AEQ1	glcG	DUF336 family protein	0.06365406	0.0141722
JW2719	P46141	ygbE	DUF3561 family inner mem	0.05987823	0.0582472
JW5164	P75962	ymfA	DUF3592 family inner mem	-0.0306749	0.05958789
JW5860	P31455	yidR	DUF3748 family protein	0.04905542	0.02508156
JW3983	P32685	yjbD	DUF3811 family protein	0.11846814	0.00059597
JW4327	P0ADD2	yjjB	DUF3815 family inner mem	0.08813346	0.00711752
JW5877	P0AD40	ypeB	DUF3820 family protein	-0.0204662	0.5001527
JW5500	Q46858	yqhG	DUF3828 family putative pe	-0.0715306	0.00063924
JW3867	P32151	yiiG	DUF3829 family lipoprotein	-0.0298872	0.25313034
JW3548	P37673	yiaL	DUF386 family protein	0.08376673	0.03629399
JW3190	P45424	yhcH	DUF386 family protein, cupi	0.02221117	0.53326654
JW5542	P46474	yhdP	DUF3971-AsmA2 domains p	0.11167476	0.07807705
JW3455	P37627	yhiJ	DUF4049 family protein	-0.012616	0.71934939
JW3365	P45804	yhgE	DUF4153 family putative in	0.20282537	0.07387697
JW5736	P0AF70	yjel	DUF4156 family lipoprotein	0.04301634	0.27897404
JW3963	P32680	yjaG	DUF416 domain protein	0.06762788	0.05219042
JW2139	P25747	yeiB	DUF418 family putative inn	-0.0326663	0.14711353
JW1516	P76148	yneG	DUF4186 family protein	-0.0249523	0.44858732
JW5083	P0AAT2	ybdF	DUF419 family protein	0.01908434	0.25163347
JW4018	P0AF50	yjbR	DUF419 family protein	0.042431	0.10485491
JW5405	P76585	yphG	DUF4380 domain-containing	-0.0259913	0.28672143
JW2763	Q46919	yqcC	DUF446 family protein	0.05656797	0.05445928
JW0457	P0AAR5	ybaN	DUF454 family inner memb	0.03173948	0.10134586
JW0516	P45570	ybcI	DUF457 family inner memb	0.0484329	0.16254168
JW1314	P76046	ycjX	DUF463 family protein, pua	0.05911032	0.24197144
JW5823	P0ACW6	ydcH	DUF465 family protein	0.06472428	0.00351407
JW4316	P0ADC8	yjiX	DUF466 family protein	-0.3353448	0.02508798
JW0591	P0AAS9	ybdD	DUF466 family protein	0.00214581	0.91830989
JW2926	P38521	yggL	DUF469 family protein	0.10125426	0.34539991
JW3783	P23305	yigA	DUF484 family protein	0.02568736	0.33268253
JW4029	P0AF54	yjcH	DUF485 family inner memb	-0.0763702	0.02160007
JW1781	P76243	yeaO	DUF488 family protein	-0.0393204	0.13127162
JW3245	P0A828	smg	DUF494 family putative per	-0.0635856	0.01837995
JW1835	P33218	yebE	DUF533 family inner memb	-0.0058339	0.8846131
JW0861	P75829	ybjX	DUF535 family protein	0.01528606	0.69821141
JW2934	Q46831	yqgA	DUF554 family putative inn	-0.1322059	0.02993192
JW1282	P45736	ycjD	DUF559 family endonucleas	-3.83E-05	0.99859432
JW1442	P76111	ydcZ	DUF606 family inner memb	0.04930989	0.02415948
JW3075	P64592	yhaI	DUF805 family inner memb	-0.1363618	1.44E-05
JW3074	P64590	yhaH	DUF805 family inner memb	-0.3771825	0.00062192
JW3892	P0AF34	yiiR	DUF805 family putative inn	0.02641415	0.15180783
JW1941	P46125	yedI	DUF808 family inner memb	0.05242676	0.16474565
JW5306	P24238	yebB	DUF830 family protein	-0.0273987	0.23964864
JW4220	P39342	yjgR	DUF853 family protein with	-0.0242112	0.88720322
JW5759	P39338	yjgN	DUF898 family inner memb	-0.0780042	0.02439597

JW2801	P65294	ygdR	DUF903 family verified lipo	-0.1008305	0.01682983
JW5448	P65292	ygdI	DUF903 family verified lipo	0.02025694	0.15356121
JW3675	P09996	ydB	DUF937 family protein	-0.0562225	0.2145313
JW3989	P32689	yjbH	DUF940 family extracellular	-0.0078983	0.56105699
JW1606	P77804	ydgA	DUF945 family protein	-0.071836	0.03001646
JW5574	P32128	yihF	DUF945 family protein	0.06370995	0.11053617
JW3225	P45566	yhdT	DUF997 family putative inn	0.08031641	8.27E-05
JW4336	P0A8Y1	yjjG	dUMP phosphatase	-0.2930035	0.07257113
JW5169	P75975	ymfT	e14 prophage; putative DNA	-0.1488336	8.57E-06
JW1133	P75976	ymfL	e14 prophage; putative DNA	0.00793713	0.83100293
JW1127	P75970	ymfG	e14 prophage; putative exci	0.02612623	0.23155649
JW5166	P75968	ymfE	e14 prophage; putative inne	0.08661394	0.00097664
JW1126	P75969	intE	e14 prophage; putative inte	0.00803087	0.68334902
JW1123	P75967	ymfD	e14 prophage; putative SAM	-0.0517199	0.01071249
JW1142	P09153	tfaE	e14 prophage; putative tail	-0.0022664	0.89778047
JW1144	P03014	pin	e14 prophage; site-specific	0.05485518	0.2687965
JW5168	P75972	ymfI	e14 prophage; uncharacteriz	-0.0856535	0.09614678
JW5171	P09154	ymfS	e14 prophage; uncharacteriz	0.01174013	0.6125904
JW1136	P75979	ymfR	e14 prophage; uncharacteriz	0.01211187	0.26518568
JW1134	P75977	ymfM	e14 prophage; uncharacteriz	0.02436317	0.11508206
JW1140	P45581	yfcK	e14 prophage; uncharacteriz	0.07686993	0.0004105
JW3151	P0AA73	yhbE	EamA family inner membra	-0.049963	0.02504077
JW3634	P31437	yicL	EamA family inner membra	-0.0114193	0.5995375
JW5557	P0ABT8	yijE	EamA-like transporter famil	0.02292883	0.46754816
JW2197	P23827	eco	ecotin, a serine protease int	-0.0145951	0.42333589
JW0287	P0AAA3	yagZ	ECP pilin	-0.0368453	0.03024642
JW0285	P77802	yagX	ECP production outer memb	0.05250268	0.321809
JW0286	P77188	yagY	ECP production pilus chaper	-0.0485698	0.13182454
JW5030	P77263	yagV	ECP production pilus chaper	0.04924576	0.11516602
JW4106	P39280	yjeK	EF-P-Lys34 lysylation protei	-0.0072197	0.81027197
JW5381	P76938	yfcM	Elongation Factor P Lys34 h	0.06556098	0.00023728
JW4116	P0A8N7	poxA	Elongation Factor P Lys34 ly	0.17301543	0.11412219
JW5362	P0A6N8	yeiP	elongation factor P-like prot	0.02147181	0.48224758
JW2459	P76562	ypfI	elongator methionine tRNA	-0.0051588	0.7151312
JW5755	P0AF93	yjgF	enamine/imine deaminase,	0.07823959	0.02484501
JW3499	P37651	bcsZ	endo-1,4-D-glucanase	-0.0976529	0.01718305
JW0773	P0AAW1	ybhP	endo/exonuclease/phospha	0.01643357	0.53907957
JW5017	P0A8U2	yafD	endo/exonuclease/phospha	0.03654027	0.31390858
JW2146	P0A6C1	nfo	endonuclease IV with intrins	0.05751488	0.0434903
JW1730	P76213	ydjQ	endonuclease of nucleotide	0.06372434	0.0152415
JW4313	P08956	hsdR	endonuclease R Type I restri	-0.0017804	0.92582106
JW5547	P68739	nfi	endonuclease V; deoxyinosi	0.00984858	0.6997964
JW0704	P50465	nei	endonuclease VIII and 5-for	-0.0674837	0.21478732
JW4354	P0A9W3	yjjK	energy-dependent translati	0.42116678	0.0102794
JW5197	P45848	yciQ	enhancer of membrane prot	-0.0541188	0.0453495

JW2338	P77399	yfcX	enoyl-CoA hydratase/epime	0.00484094	0.96487177
JW5737	P0ADB4	ecnA	entericidin A membrane lip	-0.0982875	0.13092498
JW4108	P0ADB7	ecnB	entericidin B membrane lip	0.14431223	0.00047336
JW0583	P24077	ybdA	enterobactin exporter, iron-	0.10326243	0.04651994
JW0578	P11454	entF	enterobactin synthase multi	0.00635301	0.90068585
JW0589	P0A8Y8	ybdB	enterobactin synthesis proo	-0.0111227	0.51674288
JW0576	P13039	fes	enterobactin/ferrienterobac	-0.1243346	0.29645849
JW5601	P0AG00	wzzE	Entobacterial Common Anti	0.03291272	0.52295499
JW0903	P0AB01	ycbC	envelope biogenesis factor;	-0.0459014	0.53432307
JW4124	P39288	yjeS	epoxyqueuosine reductase, r	-0.034097	0.15586496
JW2317	P05459	pdxB	erythronate-4-phosphate de	0.06179963	0.10436626
JW2437	P76553	eutG	ethanol dehydrogenase invo	-0.0261528	0.6687554
JW1474	P39451	adhP	ethanol-active dehydrogena	-0.0447586	0.37581373
JW2434	P0AEJ6	eutB	ethanolamine ammonia-lya	0.07778741	0.16265287
JW2433	P19636	eutC	ethanolamine ammonia-lya	0.0117906	0.69299957
JW2440	P0AEJ8	cchB	Ethanolamine catabolic mic	0.01576997	0.47919137
JW2436	P76552	eutH	ethanolamine transporter	0.06100231	0.0956197
JW2438	P77277	eutJ	ethanolamine utilization pro	0.05184883	0.42603025
JW2441	P0ABF4	cchA	ethanolamine utilization pro	-0.0804671	0.0007185
JW2430	P36547	yfeG	eut operon transcriptional a	0.03308098	0.20171929
JW5511	P06864	ebgA	evolved beta-D-galactosidas	-0.0111588	0.75307885
JW3048	P0AC73	ebgC	evolved beta-D-galactosidas	0.00445815	0.77782971
JW1898	P0A8G0	uvrC	excinuclease UvrABC, endor	-0.0137729	0.58542314
JW0444	P0AFP2	ybaZ	excision repair protein, alkyl	-0.0945364	0.06884467
JW0762	P0A8F8	uvrB	exision nuclease of nucleoti	0.05956034	0.17601315
JW5386	Q2EET0	ypdJ	exisonase remnant	0.04642073	0.28936631
JW1833	P0AEK0	exoX	exodeoxyribonuclease 10; D	0.05115734	0.08371461
JW1993	P04995	sbcB	exodeoxyribonuclease I; exo	0.04171338	0.23716451
JW1738	P09030	xthA	exonuclease III	0.06320276	0.08395264
JW2787	P04993	recD	exonuclease V (RecBCD corr	0.06531633	0.19486474
JW2788	P08394	recB	exonuclease V (RecBCD corr	-0.0654023	0.53217888
JW2790	P07648	recC	exonuclease V (RecBCD corr	0.09536277	0.17832185
JW0412	P0A8G9	xseB	exonuclease VII small subur	0.09219232	0.00145312
JW2493	P04994	xseA	exonuclease VII, large subur	-0.0176517	0.46628755
JW0388	P0AG76	sbcD	exonuclease, dsDNA, ATP-d	-0.0019606	0.93910108
JW0387	P13458	sbcC	exonuclease, dsDNA, ATP-d	0.11307514	0.02915587
JW2487	P0AFL6	ppx	exopolyphosphatase	0.16993963	0.01457538
JW5741	P21499	rnr	exoribonuclease R, RNase R	0.00932369	0.73293669
JW1057	P43533	flgN	export chaperone for FlgK a	-0.0432877	0.29502506
JW1836	P33219	yebF	extracellular Colicin M imm	-0.0048883	0.89733121
JW3988	P32688	yjbG	extracellular polysaccharide	0.09973044	0.06801639
JW5711	P32687	yjbF	extracellular polysaccharide	0.00149694	0.95941776
JW3986	P0AF45	yjbE	extracellular polysaccharide	0.04388413	0.16661159
JW3716	P0AB98	atpB	F0 sector of membrane-bou	-0.1718248	0.00272022
JW3714	P0ABA0	atpF	F0 sector of membrane-bou	-0.2296289	0.01308626

JW3715	P68699	atpE	F0 sector of membrane-bou	-0.2294729	0.01216519
JW3712	P0ABB0	atpA	F1 sector of membrane-bou	0.02666424	0.24054544
JW3710	P0ABB4	atpD	F1 sector of membrane-bou	-0.1362053	0.02642818
JW3713	P0ABA4	atpH	F1 sector of membrane-bou	-0.0410507	0.69078225
JW3709	P0A6E6	atpC	F1 sector of membrane-bou	0.05760011	0.33213354
JW3711	P0ABA6	atpG	F1 sector of membrane-bou	-0.0575217	0.08439156
JW1176	P0A8V6	fadR	fatty acid metabolism regul	-0.0972528	0.19575967
JW0797	P0ABT2	dps	Fe-binding and storage prot	-4.53E-05	0.99904041
JW1674	P77667	sufA	Fe-S cluster assembly prote	0.078619	0.09569786
JW2508	P0COL9	yfhJ	Fe(2+) donor and activity m	-0.0332744	0.18477699
JW5105	P75779	ybiX	Fe(II)-dependent oxygenase	-0.3293383	0.01582653
JW3377	P63020	gntY	Fe/S biogenesis protein, sca	0.05838631	0.01576421
JW0229	P04335	frsA	fermentation-respiration sw	0.00286182	0.12115095
JW1375	P52643	ldhA	fermentative D-lactate dehy	-0.0388273	0.04059079
JW2230	P0ABW3	yfaE	ferredoxin involved with rib	0.10466105	5.07E-06
JW3895	P28861	fpr	ferredoxin-NADP reductase;	-0.0132052	0.57408944
JW2193	P0AAL3	napG	ferredoxin-type protein	-0.0553546	0.26714167
JW2192	P33934	napH	ferredoxin-type protein	0.06232057	0.17629593
JW2196	P0AALO	napF	ferredoxin-type protein, role	0.03646605	0.00763576
JW4247	P15031	fecE	ferric citrate ABC transport	-0.0733647	0.0344347
JW4250	P15028	fecB	ferric citrate ABC transport	0.08037715	0.00314748
JW4249	P15030	fecC	ferric citrate ABC transport	-0.0457191	0.35121056
JW4248	P15029	fecD	ferric citrate ABC transport	0.02850485	0.42598971
JW4331	P39405	fhuF	ferric iron reductase involve	0.09033862	0.08683179
JW0669	P0A9A9	fur	ferric iron uptake regulon tr	-0.0007217	0.96372015
JW1088	P16869	fhuE	ferric-rhodotorulic acid oute	-0.0221729	0.61504798
JW0146	P06971	fhuA	ferrichrome outer membrar	0.09750538	0.07168616
JW0300	P77536	ykgF	ferridoxin-like LutB family p	0.08407146	0.03778212
JW0580	P23878	fepC	ferrienterobactin ABC transp	-0.0089194	0.86038092
JW0584	P0AEL6	fepB	ferrienterobactin ABC transp	0.02748399	0.69590593
JW0582	P23876	fepD	ferrienterobactin ABC transp	0.04581905	0.00855802
JW5086	P05825	fepA	ferrienterobactin outer men	-0.2239974	0.00016896
JW1890	P0A9A2	yecl	ferritin B, putative ferrous ir	0.01217937	0.65887904
JW1893	P0A998	ftn	ferritin iron storage protein	-0.2435806	0.03694526
JW3886	P69380	fieF	ferrous iron and zinc transp	0.03561779	0.25910966
JW3372	P33650	feoB	ferrous iron transporter prot	-0.1543398	3.67E-05
JW3371	P0AEL3	feoA	ferrous iron transporter, pro	0.00500676	0.89359734
JW2512	P0AAC8	iscA	FeS cluster assembly protei	0.08175708	0.12444601
JW0519	P0ABW5	sfmA	FimA homolog, function unk	0.01606502	0.86788624
JW5072	P38052	sfmF	FimA homolog, function unk	0.02095671	0.30995577
JW5071	P75715	sfmH	FimA homolog, function unk	0.03957781	0.38585701
JW5509	P76656	yqil	fimbrial protein	0.09322264	0.01185249
JW5780	P30130	fimD	fimbrial usher outer membr	0.03896455	0.22325141
JW3311	P0A9K9	slyD	FKBP-type peptidyl prolyl cis	-0.0323167	0.441127
JW0026	P0AEM0	fkpB	FKBP-type peptidyl-prolyl cis	-0.076262	0.40616637

JW5746	P0A9L3	fklB	FKBP-type peptidyl-prolyl cis	-0.0518945	0.03766479
JW3309	P45523	fkpA	FKBP-type peptidyl-prolyl cis	-0.0039691	0.92975388
JW1921	P0A8T5	fliE	flagellar basal-body compo	-0.111081	0.03367555
JW1922	P25798	fliF	flagellar basal-body MS-ring	0.03099985	0.26540954
JW1933	P0AC07	fliQ	flagellar biosynthesis protei	-0.0359108	0.46246878
JW5316	P22586	fliO	flagellar biosynthesis protei	0.00612816	0.85933823
JW1932	P0AC05	fliP	flagellar biosynthesis protei	0.12919508	0.0706059
JW1928	P0ABX8	fliL	flagellar biosynthesis protei	0.22455675	0.01281844
JW1881	P0A8S9	flhD	flagellar class II regulon tra	-0.0215077	0.64057652
JW1880	P0ABY7	flhC	flagellar class II regulon tra	0.01976306	0.21967314
JW1065	P0ABX5	flgG	flagellar component of cell-	0.03274014	0.4727991
JW1064	P75938	flgF	flagellar component of cell-	-0.0754173	0.17168928
JW1060	P0ABW9	flgB	flagellar component of cell-	0.01705869	0.64943312
JW1061	P0ABX2	flgC	flagellar component of cell-	0.05465055	0.37164968
JW1934	P33135	fliR	flagellar export pore proteir	0.24246982	0.00102325
JW1909	P24216	fliD	flagellar filament capping p	0.00405925	0.89869525
JW1908	P04949	fliC	flagellar filament structural	0.11408922	0.00031626
JW1062	P75936	flgD	flagellar hook assembly pro	0.13648923	0.00130123
JW1063	P75937	flgE	flagellar hook protein	0.0627334	0.33612687
JW1070	P29744	flgL	flagellar hook-filament junc	0.0562625	0.05393971
JW1069	P33235	flgK	flagellar hook-filament junc	0.12915219	0.0049966
JW1927	P52614	fliK	flagellar hook-length contro	0.01400584	0.65884297
JW1923	P0ABZ1	fliG	flagellar motor switching ar	-0.0344724	0.05512648
JW1929	P06974	fliM	flagellar motor switching ar	0.00074104	0.97235529
JW1930	P15070	fliN	flagellar motor switching ar	0.04251223	0.23122642
JW1926	P52613	fliJ	flagellar protein	0.03368886	0.29821276
JW5153	P0A6S0	flgH	flagellar protein of basal-bo	-0.1673457	0.00020912
JW1910	P26608	fliS	flagellar protein potentiates	0.02379063	0.65311737
JW1183	P76010	ycgR	flagellar velocity braking pro	0.07045177	0.0918494
JW1869	P76299	flhB	flagellin export apparatus, s	-0.1042847	0.00054627
JW1925	P52612	fliI	flagellum-specific ATP synt	0.04639969	0.04868406
JW1457	P76121	yddH	flavin reductase like-protein	-0.090401	0.06755863
JW5138	P75893	ycdH	flavin:NADH reductase	0.07745398	0.0498506
JW2865	P64559	ygfY	flavinotor of succinate dehy	0.18862529	6.20E-06
JW2863	P0ABY4	fldB	flavodoxin 2	0.1651991	0.00084915
JW5607	P0A8R9	hdfR	flhDC operon transcriptional	0.01835069	0.60549807
JW2707	Q46889	ygbK	FliA-regulated DUF1537 fan	-0.0205962	0.53959684
JW0619	P37002	crcB	fluoride efflux channel, dual	0.05411799	0.20722507
JW3720	P03817	mioC	FMN-binding protein MioC	-0.0132394	0.4292973
JW3339	P45545	yhfS	FNR-regulated pyridoxal ph	0.06335611	0.05564302
JW1659	P77147	ydhT	FNR, Nar, NarP-regulated pi	-0.0550655	0.00512131
JW1662	P77564	ydhW	FNR, Nar, NarP-regulated pi	-0.0203905	0.42461657
JW3610	P05523	mutM	formamidopyrimidine/5-for	0.00797933	0.67139151
JW0886	P09373	pflB	formate C-acetyltransferase	-0.1625003	4.33E-06
JW0887	P0AC23	focA	formate channel	0.0118807	0.64634654

JW3862	P13024	fdhE	formate dehydrogenase for	-0.0253189	0.28753693
JW3866	P32177	fdhD	formate dehydrogenase for	-0.0211382	0.64009874
JW2683	P0AAK4	hydN	formate dehydrogenase-H,	-0.1696333	0.00703752
JW4040	P07658	fdhF	formate dehydrogenase-H, s	0.0523076	0.07804438
JW1472	P0AEK7	fdnI	formate dehydrogenase-N, c	-0.0033191	0.90692213
JW1471	P0AAJ3	fdnH	formate dehydrogenase-N,	-0.021009	0.23201067
JW3863	P0AEL0	fdol	formate dehydrogenase-O, c	-0.0510119	0.01770867
JW3864	P0AAJ5	fdoH	formate dehydrogenase-O,	-0.0640597	0.36151025
JW3865	P32176	fdoG	formate dehydrogenase-O,	0.01885026	0.42644545
JW2690	P16432	hycF	formate hydrogenlyase com	0.07977039	0.00294357
JW2701	P19323	fhIA	formate hydrogenlyase tran	-0.015974	0.55596907
JW4033	P0AAK7	nrfC	formate-dependent nitrite r	-0.0240838	0.6271329
JW4034	P32709	nrfD	formate-dependent nitrite r	-0.0173824	0.56234246
JW2371	P69902	frc	formyl-CoA transferase, NA	-0.097387	2.36E-06
JW1220	P37051	purU	formyltetrahydrofolate hydr	0.23702019	0.0001016
JW1821	P76270	yebR	free methionine-(R)-sulfoxi	-0.1318278	0.02079348
JW1714	P77739	yniA	fructosamine kinase family	-0.0023304	0.9037832
JW2897	P21437	yggF	fructose 1,6 bisphosphatase	-0.213474	0.00037316
JW3896	P0A9C9	glpX	fructose 1,6-bisphosphatase	0.10742856	0.00054544
JW2155	P0AEW9	fruK	fructose-1-phosphate kinase	0.07778929	4.04E-05
JW4191	P0A993	fbp	fructose-1,6-bisphosphatase	-0.020806	0.29666202
JW5109	P78055	fsaA	fructose-6-phosphate aldola	-0.1360276	0.23016646
JW3918	P32669	fsaB	fructose-6-phosphate aldola	-0.046212	0.0891831
JW5344	P0A991	fbaB	fructose-bisphosphate aldol	0.01148133	0.64140676
JW5699	P45541	frIC	fructoselysine 3-epimerase	-0.1066013	0.05404234
JW3337	P45543	frID	fructoselysine 6-kinase	-0.0118739	0.62128714
JW5700	P0AC00	frLB	fructoselysine-6-P-deglycasc	0.03631471	0.04153448
JW4284	P0AC94	gntP	fructuronate transporter	0.04396954	0.05519298
JW4287	P39161	uxuR	fructuronate-inducible hexu	-0.0224581	0.072721
JW5125	P75862	ycbW	FtsZ stabilizer	-0.0240696	0.36883323
JW2878	P0ADS2	zapA	FtsZ stabilizer	0.00861835	0.72666536
JW0099	P36680	yacF	FtsZ stabilizer	0.06152662	0.05667264
JW3899	P0AF36	yiiU	FtsZ stabilizer, septal ring a	-0.0295305	0.31637935
JW1665	P0ACX5	ydhZ	fumarase D	0.03169234	0.05907596
JW2896	P11663	yggD	Fumarase E; MtlR family pu	-0.1884454	0.03623077
JW1604	P0AC33	fumA	fumarate hydratase (fumaric	-0.0152078	0.75024665
JW1603	P05042	fumC	fumarate hydratase (fumaric	-0.0087775	0.80976361
JW4114	P0AC47	frdB	fumarate reductase (anaerc	0.02178408	0.64790703
JW4112	P0A8Q3	frdD	fumarate reductase (anaerc	0.02389515	0.24640173
JW4113	P0A8Q0	frdC	fumarate reductase (anaerc	0.10756269	0.09830394
JW5394	P37440	ucpA	furfural resistance protein, p	-0.0703474	0.01667854
JW2804	P31119	aas	fused 2-acylglycerophospho	0.08792944	0.00666376
JW0720	P54745	mngA	fused 2-O-a-mannosyl-D-gly	0.32555888	0.00351731
JW3822	P21177	fadB	fused 3-hydroxybutyryl-CoA	0.0083335	0.7799578
JW5380	P77182	trmC	fused 5-methylaminomethy	-0.020604	0.25157093

JW1228	P0A9Q7	adhE	fused acetaldehyde-CoA dehyd	0.04383354	0.39198175
JW3700	P08722	bgfF	fused beta-glucoside-specific	-0.0492071	0.0751242
JW1877	P07363	cheA	fused chemotactic sensory h	-0.0298109	0.34501225
JW1872	P07330	cheB	fused chemotaxis regulator:	0.03192188	0.61977089
JW2581	P07023	tyrA	fused chorismate mutase T ₁	-0.0241402	0.76851621
JW3025	P30870	glnE	fused deadenyltransferase	-0.0506138	0.29910643
JW3839	P0AFB8	glnG	fused DNA-binding response	0.01377421	0.38778476
JW3968	P14375	zraR	fused DNA-binding response	0.04695835	0.07320034
JW2201	P06134	ada	fused DNA-binding transcrip	0.02722905	0.30233284
JW0999	P09546	putA	fused DNA-binding transcrip	0.16755646	0.00994584
JW2156	P69811	fruB	fused fructose-specific PTS	0.09902244	0.12612904
JW2154	P20966	fruA	fused fructose-specific PTS	-0.0880367	0.02358968
JW1087	P69786	ptsG	fused glucose-specific PTS	0.04509692	0.541791
JW1255	P00904	trpD	fused glutamine amidotrans	0.26169622	0.00291976
JW0145	P02919	mrcB	fused glycosyl transferase a	0.05311345	0.21871944
JW1806	P69797	manX	fused mannose-specific PTS	0.06064434	0.29433782
JW2536	P24232	hmp	fused nitric oxide dioxygena	-0.254114	0.01893628
JW2214	Q06065	atoC	fused response regulator of	-0.1070106	0.06233834
JW0683	P21865	kdpD	fused sensory histidine kina	0.16799472	0.04007539
JW3043	P50466	aer	fused signal transducer for	-0.0250516	0.22639024
JW3331	P0AEA8	cysG	fused siroheme synthase 1, ₂	-0.0195049	0.41872942
JW2249	P77398	yfbG	fused UDP-L-Ara4N formyltr	-0.0412748	0.10334118
JW3040	P0A9H1	ygjF	G/U mismatch-specific DNA	-0.1927541	0.0860597
JW3480	P63204	gadE	gad regulon transcriptional	0.16885527	0.00386137
JW2075	P0A9S3	gatD	galactitol-1-phosphate dehy	0.05383084	0.00652289
JW2077	P37188	gatB	galactitol-specific enzyme II	0.04215718	0.33258132
JW4186	P39325	ytfQ	galactofuranose ABC transp	0.18017634	0.19967899
JW0740	P0A6T3	galk	galactokinase	-0.0388954	0.35340134
JW3110	P42912	agal	galactosamine-6-phosphate	0.00636551	0.83840029
JW2138	P25748	galS	galactose- and fucose-induc	-0.0091553	0.79092299
JW0741	P09148	galT	galactose-1-phosphate uridy	-0.0810456	0.00059707
JW2805	P03024	galR	galactose-inducible d-galact	-0.2875592	0.01378605
JW1439	P77674	ydcW	gamma-aminobutyraldehyd	0.01216184	0.57986681
JW2638	P25527	gabP	gamma-aminobutyrate tran	-0.0599092	0.09772812
JW0232	P0A7B5	proB	gamma-glutamate kinase	0.14566583	0.0420471
JW1293	P23883	puuC	gamma-glutamyl-gamma-a	0.08303026	0.01118394
JW1291	P76038	puuD	gamma-glutamyl-gamma-a	0.06695443	0.18558577
JW0233	P07004	proA	gamma-glutamylphosphate	0.07181351	0.02081735
JW1294	P37906	puuB	gamma-glutamylputrescine	-0.0291324	0.16144282
JW3412	P18956	ggt	gamma-glutamyltranspepti	0.14996337	0.00719783
JW3677	P0A7H0	recF	gap repair protein	-0.0132621	0.78703733
JW2549	P0A7H3	recO	gap repair protein	0.01130522	0.45388022
JW0461	P0A7H6	recR	gap repair protein	0.1462997	0.00107411
JW2990	Q46865	ygiU	GCU-specific mRNA interfer	0.05639883	0.16461399
JW2038	P0AC88	gmd	GDP-D-mannose dehydratas	0.07076102	0.10097448

JW5335	P32056	nudD	GDP-mannose mannosyl hydrolase	0.13288752	0.00655889
JW2451	P37128	yffH	GDP-mannose pyrophosphatase	0.0666876	0.08819389
JW3066	P0AA63	yqjA	general envelope maintenance	-0.2654809	0.0244733
JW2976	P0AA60	yghB	general envelope maintenance	-0.0512183	0.09368421
JW5704	P36678	gspM	general secretory pathway component	-0.089427	0.04758338
JW3286	P45757	gspC	general secretory pathway component	-0.0613296	0.09066209
JW5706	P45760	gspI	general secretory pathway component	-0.0495049	0.10812495
JW3294	P45762	gspK	general secretory pathway component	-0.0354286	0.13754009
JW5705	P45763	gspL	general secretory pathway component	-0.0251544	0.6453184
JW3285	P45756	gspA	general secretory pathway component	-0.0073	0.77449535
JW5707	P45758	gspD	general secretory pathway component	0.01813911	0.73291199
JW3289	P41441	gspF	general secretory pathway component	0.05430702	0.02096763
JW3288	P45759	gspE	general secretory pathway component	0.09177608	0.12557928
JW5769	P39353	yjhC	GFO/IDH/MOCA family putative	-0.0147329	0.68203026
JW4181	P0AE48	ytfP	GGCT-like protein	0.16267921	0.33766541
JW3124	P45472	yhbQ	GIY-YIG nuclease superfamily	-0.0436567	0.34293553
JW3229	P0A6R3	fis	global DNA-binding transcription factor	-0.1567166	0.00500217
JW1225	P0ACF8	hns	global DNA-binding transcription factor	-0.1013242	0.00046188
JW1276	P76034	yciT	global regulator of transcription	0.2124415	0.00084295
JW4130	P0A6X3	hfq	global sRNA chaperone; HFY	0.07344657	0.00011986
JW0075	P10151	leuO	global transcription factor	-0.1226767	5.95E-05
JW0553	P05052	appY	global transcriptional activator	-0.0188852	0.21242847
JW5267	P0A8W2	slyA	global transcriptional regulator	0.01820252	0.53443088
JW1599	P0ACX0	ydgC	GlpM family inner membrane	-2.22E-05	0.99903164
JW2759	Q46915	gudX	glucarate dehydratase-related	-0.0139582	0.50007939
JW2673	P05706	srlB	glucitol/sorbitol-specific enzyme	0.05890419	0.26753891
JW5430	P56580	srlE	glucitol/sorbitol-specific enzyme	-0.023962	0.28829253
JW5429	P56579	srlA	glucitol/sorbitol-specific enzyme	0.05146485	0.11929514
JW2385	P0A6V8	glk	glucokinase	0.03018602	0.12001168
JW3400	P46859	gntK	gluconate kinase 2	0.01870044	0.2827496
JW5690	P39835	gntT	gluconate transporter, high-affinity	0.11404758	0.01602803
JW5686	P0AC96	gntU	gluconate transporter, low-affinity	0.04340695	0.05504855
JW1586	P50456	dgsA	glucosamine anaerobic growth	0.01174174	0.14516855
JW0664	P0A759	nagB	glucosamine-6-phosphate dehydrogenase	-0.0627266	0.12237943
JW0120	P15877	gcd	glucose dehydrogenase	-0.0185229	0.35989357
JW0987	P19926	agp	glucose-1-phosphatase/inositol	0.05066895	0.11697591
JW3393	P0A6V1	glgC	glucose-1-phosphate adenylylation	0.01940622	0.35056947
JW3763	P61887	rffH	glucose-1-phosphate thymidylate	0.03887376	0.46534428
JW2024	P37744	rfbA	glucose-1-phosphate thymidylate	0.13236712	0.03202453
JW1841	P0AC53	zwf	glucose-6-phosphate 1-dehydrogenase	-0.0263184	0.36051233
JW2410	P69783	crr	glucose-specific enzyme IIA	-0.0079966	0.75168705
JW3985	P0A6T1	pgi	glucosephosphate isomerase	0.04587997	0.09301447
JW1608	P0CE44	uidB	glucuronide transporter	0.04245462	0.14756494
JW3485	P69908	gadA	glutamate decarboxylase A, cytoplasmic	0.17948193	0.00804297
JW1488	P69910	gadB	glutamate decarboxylase B, cytoplasmic	-0.0115807	0.82818241

JW1750	P00370	gdhA	glutamate dehydrogenase, I	0.05217679	0.03264929
JW3180	P09832	gltD	glutamate synthase, 4Fe-4S	0.00716749	0.72972468
JW3179	P09831	gltB	glutamate synthase, large s	-0.0269123	0.16652918
JW3628	POAER8	gltS	glutamate transporter	-0.0085108	0.66816938
JW5201	P78061	puuA	glutamate--putrescine ligas	0.02416898	0.36846407
JW2663	POA6W9	gshA	glutamate-cysteine ligase	-0.1085057	0.00509771
JW2376	P77434	yfdZ	glutamate-pyruvate aminot	-0.0367287	0.15722412
JW2287	POA959	yfbQ	glutamate-pyruvate aminot	0.12078459	0.00084942
JW1487	P63235	gadC	glutamate:gamma-aminobu	-0.1261412	0.1392395
JW0647	POAAG3	gltL	glutamate/aspartate ABC tr	-0.025666	0.49688899
JW0648	POAER5	gltK	glutamate/aspartate ABC tr	-0.0897315	0.02687687
JW0649	POAER3	gltJ	glutamate/aspartate ABC tr	-0.0596291	0.02251307
JW5092	P37902	gltI	glutamate/aspartate peripl	0.00439814	0.88630298
JW4038	P21345	gltP	glutamate/aspartate:protor	-0.0730697	0.0405123
JW0474	P77454	ybaS	glutaminase 1	-0.0179939	0.3494154
JW1517	POA6W0	yneH	glutaminase 2	0.00201336	0.96373602
JW3841	POA9C5	glnA	glutamine synthetase	0.10340954	0.03430781
JW0795	POAEQ6	glnP	glutamine transporter subu	-0.1106432	0.12886055
JW0796	POAEQ3	glnH	glutamine transporter subu	-0.0360168	0.37045826
JW0794	P10346	glnQ	glutamine transporter subu	-0.0071981	0.77396984
JW5892	P27305	yadB	glutamyl-Q tRNA(Asp) synt	0.15068525	5.24E-05
JW0833	P68688	grxA	glutaredoxin 1, redox coenz	-0.0003753	0.99060888
JW1051	POAC59	grxB	glutaredoxin 2 (Grx2)	-0.0036886	0.95634303
JW3585	POAC62	grxC	glutaredoxin 3	-0.050622	0.02322059
JW1646	POAC69	ydhD	glutaredoxin-4	-0.0860605	0.19710527
JW5897	P75796	yliA	glutathione ABC transporter	-0.0619037	0.08361018
JW0816	P75799	yliD	glutathione ABC transporter	-0.0667549	0.53161618
JW0815	P75798	yliC	glutathione ABC transporter	0.07228133	0.02528591
JW3467	P06715	gor	glutathione oxidoreductase	0.05007208	0.00134785
JW1700	P06610	btuE	glutathione peroxidase	-0.1241475	0.00033641
JW0822	POACA7	yliJ	glutathione S-transferase	-0.0655083	0.02176714
JW2298	P77544	yfcF	glutathione S-transferase	0.00359691	0.46964533
JW1449	P76117	yncG	glutathione S-transferase h	-0.041569	0.08395449
JW3565	POACA1	yibF	glutathione S-transferase h	-0.0079134	0.84246903
JW2914	P04425	gshB	glutathione synthetase	-0.2187808	0.00015944
JW0870	P29018	cydD	glutathione/cysteine ABC tr	-0.145058	0.3941649
JW1627	POA9D2	gst	glutathionine S-transferase	-0.0674805	0.0017567
JW2956	POAES0	gss	glutathionylspermidine ami	0.15175284	0.0112014
JW3093	P23524	garK	glycerate kinase I	-0.0739433	0.00212876
JW0502	P77364	glxK	glycerate kinase II	0.01481693	0.79419578
JW5556	POA9S5	gldA	glycerol dehydrogenase, NA	0.01445983	0.6243555
JW3898	POAER0	glpF	glycerol facilitator	0.0329717	0.60575299
JW3897	POA6F3	glpK	glycerol kinase	0.02168645	0.33474577
JW3414	P10908	ugpQ	glycerophosphodiester phos	-0.0085086	0.73099809
JW2652	P14175	proV	glycine betaine/proline ABC	0.01039684	0.74381658

JW2654	P0AFM2	proX	glycine betaine/proline ABC	0.05224428	0.22454911
JW2653	P14176	proW	glycine betaine/proline ABC	0.1380526	0.00603805
JW3592	P0AB77	kbl	glycine C-acetyltransferase	0.06252246	0.16297193
JW2872	P0A6T9	gcvH	glycine cleavage system lipc	0.01722314	0.82650006
JW2779	P0A9F6	gcvA	glycine cleavage system tra	-0.0228778	0.64069995
JW2871	P33195	gcvP	glycine decarboxylase, PLP-c	-0.1392066	0.00162405
JW3530	P00961	glyS	glycine tRNA synthetase, be	-0.0616751	0.00520315
JW3394	P15067	glgX	glycogen debranching enzym	0.00809053	0.49159689
JW3391	P0AC86	glgP	glycogen phosphorylase	-0.0361989	0.19432381
JW3392	P0A6U8	glgA	glycogen synthase	0.09192618	0.00572445
JW5486	P52074	glcF	glycolate oxidase 4Fe-4S iro	0.03140449	0.40727766
JW5487	P52073	glcE	glycolate oxidase FAD bindi	0.15463023	0.0006409
JW2946	P0AEP9	glcD	glycolate oxidase subunit, F	-0.0912453	0.06119369
JW2942	Q46839	yghK	glycolate transporter	0.29293171	8.06E-05
JW1643	P0AC81	gloA	glyoxalase I, Ni-dependent	0.01453933	0.476518
JW1950	P31658	hchA	glyoxalase III and Hsp31 mo	0.04618855	0.08153676
JW0495	P0AEP7	gcl	glyoxylate carboligase	0.02924724	0.2641405
JW0494	P0ACN4	allR	glyoxylate-inducible transcri	0.05188199	0.13312869
JW5146	P75913	ycdW	glyoxylate/hydroxypyruvate	0.04326662	0.19845673
JW5656	P37666	tiaE	glyoxylate/hydroxypyruvate	-0.0654233	0.00013519
JW0101	P60560	guaC	GMP reductase	-0.1750816	0.04341929
JW2491	P04079	guaA	GMP synthetase (glutamine	-0.01983	0.2327822
JW5865	P64636	yrfG	GMP/IMP nucleotidase	-0.1369587	0.01895875
JW4269	P39368	yjhQ	GNAT family putative N-ace	-0.0518277	0.05170988
JW3519	P37664	yaC	GNAT family putative N-ace	-0.0377873	0.26410451
JW5758	P39337	yjgM	GNAT family putative N-ace	-0.0354253	0.11812965
JW2427	P76539	ypeA	GNAT family putative N-ace	-0.0307099	0.27878366
JW1917	P76319	yedL	GNAT family putative N-ace	-0.0094462	0.60874432
JW3859	P0ADQ2	yiiD	GNAT family putative N-ace	0.03518465	0.01961829
JW2262	P0AEH3	elaA	GNAT family putative N-ace	0.04723096	0.22909511
JW4088	P39274	yjD	GNAT family putative N-ace	0.05603342	0.03046088
JW0224	Q47158	yafP	GNAT family putative N-ace	0.07462559	0.01196059
JW3125	P63417	yhbS	GNAT family putative N-ace	0.11063757	0.01685735
JW3972	P09163	yjaB	GNAT-family putative N-ace	0.13495053	0.02206158
JW2299	P77526	yfcG	GSH-dependent disulfide bo	0.08472264	0.00760165
JW0700	P0AFP6	ybgI	GTP cyclohydrolase-like radi	0.02760382	0.56520056
JW2697	P0AAN3	hypB	GTP hydrolase involved in ni	0.1280879	6.78E-07
JW5571	P32132	bipA	GTP-binding protein	0.03062204	0.47359013
JW4131	P25519	hflX	GTPase, stimulated by 50S :	-0.0430378	0.2340782
JW5466	P76641	guaD	guanine deaminase	-0.0224719	0.71949023
JW5467	Q46817	ygfQ	guanine/hypoxanthine perm	0.02849768	0.3103609
JW4025	P0AF52	yjcD	guanine/hypoxanthine perm	0.05431598	0.16005626
JW5603	P25552	gpp	guanosine pentaphosphatas	0.00848009	0.64095288
JW0696	P28916	ybfD	H repeat-associated putativ	-0.0582824	0.04508633
JW1455	P28917	ydcC	H repeat-associated putativ	0.06496878	0.00023211

JW5012	P37019	clcA	H(+)/Cl(-) exchange transpo	-0.3345598	0.02255293
JW5263	P76175	clcB	H(+)/Cl(-) exchange transpo	0.10448983	0.03167715
JW2521	Q47141	hcaR	hca operon transcriptional r	-0.0614021	0.01219875
JW5117	P75824	hcr	HCP oxidoreductase, NADH-	-0.0178304	0.58679775
JW3663	POC058	ibpB	heat shock chaperone	-0.067946	0.03639274
JW3664	POC054	ibpA	heat shock chaperone	-0.0615342	0.02975138
JW5692	POA6Y5	hslO	heat shock protein Hsp33	0.08385013	0.03037071
JW0657	POA9K3	ybeZ	heat shock protein, putative	0.00692234	0.66712093
JW1374	P52644	hslJ	heat-inducible lipoprotein ir	0.02353813	0.6203534
JW5366	P33931	ccmA	heme export ABC transportε	0.00174548	0.91971648
JW2188	POABL8	ccmB	heme export ABC transportε	-0.027365	0.27031711
JW4035	P32710	nrfE	heme lyase (NrfEFG) for ins	-0.0106501	0.82146572
JW4036	P32711	nrfF	heme lyase (NrfEFG) for ins	0.29764332	0.06931751
JW4037	P32712	nrfG	heme lyase (NrfEFG) for ins	0.06853647	0.1597169
JW2184	P33927	ccmF	heme lyase, CcmF subunit	-0.0115499	0.82118262
JW2182	POABM9	ccmH	heme lyase, CcmH subunit	0.02201424	0.51124013
JW1695	POACX9	ydiE	hemin uptake protein HemP	0.047615	0.01182836
JW2922	P52062	yggW	HemN family putative oxido	-0.0709645	0.47494251
JW5181	P77335	hlyE	hemolysin E	0.07532482	0.00225655
JW2867	P67153	yqfA	hemolysin III family HylIII in	0.16942874	0.00256403
JW3024	P76658	rfaE	heptose 7-phosphate kinase	-0.050863	0.01185515
JW3725	P31473	yieN	hexameric AAA+ MoxR fami	0.02660125	0.00996505
JW5376	P77625	yfbT	hexitol phosphatase A	0.07600818	0.15124473
JW1716	P77247	yniC	hexitol phosphatase B; 2-de	0.01819324	0.65928955
JW3641	POAGC0	uhpT	hexose phosphate transport	-0.0079404	0.8709039
JW2811	Q46938	kdul	hexuronate isomerase	-0.1384766	0.10485472
JW3065	POACL2	exuR	hexuronate regulon transcrij	-0.2044673	0.00017735
JW3064	POAA78	exuT	hexuronate transporter	-0.0810606	0.05058562
JW4133	POABC3	hflC	HflB protease modulator sp	0.05054675	0.34690188
JW0450	POAAR0	ybaJ	Hha toxicity attenuator; conj	-0.0176024	0.4031729
JW2000	P60995	hisL	his operon leader peptide	-0.0057702	0.78971315
JW2303	P07109	hisP	histidine ABC transporter A1	-0.0663509	0.01015994
JW2306	POAEU0	hisJ	histidine ABC transporter pe	0.02726266	0.3428824
JW2304	POAEU3	hisM	histidine ABC transporter pe	-0.0261823	0.15004346
JW2305	P52094	hisQ	histidine ABC transporter pe	0.02975617	0.14784404
JW2004	P06987	hisB	histidinol-phosphatase and i	0.10939792	7.33E-05
JW2003	P06986	hisC	histidinol-phosphate aminot	0.0006402	0.99486207
JW0400	POAAQ2	yajD	HNH nuclease family protei	0.04219677	0.21647615
JW3979	P13009	metH	homocysteine-N5-methyltet	-0.0291487	0.56675211
JW0002	P00547	thrB	homoserine kinase	-0.0004004	0.99437098
JW0002	P00547	thrB	homoserine kinase	0.20604633	0.08974863
JW3973	P07623	metA	homoserine O-transsuccinyl	0.00875547	0.89700443
JW5585	POAG34	rhtB	homoserine, homoserine lac	0.00219015	0.89954416
JW2511	POA6L9	hscB	HscA co-chaperone, J domai	0.01111253	0.46068473
JW2054	P36928	yegD	Hsp70 chaperone family pro	-0.0568626	0.01174924

JW0645	P77319	hscC	Hsp70 family chaperone Hsc	0.0053846	0.92789437
JW3524	POA9V5	viaG	HTH_CROC1 family putative	-0.0483843	0.15504634
JW3964	POACF0	hupA	HU, DNA-binding transcripti	-0.0523385	0.01429204
JW0430	POACF4	hupB	HU, DNA-binding transcripti	-0.1817287	0.00151941
JW2367	P30855	evgS	hybrid sensory histidine kina	-0.0248471	0.5988552
JW5135	P39453	torS	hybrid sensory histidine kina	-0.0011495	0.97731564
JW2757	POAEC5	barA	hybrid sensory histidine kina	-0.1331331	0.00442916
JW2648	POAC65	nrdH	hydrogen donor for NrdEF el	0.09152405	0.00074056
JW2992	POADU5	ygiW	hydrogen peroxide and cadn	0.02246255	0.545161
JW1529	P31130	ydeI	hydrogen peroxide resistanc	0.03010047	0.01096326
JW0957	P19930	hyaD	hydrogenase 1 maturation p	-0.0369043	0.0226546
JW0956	POAAM1	hyaC	hydrogenase 1, b-type cytoc	0.11076686	3.88E-05
JW0955	POACD8	hyaB	hydrogenase 1, large subuni	-0.1018615	0.0582392
JW0954	P69739	hyaA	hydrogenase 1, small subun	0.05394926	0.16848181
JW2964	POAAJ8	hybA	hydrogenase 2 4Fe-4S ferre	0.00366945	0.88405906
JW2958	POAAM7	hybG	hydrogenase 2 accessory pro	-0.273226	0.04241794
JW2960	POAAN1	hybE	hydrogenase 2-specific chap	0.09828609	0.00652754
JW2962	POACE0	hybC	hydrogenase 2, large subuni	0.01340382	0.58242314
JW2965	P69741	hybO	hydrogenase 2, small subun	-0.1260453	0.01127402
JW2689	P16433	hycG	hydrogenase 3 and formate	0.11571361	0.18014049
JW2688	POAEV7	hycH	hydrogenase 3 maturation p	-0.1712231	0.00759312
JW2694	POAAK1	hycB	hydrogenase 3, Fe-S subunit	-0.2690236	0.0109815
JW2691	P16431	hycE	hydrogenase 3, large subuni	-0.0526538	0.02226907
JW2693	P16429	hycC	hydrogenase 3, membrane s	-0.001585	0.96388678
JW2692	P16430	hycD	hydrogenase 3, membrane s	0.00594309	0.92118791
JW2466	P23481	hyfA	hydrogenase 4, 4Fe-4S subu	-0.0308978	0.66784809
JW2473	P77423	hyfH	hydrogenase 4, Fe-S subunit	-0.0522813	0.41569065
JW5805	P77668	hyfI	hydrogenase 4, Fe-S subunit	0.02494724	0.19583003
JW2471	P77437	hyfF	hydrogenase 4, membrane s	-0.0258264	0.45498658
JW2469	P77416	hyfD	hydrogenase 4, membrane s	-0.0128621	0.70656738
JW2470	POAEW1	hyfE	hydrogenase 4, membrane s	0.00214311	0.91568672
JW2468	P77858	hyfC	hydrogenase 4, membrane s	0.07558117	0.00367145
JW2467	P23482	hyfB	hydrogenase 4, membrane s	0.11746549	0.05836853
JW2472	P77329	hyfG	hydrogenase 4, subunit	-0.0632561	0.04448813
JW2698	POAAM3	hypC	hydrogenase maturation pro	-0.0990938	0.00158379
JW2699	P24192	hypD	hydrogenase maturation pro	0.02586772	0.35943607
JW0959	P19932	hyaF	hydrogenase-1 protein nicke	0.05193215	0.10385474
JW2476	P71229	hyfR	hydrogenase-4 transcription	0.07124037	0.21490699
JW2090	P76422	thiD	hydroxy-methylpyrimidine ki	0.03121955	0.25769219
JW0202	POAC84	gloB	hydroxyacylglutathione hydr	0.00626918	0.91667824
JW0592	P45579	ybdH	hydroxycarboxylate dehydro	0.02439364	0.43597734
JW0786	P30178	ybiC	hydroxycarboxylate dehydro	0.00552196	0.89203147
JW1953	P76341	yedX	hydroxyisourate hydrolase	-0.1245759	0.0139543
JW0496	P30147	hyi	hydroxypyruvate isomerase	-0.0419809	0.03374978
JW4290	P39376	yjiE	hypochlorite-responsive trar	-0.0042551	0.90585259

JW5009	P0A9M2	hpt	hypoxanthine phosphoribosyl	-0.0239409	0.02366756
JW3647	P03061	ivbL	ilvB operon leader peptide	-0.0447425	0.05659633
JW3739	P62522	ilvL	ilvG operon leader peptide	0.02954679	0.23998338
JW2007	P60664	hisF	imidazole glycerol phosphat	0.00678782	0.97020399
JW2005	P60595	hisH	imidazole glycerol phosphat	-0.0284829	0.67817255
JW3955	O32583	thiS	immediate sulfur donor in tr	0.20023085	0.00019987
JW3970	P15639	purH	IMP cyclohydrolase and pho	0.03165136	0.47879443
JW5401	P0ADG7	guaB	IMP dehydrogenase	0.04701769	0.02213057
JW3061	P42603	ygjV	Imp-YgjV family inner mem	0.00929131	0.8132094
JW1500	P23874	hipA	inactivating GltX kinase faci	0.02727286	0.26167405
JW1774	P76236	yeal	Inactive diguanylate cyclase	0.020252	0.27378227
JW1003	P0AB24	ycdO	inactive ferrous ion transpor	-0.0195895	0.49966034
JW0765	P0AEZ9	moaB	inactive molybdopterin ader	-0.0026407	0.93217454
JW2243	P77808	yfaY	inactive PncC family protein	-0.0301373	0.14061255
JW1530	P31131	ydeJ	inactive PncC family protein	0.07681352	0.01987297
JW2254	P37590	pmrD	inactive two-component sys	-0.0783632	0.22989461
JW1254	P00909	trpC	indole-3-glycerolphosphate	0.02065952	0.74306855
JW1631	P28224	ydhA	inhibitor of c-type lysozyme,	0.05131949	0.13190538
JW0210	P0AD59	ivy	inhibitor of c-type lysozyme,	-0.0022378	0.06235247
JW0864	P0A968	cspD	inhibitor of DNA replication,	0.11406934	0.00282999
JW1165	P18196	minC	inhibitor of FtsZ ring polymε	-0.3693146	1.03E-08
JW1602	P16525	tus	inhibitor of replication at Te	0.04894132	0.02413411
JW5558	P0AE85	cpxP	inhibitor of the cpx responsε	-0.0945978	0.01007198
JW1274	P08245	yciH	initiation factor function pai	0.02276561	0.29036009
JW1156	P58034	ymgF	inner membrane division se	-0.0123571	0.35361756
JW1955	P76343	yedZ	inner membrane heme subu	0.02228242	0.40211089
JW2995	Q46867	ygiZ	inner membrane protein	-0.7512121	1.13E-08
JW3653	P31446	yidI	inner membrane protein	-0.1678587	0.08557732
JW3651	P0ADL6	yidG	inner membrane protein	-0.0956489	0.00343855
JW2344	P37327	yfdC	inner membrane protein	-0.0905216	0.00052269
JW1101	P75955	ycfT	inner membrane protein	-0.0737516	0.03440812
JW3340	P45546	yhfT	inner membrane protein	-0.0571606	0.45182991
JW0774	P0AAW5	ybhQ	inner membrane protein	-0.0404496	0.15564789
JW1405	P76090	ynbA	inner membrane protein	-0.0335001	0.34905056
JW0832	P64439	ybjM	inner membrane protein	-0.0274295	0.04786169
JW4119	P39284	yjeO	inner membrane protein	-0.0181641	0.6790428
JW5288	P76228	ynjI	inner membrane protein	-0.0171485	0.58978753
JW1829	P76278	yebZ	inner membrane protein	0.00333587	0.91765017
JW2426	P76538	yfeZ	inner membrane protein	0.04599406	0.33913171
JW1946	P76334	yedR	inner membrane protein	0.0642139	0.08690769
JW5336	P76389	yegH	inner membrane protein	0.0929903	0.00088865
JW5281	P64481	ydjM	inner membrane protein reε	-0.0646332	0.03372419
JW3834	P32129	yihG	inner membrane protein, in	-0.0360563	0.19082127
JW1264	P0AG14	sohB	inner membrane protein, S4	0.04726869	0.17952605
JW5065	P0AAS3	ybbJ	inner membrane protein; sti	0.10173559	0.01349352

JW3490	P37642	yhjD	inner membrane putative B	-0.2517948	0.00010065
JW0467	P39830	ybaL	inner membrane putative N	0.00753054	0.8084788
JW0933	P0AFL9	pqiA	inner membrane subunit of	0.10272052	0.00979228
JW1822	P0AD03	yebS	inner membrane subunit of	-0.0739614	0.05289765
JW3026	P30871	ygiF	inorganic triphosphatase	-0.1029757	0.0841358
JW0466	P0AEW6	gsk	inosine/guanosine kinase	-0.0758423	0.04142472
JW1702	P0A6X7	ihfA	integration host factor (IHF)	0.14536491	0.01026148
JW0895	P0A6Y1	ihfB	integration host factor (IHF)	0.01132752	0.56675359
JW5941	NA	yhjQ	involved in cellulose product	-0.0599961	0.01517546
JW5005	P30149	yabl	ionizing radiation survival pi	-0.0128448	0.67818851
JW5235	P76118	yncH	IPR020099 family protein	0.01862422	0.30001316
JW0479	P77279	ybbL	iron export ABC transporter	-0.1177266	0.33601244
JW5066	P77307	ybbM	iron export ABC transporter	-0.1215659	0.00859104
JW3779	P27838	cyaY	iron-dependent inhibitor of i	-0.2253173	0.10770354
JW0581	P23877	fepG	iron-enterobactin ABC trans	0.10561853	0.01079929
JW2513	P0ACD4	iscU	iron-sulfur cluster assembly	0.09325183	0.1165237
JW4167	P69506	ytfE	iron-sulfur cluster repair prc	0.06764941	0.12326233
JW2866	P0ADE8	ygfZ	iron-sulfur cluster repair prc	-0.3678441	9.53E-05
JW0147	P07821	fhuC	iron(3+)-hydroxamate impo	0.03445319	0.58034026
JW0148	P07822	fhuD	iron(3+)-hydroxamate impo	0.17163921	0.09321132
JW0149	P06972	fhuB	iron(3+)-hydroxamate impo	-0.054349	0.01969554
JW5228	P76102	ydcM	IS609 transposase B	0.01255651	0.76032773
JW2515	P0AGK8	iscR	isc operon transcriptional re	0.06883921	0.00743202
JW4291	P39377	iadA	isoaspartyl dipeptidase	-0.1755431	0.00204701
JW0812	P37595	iaaA	Isoaspartyl peptidase	0.0074397	0.75651944
JW0587	P0ADI4	entB	isochorismatase	-0.0660497	0.05352933
JW5307	P0ADI7	yecD	isochorismatase family prot	0.01009769	0.76167984
JW0585	P0AEJ2	entC	isochorismate synthase 1	0.04254695	0.28462592
JW2260	P38051	menF	isochorismate synthase 2	0.05384716	0.34478818
JW3976	P11071	aceK	isocitrate dehydrogenase ki	0.04092147	0.02212794
JW1122	P08200	icd	isocitrate dehydrogenase; e	0.12406853	0.00480969
JW3975	P0A9G6	aceA	isocitrate lyase	0.15213192	0.04569144
JW0024	P00956	ileS	isoleucyl-tRNA synthetase	0.03008493	0.4161403
JW2857	Q46822	idi	isopentenyl diphosphate iso	0.07086019	0.25486143
JW3176	P0ABU5	elbB	isoprenoid biosynthesis prot	0.01825351	0.27255234
JW1246	P0A710	yciB	IspA family inner membran	0.06027554	0.09225476
JW0644	P77359	djIC	J domain-containing HscC cc	0.01705474	0.72581107
JW1816	P76268	kdgR	KDG regulon transcriptional	-0.016921	0.42384684
JW5660	P37661	eptB	KDO phosphoethanolamine	-0.0247263	0.35115192
JW3747	P05793	ilvC	ketol-acid reductoisomerase	0.00260635	0.91703203
JW5136	P56614	ymdF	KGG family protein	-0.0658903	0.17044366
JW1251	P21361	yciG	KGG family protein	-0.0015348	0.95356633
JW1839	P0A955	eda	KHG/KDPG aldolase; 2-dehy	0.00899565	0.59715909
JW1347	P38393	kil	killing protein, Rac prophage	0.05425937	0.01627684
JW0756	P12994	ybhB	kinase inhibitor homolog, U	-0.0521922	0.02251301

JW3605	P25741	rfaP	kinase that phosphorylates c	0.03255051	0.64668055
JW2770	P0A9S1	fucO	L-1,2-propanediol oxidoredu	0.02360791	0.41145288
JW2635	P37339	ygaF	L-2-hydroxyglutarate oxidas	0.0212144	0.42349747
JW1318	P51981	ycjG	L-Ala-D/L-Glu epimerase	-0.0120404	0.39700736
JW0854	P75823	ltaE	L-allo-threonine aldolase, PI	0.00807614	0.64784011
JW3405	P46854	yhhY	L-amino acid N-acetyltransf	0.0080688	0.71961607
JW1888	P0AAF3	araG	L-arabinose ABC transporter	0.0603971	0.17165253
JW1889	P02924	araF	L-arabinose ABC transporter	0.09564365	0.07666583
JW1887	P0AE26	araH	L-arabinose ABC transporter	0.04480126	0.0348307
JW0386	P23910	araJ	L-arabinose-inducible putati	-0.0619808	0.23812982
JW3206	P0A6D0	argR	l-arginine-responsive arginin	-0.0462005	0.01314843
JW5868	P39300	ulaG	L-ascorbate 6-phosphate lac	-0.1605518	0.00088096
JW4153	P69820	ulaC	L-ascorbate-specific enzyme	-0.0219092	0.40396474
JW4152	P69822	ulaB	L-ascorbate-specific enzyme	0.01301459	0.85620164
JW5744	P39301	ulaA	L-ascorbate-specific enzyme	-0.3299432	0.03728105
JW5234	P77610	ansP	L-asparagine transporter	-0.0022749	0.85988658
JW2773	P69922	fucI	L-fucose isomerase	-0.1634974	0.08359137
JW2775	P0AEN8	fucU	L-fucose mutarotase	0.04213081	0.22401517
JW2776	P0ACK8	fucR	l-fucose operon activator	-0.0441964	0.08014656
JW2772	P11551	fucP	L-fucose transporter	-0.0481454	0.11058822
JW2774	P11553	fucK	L-fuculokinase	0.01039967	0.58530466
JW2771	P0AB87	fucA	L-fuculose-1-phosphate aldc	0.17767198	0.1234855
JW5793	P39400	yjjN	L-galactonate oxidoreductas	-0.0336291	0.26621761
JW2970	Q46851	yghZ	L-glyceraldehyde 3-phospha	-0.0278435	0.60637912
JW4224	P39346	idnD	L-idonate 5-dehydrogenase,	0.04998051	0.23532342
JW4222	P39344	idnT	L-idonate and D-gluconate t	0.03301425	0.30992429
JW2713	P0A7A5	pcm	L-isoaspartate protein carbc	-0.0509436	0.02481266
JW3580	P33232	lldD	L-lactate dehydrogenase, FM	0.03140044	0.05186192
JW3578	P33231	lldP	L-lactate permease	0.01193655	0.90135698
JW4101	P39277	yjeH	L-methionine and branched	0.01434106	0.39966272
JW2241	P77215	yfaW	L-rhamnonate dehydratase	-0.0495671	0.00376074
JW3872	P32156	yiiL	L-rhamnose mutarotase	-0.1059139	0.42468029
JW3878	P27125	rhaT	L-rhamnose:proton symport	0.01255249	0.75056146
JW4156	P39306	ulaF	L-ribulose 5-phosphate 4-ep	0.09802862	0.0025692
JW3555	P37680	sgbE	L-ribulose-5-phosphate 4-ep	-0.122316	5.46E-05
JW1803	P16095	sdaA	L-serine dehydratase 1	0.1051309	0.25959567
JW2768	P30744	sdaB	L-serine dehydratase 2	0.10466271	0.05013696
JW5520	P42630	tdcG	L-serine dehydratase 3, ana	-0.0582889	0.66869971
JW3033	P05847	ttdA	L-tartrate dehydratase, alph	-0.1129284	0.07391264
JW3034	P0AC35	ttdB	L-tartrate dehydratase, beta	-0.0795124	0.0017218
JW3035	P39414	ygjE	L-tartrate/succinate antipor	0.039963	0.40452975
JW3591	P07913	tdh	L-threonine 3-dehydrogenas	-0.0262292	0.70165585
JW5525	P11866	tdcR	L-threonine dehydratase op	0.04568888	0.01534778
JW3745	P04968	ilvA	l-threonine dehydratase, bic	0.16291469	0.15670833
JW3088	P0AGF6	tdcB	L-threonine dehydratase, ca	-0.0810919	0.01166703

JW5648	P37686	yiaY	L-threonine dehydrogenase	0.01447994	0.71269333
JW0003	P00934	thrC	L-threonine synthase	0.1293691	0.00405412
JW3087	P0AAD8	tdcC	L-threonine/L-serine transp	-0.2733692	0.01110572
JW4155	P39305	ulaE	L-xylulose 5-phosphate 3-ep	0.08191896	0.11447914
JW3552	P37677	lyxK	L-xylulose kinase	0.00348383	0.89634201
JW5820	P75954	ycfS	L,D-transpeptidase linking L	-0.0250265	0.27297562
JW0803	P0AAX8	ybiS	L,D-transpeptidase linking L	0.04203041	0.05961228
JW1968	P39176	erfK	L,D-transpeptidase linking L	0.11602659	0.02173734
JW0214	P0AA99	yafK	L,D-transpeptidase-related p	0.0750284	0.00208443
JW1313	P77615	ycjW	LacI family putative transcri	0.03826949	0.2253007
JW0334	P02920	lacY	lactose permease	0.00064989	0.17166021
JW0336	P03023	lacI	lactose-inducible lac operon	-0.0393471	0.01594329
JW2157	P33026	setB	lactose/glucose efflux syste	0.03630992	0.23332511
JW5122	P75855	ycbQ	laminin-binding fimbrin sub	-0.0033011	0.78944896
JW1041	P0ACV0	lpxL	lauryl-acyl carrier protein (A	-0.0462695	0.76703883
JW0074	P0AD79	leuL	leu operon leader peptide	0.04723363	0.07180714
JW1787	P76249	yeaS	leucine efflux protein	-0.0758719	0.1605265
JW3423	P04816	livK	leucine transporter subunit	0.00555127	0.94961602
JW0872	P0ACJ0	lrp	leucine-responsive global tr	0.07044715	0.06304309
JW0868	P0A8P1	aat	leucyl/phenylalanyl-tRNA-pi	0.0315727	0.09658693
JW5816	P0AAU7	ybfE	LexA-regulated protein, Cop	0.01355308	0.61812741
JW2162	P76445	yeiU	lipid A 1-diphosphate synth	0.02521641	0.30736992
JW1317	P0A862	tpx	lipid hydroperoxide peroxida	-0.0268272	0.15595813
JW4349	P32099	lplA	lipoate-protein ligase A	-0.0465552	0.36363675
JW3601	P27129	rfaJ	lipopolysaccharide 1,2-glucc	0.08884146	0.05267845
JW3603	P27127	rfaB	lipopolysaccharide 1,6-galac	0.01533096	0.63887927
JW2017	P37751	wbbK	lipopolysaccharide biosynthe	-0.049365	0.14403288
JW3600	P27240	rfaY	lipopolysaccharide core bios	0.12749774	0.00055164
JW3168	P0A9V1	yhbG	lipopolysaccharide export AI	0.15591501	0.00019034
JW3599	P27241	rfaZ	lipopolysaccharide KdoIII tra	-0.0179465	0.53207313
JW3604	P27126	rfaS	lipopolysaccharide rhamnos	0.04086218	0.12745898
JW5412	P11289	yfiL	lipoprotein	-0.155984	0.00615559
JW1377	P64448	ynbE	lipoprotein	-0.0575744	0.01057314
JW0206	P77339	yafT	lipoprotein	-0.0480622	0.3376041
JW1913	P31063	yedD	lipoprotein	-0.0013272	0.94691357
JW1427	P64451	ydcL	lipoprotein	0.02698945	0.34827003
JW0849	P75818	ybjP	lipoprotein	0.03839416	0.070652
JW0676	P75737	ybfP	lipoprotein	0.04221761	0.01008559
JW2598	P0A937	smpA	lipoprotein component of B	0.05119827	0.37486257
JW3132	P0AFB1	nlpl	lipoprotein involved in osmc	-0.0275371	0.25954837
JW0188	P40710	nlpE	lipoprotein involved with co	0.1924573	6.39E-05
JW5351	P33354	yehR	lipoprotein, DUF1307 family	-0.0473217	0.05952051
JW1050	P0AB26	yceB	lipoprotein, DUF1439 family	0.05513985	0.00626081
JW1892	P76308	yecR	lipoprotein, function unknow	-0.0106044	0.77559119
JW0240	P77365	yafY	lipoprotein, inner membran	0.07965139	0.04654608

JW0623	P60716	lipA	lipoyl synthase	0.02054018	0.79602264
JW1477	P0COL2	osmC	lipoyl-dependent Cys-based	0.11146957	0.00203855
JW1486	P64426	yddW	lipoprotein, glycosyl hydrolase	0.00416136	0.92886728
JW0433	P77712	ybaW	long-chain acyl-CoA thioeste	0.04170993	0.11186841
JW2341	P10384	fadL	long-chain fatty acid outer r	0.08575265	0.02776897
JW3927	P0CB39	yijP	LPS heptose I phosphoethan	-0.0492155	0.08413066
JW1272	P0AB58	yciM	LPS regulatory protein; puta	-0.062209	0.09097928
JW3590	P11290	yibD	LPS(HepIII)-glucuronic acid	0.06346644	0.00973946
JW2130	P0AD19	yohK	LrgB family inner membran	0.02264164	0.19856557
JW1505	P76141	ydeW	Isr operon transcriptional re	0.01589133	0.48529359
JW5042	P77433	ykgG	LutC family protein; putativ	0.04121907	0.00828682
JW0181	P52095	ldcC	lysine decarboxylase 2, cons	0.06702327	0.10694835
JW4092	P0A9H3	cadA	lysine decarboxylase, acid-ir	-0.2249477	0.13502578
JW2143	P25737	lysP	lysine transporter	0.03966667	0.14673016
JW2858	P0A8N3	lysS	lysine tRNA synthetase, con	-0.0758771	0.34012543
JW4090	P0A8N5	lysU	lysine tRNA synthetase, indi	-0.0619882	0.07001299
JW3984	P08660	lysC	lysine-sensitive aspartokina	-0.3474541	0.00064267
JW2307	P09551	argT	lysine/arginine/ornithine tra	-0.0783211	0.40766037
JW2833	Q46798	ygeR	LysM domain-containing M ₂	-0.0293178	0.49065088
JW5584	P07000	pldb	lysophospholipase L2	0.0005169	0.99073525
JW2803	P39196	ygeD	lysophospholipid transporte	-0.0352811	0.07289978
JW1651	P0ACR2	ydhB	LysR family putative transcr	-0.1015026	0.00855624
JW5834	P76369	yeeY	LysR family putative transcr	-0.0408004	0.08028811
JW0883	P75836	ycaN	LysR family putative transcr	-0.0099004	0.72479111
JW1587	P77559	ynfL	LysR family putative transcr	0.01877198	0.66862228
JW0198	P30864	yafC	LysR family putative transcr	0.07288782	0.01978147
JW0624	P30979	ybeF	LysR family putative transcr	0.14452779	0.08105371
JW3489	P37641	yhjC	LysR family putative transcr	0.14980357	5.46E-05
JW5821	P0C960	emtA	lytic murein endotransglyco	0.12855128	0.24817409
JW4355	P0AGC3	slt	lytic murein transglycosylas	0.07124145	0.04563592
JW5155	P0A729	yceF	m(7)GTP pyrophosphatase	-0.0098311	0.6945613
JW0909	P0AB06	ycbK	M15A protease-related fam	-0.0507522	0.03796474
JW0863	P75831	macB	macrolide ABC transporter	0.04233725	0.31078324
JW0862	P75830	macA	macrolide transporter mem	0.04901706	0.05687526
JW3738	P22787	yifB	magnesium chelatase famil	-0.0059467	0.85264534
JW4201	P0ABB8	mgtA	magnesium transporter	-0.0972116	0.00106065
JW3789	P0ABI4	corA	magnesium/nickel/cobalt tr	-0.0382631	0.42893248
JW4277	P04128	fimA	major type 1 subunit fimbri	-0.0138644	0.63488659
JW3381	P06993	malT	mal regulon transcriptional	0.00641791	0.65554434
JW5238	P26616	sfcA	malate dehydrogenase, dec	-0.0520419	0.23871781
JW2198	P33940	mgo	malate dehydrogenase, FAC	0.05605615	0.29817553
JW3205	P61889	mdh	malate dehydrogenase, NAI	0.15325356	0.01674995
JW3974	P08997	aceB	malate synthase A	-0.0034177	0.93774113
JW2943	P37330	glcB	malate synthase G	-0.1079509	0.03462347
JW2447	P76558	maeB	malic enzyme: putative oxid	0.08600969	0.08318291

JW0760	P12999	bioC	malonyl-ACP O-methyltrans	0.18502894	0.00965375
JW3155	P0ACH1	sfsB	malPQ operon transcription	0.05804529	0.0116531
JW0393	P21517	malZ	maltodextrin glucosidase	-0.0377913	0.19310284
JW5689	P00490	malP	maltodextrin phosphorylase	-0.140399	0.30270325
JW3995	P68187	malK	maltose ABC transporter AT	0.01588782	0.5248218
JW1613	P19642	malX	maltose and glucose-specific	0.01958361	0.76931097
JW0448	P77791	maa	maltose O-acetyltransferase	0.11440483	0.00090305
JW3996	P02943	lamB	maltose outer membrane p	0.03239572	0.33549007
JW3997	P03841	malM	maltose regulon periplasmic	-0.0123755	0.17054541
JW3992	P68183	malG	maltose transporter subunit	-6.29E-05	0.99903358
JW3993	P02916	malF	maltose transporter subunit	0.02413177	0.49756573
JW3994	P0AEX9	malE	maltose transporter subunit	0.20639702	0.00173406
JW2388	P0A769	mntH	manganese/divalent cation	0.01413559	0.62189725
JW3575	P0AF10	mtlR	mannitol operon repressor	-0.0398382	0.67267431
JW3574	P09424	mtlD	mannitol-1-phosphate dehy	-0.026754	0.12403212
JW3573	P00550	mtlA	mannitol-specific PTS enzym	0.06004606	0.14151385
JW0385	P23917	mak	manno(fructo)kinase	-0.0084186	0.67078636
JW4285	P24215	uxuA	mannonate hydrolase	0.06450135	0.15239466
JW2034	P24174	cpsB	mannose-1-phosphate guan	-0.0170236	0.07078438
JW1605	P00946	manA	mannose-6-phosphate isom	-0.0025813	0.90847898
JW1807	P69801	manY	mannose-specific enzyme II	0.14483357	0.20109565
JW1808	P69805	manZ	mannose-specific enzyme II	0.02233755	0.07052529
JW5308	P64515	yecN	MAPEG family inner membr	0.09580833	0.13844354
JW2961	P37182	hybD	maturation protease for hyc	-0.2096309	0.01346625
JW3252	P0A742	mscL	mechanosensitive channel ζ	0.01054192	0.69977899
JW5108	P75783	ybiO	mechanosensitive channel ζ	0.03836607	0.46966246
JW0454	P77338	kefA	mechanosensitive channel ζ	-0.1327202	0.04061312
JW0454	P77338	kefA	mechanosensitive channel ζ	0.02821634	0.59829543
JW4120	P39285	yjeP	mechanosensitive channel ζ	-0.0538297	0.00675049
JW0566	P0AAT4	ybdG	mechanosensitive channel ζ	-0.0137566	0.2491759
JW2891	P0COS1	mscS	mechanosensitive channel ζ	0.00450789	0.92177786
JW4079	P0ACH8	melR	melibiose operon transcripti	-0.0050727	0.7454346
JW4081	P02921	melB	melibiose:sodium symporte	0.11180657	0.11201779
JW0729	P19934	tolA	membrane anchored proteini	0.09924574	0.00027504
JW2885	P27254	argK	membrane ATPase/protein	0.11415735	0.07616552
JW4043	P32716	yjcR	membrane fusion protein of	-0.0107626	0.68865377
JW2093	P76425	yohM	membrane protein conferrir	0.00544939	0.74615254
JW3682	P0A8C8	ydD	membrane protein insertior	-0.052678	0.03914396
JW3642	P09836	uhpC	membrane protein regulate	-0.0554528	0.16825031
JW0728	P0ABV6	tolR	membrane spanning proteir	-0.1619955	0.14174872
JW0727	P0ABU9	tolQ	membrane spanning proteir	0.12145325	0.00011667
JW2973	P0ABV2	exbD	membrane spanning proteir	0.13657458	0.00056238
JW2974	P0ABU7	exbB	membrane spanning proteir	0.24066267	2.16E-10
JW5195	P02929	tonB	membrane spanning proteir	-0.0641839	0.10000447
JW4042	P32715	yjcQ	membrane translocase (MD	-0.0753938	0.00070282

JW0054	P31680	djIA	membrane-anchored DnaK c	0.01487521	0.39695181
JW5378	P09549	dedD	membrane-anchored peripla	-0.0097586	0.70688636
JW3069	P64581	yqjD	membrane-anchored riboso	-0.0255771	0.37295916
JW1954	P76342	yedY	membrane-anchored, peripl	0.01020501	0.78909677
JW2784	P0A935	mltA	membrane-bound lytic mur	0.00126053	0.97492344
JW2671	P41052	mltB	membrane-bound lytic mur	-0.0138309	0.56236689
JW5481	P0C066	mltC	membrane-bound lytic mur	-0.0640689	0.38005688
JW2542	P0AGC5	yfhD	membrane-bound lytic trans	-0.0067698	0.76003952
JW5790	P24203	yjiA	metal-binding GTPase	-0.1144578	0.08931386
JW4068	P16681	phnB	metalloprotein superfamily	-0.0488357	0.01558971
JW3804	P0A9F9	metR	methionine biosynthesis reg	-0.0007156	0.98010404
JW5233	P76112	ynca	methionine N-acyltransfera	0.11340599	0.01305097
JW4178	P0A744	msrA	methionine sulfoxide reduct	-0.0461722	0.20247394
JW1767	P0A746	yeaA	methionine sulfoxide reduct	-0.0525502	0.21782368
JW4318	P02942	tsr	methyl-accepting chemotax	0.03444553	0.11601639
JW1875	P07017	tar	methyl-accepting chemotax	0.04869917	0.0884849
JW1417	P05704	trg	methyl-accepting chemotax	0.03853912	0.32357721
JW1874	P07018	tap	methyl-accepting protein IV	0.07064982	0.00347143
JW4128	P23367	mutL	methyl-directed mismatch r	-0.1657736	0.00255706
JW2799	P06722	mutH	methyl-directed mismatch r	-0.0750364	0.21077381
JW2703	P23909	mutS	methyl-directed mismatch r	0.05273817	0.0996194
JW2136	P0AAG8	mgIA	methyl-galactoside ABC tra	-0.1457527	0.25552529
JW2137	P0AEE5	mgIB	methyl-galactoside transpor	-0.0443371	0.32566707
JW2135	P23200	mgIC	methyl-galactoside transpor	0.05209761	0.2836272
JW4314	P24202	mrr	methylated adenine and cyt	0.27850603	0.0634499
JW1760	P77256	ydjG	methylglyoxal reductase, NA	-0.047978	0.09758933
JW5129	P0A731	mgsA	methylglyoxal synthase	0.06859202	0.09518289
JW2886	P52045	ygfG	methylmalonyl-CoA decarbc	-0.0038982	0.85661844
JW2884	P27253	yliK	methylmalonyl-CoA mutase	-0.0669257	0.08030478
JW3227	P0A8T1	prmA	methyltransferase for 50S ri	-0.0167469	0.59223979
JW3845	P32135	yihN	MFS transporter family prot	0.00995133	0.68249242
JW3174	P64610	yrbL	Mg(2+)-starvation-stimulat	0.06287215	0.02997093
JW0337	P77569	mhpR	mhp operon transcriptional	-0.0518738	0.01654374
JW0369	P77562	yaiW	microcin Bac7 uptake protei	0.02027346	0.23871842
JW2168	P33916	yejF	microcin C ABC transporter	0.22537322	0.01757529
JW2165	P33913	yejA	microcin C ABC transporter	0.06468746	0.00057281
JW2166	P0AFU0	yejB	microcin C ABC transporter	-0.0162065	0.38928111
JW2167	P33915	yejE	microcin C ABC transporter	-0.0042871	0.85195116
JW2199	P33941	yojI	microcin J25 efflux ABC trar	0.17731745	0.01343773
JW4282	P08190	fimG	minor component of type 1	-0.0414482	0.02203667
JW4281	P08189	fimF	minor component of type 1	-0.0370226	0.19840986
JW4283	P08191	fimH	minor component of type 1	-0.0214514	0.80437108
JW0801	P0A9F1	mntR	Mn(2+)-responsive mangan	-0.0209781	0.30150803
JW3435	P0A890	yhhP	mnm(5)-s(2)U34-tRNA 2-th	-0.076019	0.0411591
JW0952	P0AB18	ycck	mnm(5)-s(2)U34-tRNA 2-th	-0.0446281	0.2200222

JW3305	P45530	yheL	mnm(5)-s(2)U34-tRNA synt	-0.0161384	0.72593424
JW3306	P45531	yheM	mnm(5)-s(2)U34-tRNA synt	-0.0011241	0.97325432
JW0277	P77183	yagQ	moco insertion factor for Pa	0.0413058	0.08435162
JW4132	P0ABC7	hflK	modulator for HflB protease	0.0518036	0.27044977
JW0953	P0AAC6	yccA	Modulator of FtsH protease,	0.08024941	0.5564287
JW0449	P0ACE3	hha	modulator of gene expressio	-0.0175313	0.44438592
JW0184	P0AFW8	rof	modulator of Rho-depender	0.19867178	0.02395734
JW3902	P0A6H5	hslU	molecular chaperone and A ⁻	-0.1314645	0.11242821
JW0743	P31060	modF	molybdate ABC transporter	-0.072224	0.18424731
JW0748	P09833	modC	molybdate ABC transporter	0.05178749	0.39943534
JW0747	P0AF01	modB	molybdate ABC transporter	0.09096031	0.00206045
JW1217	P0AF26	narJ	molybdenum-cofactor-assei	0.15646003	0.02865109
JW0008	P0AF03	mog	molybdochelataase incorpora	-0.0590224	0.00015159
JW0764	P30745	moaA	molybdopterin biosynthesis	0.05953874	0.01206801
JW0766	P0A738	moaC	molybdopterin biosynthesis,	-0.1018606	0.00060783
JW0811	P12281	moeA	molybdopterin molybdenum	-0.0419634	0.55079026
JW5287	P78067	ynjE	molybdopterin synthase sulf	0.03117146	0.25066748
JW0810	P12282	moeB	molybdopterin synthase sulf	0.00600966	0.84164222
JW0768	P30749	moaE	molybdopterin synthase, lar	0.0058592	0.82922842
JW0767	P30748	moaD	molybdopterin synthase, sm	-0.0764729	0.06873948
JW5575	P32125	mobB	molybdopterin-guanine dinu	0.13801149	0.02055006
JW3829	P32173	mobA	molybdopterin-guanine dinu	-0.3213726	0.01082477
JW3021	P26649	glgS	motility and biofilm regulat	-0.017124	0.56990892
JW2500	P27434	yfgA	MreB assembly cytoskeletal	0.00452452	0.9238429
JW5230	P76106	yncN	mRNA interferase toxin of t	0.04001231	0.15419662
JW3054	P64578	ygjN	mRNA interferase toxin of t	-0.2247337	0.01790315
JW0223	Q47157	yafO	mRNA interferase toxin of t	-0.0150967	0.51089196
JW0215	Q47149	yafQ	mRNA interferase toxin of t	-0.030338	0.43387919
JW2753	P0AE70	chpA	mRNA interferase toxin, ant	0.24572596	0.07685877
JW0119	P36649	cueO	multicopper oxidase (laccas	0.00467527	0.90038194
JW5657	P37665	yaD	multicopy suppressor of bar	0.10673436	0.06061969
JW0837	P0AAY6	ybjN	multicopy suppressor of coa	0.17133703	0.05864381
JW1039	P25738	msyB	multicopy suppressor of sec	-0.0288951	0.30591967
JW2660	P27303	emrA	multidrug efflux system	-0.0902856	0.02426054
JW0452	P0AE06	acrA	multidrug efflux system	0.08374787	0.0030007
JW3234	P24181	acrF	multidrug efflux system pro	-0.1020633	0.00020003
JW4300	P39386	yjiO	multidrug efflux system pro	-0.0906436	0.00075187
JW3688	P31462	mdtL	multidrug efflux system pro	-0.0701752	0.21280656
JW0826	P0AEY8	cmr	multidrug efflux system pro	-0.0124377	0.81927073
JW5634	P31442	emrD	multidrug efflux system pro	-0.0110332	0.67252156
JW0451	P31224	acrB	multidrug efflux system pro	0.03595378	0.3433305
JW2661	P0AEJ0	emrB	multidrug efflux system pro	0.04453505	0.08250774
JW5738	P69937	sugE	multidrug efflux system pro	0.10107606	0.01686839
JW1592	P69212	mdtJ	multidrug efflux system tra	-0.0227301	0.26735063
JW1655	P37340	mdtK	multidrug efflux system tra	-0.0105772	0.75301359

JW1591	P69210	mdtI	multidrug efflux system tra	0.02656057	0.08689146
JW5338	P76397	mdtA	multidrug efflux system, sul	0.07243404	0.01281449
JW2060	P76398	mdtB	multidrug efflux system, sul	-0.0247906	0.41086872
JW2061	P76399	mdtC	multidrug efflux system, sul	-0.001952	0.90530828
JW2365	P52599	emrK	multidrug resistance efflux	-0.0184492	0.45908717
JW1052	P69367	mdtH	multidrug resistance efflux	0.01763598	0.57986283
JW4217	P68767	pepA	multifunctional aminopeptid	0.07283637	0.13501975
JW2725	Q46896	ygbT	multifunctional endonucleas	-0.000878	0.97754665
JW2502	P0A763	ndk	multifunctional nucleoside c	0.12580761	0.02547319
JW5249	P0ACH5	marA	multiple antibiotic resistanc	-0.0504636	0.12389617
JW2325	POC0T5	mepA	murein DD-endopeptidase	-0.1090845	0.16306912
JW5270	P76190	ydhO	murein DD-endopeptidase, s	0.0659452	0.07131938
JW2163	P0AFV4	spr	murein DD-endopeptidase, s	0.00567344	0.88303791
JW5304	P0AFS9	yebA	murein DD-endopeptidase, s	0.09450357	0.01062137
JW1668	P76193	ynhG	murein L,D-transpeptidase	0.00079292	0.98845843
JW0908	P22525	ycbB	murein L,D-transpeptidase	0.00505227	0.88141455
JW1667	P69776	lpp	murein lipoprotein	-0.323474	0.00139424
JW1319	P0ACV6	mpaA	murein peptide amidase A	0.06727267	0.0448875
JW1321	P77333	ycjZ	murein peptide degradation	-0.0501441	0.02854408
JW1181	P76008	ldcA	murein tetrapeptide carboxy	0.31064148	4.96E-05
JW1322	P77348	mppA	murein tripeptide (L-ala-gar	-0.0793271	0.0027283
JW0423	P0AE16	ampG	muropeptide transporter	-0.071654	0.125991
JW2528	P76584	yphB	mutarotase superfamily pro	0.02112388	0.58621991
JW1844	P24205	lpxM	myristoyl-acyl carrier protei	0.10077869	0.03529878
JW2006	P10371	hisA	N-(5'-phospho-L-ribosyl-forr	-0.1622511	0.00509006
JW0665	P09323	nagE	N-acetyl glucosamine specif	-0.0391041	0.08691047
JW1105	P75959	ycfX	N-acetyl-D-glucosamine kin	0.03092248	0.23253269
JW3930	P11446	argC	N-acetyl-gamma-glutamylp	-0.0712095	0.02998843
JW3102	P42904	agaV	N-acetylgalactosamine-spec	-0.000206	0.99482946
JW3107	P42909	agaB	N-acetylgalactosamine-spec	0.05922367	0.37683557
JW3108	P42910	agaC	N-acetylgalactosamine-spec	0.05127042	0.29549297
JW3109	P42911	agaD	N-acetylgalactosamine-spec	0.22561169	0.0035558
JW0663	P0AF18	nagA	N-acetylglucosamine-6-pho	-0.0545076	0.10449986
JW0662	P0AF20	nagC	N-acetylglucosamine-induci	-0.0368252	0.11389276
JW5538	P45425	nanK	N-acetylmannosamine kina	0.01823396	0.53208157
JW2421	P76535	yfeU	N-acetylmuramic acid 6-ph	0.02008566	0.06130736
JW2422	P77272	murP	N-acetylmuramic acid perm	-0.0270285	0.62372789
JW5449	P63883	amiC	N-acetylmuramoyl-L-alanine	-0.0570852	0.07834368
JW2428	P36548	amiA	N-acetylmuramoyl-l-alanine	0.02336187	0.4616562
JW4127	P26365	amiB	N-acetylmuramoyl-l-alanine	-0.1819185	0.00095939
JW3194	P0A6L4	nanA	N-acetylneuraminate lyase	0.01212165	0.85090023
JW5778	P69856	yjhA	N-acetylneuraminic acid oute	-0.0141265	0.52720788
JW1267	P0A9F3	cysB	N-acetylserine-responsive c	0.01403908	0.57683461
JW1458	P77567	nhoA	N-hydroxyarylamine O-acety	-0.0657734	0.08010369
JW1046	P40874	solA	N-methyltryptophan oxidase	-0.0031477	0.93836818

JW1725	P69791	chbA	N,N'-diacetylchitobiose-spe	-0.0656896	0.11246863
JW1727	P69795	chbB	N,N'-diacetylchitobiose-spe	-0.2784278	0.00131802
JW1726	P17334	chbC	N,N'-diacetylchitobiose-spe	-0.0367249	0.22804787
JW0511	P09029	purK	N5-carboxyaminoimidazole	0.11357306	0.05464984
JW5841	P39199	prmB	N5-glutamine methyltransf	0.07738083	0.00782321
JW3251	P0AGI8	trkA	NAD-binding component of	-0.1316405	0.0150806
JW0920	P80644	ssuE	NAD(P)H-dependent FMN re	0.24212011	0.06853903
JW3820	P0AEN1	fre	NAD(P)H-flavin reductase	0.12181832	0.00763535
JW4169	P39315	ytfG	NAD(P)H:quinone oxidoredu	-0.492585	0.00063033
JW0989	P0A8G6	wrbA	NAD(P)H:quinone oxidoredu	-0.0830998	0.00234416
JW5548	P32664	nudC	NADH pyrophosphatase	-0.02965	0.3372411
JW1409	P41407	azoR	NADH-azoreductase, FMN-c	0.05277486	0.03895717
JW2681	P37596	norW	NADH:flavorubredoxin oxido	0.06717783	0.01843589
JW5875	P0AFC7	nuoB	NADH:ubiquinone oxidoredu	0.03759483	0.61678884
JW2280	P0AFD1	nuoE	NADH:ubiquinone oxidoredu	0.03878884	0.15862843
JW2279	P31979	nuoF	NADH:ubiquinone oxidoredu	0.03098449	0.11481659
JW2278	P33602	nuoG	NADH:ubiquinone oxidoredu	-0.0202347	0.37218374
JW2276	P0AFD6	nuoI	NADH:ubiquinone oxidoredu	-0.0716195	0.35320392
JW5375	P33599	nuoC	NADH:ubiquinone oxidoredu	0.06835641	0.0838706
JW2283	P0AFC3	nuoA	NADH:ubiquinone oxidoredu	0.11206978	0.00016574
JW2277	P0AFD4	nuoH	NADH:ubiquinone oxidoredu	-0.029798	0.24550689
JW2275	P0AFE0	nuoJ	NADH:ubiquinone oxidoredu	0.00685095	0.68302139
JW2274	P0AFE4	nuoK	NADH:ubiquinone oxidoredu	-0.0101347	0.87703746
JW2273	P33607	nuoL	NADH:ubiquinone oxidoredu	0.03556851	0.28885746
JW2272	P0AFE8	nuoM	NADH:ubiquinone oxidoredu	-0.0227368	0.37109666
JW2271	P0AFF0	nuoN	NADH:ubiquinone oxidoredu	-0.0269382	0.27585643
JW1532	P39831	ydfG	NADP-dependent 3-hydroxy	-0.021788	0.40824505
JW2996	P0AEY5	mdaB	NADPH quinone reductase	-0.0093446	0.80863166
JW2490	P76573	yfgI	nalidixic acid resistance pro	-0.0616424	0.1634543
JW0674	P0AFY8	seqA	negative modulator of initia	0.1028199	0.04254389
JW1924	P31068	fliH	negative regulator of Flil AT	-0.0691233	0.11479775
JW3702	P0A9K7	phoU	negative regulator of PhoR/	-0.0092721	0.60004703
JW3444	P33593	nikD	nickel ABC transporter ATPa	-0.0775663	1.78E-05
JW3445	P33594	nikE	nickel ABC transporter ATPa	0.12675486	0.00563663
JW3442	P33591	nikB	nickel ABC transporter perm	0.03243941	0.37155023
JW3443	P0AFA9	nikC	nickel ABC transporter perm	0.10728133	0.00493288
JW3441	P33590	nikA	nickel/heme ABC transporte	0.04398314	0.47425063
JW1757	P21369	pncA	nicotinamidase/pyrazinamic	0.08033097	0.10867637
JW0734	P0AFK2	pnuC	nicotinamide riboside transp	-0.0469148	0.1125887
JW2670	P0A6G3	ygaD	nicotinamide-nucleotide am	-0.0478809	0.07752817
JW0914	P18133	pncB	nicotinate phosphoribosyltra	0.10255247	0.01299794
JW1969	P36562	cobT	nicotinate-nucleotide--dime	0.01034203	0.80180614
JW1215	P09152	narG	nitrate reductase 1, alpha si	-0.0483262	0.03422309
JW1216	P11349	narH	nitrate reductase 1, beta (F	0.00778165	0.75007824
JW1218	P11350	narI	nitrate reductase 1, gamma	-0.0410851	0.33325969

JW1463	P19319	narZ	nitrate reductase 2 (NRZ), a	0.04246533	0.37421183
JW1462	P19318	narY	nitrate reductase 2 (NRZ), b	0.02285531	0.60227849
JW1461	P19317	narW	nitrate reductase 2 (NRZ), d	0.00507843	0.8596936
JW1460	P0AF32	narV	nitrate reductase 2 (NRZ), g	-0.0045013	0.87302167
JW2194	P33937	napA	nitrate reductase, periplasmic	0.01134519	0.66785725
JW5367	P0ABL3	napB	nitrate reductase, small, cytoplasmic	-0.0351482	0.25424377
JW1214	P10903	narK	nitrate/nitrite transporter	-0.0263579	0.3088196
JW1464	P37758	narU	nitrate/nitrite transporter	0.05693349	0.24383085
JW4136	P0AF63	yjeB	nitric oxide-sensitive repressor	-0.0381883	0.27740615
JW3329	P0A918	nirD	nitrite reductase (NADH) small subunit	0.09264382	0.03931376
JW4031	P0ABK9	nrfA	nitrite reductase, formate-dependent	0.03113969	0.31261132
JW4032	P0ABL1	nrfB	nitrite reductase, formate-dependent	0.10100697	0.03783549
JW3328	P08201	nirB	nitrite reductase, large subunit	-0.0874514	0.08576275
JW3330	P0AC26	nirC	nitrite transporter	0.0864007	0.03782281
JW0440	P0AC55	glnK	nitrogen assimilation regulator	-0.0048014	0.88190213
JW1967	Q47005	nac	nitrogen assimilation regulator	0.05191942	0.04711332
JW2150	P0A9E9	yeiL	nitrogen starvation viability factor	-0.0804711	0.01390528
JW0835	P17117	nfsA	nitroreductase A, NADPH-dependent	-0.0199784	0.49959314
JW5801	P39411	yjjX	non-canonical purine NTP phosphatase	-0.0645827	0.01852526
JW0403	P0A8D0	ybaD	Nrd regulon repressor	-0.0236524	0.01437568
JW2649	P0A772	nrdI	NrdEF cluster assembly factor	0.00238456	0.89500215
JW5641	P0C093	ttk	nucleoid occlusion factor, arcZ	0.10785487	0.14607317
JW1617	P64467	ydgT	nucleoid-associated oriC-binding protein	-0.0412853	0.16558528
JW2389	P0AFF2	nupC	nucleoside (except guanosine) triphosphate	-0.0606063	0.26143709
JW0401	P0A927	tsx	nucleoside channel, receptor	0.02851999	0.82298687
JW2148	P33021	yeiJ	nucleoside permease	0.00829337	0.73216552
JW5783	P39379	yjiH	nucleoside recognition pore	-0.015141	0.55296281
JW2932	P0AFF4	nupG	nucleoside transporter	-0.0461995	0.50045698
JW2085	P76417	yegT	nucleoside transporter, low affinity	-0.0528702	0.12136739
JW2245	P52006	yfaO	nucleoside triphosphatase	-0.0410385	0.02864973
JW2752	P0AEY3	mazG	nucleoside triphosphate pyrophosphatase	-0.0887173	0.02068235
JW1329	P0AFH0	ogt	O-6-alkylguanine-DNA:cysteine methyltransferase	0.1437344	0.00046745
JW1032	P0A8D6	ymdB	O-acetyl-ADP-ribose deacetylase	0.0697108	0.00897522
JW3533	P37669	yiaH	O-acetyltransferase for enterobacterial	0.03709522	0.08519538
JW5132	P0ACZ2	etp	O-antigen capsule forming protein	-0.0428317	0.60029779
JW0969	P75884	ymcC	O-antigen capsule productin	0.05122615	0.06865251
JW5133	P75885	ymcD	O-antigen capsule productin	-0.0523352	0.17096504
JW3597	P27243	rfaL	O-antigen ligase	-0.1160641	0.00280508
JW2020	P37748	wbbH	O-antigen polymerase	0.03313119	0.28938409
JW3766	P0AAA7	wzxE	O-antigen translocase	0.07495826	0.02829435
JW2255	P37353	menE	O-succinylbenzoate-CoA ligase	0.04029751	0.23616053
JW2256	P29208	menC	O-succinylbenzoyl-CoA synthetase	0.10615593	0.01170319
JW5745	P39310	ytfB	OapA family protein	0.11045976	0.01869657
JW5089	P60720	lipB	octanoyltransferase; octanoate	0.16247174	0.00069539
JW3465	P27298	prlC	oligopeptidase A	-0.0361299	0.50681854

JW1239	P77737	oppF	oligopeptide ABC transporte	-0.0005953	0.98364717
JW1238	P76027	oppD	oligopeptide ABC transporte	0.03042887	0.4045384
JW1235	P23843	oppA	oligopeptide ABC transporte	0.00383713	0.79494961
JW1237	P0AFH6	oppC	oligopeptide ABC transporte	-0.0153607	0.67640695
JW1236	P0AFH2	oppB	oligopeptide ABC transporte	0.02473937	0.28175051
JW3160	P64604	yrbD	OM lipid asymmetry mainte	-0.0209983	0.52878334
JW3116	P45464	yraM	OM lipoprotein stimulator o	0.00053034	0.98749858
JW5157	P0AB38	ycfM	OM lipoprotein stimulator o	0.00536734	0.8209396
JW2479	P66948	yfgC	OM protein maintenance ar	0.07835627	0.00886391
JW5127	P0AB10	ymbA	OM-anchored periplasmic li	0.01799912	0.24971893
JW1037	P62517	mdoH	OPG biosynthetic ACP-depei	-0.0044517	0.87888474
JW1035	P33136	mdoG	OPG biosynthetic periplasm	-0.0512314	0.15997013
JW1420	P40120	mdoD	OPG biosynthetic periplasm	0.02019877	0.67916886
JW0800	P75785	ybiP	OPG biosynthetic transmem	0.00807118	0.82604381
JW1034	P75920	mdoC	OPG biosynthetic transmem	0.0229239	0.1295136
JW5794	P39401	mdoB	OPG periplasmic biosynthet	-0.0202027	0.27694675
JW4211	P04391	argI	ornithine carbamoyltransfer	0.04713135	6.38E-05
JW0266	P06960	argF	ornithine carbamoyltransfer	0.11878647	0.00029293
JW0680	P24169	speF	ornithine decarboxylase isoz	0.0675346	0.08034506
JW5482	P21169	speC	ornithine decarboxylase, cor	-0.046929	0.08608358
JW3617	P0A7E3	pyrE	orotate phosphoribosyltrans	0.06569758	0.42358795
JW1273	P08244	pyrF	orotidine-5'-phosphate deca	0.15465675	0.00164473
JW2067	P37057	ogrK	orphan Ogr protein, positive	0.19229953	3.34E-06
JW3319	P0ADX1	yhfA	OsmC family protein	0.04718426	0.0160007
JW1275	P0ADA7	osmB	osmotically and stress induc	0.13224194	0.00171465
JW1728	P0ADB1	osmE	osmotically-inducible lipopr	-0.0738931	0.18786858
JW4041	P32714	yjcP	outer membrane factor of e	-0.0858741	0.00264475
JW5400	P65290	yfgH	outer membrane integrity li	-0.0687831	0.00091151
JW5151	P0AB31	yceK	outer membrane integrity li	-0.0057195	0.8434764
JW3119	P64596	yraP	outer membrane lipoproteir	-0.1795882	0.00487858
JW3474	P37194	slp	outer membrane lipoproteir	-0.0126875	0.51621492
JW0443	P77717	ybaY	outer membrane lipoproteir	0.03567078	0.07878108
JW1633	P0A905	slyB	outer membrane lipoproteir	0.05359335	0.01607561
JW4110	P0A901	blc	outer membrane lipoproteir	-0.0982672	0.06179854
JW2982	P65298	yqhH	outer membrane lipoproteir	0.03460728	0.0858977
JW3794	P0A921	pldA	outer membrane phospholip	-0.026503	0.15799453
JW0231	P02932	phoE	outer membrane phosphop	0.0558625	0.24379164
JW1371	P77747	ompN	outer membrane pore prote	-0.0074705	0.80324849
JW0912	P02931	ompF	outer membrane porin 1a (I	0.0161725	0.42829463
JW1312	P76045	ompG	outer membrane porin G	0.20349447	0.00600751
JW3846	P76773	ompL	outer membrane porin L; pu	0.07677241	0.01205487
JW2203	P06996	ompC	outer membrane porin prote	0.10316496	0.1079769
JW0349	Q47534	yaiO	outer membrane protein	0.04718511	0.07626184
JW0940	P0A910	ompA	outer membrane protein A (0.16885279	0.01126621
JW1248	P0A915	ompW	outer membrane protein W	0.12610095	0.00344454

JW0799	P0A917	ompX	outer membrane protein X	-0.0648382	0.01845254
JW5371	P76471	yfaZ	outer membrane protein, pu	-0.0292468	0.30940161
JW2370	P0AF10	oxc	oxalyl CoA decarboxylase, TI	-0.1448216	0.44617403
JW1382	P77455	maoC	oxepin-CoA hydrolase and 3-	-0.0941277	0.00327566
JW3933	P0ACQ4	oxyR	oxidative and nitrosative str	-0.021297	0.28110926
JW2929	P0A8P3	yggX	oxidative damage protective	-0.4504024	0.00251737
JW2200	P05050	alkB	oxidative demethylase of N:	-0.0664521	0.00831667
JW2889	P0ADS6	yggE	oxidative stress defense pro	0.25264991	0.02750517
JW4004	P28303	dinF	oxidative stress resistance p	0.15630347	0.07066815
JW5057	Q46948	yajL	oxidative-stress-resistance c	-0.1063087	0.01493959
JW5182	P0A6M2	dsbB	oxidoreductase that catalyz	0.36769433	0.07969702
JW1581	P0AAJ1	ynfG	oxidoreductase, Fe-S subuni	0.01192968	0.52366472
JW5261	P76173	ynfH	oxidoreductase, membrane	-0.0466429	0.12717402
JW1484	P76129	dos	oxygen sensor, c-di-GMP ph	-0.0222841	0.32595459
JW1328	P0A9E5	fnr	oxygen-sensing anaerobic g	-0.1485757	0.00277687
JW0380	P0AAN5	yaiA	OxyR-regulated conserved p	0.09564959	0.04180369
JW1331	P76052	abgB	p-aminobenzoyl-glutamate	0.0188714	0.09015804
JW5822	P46133	abgT	p-aminobenzoyl-glutamate	0.10821006	0.00300071
JW3210	P46482	aaeA	p-hydroxybenzoic acid efflu	-0.0498045	0.15685825
JW3209	P46481	aaeB	p-hydroxybenzoic acid efflu	0.06969865	0.00068493
JW3042	P64588	yqjI	PadR family putative transci	-0.0829401	0.25290903
JW2375	P0ACV2	ddg	palmitoleoyl-acyl carrier prc	0.00581154	0.75226507
JW5396	P76561	yphH	palmitoyl-CoA esterase acti	-0.064325	0.0510992
JW3424	P37613	yhhK	PanD autocleavage accelera	0.01692065	0.76441598
JW3942	P0A6I3	coaA	pantothenate kinase	-0.0750515	0.09531787
JW0129	P31663	panC	pantothenate synthetase	-0.0502308	0.1272813
JW3226	P16256	panF	pantothenate:sodium sympr	-0.0220287	0.72773776
JW0280	P77165	yagT	PaoABC aldehyde oxidoredu	0.11392954	0.00606228
JW0279	P77324	yagS	PaoABC aldehyde oxidoredu	0.01309472	0.62447154
JW0278	P77489	yagR	PaoABC aldehyde oxidoredu	0.03375097	8.41E-05
JW0595	P77216	ybdN	PAPS reductase-like domain	0.00764004	0.68939851
JW3284	P03825	pioO	part of gsp divergon involve	-0.1055472	0.0175367
JW1223	P0AEV1	rssB	PcnB-degradosome interact	0.11368021	0.00023153
JW0186	P0AA97	yaeQ	PDDEXK superfamily protein	-0.0213186	0.60302454
JW3749	P56259	yifO	PemK toxin family pseudoge	-0.0945232	0.0003495
JW5395	P77619	yfeW	penicillin binding protein PB	-0.0288802	0.36598367
JW3359	P02918	mrcA	penicillin-binding protein 1a	-0.0539098	0.14925346
JW4111	P00811	ampC	penicillin-binding protein; b	0.05449339	0.02180694
JW2503	P76577	pbpC	penicillin-insensitive mureir	0.04438833	0.10137898
JW3092	P11864	yhaC	pentapeptide repeats-relatec	-0.1019286	0.01291475
JW1693	P0A8A4	ydiA	PEP synthase kinase and PEI	-0.0028748	0.86673665
JW2797	P37177	ptsP	PEP-protein phosphotransfe	-0.0546375	0.21011522
JW2409	P08839	ptsI	PEP-protein phosphotransfe	0.03201674	0.2443297
JW3903	P0A7B8	hslV	peptidase component of the	0.13463581	0.09650108
JW3981	P0A7C6	pepE	peptidase E, alpha-aspartyl	-0.0380761	0.31589865

JW1113	P29745	pepT	peptidase T	-0.0333423	0.43371087
JW0368	P0AFY6	sbmA	peptide antibiotic transport	-0.1435155	6.32E-05
JW5847	P07012	prfB	peptide chain release factor	-4.12E-05	0.99865714
JW5873	P0A714	prfC	peptide chain release factor	-0.25275	0.00014051
JW0731	P0A912	pal	peptidoglycan-associated ou	-0.0697368	0.12714096
JW0052	P0ABZ6	surA	peptidyl-prolyl cis-trans isor	0.04197145	0.10531372
JW3326	P0AFL3	ppiA	peptidyl-prolyl cis-trans isor	-0.0596505	0.02506679
JW0514	P23869	ppiB	peptidyl-prolyl cis-trans isor	0.05624658	0.15579947
JW3748	P0A9L5	ppiC	peptidyl-prolyl cis-trans isor	-0.0083295	0.78118711
JW0426	P0A850	tig	peptidyl-prolyl cis/trans isor	-0.0523414	0.17493234
JW1300	P0AFV8	pspD	peripheral inner membrane	-0.0473913	0.29258248
JW1732	P77754	spy	periplasmic ATP-independe	-0.0659784	0.05566246
JW0173	P0AEU7	hlpA	periplasmic chaperone	-0.0013793	0.96965997
JW4279	P31697	fimC	periplasmic chaperone	0.00054084	0.99400461
JW0562	P77214	cusF	periplasmic copper- and silv	0.01661919	0.46685208
JW3300	P13656	chiA	periplasmic endochitinase	-0.0319502	0.47557764
JW0431	P0ADY1	ppiD	periplasmic folding chapero	0.02879779	0.58533916
JW2233	P09394	glpQ	periplasmic glycerophospho	0.03883328	0.51438963
JW2185	P69490	ccmE	periplasmic heme chaperon	0.05100394	0.03035124
JW1043	P0A8X2	ycel	periplasmic high pH-inducib	0.13653199	0.00079762
JW1167	P76002	ycgK	periplasmic inhibitor of g-ty	-0.194764	0.06398894
JW2924	P00805	ansB	periplasmic L-asparaginase	-0.0767186	0.02843212
JW1525	P31121	marB	periplasmic mar operon reg	-0.0670667	0.04363315
JW0934	P43671	pqiB	periplasmic MCE subunit of	-0.0925104	0.00386386
JW1823	P76272	yebT	periplasmic MCE subunit of	-0.0879027	0.0802187
JW5346	P64534	yohN	periplasmic modulator of Ni	0.01852397	0.51139789
JW5100	P0A855	tolB	periplasmic protein	-0.2806429	0.04782354
JW3181	P28721	gltF	periplasmic protein	-0.0105533	0.66358721
JW0321	P75694	yahO	periplasmic protein, functio	-0.0505254	0.04007076
JW5177	P0AB46	ymgD	periplasmic protein, HdeA st	-0.0102113	0.83766086
JW2183	P0AA86	ccmG	periplasmic thioredoxin of c	0.136489	0.01251671
JW0732	P45955	ybgF	periplasmic TolA-binding pr	-0.0864863	0.0036774
JW1186	P13482	treA	periplasmic trehalase	0.04992602	0.0069145
JW0900	P0AAZ7	ycaR	peroxide and acid resistance	-0.0411222	0.41080919
JW0005	P0A813	yaaA	peroxide resistance protein,	0.02699066	0.06854422
JW2465	P0AE52	bcp	peroxiredoxin; thiol peroxid	0.07999091	0.02169277
JW5058	P0A8E7	yajQ	phage Phi6 host factor, ATP,	0.06579446	0.09360094
JW5716	P32696	yjbO	phage shock protein G	0.01169838	0.70799685
JW5209	P38392	sieB	phage superinfection exclus	0.05590796	0.00309302
JW0478	P0AA53	ybbK	PHB domain membrane-anc	0.11771313	0.00131391
JW3023	P77306	yqiK	PHB family membrane prote	0.10085439	0.0776373
JW2903	P25894	yggG	Phe-Phe periplasmic metall	-0.062503	0.17260206
JW2579	P0AD72	pheL	pheA gene leader peptide	0.03172564	0.01434828
JW1380	P80668	feaB	phenylacetaldehyde dehydr	0.04631167	0.14981844
JW0565	P24207	pheP	phenylalanine transporter	0.02408976	0.20989747

JW1705	P0AD74	pheM	phenylalanyl-tRNA syntheta	-0.0360907	0.15826632
JW2526	P77650	hcaD	phenylpropionate dioxygena	-0.7065354	0.00011813
JW1593	P0AFS5	ydgG	pheromone AI-2 transporter	-0.157493	0.19282732
JW3310	P0A8R4	slyX	phi X174 lysis protein	-0.0751257	0.21976736
JW4358	P0A7A2	ytjC	phosphatase	0.00739525	0.84712826
JW3703	P0AAH0	pstB	phosphate ABC transporter ,	0.00742424	0.82245408
JW3706	P0AG82	pstS	phosphate ABC transporter	-0.1685372	0.06322353
JW3704	P07654	pstA	phosphate ABC transporter	-0.0127592	0.78478558
JW3705	P0AGH8	pstC	phosphate ABC transporter	0.07026381	0.35905052
JW2294	P0A9M8	pta	phosphate acetyltransferase	-0.0026176	0.94665695
JW2442	P77218	eutI	phosphate acetyltransferase	0.00500185	0.82884811
JW3990	P0A7C8	yjbA	phosphate starvation induci	0.11464105	0.00170135
JW2955	P43676	pitB	phosphate transporter	0.0032901	0.91996311
JW3460	P0AFJ7	pitA	phosphate transporter, low-	0.09075067	0.00642774
JW2070	P76407	yegS	phosphatidylglycerol kinase,	0.01282406	0.43517111
JW0408	P18200	pgpA	phosphatidylglycerophospha	0.00330464	0.97854127
JW1270	P0A924	pgpB	phosphatidylglycerophospha	0.04346263	0.02677031
JW5408	P0AD42	yfhB	phosphatidylglycerophospha	-0.1043273	0.05584092
JW1723	P17411	chbF	phospho-chitobiase; general	-0.113751	0.00574875
JW2732	P17854	cysH	phosphoadenosine phospho:	0.3604491	2.09E-07
JW0963	P07102	appA	phosphoanhydride phosphor	-0.0412676	0.12626814
JW5377	P67095	yfcE	phosphodiesterase activity c	0.06389857	0.10525894
JW5014	P37049	yael	phosphodiesterase with mo	-0.0733843	0.36593497
JW3693	P31467	yieH	phosphoenolpyruvate and 6-	-0.0417521	0.18860285
JW3366	P22259	pck	phosphoenolpyruvate carbo:	-0.0516203	0.06308885
JW3928	P00864	ppc	phosphoenolpyruvate carbo:	0.07142807	0.29076458
JW1692	P23538	pps	phosphoenolpyruvate syntha	-0.0101672	0.81377181
JW0675	P36938	pgm	phosphoglucomutase	0.01976291	0.36499654
JW3143	P31120	glmM	phosphoglucosamine mutas	0.03826709	0.41949641
JW3587	P37689	gpml	phosphoglycero mutase III, c	0.11762752	0.00614518
JW0738	P62707	gpmA	phosphoglyceromutase 1	-1.39E-05	0.99898289
JW3348	P32662	gph	phosphoglycolate phosphata	0.01776661	0.49830027
JW2337	P76502	sixA	phosphohistidine phosphata	0.07554597	0.17371814
JW3173	P0A9N0	npr	phosphohistidinoprotein-he:	-0.0303818	0.66817319
JW0617	P37001	crcA	phospholipid:lipid A palmito	-0.0338864	0.21197409
JW2033	P24175	cpsG	phosphomannomutase	0.09491294	0.25447561
JW3958	P30136	thiC	phosphomethylpyrimidine s'	0.09924648	0.07175175
JW4067	P16677	phnC	phosphonate ABC transport	-0.1183596	0.01852312
JW4066	P16682	phnD	phosphonate ABC transport	0.06551852	0.01975677
JW3690	P0ADM8	yieE	phosphopantetheinyl transfe	-0.0111967	0.6139091
JW4346	P0A6K6	deoB	phosphopentomutase	-0.0665311	0.04936641
JW3343	P45549	yhfW	phosphopentomutase-relate	0.04310193	0.07948773
JW2008	P06989	hisI	phosphoribosyl-AMP cyclohy	0.02872671	0.60025966
JW2484	P08178	purM	phosphoribosylaminoimidaz	-0.0056076	0.80312938
JW2461	P0A7D7	purC	phosphoribosylaminoimidaz	0.01369206	0.72508377

JW2541	P15254	purL	phosphoribosylformyl-glycin	-0.0006112	0.98778406
JW2485	P08179	purN	phosphoribosylglycinamide	-0.0612679	0.33662846
JW1838	P33221	purT	phosphoribosylglycinamide	0.11542218	0.06990528
JW3969	P15640	purD	phosphoribosylglycinamide	0.12484411	0.02156046
JW2204	P39838	rcsD	phosphotransfer intermedia	-0.0766671	0.02110066
JW3342	P45548	php	phosphotriesterase homolog	-0.0077716	0.89927944
JW1258	P77766	yciV	PHP domain protein	0.02431453	0.36010018
JW1459	P37757	yddE	PhzC-PhzF family protein	0.00821342	0.70423814
JW3375	P13001	bioH	pimeloyl-ACP methyl ester c	0.09641716	0.00260134
JW1614	P23256	malY	PLP-dependent beta-cystath	0.02478024	0.32750969
JW5142	P75906	ycdR	poly-beta-1,6-N-acetyl-D-glu	-0.0975639	0.01191819
JW5808	P0ABF1	pcnB	poly(A) polymerase	-0.0322127	0.27404538
JW0284	P77694	yagW	polymerized tip adhesin of E	-0.0370437	0.19295843
JW5851	P05055	pnp	polynucleotide phosphorylas	0.11939261	0.1586739
JW2486	P0A7B1	ppk	polyphosphate kinase, comp	-0.0135308	0.48106603
JW4107	P0A6N4	efp	polyproline-specific translat	-0.0542991	0.35463607
JW0555	P10805	envY	porin thermoregulatory tran	-0.0212099	0.1416467
JW2424	P76536	yfeX	porphyrinogen oxidase, cyto	-0.0339338	0.03645206
JW0687	P36937	kdpF	potassium ion accessory tra	0.03402565	0.26864277
JW0686	P03959	kdpA	potassium translocating ATI	-0.0379391	0.1112422
JW0685	P03960	kdpB	potassium translocating ATI	0.00461307	0.80266879
JW0684	P03961	kdpC	potassium translocating ATI	-0.1064159	0.24692222
JW5576	P0AFZ7	trkH	potassium transporter	-0.1565231	3.95E-06
JW5609	P63183	trkD	potassium transporter	0.05844174	0.29792548
JW3314	P0A756	kefG	potassium-efflux system an	-0.0963682	0.00081232
JW0045	P0A754	kefF	potassium-efflux system an	-0.0351945	0.36350877
JW1425	P25396	tehA	potassium-tellurite ethidiu	0.05750411	0.10785133
JW3313	P45522	kefB	potassium:proton antiporter	-0.0473166	0.25668845
JW0046	P03819	kefC	potassium:proton antiporter	-0.016348	0.54605018
JW5696	P45551	yhfY	PRD domain protein	0.02327396	0.32891041
JW3142	P0AG99	secG	preprotein translocase merr	0.05403445	0.25197678
JW4159	P07013	priB	primosomal protein N	0.02427817	0.20864251
JW0456	P23862	priC	primosomal replication prot	-0.0336106	0.31128044
JW3906	P17888	priA	Primosome factor n' (replica	-0.1203372	0.25632097
JW0986	P36661	yccE	PRK09784 family protein	0.32639833	2.37E-10
JW3694	P31468	yieI	PRK09823 family inner men	-0.0577787	0.05887765
JW0556	P37325	ybcH	PRK09936 family protein	0.00601589	0.78269917
JW5590	P27843	yigG	PRK11371 family inner men	0.13268055	0.00251187
JW1139	P75982	ymfQ	prohage e14 tail protein hor	-0.0319588	0.03319849
JW2876	P15034	pepP	proline aminopeptidase P II	0.03422667	0.46812896
JW3823	P21165	pepQ	proline dipeptidase	-0.1423618	0.00065452
JW5055	P0AAE2	proY	proline-specific permease	-0.0105931	0.54437008
JW1001	P07117	putP	proline:sodium symporter	-0.0245946	0.38109583
JW4072	P0COL7	proP	proline/glycine betaine tran	0.006699	0.7755258
JW0322	P77743	prpR	propionate catabolism oper	-0.044701	0.05138556

JW5806	P11868	tdcD	propionate kinase/acetate k	-0.0520308	0.12583543
JW0326	P77495	prpE	propionate--CoA ligase	0.03987583	0.01914843
JW2887	P52043	ygfH	propionyl-CoA:succinate CoA	-0.0038691	0.82797113
JW1219	P02338	tpr	protamine-like protein	0.01453534	0.63703141
JW1834	P24555	ptrB	protease II	0.06987503	0.31001781
JW2687	P0AEV9	hycl	protease involved in process	0.01255455	0.70050553
JW1755	P08395	sppA	protease IV (signal peptide	-0.0337033	0.33272446
JW5840	Q47013	elaD	protease, capable of cleavin	-0.0031182	0.9000944
JW0049	P62672	apaG	protein associated with Co2	0.00976221	0.88307251
JW2861	P0AEG6	dsbC	protein disulfide isomerase	0.05410264	0.05709243
JW3584	P0AG86	secB	protein export chaperone	0.0452388	0.16772081
JW4212	P0AF90	yjgD	protein inhibitor of RNase E	-0.4521861	0.00244417
JW2696	P0A700	hypA	protein involved in nickel ins	0.02754122	0.32169568
JW5493	P0A703	hybF	protein involved with the m	0.05352137	0.06133578
JW2055	P76393	yegl	protein kinase-related putat	-0.0302025	0.49445811
JW1772	P0ACY3	yeaG	protein kinase, endogenous	0.04602333	0.03280754
JW2568	P76594	yfiQ	protein lysine acetyltransfer	-0.0360825	0.18845728
JW0462	P0A6Z3	htpG	protein refolding molecular	0.02540056	0.07425457
JW1878	P0AF06	motB	protein that enables flagella	0.10430839	0.10335853
JW0427	P0A6G7	clpP	proteolytic subunit of ClpA-(0.00149619	0.9782234
JW0418	P0AEA5	cyoE	protoheme IX farnesyltransf	0.14882748	0.01310418
JW1879	P09348	motA	proton conductor componen	0.01308773	0.76703862
JW1867	P76297	flhE	proton seal during flagellar	-0.1315962	0.15538019
JW2232	P45505	yfaH	pseudogene	-0.2269295	1.00E-04
JW5787	P39391	yjiT	pseudogene	-0.0801456	0.07701607
JW5145	NA	ymdE	pseudogene	-0.0646489	0.03120621
JW2818	Q46786	ygeF	pseudogene	-0.0540512	0.16193747
JW2110	P33353	yehQ	pseudogene	-0.0536976	0.0010836
JW0225	P75675	ykfJ	pseudogene	-0.0459849	0.05038487
JW2629	P76612	ypjB	pseudogene	-0.0456989	0.05086358
JW1453	NA	yncl	pseudogene	-0.0398437	0.15103581
JW5960	Q2EER5	ymjC	pseudogene	-0.0298628	0.08212008
JW0207	P77354	yafU	pseudogene	-0.0209684	0.13965512
JW1499	P76137	ydeT	pseudogene	0.00394479	0.9347305
JW1162	NA	ycgl	pseudogene	0.01830693	0.07915079
JW3471	P37635	yhiS	pseudogene	0.02785879	0.35105877
JW5094	NA	ybfG	pseudogene	0.05461676	0.16596363
JW5838	NA	yohG	pseudogene	0.05825984	0.08891381
JW3658	NA	glvG	pseudogene	0.06496043	0.15352827
JW0489	P33669	ybbD	pseudogene	0.06733726	0.00026219
JW1311	NA	ycjV	pseudogene	0.06870515	0.06592771
JW0383	P75704	ykiA	pseudogene	0.14790212	0.00020178
JW5678	NA	yrhC	pseudogene fragment	0.04275027	0.29782175
JW3236	P45766	yhdW	pseudogene, ABC transporte	-0.0552233	0.02145234
JW1503	P32051	ydeK	pseudogene, AidA homolog	-0.0646222	6.23E-05

JW5244	P76138	yneL	pseudogene, AraC family	-0.0261025	0.40314296
JW5037	P77601	ykgA	pseudogene, AraC family	0.05498403	0.0641741
JW3659	P69789	glvB	pseudogene, arbutin specific	-0.1737336	0.00065655
JW0291	P36943	eaeh	pseudogene, attaching and	-0.0137232	0.41970043
JW0362	NA	yaiT	pseudogene, autotransporte	0.03440671	0.33117491
JW5839	P33924	yejO	pseudogene, autotransporte	0.14680673	0.08701187
JW5964	NA	ypaA	pseudogene, C-terminal frag	0.02219015	0.71472013
JW5327	P76359	yeeP	pseudogene, CP4-44 proph	-0.0338762	0.5977028
JW5328	Q2EES3	yoeF	pseudogene, CP4-44 putativ	-0.0410879	0.10846603
JW5922	NA	ypjL	pseudogene, CP4-57 proph	-0.0967601	0.00051598
JW0259	P37008	yagB	pseudogene, CP4-6 prophag	-0.0500832	0.05511311
JW0255	P75681	afuB	pseudogene, CP4-6 prophag	0.01460224	0.39203605
JW5384	P76508	yfdL	pseudogene, CPS-53 (KpLE1	-0.0240866	0.3398371
JW2355	P0AD35	yfdO	pseudogene, CPS-53 (KpLE1	-0.0537855	0.29306188
JW5383	P77326	tfaS	pseudogene, CPS-53 (KpLE1	-0.0743034	0.00537258
JW0695	P75741	ybfL	pseudogene, DDE domain tr	0.06617947	0.12555097
JW5926	NA	yghX	pseudogene, dienlactone hy	-0.0205278	0.55169484
JW0530	P75718	renD	pseudogene, DLP12 prophag	0.0124993	0.53122148
JW0552	P77087	ylcE	pseudogene, DLP12 prophag	0.03892641	0.21715399
JW0551	P77460	ybcY	pseudogene, DLP12 prophag	-0.0503675	0.0206592
JW0526	P75717	ybcC	pseudogene, DLP12 prophag	-0.1280918	0.24377449
JW5815	NA	tfaD	pseudogene, DLP12 prophag	-0.0596474	0.00272608
JW3386	P0ACLO	glpR	pseudogene, DNA-binding tr	-0.0420627	0.04111054
JW5674	NA	yhiK	pseudogene, DUF4049 fami	0.02455414	0.19825077
JW5170	P75981	ymfP	pseudogene, e14 prophage	0.00243048	0.90286677
JW5172	P33227	stfE	pseudogene, e14 prophage;	-0.0953921	0.0195033
JW2334	NA	yfcT	pseudogene, FimD fimbrial	0.02091975	0.70457257
JW5811	Q47153	fhiA	pseudogene, flagellar syste	-0.0168881	0.41124139
JW2076	P69831	gatC	pseudogene, galactitol-spec	-0.0012601	0.96733881
JW2831	Q46796	ygeP	pseudogene, glycosyl hydrol	-0.0195909	0.12734879
JW4271	P39369	yjhR	pseudogene, helicase family	0.22692425	0.19580864
JW1559	P76164	ydfW	pseudogene, integrase frag	0.14572961	0.00365262
JW4227	P39347	intB	pseudogene, integrase hom	-0.0405328	0.09667537
JW5864	P46856	yrhA	pseudogene, interrupted by	0.18361783	0.04934727
JW0350	NA	yaiX	pseudogene, interrupted by	0.03007124	0.20865248
JW5423	P76611	pinH	pseudogene, invertase resol	-0.0604626	0.61677797
JW5848	Q46840	yghO	pseudogene, IS-interrupted	-0.017191	0.52536389
JW5173	NA	icdC	pseudogene, isocitrate dehy	0.08229539	4.78E-06
JW4246	Q47719	yjhV	pseudogene, KpLE2 phage-li	-0.053789	0.61430775
JW5770	NA	yjhD	pseudogene, KpLE2 phage-li	-0.0464238	0.10113059
JW4242	NA	yjhE	pseudogene, KpLE2 phage-li	-0.0398346	0.25028438
JW5812	Q47154	mbhA	pseudogene, lateral flagella	0.02149795	0.40546294
JW1467	P76123	yddK	pseudogene, leucine-rich pr	-0.0449155	0.08947522
JW2882	P64562	yqfE	pseudogene, LysR family	0.00514232	0.92157124
JW0276	P75684	yagP	pseudogene, LysR family, fr	0.05012044	0.07765379

JW2655	P76628	ygaX	pseudogene, major facilitator	0.11400914	0.01739862
JW1536	P77228	ydfJ	pseudogene, MFS transport	0.05141826	0.06079616
JW5527	P42906	agaA	pseudogene, N-acetylgalact	0.10783195	0.03753141
JW3103	NA	agaW	pseudogene, N-acetylgalact	-0.0762902	0.065073
JW5846	Q46795	ygeO	pseudogene, orgA family, p	0.2286492	0.03260024
JW5459	NA	ygeM	pseudogene, orgB family, p	-0.0031739	0.90060438
JW0055	P39220	yabP	pseudogene, pentapeptide r	-0.0132549	0.64806947
JW5457	NA	pbl	pseudogene, peptidoglycan-	0.08506544	0.02391834
JW3390	P76692	yzgL	pseudogene, periplasmic so	0.30858361	0.01654055
JW5913	NA	intG	pseudogene, phage integras	0.01921816	0.40389815
JW1135	P75978	ymfN	pseudogene, phage termina	-0.004207	0.91751308
JW1137	P75980	ymfO	pseudogene, portal protein	0.00639032	0.73866117
JW1560	P76165	ydfX	pseudogene, Qin prophage	0.04051872	0.14736596
JW1541	P31061	nohA	pseudogene, Qin prophage;	-0.1493999	0.00097038
JW1571	P76168	intQ	pseudogene, Qin prophage;	0.01612601	0.4883966
JW5212	P77551	rzpR	pseudogene, Rac prophage;	-0.0077924	0.88981482
JW4163	P39309	ytfA	pseudogene, related to tran	-0.0197362	0.26769355
JW5458	NA	ygeK	pseudogene, response regul	-0.0287958	0.35071214
JW0692	P77779	ybfO	pseudogene, Rhs family	-0.0124774	0.65877341
JW1451	P24211	rhsE	pseudogene, Rhs family	0.01482521	0.69931412
JW0488	P77759	ylbH	pseudogene, Rhs family C-ter	0.00473588	0.80862031
JW5484	Q46834	yghF	pseudogene, secretion path	-0.0212885	0.57494618
JW5924	NA	yghE	pseudogene, secretion path	-0.0162112	0.50965935
JW0230	P24251	crl	pseudogene, sigma factor-b	-0.0158841	0.43997418
JW3998	P32690	yjbl	pseudogene, SopA-related,	-0.1504199	0.00086912
JW5953	NA	yjiP	pseudogene, transposase_3	0.03005928	0.44813718
JW4195	NA	cybC	pseudogene, truncated cyto	-0.0094355	0.65375737
JW0527	NA	ybcD	pseudogene; DLP12 prophag	-0.0170349	0.55638148
JW5507	P76655	yqiG	pseudogene; fimbrial export	0.09552774	0.04975005
JW3290	P41442	gspG	pseudopilin, cryptic, general	-0.0499442	0.41552753
JW2152	P33025	yeiN	pseudouridine 5'-phosphate	0.02166741	0.60148975
JW2153	P30235	yeiC	pseudouridine kinase	-0.0515791	0.05852789
JW5054	P0AFM4	psiF	PsiF family protein	0.019598	0.50995142
JW1298	P0AFM9	pspB	psp operon transcription co-	0.01011261	0.70892981
JW1299	P0AFN2	pspC	psp operon transcription co-	0.02867825	0.33066481
JW1296	P37344	pspF	psp operon transcriptional a	0.03994823	0.1913925
JW4140	P0AF78	yjfJ	PspA/IM30 family protein	0.03473077	0.20071623
JW0118	P0AA95	yacC	PulS_OutS family protein	0.00840656	0.64829247
JW4347	P0ABP8	deoD	purine nucleoside phosphor	-0.0232342	0.50242918
JW2398	P45563	xapA	purine nucleoside phosphor	0.04628553	0.22648534
JW1876	P0A964	cheW	purine-binding chemotaxis p	-0.0090862	0.78027129
JW3096	P0AA80	garP	putative (D)-galactarate tra	0.03922307	0.15714805
JW3924	P32675	pflC	putative [formate-C-acetyl	0.14490878	0.04142501
JW5786	P39384	yjiM	putative 2-hydroxyglutaryl-C	-0.0082928	0.71199919
JW3848	P32137	yihP	putative 2,3-dihydroxypropa	0.02024724	0.36936327

JW2520	Q47142	hcaT	putative 3-phenylpropionic t	0.00028235	0.99159335
JW2546	P52102	yfhL	putative 4Fe-4S cluster-cont	0.0397992	0.03169373
JW2737	Q46905	ygcO	putative 4Fe-4S cluster-cont	0.31234591	0.00077918
JW5468	Q46819	ygfS	putative 4Fe-4S ferredoxin-t	-0.3040466	0.04085264
JW0043	P68646	fixX	putative 4Fe-4S ferredoxin-t	0.00647067	0.85223856
JW1664	P0AAL6	ydhY	putative 4Fe-4S ferridoxin-t	-0.118323	0.17899597
JW5271	P77375	ydhX	putative 4Fe-4S ferridoxin-t	-0.0746313	0.00178133
JW0977	P52636	yccM	putative 4Fe-4S membrane	-0.0740313	0.1438878
JW4087	P0AF59	yjdl	putative 4Fe-4S mono-clust	-0.0203816	0.46675984
JW1145	P24200	mcrA	putative 5-methylcytosine/5	-0.1291381	0.05482716
JW5613	P31470	yieK	putative 6-phosphogluconol	0.011046	0.80212627
JW1303	P76042	ycjN	putative ABC sugar transpor	-0.0029778	0.95768843
JW0123	P36879	yadG	putative ABC transporter AT	-0.1330573	0.02296611
JW5286	P76909	ynjD	putative ABC transporter AT	-0.0209063	0.10534357
JW1902	P37774	yecC	putative ABC transporter AT	-0.0051584	0.88151206
JW5104	P0A9U1	ybhF	putative ABC transporter AT	0.01854708	0.56564932
JW2117	P33360	yehX	putative ABC transporter AT	0.02361231	0.51975091
JW1436	P77795	ydcT	putative ABC transporter AT	0.02924623	0.52754993
JW0484	P0A9T8	ybbA	putative ABC transporter AT	0.03411981	0.29212332
JW2119	P33362	yehZ	putative ABC transporter pe	-0.0120657	0.3580861
JW0435	P46890	ybaE	putative ABC transporter pe	0.04333749	0.03445164
JW5284	P76223	ynjB	putative ABC transporter pe	0.10421235	0.00094164
JW1435	P76108	ydcS	putative ABC transporter pe	0.11647204	0.0036437
JW1438	P0AFR9	ydcV	putative ABC transporter pe	-0.1654549	0.00128609
JW0124	P0AFN6	yadH	putative ABC transporter pe	-0.1004577	0.00539728
JW0777	P0AFQ2	ybhS	putative ABC transporter pe	-0.0953913	0.07103686
JW0485	P77504	ybbP	putative ABC transporter pe	-0.0355436	0.17296275
JW5803	P0AFP9	ybhR	putative ABC transporter pe	-0.0006664	0.97652432
JW2988	Q46863	ygiS	putative ABC transporter pe	0.00173524	0.94382134
JW5285	P76224	ynjC	putative ABC transporter pe	0.00313477	0.94077815
JW1437	P77156	ydcU	putative ABC transporter pe	0.00649463	0.87215497
JW2116	P33359	yehW	putative ABC transporter pe	0.01989847	0.57955188
JW2118	P33361	yehY	putative ABC transporter pe	0.07624006	0.04048154
JW5677	P0AGH1	yhhJ	putative ABC transporter pe	0.09480126	0.07545539
JW0769	P0AAC4	ybhL	putative acetate transporter	-0.059409	0.67386362
JW1684	P37766	ydiF	putative acetyl-CoA:acetoac	-0.0269666	0.41126807
JW3222	P26646	yhdH	putative acryloyl-CoA reduct	-0.0314935	0.22968783
JW2043	P0ACC9	wcaB	putative acyl transferase	-0.0353463	0.61639584
JW2039	P0ACD2	wcaF	putative acyl transferase	0.14999323	0.11804306
JW5275	P0A9U8	ydiO	putative acyl-CoA dehydroge	0.01265337	0.69448968
JW1193	P76017	ycgV	putative adhesin	-0.1178977	0.11230988
JW5833	P76347	yeeJ	putative adhesin	0.0349547	0.46853204
JW1762	P77704	ydjI	putative aldolase	-0.0285259	0.02765038
JW5721	P32717	yjcS	putative alkylsulfatase; SDS	-0.0144222	0.48098918
JW0499	P75712	ybbW	putative allantoin transport	0.12125223	0.01696492

JW0701	P0AAV4	ybgJ	putative allophanate hydroly	0.1015428	0.00254704
JW0702	P75745	ybgK	putative allophanate hydroly	-0.0544638	0.04156178
JW3631	P31434	yicl	putative alpha-glucosidase	0.06378463	0.04898914
JW0633	P52086	cobC	putative alpha-ribazole-5'-P	-0.1092508	0.34672898
JW3239	P45769	yhdZ	putative amino acid ABC tra	-0.0091339	0.75702056
JW5545	P45768	yhdY	putative amino acid ABC tra	0.04191528	0.27074208
JW5544	P45767	yhdX	putative amino acid ABC tra	0.06251684	0.02794404
JW2842	Q46807	yqeA	putative amino acid kinase	0.03729135	0.61397347
JW0475	P77400	ybaT	putative amino acid transpo	-0.0641544	0.19499158
JW0995	P0AFQ5	ycdK	putative aminoacrylate dear	-0.0161426	0.72699933
JW0509	P0AAS5	ylbF	putative anaerobic allantoin	0.08767557	0.00414932
JW4194	P0AFK0	pmbA	putative antibiotic peptide M	0.11504421	0.00541712
JW2738	Q46906	ygcP	putative antiterminator regi	0.02472469	0.44824846
JW3325	P0ADX5	yhfG	putative antitoxin for Fic	-0.0303464	0.3804187
JW5595	P27837	yifK	putative APC family amino a	0.15835282	0.00026346
JW2319	P77549	yfcJ	putative arabinose efflux tra	-0.056966	0.00143463
JW1588	P43531	ynfM	putative arabinose efflux tra	0.03849272	0.46740014
JW3633	P31436	setC	putative arabinose efflux tra	0.05639858	0.12179378
JW1652	P37597	ydhC	putative arabinose efflux tra	0.06728382	0.18557457
JW5945	P37621	yhhS	putative arabinose efflux tra	0.08820472	0.10997151
JW1597	P0AAE5	ydgl	putative arginine/ornithine :	-0.0741283	0.23965001
JW0802	P75788	ybiR	putative ArsB family transpo	-0.0449192	0.04791122
JW2455	P24178	yffB	putative ArsC family reducta	-0.0513054	0.20357056
JW5594	P25550	aslB	putative AsIA-specific sulfat	0.08214201	0.02346683
JW2954	Q46844	yghT	putative ATP-binding protei	-0.1635727	0.00030701
JW5491	Q46843	yghS	putative ATP-binding protei	-0.0754496	0.00074835
JW2952	P64572	yghR	putative ATP-binding protei	0.22177113	0.06872797
JW2172	P33919	yejH	putative ATP-dependent DN	0.02566989	0.47630873
JW1645	P30015	lhr	putative ATP-dependent hel	-0.0173688	0.60652832
JW5905	P43329	hrpA	putative ATP-dependent hel	0.00028329	0.98983756
JW0144	P37024	hrpB	putative ATP-dependent hel	0.09791296	0.00131099
JW1797	P76257	yoaA	putative ATP-dependent hel	0.00430115	0.83619491
JW5785	P39383	yjiL	putative ATPase, activator o	0.01140206	0.41752632
JW1510	P76143	lsrF	putative autoinducer-2 (AI-2	-0.3726163	0.00136886
JW3208	P64616	yhcO	putative barnase inhibitor	0.16503239	0.07512291
JW1698	P23898	nlpC	putative C40 clan peptidase	0.11848535	0.00177869
JW3163	P45394	yrbG	putative calcium/sodium:pr	0.04090383	0.29333046
JW5463	Q46803	ygeW	putative carbamoyltransfera	0.02009535	0.32429606
JW0510	P37306	ybcF	putative carbonate kinase	0.1383427	0.00279805
JW5853	P56262	ysgA	putative carboxymethylenek	-0.1315834	6.09E-06
JW4026	P32703	yjcE	putative cation/proton antiq	-0.006064	0.83262527
JW5184	P76007	cvrA	putative cation/proton antiq	-0.0049305	0.90469812
JW1406	P76091	ynbB	putative CDP-diglyceride syr	0.01431577	0.6866187
JW5589	P27844	rarD	putative chloramphenical re	0.02325645	0.55455866
JW2062	P36554	mdtD	putative citrate/iron-citrate,	-0.0086845	0.78999013

JW2708	Q46890	ygbL	putative class II aldolase	-0.0284157	0.43455894
JW1802	P43337	yeaB	putative CoA pyrophosphohy	-0.0041694	0.88297607
JW5130	P75874	yccU	putative CoA-binding protei	0.0406348	0.06598855
JW0763	P75767	ybhK	putative CofD superfamily tr	0.01694272	0.58424001
JW2031	P77377	wzxC	putative colanic acid export	-0.022303	0.74930624
JW2041	P71238	wcaD	putative colanic acid polym	-0.0079279	0.60242664
JW0432	P0AAR8	ybaV	putative competence-suppre	0.06044793	0.05725674
JW1863	P67826	cutC	putative copper homeostasi	-0.0158988	0.72429409
JW0036	P31552	caiC	putative crotonobetaine/car	-0.2512473	0.00022118
JW0332	P17583	cynX	putative cyanate transport	-0.0477576	0.17133593
JW3650	P31443	yidF	putative Cys-type oxidative `	0.10736319	0.00434012
JW1660	P77409	ydhU	putative cytochrome b subu	0.00275565	0.92626687
JW1044	P75925	yceJ	putative cytochrome b561	0.00775854	0.72469953
JW2760	Q46916	gudP	putative D-glucarate transp	0.0190599	0.39573445
JW0753	P75763	ybhI	putative DASS family tricart	0.0453214	0.04158173
JW4259	P39358	yjhG	putative dehydratase	0.3225947	0.00542989
JW2706	Q46888	ygbJ	putative dehydrogenase	-0.0396737	0.42283893
JW5264	P0A6E9	ynfK	putative dethiobiotin synthe	-0.0056165	0.87223221
JW1243	P0AB55	ycil	putative DGPF domain-cont	-0.0420424	0.06496693
JW5391	P23842	yfeA	putative diguanylate cyclase	-0.0252925	0.65358135
JW2052	P38097	yegE	putative diguanylate cyclase	0.02090288	0.40036566
JW5291	P76237	yeaJ	putative diguanylate cyclase	0.03042739	0.19097397
JW2328	P0A8B2	yfcN	putative DNA endonuclease	-0.0059702	0.83522223
JW2379	P77396	ypdC	putative DNA-binding protei	-0.0453408	0.03449382
JW3843	P0ACM9	yihL	putative DNA-binding transc	-0.2495084	0.05715319
JW0472	P0A9T6	ybaQ	putative DNA-binding transc	-0.0915726	0.00426587
JW5948	P45552	yhfZ	putative DNA-binding transc	-0.0627673	0.10272002
JW5226	P77171	ydcl	putative DNA-binding transc	-0.0610899	0.01823802
JW1519	P77309	yneJ	putative DNA-binding transc	-0.0531409	0.03737708
JW5896	P52696	ybhD	putative DNA-binding transc	-0.0468614	0.24258192
JW3689	P31463	yidZ	putative DNA-binding transc	-0.0383964	0.20423236
JW5698	P45544	frlR	putative DNA-binding transc	-0.0381329	0.11578156
JW3373	P64638	yhgG	putative DNA-binding transc	-0.037838	0.03429048
JW4262	P39361	sgcR	putative DNA-binding transc	-0.0242254	0.20799259
JW2144	P0ACR4	yeiE	putative DNA-binding transc	-0.0127686	0.60394387
JW2088	P0ACM5	yegW	putative DNA-binding transc	-0.0079952	0.70822708
JW1686	P77402	ydiP	putative DNA-binding transc	-0.0037713	0.92259665
JW1430	P77626	ydcN	putative DNA-binding transc	-0.0027609	0.95952029
JW3557	P37682	yiaU	putative DNA-binding transc	0.00203252	0.91018993
JW1779	P76241	yeaM	putative DNA-binding transc	0.00728205	0.74943324
JW2561	P33634	yfiE	putative DNA-binding transc	0.02094195	0.46439994
JW5908	P67699	yddM	putative DNA-binding transc	0.02684108	0.13659056
JW4261	P39360	yjhl	putative DNA-binding transc	0.02887004	0.34760062
JW0596	P77746	ybdO	putative DNA-binding transc	0.03648621	0.02074074
JW0437	P0ACJ5	ybaO	putative DNA-binding transc	0.03697054	0.15083189

JW1759	P77721	ydjF	putative DNA-binding transc	0.04218973	0.1124546
JW5406	P76586	yphH	putative DNA-binding transc	0.05242356	0.05762134
JW1842	P46118	yebK	putative DNA-binding transc	0.05454151	0.1307829
JW5476	P52044	ygfl	putative DNA-binding transc	0.07168518	0.19623066
JW2545	P37767	yfhH	putative DNA-binding transc	0.08877813	0.0021628
JW1434	P77730	ydcR	putative DNA-binding transc	0.04269952	0.40319393
JW2242	P77732	yfaX	putative DNA-binding transc	-0.0470186	0.05153884
JW1333	P77744	abgR	putative DNA-binding transc	-0.0677731	0.00044201
JW4063	P16684	phnF	putative DNA-binding transc	0.03494891	0.13662184
JW5952	P39356	yjhU	putative DNA-binding transc	-0.0382415	0.10613324
JW4303	P39389	yjiR	putative DNA-binding transc	0.16053886	0.00092658
JW3488	P37640	yhjB	putative DNA-binding transc	0.40251143	0.00734345
JW0308	P77700	yahB	putative DNA-bindng transc	-0.0697894	0.02514041
JW4341	P39408	yjjV	putative DNase	-0.0076748	0.77729255
JW1086	P0AFQ7	ycfH	putative DNase	0.14079889	4.68E-05
JW0829	P75810	ybjJ	putative drug efflux MFS tra	0.00386122	0.92347373
JW1040	P25744	mdtG	putative drug efflux system	-0.0557043	0.23668461
JW5795	P18390	yjJA	putative DUF2501 family pe	0.0013343	0.95527834
JW1637	P76186	ydhK	putative efflux protein (PET)	-0.0121635	0.67874459
JW5276	P76201	ydiQ	putative electron transfer fl	0.01472431	0.57499968
JW1688	P77378	ydiR	putative electron transfer fl	0.14477934	0.00653264
JW0041	P31574	fixB	putative electron transfer fl	0.09146419	0.00372271
JW1263	P31808	yciK	putative EmrKY-TolC system	-0.1168176	4.05E-06
JW5776	P39366	sgcX	putative endoglucanase witi	-0.0911871	0.31619654
JW1818	P23894	htpX	putative endopeptidase	0.05396895	0.64516784
JW3922	P69816	frwB	putative enzyme IIB compor	0.04169857	0.25058818
JW5967	P58035	sgcB	putative enzyme IIB compor	0.04814305	0.00977953
JW5389	P69808	ypdH	putative enzyme IIB compor	0.06041487	0.04663753
JW3925	P32676	frwD	putative enzyme IIB compor	0.06832127	0.01690989
JW2383	P77579	ypdG	putative enzyme IIC compor	-0.003317	0.91157998
JW3921	P32672	frwC	putative enzyme IIC compor	0.06811878	0.32177949
JW4263	P39362	sgcE	putative epimerase	-0.0476879	0.01324383
JW1998	P0AD12	yeeZ	putative epimerase	0.37113411	0.00860797
JW5534	P42640	yhbX	putative EptAB family phosp	-0.0948024	0.01635088
JW1407	P76092	ynbC	putative esterase	0.00132403	0.96477761
JW2432	P76541	eutL	putative ethanol utilization	0.00609971	0.94664906
JW2446	P63746	ypfE	putative ethanol utilization	0.05478788	0.08670759
JW2431	P76540	yffl	putative ethanol utilization	0.05608981	0.17847016
JW1677	P77748	ydiJ	putative FAD-linked oxidore	-0.0547352	0.03884334
JW5442	Q46911	ygcU	putative FAD-linked oxidore	0.01891715	0.31516568
JW0355	Q47536	yaiP	putative family 2 glycosyltra	0.20362532	0.00017499
JW5345	P76421	yegX	putative family 25 glycosyl t	0.11110348	0.06854987
JW0785	P30177	ybiB	putative family 3 glycosyltra	0.00626808	0.81323972
JW1309	P77154	ycjT	putative family 65 glycosyl t	-0.0595731	0.09777782
JW3178	P0ADW6	yhcC	putative Fe-S oxidoreductas	-0.0583918	0.03857262

JW5923	Q46811	ygfK	putative Fe-S subunit oxidor	-0.0001786	0.99220316
JW5283	P76220	ydjY	putative ferredoxin-like lipo	0.00995335	0.50717272
JW0925	P75859	ycbU	putative fimbriae protein	-0.056251	0.02801702
JW0925	P75859	ycbU	putative fimbriae protein	-0.0337992	0.22857332
JW5098	P75748	ybgO	putative fimbrial protein	-0.0285377	0.34415922
JW2331	P76500	yfcQ	putative fimbrial-like adhesi	-0.1596605	0.00180843
JW3111	P42913	yraH	putative fimbrial-like adhesi	-0.1487481	0.30131963
JW0709	P37909	ybgD	putative fimbrial-like adhesi	-0.0945902	0.00101195
JW0924	P75858	ycbT	putative fimbrial-like adhesi	-0.0924977	0.00065467
JW0134	P37018	yadM	putative fimbrial-like adhesi	-0.0753384	0.00179109
JW1496	P77588	ydeQ	putative fimbrial-like adhesi	-0.0543751	0.04324689
JW0137	P37050	yadN	putative fimbrial-like adhesi	-0.0433781	0.00733627
JW5123	P75860	ycbV	putative fimbrial-like adhesi	-0.0357935	0.53157713
JW0131	P31058	yadC	putative fimbrial-like adhesi	-0.0326513	0.10333073
JW2098	P33343	yehD	putative fimbrial-like adhesi	-0.0260646	0.30971363
JW2332	P76501	yfcR	putative fimbrial-like adhesi	-0.0240581	0.6113888
JW0133	P37017	yadL	putative fimbrial-like adhesi	-0.0162096	0.67962038
JW2095	P33340	yehA	putative fimbrial-like adhesi	-0.0144287	0.3938572
JW3011	P39834	ygiL	putative fimbrial-like adhesi	-0.0040404	0.87941971
JW1498	P77789	ydeS	putative fimbrial-like adhesi	0.00288818	0.87546873
JW0132	P37016	yadK	putative fimbrial-like adhesi	0.03669332	0.0808734
JW2330	P76499	yfcP	putative fimbrial-like adhesi	0.04110653	0.3135951
JW2336	P77288	yfcV	putative fimbrial-like adhesi	0.08357046	0.0899878
JW1497	P77294	ydeR	putative fimbrial-like adhesi	0.09194883	0.0005691
JW3114	P43319	yraK	putative fimbrial-like adhesi	0.15475406	0.00864245
JW2318	P15286	flk	putative flagella assembly p	0.01320526	0.4068271
JW1067	P0A6S3	flgI	putative flagellar basal body	-0.0011128	0.98173219
JW1868	P76298	flhA	putative flagellar export por	-0.0009723	0.97595888
JW1911	P0ABY2	fliT	putative flagellar synthesis :	0.07195579	0.15778424
JW5440	Q46907	ygcQ	putative flavoprotein	-0.0618789	0.00753291
JW5441	Q46908	ygcR	putative flavoprotein	0.01632674	0.57637123
JW2477	P77733	focB	putative formate transporte	-0.0035172	0.86719941
JW0468	P52067	fsr	putative fosmidomycin efflu	-0.1783321	0.11778289
JW3333	P45539	frlA	putative fructoselysine trans	0.09024409	0.0002544
JW3868	P32152	frvR	putative frv operon regulato	0.10785083	0.00093667
JW3291	P41443	gspH	putative general secretory p	-0.0660274	0.07541444
JW3293	P45761	gspJ	putative general secretory p	0.14555793	0.0176751
JW5653	P27297	bax	putative glucosaminidase	-0.0456818	0.59343243
JW3031	P60782	ygiH	putative glycerol-3-phospha	-0.0358857	0.08807798
JW3923	P32674	pflD	putative glycine radical dom	-0.0315936	0.74032892
JW2044	P77414	wcaA	putative glycosyl transferase	-0.0195635	0.38115532
JW2040	P71239	wcaE	putative glycosyl transferase	0.01660287	0.20444045
JW2029	P71243	wcaL	putative glycosyl transferase	0.10346894	0.03026393
JW2042	P71237	wcaC	putative glycosyl transferase	0.13448348	0.03973192
JW2035	P32057	wcaI	putative glycosyl transferase	0.26252625	0.0051369

JW3406	P46855	yhhZ	putative Hcp1 family polym	0.00318981	0.9525779
JW1945	P46144	yedJ	putative HD superfamily phc	0.02369253	0.53610538
JW5349	P33348	yehL	putative hexameric AAA+ M	0.00263591	0.89707577
JW0641	P77381	djlB	putative HscC co-chaperone,	0.01897045	0.30048732
JW0958	P19931	hyaE	putative HyaA chaperone	0.00742411	0.75376935
JW5494	P37180	hybB	putative hydrogenase 2 cyto	0.01724669	0.67780612
JW3545	P56256	yiaI	putative hydrogenase, 4Fe-4	-0.0384735	0.15364581
JW2709	Q46891	ygbM	putative hydroxypyruvate isc	-0.0108844	0.73378976
JW2849	Q46814	xdhD	putative hypoxanthine oxida	0.04059429	0.07359263
JW0487	P33668	ybbC	putative immunity protein	0.09288378	0.0002735
JW3568	P0ADK6	yibA	putative immunity protein fi	-0.0701074	0.09299092
JW1452	P31991	ydcD	putative immunity protein fi	-0.0027349	0.89157981
JW3803	P0ADP5	yigM	putative inner membrane E ₂	0.05802743	0.32859553
JW3120	P45468	yraQ	putative inner membrane p ₆	0.0857643	0.28227715
JW5490	Q46841	yghQ	putative inner membrane p ₆	-0.0544279	0.14140635
JW1715	P76208	yniB	putative inner membrane p ₆	-0.109932	0.00024674
JW1814	P64499	yebO	putative inner membrane p ₆	-0.0553416	0.21235627
JW5718	P32700	yjcB	putative inner membrane p ₆	-0.007137	0.76716299
JW0302	P77180	ykgH	putative inner membrane p ₆	-0.0007253	0.97851714
JW0309	P77219	yahC	putative inner membrane p ₆	0.00706816	0.74659157
JW1015	P75910	ycdU	putative inner membrane p ₆	0.02594947	0.39118631
JW0725	P0AAV0	ybgE	putative inner membrane p ₆	-0.0311578	0.11265541
JW2919	P64564	yggT	putative inner membrane p ₆	-0.0362997	0.19855304
JW2295	P39263	yfcC	putative inner membrane tr	-0.1218204	0.00024086
JW3630	P31433	yicH	putative inner membrane-al	-0.0079601	0.69938429
JW3492	P37645	yhjG	putative inner membrane-al	0.03912014	0.09931586
JW5876	P39836	yfeH	putative inorganic ion transp	-0.0012791	0.95652881
JW1211	P39165	ychP	putative invasins	0.02617274	0.51822849
JW2386	P67729	yfeO	putative ion channel protein	0.01755864	0.59004351
JW0655	P0AE78	ybeX	putative ion transport	-0.1587259	0.04316806
JW1446	P76115	yncD	putative iron outer membra	-0.0180917	0.47546796
JW0880	P21367	ycaC	putative isochorismatase fa	0.03166047	0.0702028
JW1169	P76004	ycgM	putative isomerase/hydrola:	-0.0005625	0.99157485
JW5444	P55138	ygcE	putative kinase	-0.061243	0.08715976
JW2087	P76419	yegV	putative kinase	0.01390739	0.66740113
JW5289	P77493	ydjH	putative kinase	0.02305088	0.17688192
JW2147	P33020	yeiI	putative kinase	0.04826466	0.12119491
JW4319	P39398	yjiZ	putative L-galactonate:H ⁺ sy	-0.0038538	0.85437894
JW2240	P76470	yfaV	putative L-rhamnonate tran:	-0.1334424	0.45857982
JW5518	P42626	yhaM	putative L-serine dehydrata:	0.03630154	0.38051644
JW2657	P76630	ygaZ	putative L-valine exporter, n	0.06288763	0.07139218
JW2658	P43667	ygaH	putative L-valine exporter, n	0.06643352	0.00400374
JW5650	P37679	sgbU	putative L-xylulose 5-phosph	-0.0578126	0.09410043
JW3908	P32167	yiiX	putative lipid binding hydrol	0.04306211	0.30672027
JW2018	P37750	wbbJ	putative lipopolysaccharide	-0.032753	0.27548589

JW5682	P0AEE1	dcrB	putative lipoprotein	-0.0927864	0.01263316
JW3781	P0ADN6	yifL	putative lipoprotein	-0.0295788	0.25503869
JW1468	P77519	yddL	putative lipoprotein	-0.0162178	0.81991445
JW2570	P46126	yfiM	putative lipoprotein	-0.0132228	0.61381245
JW0424	P0ADA5	yajG	putative lipoprotein	0.02256363	0.34477023
JW5016	P37056	yaeF	putative lipoprotein	0.02916971	0.2045982
JW5858	P0ADM6	ydX	putative lipoprotein	0.0492979	0.00646638
JW5056	P46122	yajI	putative lipoprotein	0.06868809	0.01383267
JW0217	Q47151	yafL	putative lipoprotein and C4C	-0.0215477	0.47746465
JW2373	O32528	yplI	putative lipoprotein involvec	0.03706881	0.12835192
JW2246	P45565	ais	putative LPS core heptose(II	0.03558236	0.11494188
JW3129	P0ADV5	yhbW	putative luciferase-like mon	0.15833027	0.04008035
JW3475	P37195	yhiF	Putative LuxR family repres	-0.0522496	0.35173071
JW5454	Q46941	yqeH	putative LuxR family transcr	-0.0452779	0.54830121
JW0182	P52096	yaeR	putative lyase	0.07538994	0.00807191
JW5775	P39359	yjhH	putative lyase/synthase	0.02536652	0.28317794
JW4093	P0AAE8	cadB	putative lysine/cadaverine t	0.02063874	0.58720053
JW5165	P25746	hflD	putative lysogenization regu	0.03250452	0.43571801
JW2266	P76482	yfbL	putative M28A family peptic	-0.0495482	0.10487246
JW0993	P75894	ycdI	putative malonic semialdeh	-0.0158503	0.55064992
JW2901	P69824	cmtB	putative mannitol-specific e	0.0422928	0.52843688
JW2900	P69826	cmtA	putative mannitol-specific P	0.01457951	0.28883516
JW1938	P76329	yedP	putative mannosyl-3-phosph	0.0641564	0.0374198
JW3571	P0AFV0	yibH	putative membrane fusion p	-0.0604827	0.00542688
JW0779	P75777	ybhG	putative membrane fusion p	0.014742	0.58103554
JW3454	P37626	yhiI	putative membrane fusion p	0.03414484	0.11545626
JW1636	P76185	ydhJ	putative membrane fusion p	0.05251129	0.24292003
JW0691	P0AAU5	ybfB	putative membrane protein	-0.0356102	0.17964656
JW5354	Q2EES6	yohO	putative membrane protein	-0.0086013	0.8037564
JW3231	P64619	yhdU	putative membrane protein	0.07182595	0.10663189
JW2457	Q2EET2	yfpN	putative membrane protein,	-0.1107354	0.0030112
JW1805	P0AEC0	yoaE	putative membrane protein,	-0.043363	0.47894048
JW4022	P32701	yjcC	putative membrane-anchore	-0.1103427	7.48E-06
JW0817	P75800	yliE	putative membrane-anchore	-0.071009	0.02530965
JW5062	P77473	ylaB	putative membrane-anchore	-0.0150151	0.52852371
JW5174	P75995	ycgG	putative membrane-anchore	0.08124573	0.00020649
JW1804	P76261	yoaD	putative membrane-anchore	0.0015598	0.92293526
JW0818	P75801	yliF	putative membrane-anchore	-0.0393998	0.19550751
JW5832	P76330	yedQ	putative membrane-anchore	0.01549304	0.42039602
JW2585	P46139	yfiN	putative membrane-anchore	0.05267193	0.01487938
JW2261	P0AEH5	elaB	putative membrane-anchore	-0.0787808	0.0435085
JW2647	P0ADQ7	ygaM	putative membrane-anchore	0.09259385	0.0003785
JW1376	P52645	ydbH	putative membrane-anchore	0.03259625	0.28563444
JW2935	Q46832	yghD	putative membrane-anchore	-0.1545796	0.00102508
JW5825	P76147	yneF	putative membrane-bound c	-0.179097	0.17953482

JW5018	P0AEZ7	mltD	putative membrane-bound l	0.07798416	0.00560012
JW5515	P42601	alx	putative membrane-bound r	0.001223	0.95534237
JW0910	P75849	ycbL	putative metal-binding enzy	-0.1061017	0.30132095
JW5309	P52007	yecM	putative metal-binding enzy	-0.0880338	0.05185049
JW0316	P77554	yahJ	putative metallo-dependent	0.16982818	0.01523017
JW1419	P76097	ydcJ	putative metalloenzyme	0.01192202	0.71836051
JW4268	P39367	yjhP	putative methyltransferase	-0.1242676	0.00750122
JW2565	P0AGJ5	yfiF	putative methyltransferase	0.00715709	0.79191946
JW4366	P37005	yjtD	putative methyltransferase	0.24876662	0.01931277
JW1758	P38055	ydjE	putative MFS sugar transpo	-0.1396655	0.03718696
JW5290	P76230	ydjK	putative MFS sugar transpo	-0.02037	0.43072184
JW5845	Q46909	ygcS	putative MFS sugar transpo	0.01224593	0.66136672
JW0044	P31679	yaaU	putative MFS sugar transpo	0.17366024	0.28683542
JW0881	P21503	ycaD	putative MFS transporter, ir	-0.2113019	0.10242203
JW1780	P76242	yeaN	putative MFS transporter, ir	-0.0147745	0.53857861
JW1649	P77389	ydhP	putative MFS transporter, ir	0.02090699	0.35388258
JW2746	P77031	yqcE	putative MFS transporter, ir	0.08664423	0.00018499
JW5768	P39352	yjhB	putative MFS transporter, r	-0.0012156	0.96503937
JW5274	P76198	ydiN	putative MFS transporter, r	0.04896399	0.19240792
JW3491	P37643	yhjE	putative MFS transporter; r	0.00342484	0.88825647
JW5670	P0AFV2	yhiD	putative Mg(2+) transport A	0.10545113	0.18649796
JW5830	P76264	yebN	putative Mn(2+) efflux pum	-0.0894141	0.01922216
JW1657	P0ACX3	ydhR	putative monooxygenase	-0.0057087	0.87753213
JW1965	P76352	yeeO	putative multidrug exporter,	0.09513736	0.00278418
JW5061	P0AAG5	mdlB	putative multidrug ABC tran	-0.0161356	0.52441357
JW0438	P77265	mdlA	putative multidrug ABC tran	0.04927702	0.03556053
JW5242	P31826	yddA	putative multidrug ABC tran	0.00673659	0.84693734
JW2364	P52600	emrY	putative multidrug efflux sy	-0.0890003	0.32150932
JW3733	P31474	hsrA	putative multidrug or homo	-0.1364881	0.09419057
JW3192	P0A761	nanE	putative N-acetylmannosarr	0.01550169	0.45141823
JW3980	P0AF43	yjbB	putative Na ⁺ /Pi-cotransport	0.11826522	0.00107307
JW1535	P77260	ydfI	putative NAD-dependent D-ri	0.00155788	0.96178148
JW2160	P33029	yeiQ	putative NAD-dependent D-ri	0.08874453	0.02147387
JW2301	P77775	yfch	putative NAD-dependent nu	-0.0944417	0.07308971
JW5116	P75822	ybjT	putative NAD-dependent oxi	0.01260333	0.54947259
JW0506	Q47208	fdrA	putative NAD(P)-binding acy	0.02763341	0.04649904
JW5019	Q47679	yafV	putative NAD(P)-binding C-ri	0.01391878	0.53964865
JW0312	P77187	yahF	putative NAD(P)-binding suc	0.05803173	0.06817306
JW3058	P42599	ygjR	putative NAD(P)-dependent	0.00480583	0.74552259
JW2870	P52037	ygfF	putative NAD(P)-dependent	-0.0052995	0.81610428
JW0884	P43340	ycaK	putative NAD(P)H-depender	-0.0808522	0.08598027
JW5819	P75821	ybjS	putative NAD(P)H-depender	0.02981927	0.30203429
JW1308	P77503	ycjS	putative NADH-binding oxid	-0.0076196	0.84057544
JW2802	P0A9T4	tas	putative NADP(H)-depender	0.02053292	0.57719315
JW2460	P64429	ypfJ	putative neutral zinc metall	0.00141411	0.91233565

JW3449	P28911	yhhH	putative NTF2 fold immunit	-0.0594074	0.00760508
JW2151	P33024	yeiM	putative nucleoside transpo	-0.0076745	0.66278818
JW4265	P39364	sgcQ	putative nucleoside triphosp	0.06560685	0.13039244
JW5528	P45469	yraR	putative nucleoside-diphosp	0.00843333	0.78496324
JW2296	P65556	yfcD	putative NUDIX hydrolase	-0.1432556	0.00917797
JW0966	P0A932	yccZ	putative O-antigen capsule	0.07879354	0.0059091
JW0968	P75883	ymcB	putative O-antigen capsule	-0.072007	0.04621196
JW0967	P75882	ymcA	putative O-antigen capsule	-0.0117945	0.6588092
JW0860	P75828	ybjD	putative OLD family ATP-de	-0.0163444	0.57257525
JW0521	P77468	sfmD	putative outer membrane e	-0.0567586	0.02566928
JW0923	P75857	ycbS	putative outer membrane fi	0.01794147	0.60488807
JW3183	P45420	yhcD	putative outer membrane fi	-0.0242407	0.53754146
JW1607	Q47706	uidC	putative outer membrane pi	0.08562043	0.00254711
JW2399	P45564	yfeN	putative outer membrane pi	-0.0816818	0.01841876
JW3113	P42915	yraJ	putative outer membrane pi	-0.0284978	0.29483495
JW3556	P37681	yaT	putative outer membrane pi	0.01082327	0.66981629
JW5099	P75750	ybgQ	putative outer membrane pi	0.04680955	0.60017226
JW2096	P33341	yehB	putative outer membrane pi	0.05935472	0.12574359
JW3235	P64622	yhdV	putative outer membrane pi	0.11589843	0.00045489
JW0192	P69411	rscF	putative outer membrane pi	0.20898133	0.0274235
JW2539	P0AD44	yfhG	putative outer membrane pi	0.06378634	0.18939852
JW0135	P33129	htrE	putative outer membrane u	0.05009339	0.36539218
JW2848	P64557	ygfM	putative oxidoreductase	-0.0558382	0.14598418
JW2736	Q46904	ygcN	putative oxidoreductase	-0.0508337	0.00916931
JW0042	P68644	fixC	putative oxidoreductase	-0.0490017	0.03032082
JW1055	P75931	mviM	putative oxidoreductase	-0.0329864	0.14213479
JW3459	P37631	yhiN	putative oxidoreductase	-0.010631	0.78716016
JW2125	P33368	yohF	putative oxidoreductase	-0.0060029	0.76197906
JW1689	P77337	ydiS	putative oxidoreductase	-0.0048594	0.84926432
JW1495	P77561	ydeP	putative oxidoreductase	0.00101376	0.90938368
JW5265	P77376	ydgJ	putative oxidoreductase	0.00970564	0.70875662
JW2480	P76569	yfgD	putative oxidoreductase	0.01638277	0.43516646
JW1639	P76187	ydhF	putative oxidoreductase	0.02365186	0.20595332
JW2972	P0AG84	yghA	putative oxidoreductase	0.04862665	0.16697751
JW1754	P0ACY1	ydjA	putative oxidoreductase	0.05203435	0.23300387
JW5200	P76035	yciW	putative oxidoreductase	0.15721753	5.30E-05
JW3403	P46853	yhhX	putative oxidoreductase	-0.0207634	0.08856744
JW5272	P76192	ydhV	putative oxidoreductase sub	0.001236	0.95829703
JW5469	Q46820	ygfT	putative oxidoreductase, Fe	0.03026037	0.49488602
JW2452	P37127	aegA	putative oxidoreductase, Fe	-0.1646562	0.09178184
JW2445	P76556	eutP	putative P-loop NTPase eth	-0.0010418	0.9353652
JW2895	P11664	yggC	putative PanK family P-loop	-0.0970449	0.48217854
JW5703	P64624	yheO	putative PAS domain-contai	0.06566589	0.05505167
JW1222	P0AFR0	rssA	putative patatin-like family	-0.0664904	0.02925855
JW4340	P39407	yjjU	putative patatin-like family	0.06497542	0.02089353

JW2840	P65807	ygeY	putative peptidase	-0.1932567	0.00964714
JW0938	P75867	ycbZ	putative peptidase	-0.0612527	0.11701067
JW1431	P76104	ydcP	putative peptidase	0.01908069	0.44110628
JW1590	P76176	ydgD	putative peptidase	0.050025	0.11689803
JW2066	P76403	yegQ	putative peptidase	0.08217468	0.07971535
JW3869	P32153	frvX	putative peptidase	0.09202449	0.01376894
JW3213	P0AGG8	tldD	putative peptidase	0.10361017	0.17730133
JW0892	P43674	ycaL	putative peptidase-related c	0.0121016	0.60228118
JW3182	P28722	yhcA	putative periplasmic chaper	0.02419042	0.26567128
JW2584	P64548	yfiR	putative periplasmic inhibito	-0.1375249	0.03771657
JW3495	P37648	yhjJ	putative periplasmic M16 fa	-0.0326165	0.54916234
JW1489	P31828	pqqL	putative periplasmic M16 fa	-0.3705759	0.00948121
JW0136	P33128	ecpD	putative periplasmic pilin ch	-0.0506828	0.06693408
JW5124	P40876	ycbF	putative periplasmic pilin ch	-0.017288	0.47479632
JW0922	P75856	ycbR	putative periplasmic pilin ch	-0.0167738	0.55214006
JW2333	P77599	yfcS	putative periplasmic pilin ch	-0.0127241	0.52035459
JW2097	P33342	yehC	putative periplasmic pilin ch	-0.0108586	0.61434909
JW5508	P77616	yqiH	putative periplasmic pilin ch	-0.0003972	0.98809608
JW0707	P75749	ybgP	putative periplasmic pilin ch	0.00601228	0.87911768
JW3112	P42914	yral	putative periplasmic pilin ch	0.06451145	0.06524627
JW0520	P77249	sfmC	putative periplasmic pilus cl	0.01026554	0.80827578
JW0736	P0AAV6	ybgS	putative periplasmic proteir	-0.0452156	0.0762374
JW3050	P42591	ygjJ	putative periplasmic proteir	-0.0341744	0.40582917
JW5965	Q2M7X4	yicS	putative periplasmic proteir	0.04210155	0.074437
JW1416	P0ACW4	ydcA	putative periplasmic proteir	0.05315494	0.01958436
JW4360	P0AE91	creA	putative periplasmic proteir	0.10562991	4.28E-05
JW1408	P76093	ynbD	putative phosphatase inner	0.02058781	0.31648002
JW5156	P27247	plsX	putative phosphate acyltran	0.0034861	0.68254554
JW0976	P0AC92	gnsA	putative phosphatidylethanc	-0.0813284	0.05287968
JW3318	P0AEX5	prkB	putative phosphoribulokinas	-0.0389767	0.12540975
JW4264	P39363	sgcA	putative phosphotransferase	0.10482755	0.00381597
JW0356	P71311	yaiS	putative PIG-L family deace	-0.0172188	0.59962432
JW2917	P52052	yggR	putative PilT family AAA+ A	0.03434987	0.27934827
JW2022	P37746	rfbX	putative polisoprenol-linked	0.0187216	0.74702154
JW5645	P37691	yibQ	putative polysaccharide dea	0.15867701	0.00697995
JW0126	P31666	yadE	putative polysaccharide dea	-0.0886784	0.00271893
JW0104	P36647	ppdD	putative prepilin peptidase-	0.00234571	0.93550075
JW5451	P08371	ppdB	putative prepilin peptidase-	-0.2421545	0.00082636
JW2791	P08372	ppdC	putative prepilin peptidase-	0.02070003	0.44338262
JW2794	P33554	ppdA	putative prepilin peptidase-	0.05568438	0.10466731
JW2475	P77453	hyfJ	putative processing elemen	0.02691142	0.44460449
JW4348	P39410	yjjJ	putative protein kinase	0.07203571	0.08440685
JW3774	P0ACB7	hemY	putative protoheme IX synt	0.0236799	0.29096118
JW0752	P0AAV8	ybhH	putative PrpF family isomer	0.00476181	0.79572279
JW0125	P36881	yadI	putative PTS Enzyme IIA	-0.0348212	0.05405472

JW5562	P32154	frvB	putative PTS enzyme, IIB co	0.02698986	0.456256
JW5555	P32670	ptsA	putative PTS enzyme: Hpr, e	-0.0159856	0.5629855
JW2380	P77439	ypdD	putative PTS enzyme: Hpr, e	-0.0546876	0.1262231
JW4266	P39365	sgcC	putative PTS system EIIIC pe	0.10942207	6.72E-05
JW3344	P45550	yhfX	putative pyridoxal 5'-phosph	0.00274539	0.87588448
JW0807	P75793	ybiW	putative pyruvate formate ly	0.08717893	0.00173634
JW0808	P75794	ybiY	putative pyruvate formate ly	-0.057898	0.04647227
JW4342	P39409	yjjW	putative pyruvate formate ly	0.13276892	0.17009208
JW5850	P42619	yqjF	putative quinol oxidase subu	0.01465948	0.65931923
JW5295	P0AEB7	yoaB	putative reactive intermedi	0.07619437	0.02334101
JW0994	P75895	rarA	putative reactive intermedi	-0.1506639	0.07370569
JW2027	P0AAB6	galF	putative regulatory subunit	-0.0052577	0.82004383
JW3586	P0AG27	yibN	putative rhodanese-related	-0.3068007	0.00015989
JW1042	P24188	yceA	putative rhodanese-related	-0.0728045	0.20540527
JW1384	P76078	paaB	putative ring 1,2-phenylacet	0.01138171	0.90128764
JW5196	P0AFR4	yciO	putative RNA binding protei	0.03717314	0.31803841
JW1249	P21363	yciE	putative rubrerythrin/ferriti	-0.0362789	0.04186484
JW1250	P21362	yciF	putative rubrerythrin/ferriti	-0.0047388	0.83745878
JW0904	P36566	smtA	putative S-adenosyl-L-methi	0.01923201	0.18251291
JW0200	P30866	yafE	putative S-adenosyl-L-methi	0.02643438	0.02829882
JW0203	P75672	yafS	putative S-adenosyl-L-methi	0.09418659	0.00879603
JW5492	Q46845	yghU	putative S-transferase	-0.0719663	0.02812177
JW3073	P42620	yqjG	putative S-transferase	-0.0343519	0.47319372
JW2518	P77538	yfhR	putative S9 family prolyl olig	-0.007245	0.42998518
JW5443	P76633	ygcW	putative SDR family oxidore	0.05311544	0.09418009
JW5925	P0CK95	yghJ	putative secreted and surfac	-0.067223	0.07052303
JW0693	P28915	ybfC	putative secreted protein	0.00978269	0.43173955
JW1579	P77374	ynfE	putative selenate reductase	-0.0173428	0.36841389
JW5464	Q46809	yqeC	putative selenium-dependen	-0.0136744	0.67440424
JW2316	P08390	usg	putative semialdehyde dehy	0.02209122	0.28798945
JW1951	P76339	yedV	putative sensory kinase in tv	0.03403782	0.1489824
JW3773	P25549	aslA	putative Ser-type periplasm	-0.0557629	0.09509389
JW5243	P77318	ydeN	putative Ser-type periplasm	-0.0264443	0.37325408
JW2767	P0AAD6	sdaC	putative serine transporter	0.10219099	0.01371067
JW3041	Q46871	yqjH	putative siderophore interac	0.00174286	0.96177282
JW2837	Q46802	ygeV	putative sigma-54-interacti	0.01384363	0.65245951
JW3655	P31448	yidK	putative SSF family symport	0.05104235	0.0315887
JW2531	P77509	yphE	putative sugar ABC transpor	-0.0060719	0.86548188
JW5752	Q6BEX0	ytfR	putative sugar ABC transpor	0.02165993	0.24340793
JW1305	P77716	ycjP	putative sugar ABC transpor	-0.073939	0.06044424
JW5754	P37772	yjfF	putative sugar ABC transpor	0.03142149	0.1451952
JW5753	P39328	ytfT	putative sugar ABC transpor	0.06224997	0.05939452
JW2530	P77315	yphD	putative sugar ABC transpor	0.09856838	0.00110608
JW1304	P0AFR7	ycjO	putative sugar ABC transpor	0.1201285	0.29843493
JW3844	P32134	yihM	putative sugar phosphate is	-0.0213723	0.54246182

JW3849	P32138	yihQ	putative sulpholipid alpha-g	0.00255053	0.91601598
JW5852	P32136	yihO	putative sulphoquinovose in	0.02275242	0.36112742
JW3850	P32139	yihR	putative sulphoquinovose m	-0.0725983	0.00212785
JW5368	P0AB85	yojL	putative thiamine-synthetic	0.10418309	0.00030619
JW5563	P0AFU6	yiiF	putative thymol sensitivity p	0.34706028	0.01541678
JW5202	P76044	ycjR	putative TIM alpha/beta bar	0.09614469	0.03901057
JW1490	P31827	yddb	putative TonB-dependent ou	-0.0472719	0.19379165
JW3370	P46837	yhgF	putative transcriptional acc	-0.0367405	0.32713751
JW5792	P39399	yjjM	putative transcriptional acti	-0.0489689	0.08665467
JW4175	P39187	ytfJ	putative transcriptional regu	-0.2524648	1.82E-05
JW4329	P0ADD7	yjjQ	putative transcriptional regu	-0.1857018	0.24933499
JW3188	P45422	yhcF	putative transcriptional regu	-0.0339	0.02618199
JW5608	P31475	yieP	putative transcriptional regu	-0.0017648	0.94319524
JW2815	Q46942	yqel	putative transcriptional regu	0.00435916	0.91601822
JW0366	P0AAP5	yaiV	putative transcriptional regu	0.01333773	0.65671209
JW2820	P76639	ygeH	putative transcriptional regu	0.01706017	0.22441849
JW5733	P0ACU7	yjdC	putative transcriptional regu	0.23745563	0.19313273
JW5567	P32144	yihW	putative transcriptional regu	-0.0311729	0.1580479
JW5031	P71301	ykgK	putative transcriptional regu	0.01727508	0.38991264
JW5512	P42590	ygiI	putative transporter	-0.078707	0.08827991
JW2289	P0AFU2	yfbS	putative transporter	-0.0589427	0.05696225
JW1527	P31126	ydeE	putative transporter	-0.0533051	0.00643825
JW5939	P31435	yicJ	putative transporter	-0.0413053	0.07930722
JW0831	P60869	ybjL	putative transporter	-0.035689	0.51338732
JW5938	P0ADL1	yicM	putative transporter	-0.0213132	0.39476846
JW3196	P45428	dcuD	putative transporter	-0.0172687	0.69187777
JW3662	P60872	yidE	putative transporter	-0.0106802	0.62269925
JW5293	P0ABD1	yeaV	putative transporter	-0.0024674	0.91246255
JW2369	P0AA49	yfdV	putative transporter	0.00166209	0.90662702
JW0858	P75826	ybjE	putative transporter	0.00779418	0.84274105
JW0039	P31553	caiT	putative transporter	0.01462494	0.8119343
JW5739	P39282	yjeM	putative transporter	0.01844875	0.50069885
JW5059	P77726	yajR	putative transporter	0.04147807	0.02381398
JW5299	P76269	yebQ	putative transporter	0.04780816	0.01358442
JW2813	P63340	yqeG	putative transporter	0.05670342	0.30515795
JW3508	P37660	yhjV	putative transporter	0.06429026	0.15556419
JW2710	Q46892	ygbN	putative transporter	0.07550271	0.13038126
JW3327	P60778	tsgA	putative transporter	0.07557436	0.12949486
JW5519	P42628	yhaO	putative transporter	0.07622061	0.01137921
JW0006	P30143	yaaJ	putative transporter	0.09008959	0.00023434
JW1718	P77529	ydjN	putative transporter	0.11262705	0.09099185
JW5119	P75835	ycaM	putative transporter	0.13669505	0.02478943
JW4258	P39357	yjhF	putative transporter	0.14445933	0.14660833
JW1990	P33011	yeeA	putative transporter, FUSC f	0.02398526	0.19626355
JW5128	P75870	yccS	putative transporter, FUSC s	0.00830468	0.68263414

JW5701	P45537	yhfK	putative transporter, FUSC s	0.03196612	0.5296651
JW3451	P28912	yhhI	putative transposase	-0.0400797	0.13774492
JW3045	P42589	ygjH	putative tRNA binding prote	-0.0140279	0.76792623
JW1994	P33014	yeeD	putative TusA family sulfurt	0.04707234	0.21698788
JW1915	P0AA31	yedF	putative TusA family sulfurt	0.06610638	0.00818792
JW2478	P0AF19	yfgO	putative UPF0118 family inr	0.00790487	0.53293261
JW5158	P0A8E1	ycfP	putative UPF0227 family es	0.00931511	0.67485304
JW0501	P77328	ybbY	putative uracil/xanthine tra	0.00085772	0.97641411
JW3775	P09127	hemX	putative uroporphyrinogen II	-0.0430073	0.41497483
JW5612	P31471	yieL	putative xylanase	-0.0323332	0.28800211
JW1492	P76134	ydeM	putative YdeN-specific sulfa	-0.0305536	0.59579048
JW5294	P0ABR7	yeaW	putative YeaWX dioxygenas	0.05043684	0.05725752
JW1792	P76254	yeaX	putative YeaWX dioxygenas	0.03166296	0.28109308
JW5477	P52048	yggP	putative Zn-binding dehydro	-0.0496505	0.00220056
JW1572	P38105	rspB	putative Zn-dependent NAD	0.00895609	0.75693178
JW1306	P76043	ycjQ	putative Zn-dependent NAD	0.01726017	0.40677206
JW5842	P77360	yphC	putative Zn-dependent NAD	0.03400861	0.18619849
JW1765	P77539	ydjL	putative Zn-dependent NAD	0.09598055	0.00959021
JW1763	P77280	ydjJ	putative Zn-dependent NAD	0.10292572	0.02458303
JW1336	P64423	ydaN	putative Zn(II) transporter	0.03480134	0.18222907
JW5818	P31134	potG	putrescine ABC transporter ,	0.01547179	0.71250401
JW0838	P31133	potF	putrescine ABC transporter	-0.0625101	0.0001853
JW0840	P31135	potH	putrescine ABC transporter	0.07720669	0.13729742
JW0841	P0AFL1	potI	putrescine ABC transporter	0.16760305	0.17321909
JW1289	P76037	puuP	putrescine importer	-0.0036552	0.94816788
JW5330	P0AA47	yeeF	putrescine importer, low afl	0.03645784	0.07885964
JW5510	P42588	ygjG	putrescine:2-oxoglutaric aci	-0.0168403	0.53988695
JW0679	P0AAF1	potE	putrescine/proton symporte	-0.0681425	0.07904014
JW4205	P0AD83	pyrL	pyrBI operon leader peptide	-0.2199883	0.04526419
JW1595	P07001	pntA	pyridine nucleotide transhyc	-0.0614139	0.03355609
JW1594	P0AB67	pntB	pyridine nucleotide transhyc	0.03432859	0.3994815
JW5551	P27306	sthA	pyridine nucleotide transhyc	-0.0684333	0.00484751
JW0749	P21829	ybhA	pyridoxal phosphate (PLP) pl	0.06951983	0.01074118
JW5854	P27848	yigL	pyridoxal phosphate phosph	0.16984126	0.02000189
JW2411	P40191	pdxK	pyridoxal-pyridoxamine kina	0.03511849	0.20461869
JW1628	P77150	pdxY	pyridoxamine kinase	0.04371006	0.2923123
JW1403	P25906	ydbC	pyridoxine 4-dehydrogenase	0.06168633	0.23763665
JW1630	P0AF17	pdxH	pyridoxine 5'-phosphate oxi	-0.18665	0.02347154
JW2548	P0A794	pdxJ	pyridoxine 5'-phosphate syn	0.06618113	0.1345236
JW0997	P75898	ycdM	pyrimidine oxygenase, FMN	-0.0211073	0.33750403
JW5137	P75892	ycdG	pyrimidine permease	0.02804578	0.10285522
JW0382	P0C037	yaiE	pyrimidine/purine nucleosid	-0.0293939	0.28411023
JW2766	P0ADR8	ygdH	pyrimidine/purine nucleotid	0.0349055	0.03140738
JW0377	P0A9L8	proC	pyrroline-5-carboxylate redu	0.37481248	0.00045712
JW0109	P0ACL9	pdhR	pyruvate dehydrogenase cor	0.02466777	0.57383331

JW0110	P0AFG8	aceE	pyruvate dehydrogenase, de	0.03639203	0.21345702
JW0111	P06959	aceF	pyruvate dehydrogenase, dil	-0.0775267	0.01398032
JW0855	P07003	poxB	pyruvate dehydrogenase, thi	0.04821455	0.09934985
JW0885	P0A9N4	pflA	pyruvate formate-lyase 1-ac	-0.3423231	5.77E-06
JW5522	P42632	tdcE	pyruvate formate-lyase 4/2-	0.07220738	0.03716549
JW1666	P0AD61	pykF	pyruvate kinase I	0.01000625	0.91709201
JW1843	P21599	pykA	pyruvate kinase II	-0.036947	0.59013333
JW1372	P52647	ydbK	pyruvate-flavodoxin oxidore	-0.0103038	0.6843176
JW5791	P39396	yjiY	pyruvate/H ⁺ symporter	0.04552455	0.277385
JW1566	P09557	dicB	Qin prophage; cell division i	0.08143546	0.12500578
JW1550	P0A976	cspF	Qin prophage; cold shock pr	-0.0713974	0.09053566
JW1549	P36995	cspB	Qin prophage; cold shock pr	-0.0242538	0.126759
JW5254	P76157	ynfN	Qin prophage; cold shock-in	-0.0305358	0.17624926
JW1561	P06965	dicC	Qin prophage; DNA-binding	0.22093275	0.01511577
JW1547	P76160	ydfR	Qin prophage; DUF1327 fan	0.00819326	0.65111399
JW1563	P0ACW8	ydfA	Qin prophage; DUF1391 fan	8.03E-05	0.9952303
JW5252	P76156	ydfO	Qin prophage; DUF1398 fan	0.05890027	0.16799738
JW1567	P29010	ydfD	Qin prophage; DUF1482 fan	-0.0131361	0.55107055
JW5909	P76162	ydfU	Qin prophage; DUF968 fami	0.05633078	0.00402836
JW5253	P77695	gnsB	Qin prophage; multicopy sup	-0.0034927	0.91358447
JW1568	Q47138	ydfE	Qin prophage; pseudogene	-0.0077699	0.7687078
JW1551	P76161	ydfT	Qin prophage; putative antit	0.09869991	0.0006364
JW1546	P76159	ydfQ	Qin prophage; putative lyso	0.02396325	0.24523476
JW5255	P77237	essQ	Qin prophage; putative S lys	-0.0149204	0.61611166
JW1540	P77515	stfQ	Qin prophage; putative side	0.05024358	0.0222893
JW1538	P77170	pinQ	Qin prophage; putative site-	0.00757982	0.70025899
JW1539	P76155	tfaQ	Qin prophage; putative tail f	-0.0757266	0.02904037
JW1545	P76158	ydfP	Qin prophage; Rz-like protei	-0.0071957	0.73738214
JW1554	P0ACG6	hokD	Qin prophage; small toxic pr	-0.1910085	0.00669464
JW1555	P0C077	relE	Qin prophage; toxin of the R	0.02670047	0.23296047
JW1553	P07010	rem	Qin prophage; uncharacteriz	-0.0385285	0.4730115
JW1565	P21418	ydfC	Qin prophage; uncharacteriz	-0.0188926	0.41241228
JW1557	P76163	ydfV	Qin prophage; uncharacteriz	0.04314314	0.08194049
JW1558	P77609	flxA	Qin prophage; uncharacteriz	0.11941612	0.00878472
JW5931	P27859	tatD	quality control of Tat-export	-0.011027	0.78024968
JW3402	P46852	yhhW	quercetinase activity in vitrc	-0.029411	0.01653708
JW1682	NA	ydiB	quininate/shikimate 5-dehydr	-0.0162907	0.68848871
JW2190	P0ABL5	napC	quinol dehydrogenase, elect	0.12871818	0.17277022
JW2997	P0ADU2	ygiN	quinol monooxygenase	-0.101548	0.01650314
JW0105	P30011	nadC	quinolinate phosphoribosylt	0.42573367	5.84E-10
JW2558	P10902	nadB	quinolinate synthase, L-aspæ	0.3788206	2.61E-06
JW0733	P11458	nadA	quinolinate synthase, subun	0.25202458	8.73E-05
JW4011	P28304	qor	quinone oxidoreductase, NA	-0.0081262	0.53121933
JW2993	P52076	qseB	quorum sensing DNA-bindin	-0.1000081	0.00227916
JW2994	P40719	qseC	quorum sensing sensory his	-0.0205239	0.18611507

JW1901	P07026	sdiA	quorum-sensing transcriptic	0.05633952	0.00191145
JW1359	P76068	ynaK	Rac prophage; conserved pr	-0.0328938	0.1100369
JW5207	P76057	ydaQ	Rac prophage; conserved pr	-0.0321533	0.47100804
JW1354	P76065	ydaU	Rac prophage; conserved pr	0.00316786	0.83086923
JW1344	P15032	recE	Rac prophage; exonuclease	0.08575252	0.04322974
JW1339	P76056	intR	Rac prophage; integrase	-0.0251605	0.26257597
JW1358	P23849	trkG	Rac prophage; potassium tr	-0.0990695	0.07809933
JW5211	P76066	ydaW	Rac prophage; pseudogene,	-0.0377674	0.08652303
JW1361	P77658	ynaA	Rac prophage; pseudogene,	-0.0284639	0.26353229
JW1355	P77546	ydaV	Rac prophage; putative DNA	0.06153577	0.33591171
JW1352	P76063	ydaS	Rac prophage; putative DNA	0.21636087	4.93E-06
JW5213	P58042	rzoR	Rac prophage; putative lipo	0.08747016	0.01140867
JW1368	P0ADI0	pinR	Rac prophage; putative site-	-0.074132	0.08077887
JW1367	P77163	tfaR	Rac prophage; putative tail	0.03999898	0.1028892
JW1366	P76072	stfR	Rac prophage; putative tail	0.02869916	0.10340435
JW1343	P33228	recT	Rac prophage; recombinatic	0.24701791	0.02214644
JW5208	P33229	lar	Rac prophage; restriction all	-0.0412845	0.12480896
JW1345	P15033	racC	Rac prophage; uncharacteri	-0.025181	0.44579271
JW1353	P76064	ydaT	Rac prophage; uncharacteri	-0.0234389	0.19247611
JW2608	P52126	yfjK	radiation resistance protein	0.06985384	0.04912878
JW5501	Q46861	ygiQ	Radical SAM superfamily pr	-0.1169011	0.05249493
JW0218	Q47152	yafM	RAYT REP element-mobilizi	-0.0478677	0.18519709
JW1152	P75992	ymgA	RcsB connector protein for r	0.00855018	0.66601586
JW1151	P75991	ycgZ	RcsB connector protein for r	0.02402485	0.46900398
JW1153	P75993	ymgB	RcsB connector protein for r	0.04876631	0.11300701
JW2435	P76551	eutA	reactivating factor for ethar	-0.0701003	0.03462438
JW5038	P75685	ykgB	reactive chlorine species (R	0.03800411	0.0659804
JW5039	P75687	ykgI	reactive chlorine species (R	0.00937985	0.42343084
JW0298	P77379	ykgD	reactive chlorine species (R	-0.0583189	0.00823341
JW5040	P77212	ykgC	reactive chlorine stress spec	0.06392866	0.01867887
JW5416	P05824	recN	recombination and repair pr	-0.116335	0.20956868
JW0875	P0AAZ4	ycaJ	recombination intermediate	0.12408486	0.00251347
JW1018	P75915	ycdY	redox enzyme maturation p	-0.0180789	0.40214557
JW4024	P0ACS2	soxR	redox-sensitive transcrip	0.0624052	0.01302868
JW5097	P75747	abrB	regulator of aidB expressio	0.00808689	0.82877839
JW0579	P26266	fepE	regulator of length of O-ant	-0.0951842	0.02605869
JW5836	P76372	cld	regulator of length of O-ant	0.05405395	0.00045947
JW0602	P0AFW4	rnk	regulator of nucleoside diph	0.02224879	0.44382907
JW2695	P0AEV4	hycA	regulator of the transcrip	0.04617768	0.1138899
JW0348	P0AAP3	frmR	regulator protein that repre	-0.0097893	0.54587591
JW1815	P64512	yobG	regulatory peptide for PhoP	-0.0366169	0.21290957
JW0865	P0A8Q6	clpS	regulatory protein for ClpA s	-0.016713	0.6504921
JW1297	P0AFM6	pspA	regulatory protein for phage	-0.1176227	0.01695897
JW2668	P33596	recX	regulatory protein for RecA	-0.2204261	0.03741944
JW2537	P0A9Z1	glnB	regulatory protein P-II for gl	0.02586015	0.79611625

JW0932	P43672	uup	replication regulatory ABC-F	0.05140106	0.16823219
JW5159	P75952	ycfQ	repressor for bhsA(ycfR)	-0.1302528	0.13095785
JW2420	P77245	yfeT	repressor for murPQ, MurN/	0.01962336	0.39061898
JW1292	P0A9U6	puuR	repressor for the divergent p	-0.0821044	0.02000714
JW0820	P0AAY1	yliH	repressor of biofilm formati	-0.0321835	0.38645546
JW1149	P75989	ycgE	repressor of blue light-respc	-0.0436668	0.13215879
JW1724	P17410	chbR	repressor of chb operon for	-0.008919	0.59604394
JW2164	P76446	rtn	resistance protein for phage	0.09083302	0.05713429
JW1095	P00393	ndh	respiratory NADH dehydroge	-0.0550545	0.00296496
JW2378	P0AE39	ypdB	response regulator activatin	0.02135042	0.40016383
JW5322	P76340	yedW	response regulator family p	0.00319557	0.83164394
JW5073	P0AEL8	fimZ	response regulator family p	0.1138735	0.01104509
JW4364	P0A9Q1	arcA	response regulator in two-c	0.11832508	0.1978893
JW2064	P69228	baeR	response regulator in two-c	0.07098477	0.03038577
JW1899	P0AED5	uvrY	response regulator in two-c	0.02864298	0.4486024
JW4074	P30843	basR	response regulator in two-c	0.03242236	0.13391229
JW0612	P0AEF4	citB	response regulator in two-c	-0.0070696	0.7523159
JW3883	P0AE88	cpxR	response regulator in two-c	-0.0319401	0.0668303
JW4361	P08368	creB	response regulator in two-c	-0.0779847	0.00012941
JW0560	P0ACZ8	cusR	response regulator in two-c	0.00085008	0.95795946
JW4085	P0AD01	dcuR	response regulator in two-c	-0.0109941	0.66270944
JW3368	P0AA16	ompR	response regulator in two-c	-0.0032384	0.87915069
JW2366	P0ACZ4	evgA	response regulator in two-c	-0.0551988	0.05409732
JW5096	P21866	kdpE	response regulator in two-c	-0.0904066	0.00267736
JW2181	P31802	narP	response regulator in two-c	0.006173	0.78276472
JW1212	P0AF28	narL	response regulator in two-c	0.01676197	0.51889635
JW1116	P23836	phoP	response regulator in two-c	0.01372839	0.49790811
JW0389	P0AFJ5	phoB	response regulator in two-c	-0.0424277	0.21027048
JW2205	P0DMC7	rcsB	response regulator in two-c	0.05752314	0.02273886
JW0980	P38684	torR	response regulator in two-c	0.04434276	0.21535467
JW3644	P0AGA6	uhpA	response regulator in two-c	0.04918101	0.06233808
JW5352	P0AFT5	yehT	response regulator inducing	-0.0511266	0.04086518
JW5387	Q2EES9	torI	response regulator inhibitor	0.00135455	0.96342488
JW1600	P52108	rstA	response regulator of RstAB	0.08470992	0.00171244
JW2538	P0AFU4	yfhA	response regulator regulatir	0.07005687	0.16376997
JW5404	P0AFZ1	sseB	rhodanase-like enzyme, sulf	0.08536765	0.00798195
JW5687	P09391	glpG	rhomboid intramembrane si	-0.0437123	0.01973575
JW0486	P16919	rhsD	Rhs protein with DUF4329 f	-0.0009619	0.96419516
JW5679	P16917	rhsB	Rhs protein with DUF4329 f	0.1703525	3.4E-07
JW3566	P16916	rhsA	Rhs protein with putative to	-0.0918538	0.41792963
JW0689	P16918	rhsC	Rhs protein with putative to	-0.0503221	0.24421027
JW3731	P0A9J6	rbsK	ribokinase	-0.0600988	0.00129448
JW1793	P09155	rnd	ribonuclease D	0.07762405	0.00703591
JW3900	P0A8R0	rraA	ribonuclease E (RNase E) in	0.05574836	0.17633659
JW3216	P0A9J0	rng	ribonuclease G	0.05711034	0.01184211

JW0204	P0A7Y4	rnhA	ribonuclease HI, degrades R	-0.0281731	0.41029127
JW0178	P10442	rnhB	ribonuclease HII, degrades F	0.13800531	0.04452079
JW0603	P21338	rna	ribonuclease I	-0.055621	0.0300124
JW1279	P30850	rnb	ribonuclease II	0.03261485	0.01250496
JW3618	P0CG19	rph	ribonuclease PH (defective)	-0.0285718	0.10489416
JW0646	P41409	rihA	ribonucleoside hydrolase 1	-0.0648521	0.10935656
JW2149	P33022	rihB	ribonucleoside hydrolase 2	0.02976132	0.15675409
JW0028	P22564	rihC	ribonucleoside hydrolase 3	0.02198413	0.11711232
JW2650	P39452	nrdE	ribonucleoside-diphosphate	-0.1749591	0.26526711
JW2651	P37146	nrdF	ribonucleoside-diphosphate	-0.0176426	0.45537237
JW4056	P16689	phnM	ribophosphonate triphospha	-0.001168	0.9414132
JW4060	P16687	phnI	ribophosphonate triphospha	-0.0220464	0.11689978
JW4062	P16685	phnG	ribophosphonate triphospha	-0.1132668	0.00049676
JW4061	P16686	phnH	ribophosphonate triphospha	-0.0096241	0.74880631
JW4057	P16679	phnL	ribophosphonate triphospha	0.04850652	0.12804127
JW4055	P16690	phnN	ribose 1,5-bisphosphokinase	0.0786435	0.01977941
JW4051	P37351	rpiB	ribose 5-phosphate isomera	-0.1188911	0.00315339
JW5475	P0A7Z0	rpiA	ribose 5-phosphate isomera	-0.2373834	0.00039234
JW0819	P0AEI4	yliG	ribosomal protein S12 meth	0.12655282	0.02926027
JW0888	P75838	ycaO	ribosomal protein S12 meth	0.08217492	0.01250286
JW0836	P0COU4	rimK	ribosomal protein S6 modifi	0.04383517	0.0245013
JW5090	P0AAT6	ybeB	ribosomal silencing factor	0.03146105	0.09794151
JW1423	P13857	rimL	ribosomal-protein-L7/L12-s	0.19985522	0.03796069
JW4335	P0A944	rimI	ribosomal-protein-S18-alani	-0.0744084	0.0278112
JW1053	P0A948	rimJ	ribosomal-protein-S5-alanir	0.03225836	0.60006167
JW3170	P0AFX0	yhbH	ribosome hibernation prom	0.05665961	0.22316689
JW5413	P0A7X6	rimM	ribosome maturation factor	-0.1516336	0.11698405
JW5533	P0A8A8	yhbC	ribosome maturation factor	-0.0189509	0.35943485
JW0936	P0AFW2	rmf	ribosome modulation factor	-0.0527503	0.02961191
JW4122	P39286	rsgA	ribosome small subunit-dep	0.06013544	0.16883761
JW5676	P37624	rbbA	ribosome-associated ATPase	-0.0314135	0.24959165
JW3577	P0ADK8	yibL	ribosome-associated DUF28	-0.0285967	0.30148979
JW3363	P0ACG8	hslR	ribosome-associated heat s	-0.0547184	0.00682382
JW5070	P0AAS7	ybcJ	ribosome-associated protei	0.04355415	0.18550395
JW4193	P0A8X0	yjgA	ribosome-associated UPF03	-0.2700341	0.03585642
JW4359	P0ACI0	rob	right oriC-binding transcripti	0.00603833	0.90809647
JW1383	P76077	paaA	ring 1,2-phenylacetyl-CoA e	-0.1905333	0.06920138
JW5217	P76080	paaD	ring 1,2-phenylacetyl-CoA e	0.04399959	0.13437982
JW1385	P76079	paaC	ring 1,2-phenylacetyl-CoA e	0.11054132	0.06562218
JW1387	P76081	paaE	ring 1,2-phenylacetyl-CoA e	0.07478786	0.03127395
JW2444	P76555	eutQ	RmlC-like cupin domain pro	0.09264378	0.08889454
JW5784	P39380	kptA	RNA 2'-phosphotransferase	0.08141263	0.08059704
JW5688	P46849	rtcA	RNA 3'-terminal phosphate	-0.1278524	0.00670502
JW3147	P0AGK4	yhbY	RNA binding protein associa	0.01238915	0.76356228
JW3525	P0A9X9	cspA	RNA chaperone and antiterr	-0.0458761	0.09458008

JW0058	P60240	hepA	RNA polymerase remodeling	-0.1693112	0.00630587
JW4253	P23484	fecl	RNA polymerase sigma-19 f	0.01878708	0.6022791
JW3624	POA800	rpoZ	RNA polymerase, omega su	-0.0726301	0.00356548
JW1907	POAEM6	fliA	RNA polymerase, sigma 28	-0.093683	0.00020532
JW3169	P24255	rpoN	RNA polymerase, sigma 54	0.03553146	0.00167239
JW3039	P00579	rpoD	RNA polymerase, sigma 70	0.11549495	0.00020496
JW5437	P13445	rpoS	RNA polymerase, sigma S (s	0.13663472	0.10035541
JW2798	POA776	nudH	RNA pyrophosphohydrolase	-0.1258146	0.32067196
JW3384	P46850	rtcB	RNA-splicing ligase	0.02050676	0.66527509
JW2263	POA8V0	elaC	RNase BN, tRNA processing	-0.0197318	0.33803662
JW1644	P30014	rnt	RNase T; exoribonuclease T,	-0.0474555	0.32708128
JW5034	Q2EEQ2	ykgM	RpmJ-like protein	-0.0394055	0.05716485
JW2425	P76537	yfeY	RpoE-regulated lipoprotein	0.07370491	0.00512398
JW1906	P52627	fliZ	RpoS antagonist; putative re	0.0848768	0.32571386
JW5782	P39375	yjiD	RpoS stabilizer after DNA da	-0.0268245	0.16067555
JW1147	P75987	elbA	RpoS stabilizer during Mg st	-0.0423577	0.07617118
JW0079	P22186	mraZ	RsmH methyltransferase inh	-0.0570576	0.04206434
JW0998	POACU2	ycdC	rut operon transcriptional re	-0.0074865	0.84021383
JW5260	P77783	ynfF	S- and N-oxide reductase, A	-0.032777	0.24914274
JW0116	POA7F6	speD	S-adenosylmethionine decal	-0.1069783	0.00597327
JW0395	POA7F9	queA	S-adenosylmethionine:tRNA	0.10782847	0.0746286
JW2141	P33018	yeiG	S-formylglutathione hydrola	-0.0680362	0.15096574
JW0346	P51025	frmB	S-formylglutathione hydrola	-0.0195604	0.42501905
JW2662	P45578	luxS	S-ribosylhomocysteine lyase	-0.0338015	0.73380891
JW0503	P75713	ylbA	S-ureidoglycine aminohydro	-0.04862	0.01310268
JW5804	P76049	ycjY	S9 homolog non-peptidase f	-0.0825457	0.00454077
JW4338	POAFH8	osmY	salt-inducible putative ABC t	-0.0984046	0.01724264
JW1771	POA908	mipA	scaffolding protein for mure	0.01760368	0.59729359
JW5869	P39382	yjiK	SdiA-regulated family putat	-0.0780163	0.00199882
JW2938	Q46835	yghG	secretin (GspDbeta) OM loc	-0.0568916	0.00968312
JW2764	POA8U0	syd	SecY-interacting protein	0.00476942	0.91612166
JW0397	POADZ7	yajC	SecYEG protein translocase	-0.0460256	0.20119526
JW4039	POAF56	yjcO	Sel1 family TPR-like repeat	-0.0687473	0.0071697
JW5091	P77234	ybeQ	Sel1 family TPR-like repeat	-0.0357502	0.12278889
JW0642	P77296	ybeT	Sel1 family TPR-like repeat	-0.0348182	0.09646468
JW3564	POA821	selA	selenocysteine synthase	0.05211789	0.08585137
JW3563	P14081	selB	selenocysteinyl-tRNA-specif	0.01488195	0.65975222
JW1753	P16456	selD	selenophosphate synthase	0.01042086	0.52098519
JW1534	P64463	ydfZ	selenoprotein, function unkr	0.00388864	0.88882379
JW5388	POAA93	ypdA	sensor kinase regulating yhj	0.00018026	0.99525728
JW5407	P52101	yfhK	sensor protein kinase regula	-0.0064058	0.87364405
JW2213	Q06067	atoS	sensory histidine kinase in t'	0.03709838	0.26550676
JW2063	P30847	baeS	sensory histidine kinase in t'	-0.0377551	0.13467902
JW4073	P30844	basS	sensory histidine kinase in t'	0.10201415	2.92E-06
JW0611	P77510	citA	sensory histidine kinase in t'	-0.0912437	0.20573598

JW3882	P0AE82	cpxA	sensory histidine kinase in t	-0.0049547	0.77477393
JW4362	P08401	creC	sensory histidine kinase in t	-0.0136975	0.10192247
JW4086	P0AEC8	dcuS	sensory histidine kinase in t	-0.0183704	0.33250146
JW3840	P0AFB5	glnL	sensory histidine kinase in t	-0.1649253	0.00763523
JW1213	P0AFA2	narX	sensory histidine kinase in t	-0.0551858	0.29816086
JW2453	P27896	narQ	sensory histidine kinase in t	0.01979471	0.52781478
JW3367	P0AEJ4	envZ	sensory histidine kinase in t	0.15204692	0.00041798
JW0390	P08400	phoR	sensory histidine kinase in t	-0.0249599	0.48786093
JW1115	P23837	phoQ	sensory histidine kinase in t	0.02179767	0.59197313
JW3967	P14377	zraS	sensory histidine kinase in t	0.03840619	0.46277239
JW3643	P09835	uhpB	sensory histidine kinase in t	0.00092604	0.95042095
JW1601	P18392	rstB	sensory histidine kinase of F	0.00146299	0.92543466
JW0628	P10100	rlpA	septal ring protein, suppres	0.03213194	0.54824796
JW1083	P28306	yceG	septation protein, ampicillir	-0.0117427	0.72752816
JW2057	P76395	yegK	ser/thr phosphatase-relatec	-0.0940993	0.00106081
JW3582	P0A9D4	cysE	serine acetyltransferase	0.01527131	0.54301893
JW0157	P0COV0	degP	serine endoprotease (prote	0.01775189	0.67975769
JW3203	P39099	degQ	serine endoprotease, peripl	-0.0569087	0.24027095
JW2535	P0A825	glyA	serine hydroxymethyltransfe	0.29740439	0.04980452
JW2535	P0A825	glyA	serine hydroxymethyltransfe	0.34328821	0.03549728
JW1827	P55798	pphA	serine/threonine-specific pr	-0.0261862	0.4262308
JW2704	P55799	pphB	serine/threonine-specific pr	0.05911131	0.00594697
JW5382	P76507	yfdI	serotype-specific glucosyl tr	0.01219599	0.67150909
JW3027	P0ADT8	htrG	SH3 domain protein	0.14961259	0.00817478
JW0379	P0A6E1	aroL	shikimate kinase II	-0.26535	0.0161774
JW1962	P76350	shiA	shikimate transporter	-0.0197004	0.67147601
JW5453	Q46939	yqeF	short chain acyltransferase	-0.0338401	0.13122133
JW2217	P76460	atoE	short chain fatty acid transp	0.01159123	0.45783005
JW2761	P65367	yqcA	short-chain flavodoxin, FMN	0.03541727	0.32794421
JW3193	P41036	nanT	sialic acid transporter	0.12966577	0.00047212
JW3195	P0A8W0	nanR	sialic acid-inducible nan ope	0.01338773	0.64770956
JW3385	P38035	rtcR	sigma 54-dependent transcr	0.02281222	0.14348288
JW3558	P37683	yiaV	signal-anchored membrane	-0.0096708	0.8345498
JW1204	Q46755	yhcQ	SIRB family inner membran	-0.060208	0.00219535
JW3784	P0A8P6	xerC	site-specific tyrosine recoml	0.00842944	0.80767676
JW2862	P0A8P8	xerD	site-specific tyrosine recoml	0.03185736	0.33099944
JW1795	P0AA91	yeaY	Slp family lipoprotein, RpoE	0.02028074	0.35640227
JW3332	P64627	yhfL	small lipoprotein	-0.0170398	0.73249703
JW4350	P0AGC7	ytjB	SMP_2 family putative men	-0.0089579	0.77814894
JW3416	P10906	ugpE	sn-glycerol-3-phosphate AB	-0.0238252	0.40203023
JW3415	P10907	ugpC	sn-glycerol-3-phosphate AB	0.15182905	0.20175996
JW3417	P10905	ugpA	sn-glycerol-3-phosphate AB	-0.0791546	0.00070666
JW3389	P13035	glpD	sn-glycerol-3-phosphate del	0.02581156	0.34681779
JW2234	P08194	glpT	sn-glycerol-3-phosphate tra	0.08052485	0.35879177
JW0018	P13738	nhaA	sodium-proton antiporter	-0.0471675	0.29632047

JW1175	P0AFA7	nhaB	sodium:proton antiporter	0.18423553	0.01162633
JW0821	P75804	ylil	soluble aldose sugar dehydr	0.02783397	0.38559036
JW5757	P39336	yjgL	SopA-central-domain-like h	-0.0593267	1.92E-06
JW2674	P05707	srlD	sorbitol-6-phosphate dehydr	0.01364465	0.36034071
JW2676	P15082	srlR	sorbitol-inducible srl operon	-0.0793935	0.00222391
JW2675	P15081	gutM	sorbitol-responsive srl oper	-0.0080167	0.79563515
JW0941	P0AFZ5	sulA	SOS cell division inhibitor	-0.0278496	0.12791885
JW2554	P46187	rseC	SoxR iron-sulfur cluster redu	-0.0221206	0.45161879
JW1624	P77179	rsxE	SoxR iron-sulfur cluster redu	-0.0258347	0.17313745
JW1619	P0A766	rsxA	SoxR iron-sulfur cluster redu	-0.0262531	0.2174523
JW1620	P77223	rsxB	SoxR iron-sulfur cluster redu	0.14153141	0.13640993
JW1622	P76182	rsxD	SoxR iron-sulfur cluster redu	-0.0151889	0.46410655
JW1623	P77285	rsxG	SoxR iron-sulfur cluster redu	-0.0066232	0.91983753
JW1621	P77611	rsxC	SoxR iron-sulfur cluster redu	-0.0566341	0.00207429
JW4311	P05719	hsdS	specificity determinant for h	-0.237212	0.01213605
JW1576	P0A951	speG	spermidine N(1)-acetyltrans	0.03994931	0.70599139
JW0117	P09158	speE	spermidine synthase (putres	0.28873174	0.04689174
JW1112	P69874	potA	spermidine/putrescine ABC	-0.0219026	0.46070458
JW1109	P0AFK9	potD	spermidine/putrescine ABC	0.00961282	0.71836401
JW1110	P0AFK6	potC	spermidine/putrescine ABC	0.02374758	0.55221996
JW1111	P0AFK4	potB	spermidine/putrescine ABC	0.03173233	0.3690153
JW4292	P0AEH8	yjiG	SpmB family inner membra	-0.4030424	0.00281144
JW0594	P77174	ybdM	Spo0J family protein, ParB-I	-0.0234722	0.03899842
JW1177	P29013	ycgB	SpoVR family stationary pha	-0.0531242	0.20881527
JW5446	P38506	exo	Ssb-binding protein, misider	-0.0082413	0.7352811
JW2860	P21893	recJ	ssDNA exonuclease, 5' --> 3	-0.0459255	0.14377547
JW5949	P45771	yrdD	ssDNA-binding protein, func	-0.0135701	0.67313559
JW0656	P0A898	ybeY	ssRNA-specific endoribonuc	-0.4173351	0.00729602
JW1966	Q47083	cbl	ssuEADCB/tauABCD operon	0.03900897	0.26344238
JW3411	P46857	yrhB	stable heat shock chaperone	0.16587879	0.00882846
JW5150	P75919	ymdC	stationary phase cardiolipin	0.01408403	0.21531686
JW3952	P27375	htrC	stationary phase growth ad	0.00520037	0.83467035
JW5878	P54901	csiE	stationary phase inducible p	-0.0257745	0.50257629
JW3959	P0AFX4	rsd	stationary phase protein, bi	0.03640085	0.19667524
JW3324	P20605	fic	stationary phase-induced pr	0.04410193	0.09482882
JW5060	P0ABE2	bolA	stationary-phase morphoge	-0.1315026	0.00540287
JW5962	P68191	sra	stationary-phase-induced ril	-0.0318951	0.13664129
JW5004	P39206	caiE	stimulator of CaiD and CaiB	-0.0021622	0.8914261
JW0577	P18393	ybdZ	stimulator of EntF adenylati	0.00721267	0.77953721
JW5610	P0ADN0	yieM	stimulator of RavA ATPase	0.01223313	0.38996147
JW1812	P0A9Y6	cspC	stress protein, member of t	0.00209809	0.00045369
JW3478	P0AES9	hdeA	stress response protein acid	0.14072122	0.00041369
JW3894	P0AAB8	yiiT	stress-induced protein	-0.0500366	0.37467406
JW1327	P0AAC0	uspE	stress-induced protein	-0.0154694	0.58426559
JW3971	P09162	yjaA	stress-induced protein	0.02084569	0.50922727

JW1370	P37903	uspF	stress-induced protein, ATP-	0.04705251	0.05706963
JW4005	P68206	yjbj	stress-induced protein, UPF1	0.13857355	0.00701485
JW5529	P45470	yhbO	stress-resistance protein	0.03473724	0.50379837
JW3198	P0ACA3	sspA	stringent starvation protein	-0.2711932	0.00035645
JW0714	P07014	sdhB	succinate dehydrogenase, Fd	-0.0289012	0.14763696
JW0713	P0AC41	sdhA	succinate dehydrogenase, fl	0.08699702	0.01981426
JW0711	P69054	sdhC	succinate dehydrogenase, r	-0.0042825	0.7546931
JW0712	P0AC44	sdhD	succinate dehydrogenase, r	0.06523532	0.09015875
JW5247	P76149	yneI	succinate semialdehyde de	-0.0188979	0.6385761
JW0009	P0AC98	yaaH	succinate-acetate transport	0.04931519	0.1510732
JW2636	P25526	gabD	succinate-semialdehyde de	0.01837657	0.45205663
JW0717	P0A836	sucC	succinyl-CoA synthetase, be	0.05624871	0.16787423
JW0718	P0AGE9	sucD	succinyl-CoA synthetase, NA	0.12768341	0.034742
JW1734	P76216	astB	succinylarginine dihydrolase	-0.1289145	0.00044962
JW1733	P76215	astE	succinylglutamate desucciny	0.10872199	0.01252042
JW5282	P76217	astD	succinylglutamic semialdeh	-0.0432048	0.10930064
JW1737	P77581	astC	succinylornithine transamin	-0.005446	0.71571384
JW1672	P77499	sufC	SufBCD Fe-S cluster assembl	0.11878787	0.00907824
JW0142	P0A823	sfsA	sugar fermentation stimula	-0.0038225	0.80514509
JW0806	P75792	ybiV	sugar phosphatase; fructose	-0.0445063	0.25087466
JW3674	P0A8Y5	ydA	sugar phosphate phosphata	-0.4830129	0.00164208
JW3171	P69829	ptsN	sugar-specific enzyme IIA c	0.06753583	0.13692958
JW3654	P31447	ydJ	sulfatase/phosphatase supe	-0.0674815	0.03686009
JW2721	P23845	cysN	sulfate adenylyltransferase,	0.08923717	0.35712641
JW2722	P21156	cysD	sulfate adenylyltransferase,	0.17206671	0.0091272
JW3888	P0AG78	sbp	sulfate transporter subunit	0.06031218	0.06233854
JW2406	P0A6J3	cysZ	sulfate transporter, sulfite i	-0.0241843	0.6761156
JW2416	P0AEB0	cysW	sulfate/thiosulfate ABC trar	-0.0337152	0.20677202
JW2417	P16701	cysU	sulfate/thiosulfate ABC trar	-0.0023507	0.92840924
JW2415	P16676	cysA	sulfate/thiosulfate transpor	-0.239963	0.01595823
JW2734	P38038	cysJ	sulfite reductase, alpha sub	0.13262591	0.15539456
JW2733	P17846	cysI	sulfite reductase, beta subu	0.17737334	8.21E-07
JW1669	P76194	sufE	sulfur acceptor protein	-0.0245968	0.31318446
JW3307	P45532	yheN	sulfurtransferase for 2-thiol	-0.155723	0.22847905
JW5569	P32140	yihS	sulphoquinovose isomerase	0.0243501	0.51161169
JW1638	P0AGD1	sodC	superoxide dismutase, Cu, Z	0.04261898	0.00230213
JW1648	P0AGD3	sodB	superoxide dismutase, Fe	-0.0436154	0.312906
JW3879	P00448	sodA	superoxide dismutase, Mn	0.1590475	6.97E-08
JW4023	P0A9E2	soxS	superoxide response regulor	0.12930641	2.91E-09
JW4100	P37147	fxsA	suppressor of F exclusion of	0.04430717	0.35696547
JW2049	P28249	asmA	suppressor of OmpF assembl	0.12490052	0.00011413
JW2819	Q46787	ygeG	SycD-like chaperone family	0.07439454	0.08978379
JW0103	P36645	hofB	T2SE secretion family protei	0.09462784	0.4870557
JW1125	P11072	lit	T4 phage exclusion protein;	-0.0496092	0.14725069
JW3106	P0AB74	kbaY	tagatose 6-phosphate aldol	0.09471197	0.04045317

JW3101	P0C8K0	kbaZ	tagatose 6-phosphate aldolase	-0.0315375	0.39155816
JW3105	P42907	agaS	tagatose-6-phosphate ketolase	-0.1152846	0.00789388
JW2220	P76463	yfaQ	tandem DUF2300 domain protein	-0.0092677	0.75214874
JW3221	P13518	yhdA	targeting factor for csrBC sigma factor	0.10650297	2.64E-05
JW5526	P0ABQ2	garR	tartronate semialdehyde reductase	-0.0252633	0.37791057
JW0497	P77161	glxR	tartronate semialdehyde reductase	-0.0507791	0.41119092
JW5580	P69425	tatB	TatABCE protein translocator	-0.1520483	0.07885885
JW3815	P69423	tatC	TatABCE protein translocator	-0.0346632	0.40807687
JW0622	P0A843	tatE	TatABCE protein translocator	0.00605239	0.83930797
JW3813	P69428	tatA	TatABCE protein translocator	0.13469902	0.08393848
JW2324	P0AD30	yfcA	TauE/TSUP family inner membrane protein	-0.0723085	0.00369914
JW0358	Q47538	tauB	taurine ABC transporter ATPase	-0.0476467	0.2845512
JW0357	Q47537	tauA	taurine ABC transporter permease	0.06369475	0.10945525
JW0359	Q47539	tauC	taurine ABC transporter permease	0.02726936	0.71548536
JW0360	P37610	tauD	taurine dioxygenase, 2-oxoglutarate dependent	0.04862466	0.11103281
JW3089	P0ACQ7	tdcA	tdc operon transcriptional activator	0.02622014	0.24069155
JW5596	P56258	rffT	TDP-Fuc4NAc:lipidIIIFuc4NAc transferase	0.03264236	0.47186706
JW5597	P27832	rffC	TDP-fucosamine acetyltransferase	0.10920227	0.04884645
JW1426	P25397	tehB	tellurite, selenium methyltransferase	-0.0348419	0.19045962
JW0939	P0A8N0	ycbG	Ter macrodomain organizer	-0.0641224	0.03681422
JW5549	P30139	thiG	thiamine biosynthesis ThiG-like protein	0.0838632	0.08113572
JW1092	P75948	ycfN	thiamine kinase	0.09771914	0.00409389
JW4017	P0AF48	yjbQ	thiamine phosphate synthase	-0.0361198	0.1725239
JW3957	P30137	thiE	thiamine phosphate synthase	0.0969912	0.05389559
JW0436	P46891	cof	thiamine pyrimidine pyrophosphorylase	-0.030029	0.16774385
JW0065	P31548	thiQ	thiamine/thiamine pyrophosphorylase	-0.0574507	0.00119224
JW0066	P31549	thiP	thiamine/thiamine pyrophosphorylase	-0.0544648	0.08558209
JW0067	P31550	tbpA	thiamine/thiamine pyrophosphorylase	-0.0160206	0.53732618
JW1395	P77181	paaY	thioesterase required for phosphotransferase	0.07093481	0.00742844
JW0333	P07464	lacA	thiogalactoside acetyltransferase	-0.0012768	0.9685292
JW5734	P36655	dipZ	thiol:disulfide interchange protein	9.68E-05	0.9975407
JW0597	P77202	dsbG	thiol:disulfide interchange protein	-0.1460856	7.09E-05
JW5856	P0AA25	trxA	thioredoxin 1	-0.022518	0.65524429
JW2566	P0AGG4	trxC	thioredoxin 2	-0.0800877	0.1057567
JW0871	P0A9P4	trxB	thioredoxin reductase, FAD-dependent	0.05283285	0.13839382
JW2418	P16700	cysP	thiosulfate-binding protein	-0.2475981	0.00054146
JW1301	P23857	pspE	thiosulfate:cyanide sulfurtransferase	0.00886282	0.73217225
JW3388	P0A6V5	glpE	thiosulfate:cyanide sulfurtransferase	0.02377835	0.1449828
JW4367	P0AD86	thrL	thr operon leader peptide	-0.0924491	0.00010342
JW0798	P0AA67	rhtA	threonine and homoserine efflux pump	0.06545636	0.05804647
JW5586	P0AG38	rhtC	threonine efflux pump	0.00841843	0.720795
JW1226	P23331	tdk	thymidine kinase/deoxyuridine kinase	0.10060185	0.0050433
JW4345	P07650	deoA	thymidine phosphorylase	0.07654538	0.0347986
JW2795	P0A884	thyA	thymidylate synthetase	-0.0133837	0.06256836
JW1862	P52005	torY	TMAO reductase III (TorYZ),	0.01754017	0.18079845

JW3433	P0ADI9	yhhN	TMEM86 family putative intr	-0.0048266	0.74146856
JW2601	POA832	smpB	tmRNA-binding trans-transl	-0.0465835	0.04666256
JW4251	P13036	fecA	TonB-dependent outer mem	-0.1458511	0.01561809
JW0983	P36662	torD	TorA-maturation chaperone	-0.0237649	0.37854642
JW4310	P39394	yjiW	toxic peptide regulated by a	0.02275138	0.5048933
JW5084	P77091	hokE	toxic polypeptide, small	-0.1767943	0.13275829
JW3526	P37305	hokA	toxic polypeptide, small	-0.0917341	0.01501169
JW5225	P77494	hokB	toxic polypeptide, small	0.03666302	0.28848257
JW2600	P0AGL5	yfjG	toxic UPF0083 family protei	0.0622136	0.05240625
JW4184	P33647	chpB	toxin of the ChpB-ChpS toxir	0.09307525	0.02686462
JW3099	P64594	yhaV	toxin of the SohB(PrfF)-Yha\	-0.0282086	0.56921552
JW5331	P69348	yoeB	toxin of the YoeB-YefM toxi	0.01613459	0.54836343
JW5445	P55140	ygcG	TPM domain protein, putati	0.02273645	0.59697707
JW3570	P32106	yibG	TPR-like repeat protein	0.0383775	0.02277968
JW2270	P76486	yfbP	TPR-like repeats-containing	-0.0488565	0.17555872
JW0471	P77301	ybaP	TraB family protein	0.03689213	0.12299107
JW1512	P76145	tam	trans-aconitate methyltrans	-0.0479082	0.02871787
JW2448	POA867	talA	transaldolase A	-0.0679157	0.02935148
JW0007	POA870	talB	transaldolase B	-0.1347499	0.00092605
JW3369	P30128	greB	transcript cleavage factor	-0.1409656	1.89E-05
JW3148	POA6W5	greA	transcript cleavage factor	0.07193806	0.09925701
JW3818	POAFW0	rfaH	transcription antiterminatio	-0.2129053	0.00715896
JW0406	POA780	nusB	transcription antiterminatio	-0.0004519	0.98766628
JW3076	P67660	yhaJ	transcription regulator of qu	0.0433406	0.15142711
JW3756	P0AG30	rho	transcription termination fa	0.05714831	0.35797751
JW1100	P30958	mfd	transcription-repair coupling	-0.2756096	0.2020916
JW1379	Q47129	feaR	transcriptional activator for	0.03661451	0.23566904
JW3721	P0ACI6	asnC	transcriptional activator of a	-0.0154676	0.55157691
JW2115	P33358	mlrA	transcriptional activator of c	-0.0270464	0.51314183
JW5894	P27111	cynR	transcriptional activator of c	-0.0141617	0.54303788
JW1788	P76250	yeaT	transcriptional activator of c	0.06785778	0.08415819
JW3483	P63201	gadW	transcriptional activator of g	-0.1016218	0.30637899
JW3746	P05827	ilvY	transcriptional activator of i	0.06462916	0.42306728
JW2807	P03030	lysR	transcriptional activator of l	0.1592415	9.93E-05
JW0019	POA9G2	nhaR	transcriptional activator of r	-0.0015948	0.94837847
JW3876	P09377	rhaS	transcriptional activator of r	-0.1041455	0.00835012
JW3877	P09378	rhaR	transcriptional activator of r	0.00682869	0.82731374
JW3032	P45463	ygiP	transcriptional activator of t	0.01815144	0.60337031
JW2396	P23841	xapR	transcriptional activator of x	-0.0500005	0.10446075
JW5849	Q46855	yqhC	transcriptional activator of y	0.09644089	0.00520296
JW3701	P11989	bgIG	transcriptional antiterminat	0.00725098	0.70746046
JW0068	P33595	sgrR	transcriptional DNA-binding	-0.048686	0.05620032
JW3212	P67662	aaeR	transcriptional regulator for	0.04761059	0.11607624
JW2883	POA8S1	argP	transcriptional regulator for	-0.0008706	0.96031677
JW1935	P0DMC9	rcaA	transcriptional regulator of r	0.03391231	0.2451254

JW5114	P75811	ybjK	transcriptional regulator of	-0.1110033	1.13E-05
JW0141	P0ABS1	dkxA	transcriptional regulator of	0.20415718	1.52E-05
JW2400	P0ACR7	yfeR	transcriptional regulator of	-0.0188475	0.39397504
JW1610	P0ACT6	uidR	transcriptional repressor	-0.0391027	0.05070258
JW3978	P16528	iclR	transcriptional repressor	-0.0184028	0.37660365
JW0453	P0ACS9	acrR	transcriptional repressor	0.05167731	0.02341472
JW4208	P39334	yjgJ	transcriptional repressor for	-0.0107484	0.84952743
JW1533	P0ACM2	ydfH	transcriptional repressor for	-0.0477052	0.03071992
JW4149	P0A9W0	ulaR	transcriptional repressor for	-0.2324161	0.27208283
JW0719	P13669	mngR	transcriptional repressor for	-0.1340599	0.00566693
JW0744	P0A9G8	modE	transcriptional repressor for	-0.0410362	0.52481365
JW5874	P67430	ydhM	transcriptional repressor for	-0.0379214	0.06585838
JW3546	P37671	yiaJ	transcriptional repressor for	0.04445486	0.00568326
JW2639	P37338	csiR	transcriptional repressor of	-0.0333525	0.50594563
JW3935	P0ACU5	fabR	transcriptional repressor of	-0.0230134	0.28399599
JW2284	P36771	lrhA	transcriptional repressor of	0.04658383	0.23931165
JW1612	P18811	mall	transcriptional repressor of	-0.0734104	0.03233074
JW2659	P0ACR9	mprA	transcriptional repressor of	0.02123211	0.121608
JW5248	P27245	marR	transcriptional repressor of	-0.1747283	0.10780627
JW1394	P76086	paaX	transcriptional repressor of	0.02206341	0.75237541
JW2092	P64530	yohL	transcriptional repressor of	-0.0072525	0.83541068
JW3732	P0ACQ0	rbsR	transcriptional repressor of	-0.0898784	0.00112616
JW3100	P0ACK2	agaR	transcriptional repressor of	-0.0491637	0.42346113
JW0078	P0ACP1	fruR	transcriptional repressor-ac	0.06084054	0.00290686
JW4221	P39343	idnR	transcriptional repressor, 5-	-0.0077505	0.48054134
JW1650	P0ACP7	purR	transcriptional repressor, hy	0.06224869	0.02330476
JW3446	P0A6Z6	nikR	transcriptional repressor, Ni	0.04661331	0.03552495
JW2464	P0A9I3	gcvR	transcriptional repressor, re	0.19894307	0.00029715
JW3909	P0A8U6	metJ	transcriptional repressor, S-	0.01993194	0.36478037
JW4356	P0A881	trpR	transcriptional repressor, tr	-0.1192024	0.00186837
JW5714	P0AC51	zur	transcriptional repressor, Zr	-0.070122	0.1864617
JW1205	P0AGM5	ycaA	transglutaminase-like TPR-r	-0.0021789	0.95294943
JW5478	P27302	tktA	transketolase 1, thiamine tr	0.02871239	0.34565737
JW2449	P33570	tktB	transketolase 2, thiamine tr	-0.0497446	0.44700436
JW3301	P0CE47	tufA	translation elongation facto	0.08202141	0.00907163
JW3943	P0CE48	tufB	translation elongation facto	-0.1794856	0.01667789
JW1173	P04152	umuC	translesion error-prone DNA	-0.0076242	0.76981855
JW4180	P39321	ytfN	translocation and assembly	-0.0401211	0.82725514
JW4179	P0ADE4	ytfM	translocation and assembly	-0.1531069	0.17181194
JW5503	P02930	tolC	transport channel	-0.3113663	6.98E-05
JW2238	P37014	yfaD	transposase_31 family prote	-0.3210149	0.04227924
JW2302	P77768	yfcl	transposase_31 family prote	-0.0194106	0.59759824
JW3374	P31667	yhgA	transposase_31 family prote	0.00505071	0.92425898
JW4200	P36673	treR	trehalose 6-phosphate-indu	0.0273254	0.43228647
JW4198	P28904	treC	trehalose-6-P hydrolase	0.03699784	0.47795203

JW1886	P31678	otsB	trehalose-6-phosphate phos	0.13202971	0.00147991
JW5312	P31677	otsA	trehalose-6-phosphate syntl	-0.065845	0.00571999
JW2642	P77295	ygaV	tributyltin-inducible repress	0.12321244	0.07505892
JW5800	P27278	nadR	trifunctional protein: nicotin	-0.0170952	0.30585751
JW0982	P33225	torA	trimethylamine N-oxide (TM	0.09766035	0.00266709
JW0981	P33226	torC	trimethylamine N-oxide (TM	0.09080191	0.19515007
JW1861	P46923	torZ	trimethylamine N-oxide red	-0.0389907	0.30811702
JW3890	POA858	tpiA	triosephosphate isomerase	-0.0104991	0.58249048
JW0491	P33667	ybbB	tRNA 2-selenouridine synth	0.01887508	0.21983382
JW3581	POAGJ7	yibK	tRNA Leu mC34,mU34 2'-O-	0.17248341	7.98E-06
JW3937	P23003	trmA	tRNA m(5)U54 methyltransi	-0.0140616	0.75036129
JW2927	POA815	yggH	tRNA m(7)G46 methyltransi	0.11982077	0.02206119
JW2516	POAE01	yfhQ	tRNA mC32,mU32 2'-O-met	-0.0152043	0.54302146
JW3626	POAGJ2	trmH	tRNA mG18-2'-O-methyltra	-0.0669794	0.0820965
JW3135	P60340	truB	tRNA pseudouridine synthas	-0.0902032	0.00162468
JW2315	P07649	truA	tRNA pseudouridine(38-40)	0.05451971	0.22142157
JW1338	P76055	ydaO	tRNA s(2)C32 thioltransfera	0.16798205	0.09053308
JW0413	P77718	thiI	tRNA s(4)U8 sulfurtransfera	0.16936878	0.02864603
JW3684	P25522	trmE	tRNA U34 5-methylaminom	0.07827323	0.04862246
JW5950	P32695	yjbN	tRNA-dihydrouridine syntha:	0.11723578	0.0094334
JW3228	POABT5	dusB	tRNA-dihydrouridine syntha:	-0.0152913	0.76692459
JW2128	P33371	dusC	tRNA-dihydrouridine syntha:	-0.046408	0.06754893
JW0396	POA847	tgt	tRNA-guanine transglycosyl:	0.01131664	0.87402866
JW0658	POAE11	miaB	tRNA-i(6)A37 methylthiotra	-0.0329253	0.07249702
JW0191	P28634	yaeB	tRNA-Thr(GGU) m(6)t(6)A3	0.02514594	0.06436889
JW1119	P25745	trmU	tRNA(Gln,Lys,Glu) U34 2-thi	-0.2376417	0.04422516
JW2715	Q57261	truD	tRNA(Glu) pseudouridine(13	0.0435355	0.0610089
JW2762	POAA41	yqcB	tRNA(Ile1,Asp) pseudouridir	0.00225235	0.90981703
JW2559	P31825	yfiC	tRNA1(Val) (adenine(37)-N(-0.0827407	0.00074007
JW1257	POAD92	trpL	trp operon leader peptide	-0.0078822	0.67062882
JW1252	POA877	trpA	tryptophan synthase, alpha :	-0.3403034	0.11711307
JW1253	POA879	trpB	tryptophan synthase, beta s	0.28083277	0.00083002
JW3130	POAAD2	mtr	tryptophan transporter of hi	0.01482073	0.62904922
JW3685	POAD89	tnaC	tryptophanase leader peptic	-0.0717331	0.10923211
JW3686	POA853	tnaA	tryptophanase/L-cysteine de	-0.0098117	0.65938039
JW1741	P76221	ydjZ	TVP38/TMEM64 family inne	-0.1927806	0.00383307
JW1739	P76219	ydjX	TVP38/TMEM64 family inne	0.10141473	0.00178271
JW5262	P69853	dmsD	twin-arginine leader-bindin	0.01987279	0.33632125
JW0213	Q47147	yafJ	type 2 glutamine amidotran	0.06200525	0.05235562
JW1381	P46883	tynA	tyramine oxidase, copper-re	0.09204531	0.00099624
JW4014	P04693	tyrB	tyrosine aminotransferase, †	0.07436512	0.07095943
JW3953	P30140	thiH	tyrosine lyase, involved in th	-0.0042837	0.91732397
JW4275	POADH5	fimB	tyrosine recombinase/inver	0.06524443	0.06124267
JW1895	POAAD4	tyrP	tyrosine transporter	-0.3165626	0.01433382
JW0964	P38134	yccC	tyrosine-protein kinase, role	-0.0891069	0.00091538

JW3127	P45527	yhbU	U32 peptidase family protei	-0.0549879	0.14598948
JW3602	P27128	rfaI	UDP-D-galactose:(glucosyl)l	-0.1378011	0.0004713
JW2021	P37747	glf	UDP-galactopyranose muta	-0.0934357	0.02189281
JW0742	P09147	galE	UDP-galactose-4-epimerase	0.00970189	0.82697256
JW3758	P0AC78	rfe	UDP-GlcNAc:undecaprenylpl	-0.2723732	0.01035952
JW2010	P76373	ugd	UDP-glucose 6-dehydrogena	-0.0940627	0.38580234
JW3606	P25740	rfaG	UDP-glucose:(heptosyl)lipo	-0.6413405	2.93E-05
JW5600	P27828	rffE	UDP-N-acetyl glucosamine-	0.14644301	0.00156327
JW5599	P27829	rffD	UDP-N-acetyl-D-mannosam	0.10001622	0.0073069
JW3770	P27836	rffM	UDP-N-acetyl-D-mannosam	-0.0020684	0.95694275
JW4192	P37773	mpl	UDP-N-acetylmuramate:L-a	0.02007869	0.59216871
JW0661	P0AF24	nagD	UMP phosphatase	-0.0773044	0.06869439
JW4365	P0ADD9	yjjY	uncharacterized protein	-0.392086	0.00704162
JW2817	P77136	yqeK	uncharacterized protein	-0.3085202	0.05023875
JW5517	P42625	yhaL	uncharacterized protein	-0.3010681	0.03321552
JW1432	P64459	yncJ	uncharacterized protein	-0.2186003	0.0596386
JW2372	P76520	yfdX	uncharacterized protein	-0.1949469	0.00537113
JW2169	P0AD21	yejG	uncharacterized protein	-0.179505	0.11142972
JW4288	P39374	yjiC	uncharacterized protein	-0.1218823	0.37018142
JW1045	P64442	yceO	uncharacterized protein	-0.114092	0.00025433
JW3071	Q47710	yqjK	uncharacterized protein	-0.1002627	0.00048692
JW5003	P75620	yaaY	uncharacterized protein	-0.0995072	0.00898093
JW2412	Q47702	yfeK	uncharacterized protein	-0.0988649	0.03299373
JW4007	P32693	yjbL	uncharacterized protein	-0.0816835	0.01861529
JW1166	P76001	ycgJ	uncharacterized protein	-0.0656403	0.02216741
JW1719	P76210	ydjO	uncharacterized protein	-0.0631958	0.01992505
JW5425	NA	ygaQ	uncharacterized protein	-0.0590884	0.0382873
JW2342	P76505	yfdF	uncharacterized protein	-0.0585204	0.0511058
JW2906	P64567	yqgB	uncharacterized protein	-0.0525995	0.0516939
JW1520	P76150	yneK	uncharacterized protein	-0.0438112	0.11447808
JW2269	P76485	yfbO	uncharacterized protein	-0.0406158	0.46434064
JW5911	Q2EES1	yniD	uncharacterized protein	-0.0336863	0.17594531
JW5748	P39317	ytfI	uncharacterized protein	-0.0253685	0.05035699
JW1940	P64517	yodC	uncharacterized protein	-0.0235102	0.14282171
JW1185	P76012	ycgY	uncharacterized protein	-0.0222291	0.41174782
JW4236	P39351	yjgZ	uncharacterized protein	-0.0211553	0.37920046
JW5399	P64545	yfgG	uncharacterized protein	-0.0208919	0.35893254
JW5298	Q2MB16	yobH	uncharacterized protein	-0.0191989	0.52327735
JW5797	P55914	yjjZ	uncharacterized protein	-0.0190557	0.33126166
JW1424	P76100	ydcK	uncharacterized protein	-0.0174284	0.39370172
JW5956	Q9XB42	ykfH	uncharacterized protein	-0.0172511	0.48815283
JW5317	P64519	yodD	uncharacterized protein	-0.0120892	0.61341362
JW5456	Q46789	ygeI	uncharacterized protein	-0.0081115	0.76190858
JW1713	P64479	ydiZ	uncharacterized protein	-0.0042183	0.777311
JW2640	P0ADE6	ygaU	uncharacterized protein	0.00081388	0.97692068

JW0827	P0AAY4	ybjH	uncharacterized protein	0.00352551	0.81472842
JW1785	P64496	yoaG	uncharacterized protein	0.00666732	0.91264915
JW5033	P56257	ykgL	uncharacterized protein	0.01003137	0.3456222
JW1675	P64476	ydiH	uncharacterized protein	0.01169898	0.57229137
JW2108	P33349	yehM	uncharacterized protein	0.01866575	0.11455223
JW5421	P58033	ypjJ	uncharacterized protein	0.02393103	0.44632625
JW1936	P0AEG8	dsrB	uncharacterized protein	0.02558795	0.22596385
JW0988	P0AB14	yccJ	uncharacterized protein	0.02577656	0.15249993
JW5044	P75692	yahM	uncharacterized protein	0.03281284	0.15623776
JW2702	P25728	ygbA	uncharacterized protein	0.03461285	0.19038793
JW2907	P64570	yqgC	uncharacterized protein	0.03517732	0.27478326
JW2915	P0A8W5	yqgE	uncharacterized protein	0.03605388	0.21991729
JW2646	P0AD53	ygaC	uncharacterized protein	0.03778584	0.35632025
JW5303	P76275	yebW	uncharacterized protein	0.03972809	0.18552089
JW1031	P75917	ymdA	uncharacterized protein	0.04272844	0.14412722
JW5310	P76296	yecT	uncharacterized protein	0.04927422	0.21936458
JW1090	P75946	ycfL	uncharacterized protein	0.05786885	0.01774305
JW3576	Q2M7R5	yibT	uncharacterized protein	0.06488786	0.06488527
JW4008	P32694	yjbM	uncharacterized protein	0.06629453	0.04544472
JW2268	P76484	yfbN	uncharacterized protein	0.0708686	0.44762197
JW3532	Q2M7M3	ysaB	uncharacterized protein	0.07472417	0.03064231
JW4118	P39283	yjeN	uncharacterized protein	0.07542671	0.04716319
JW2106	P33347	yehK	uncharacterized protein	0.07809777	0.0046033
JW0318	P77393	yahL	uncharacterized protein	0.08396966	0.00010551
JW3091	P11865	yhaB	uncharacterized protein	0.10166599	0.00144093
JW5302	P64503	yebV	uncharacterized protein	0.10267367	0.01767971
JW5837	P76406	yegR	uncharacterized protein	0.10534201	0.00043512
JW5455	Q46943	yqeJ	uncharacterized protein	0.12013192	0.22906288
JW1096	P0AB35	ycfJ	uncharacterized protein	0.14014211	0.19899347
JW4162	P39308	yjfZ	uncharacterized protein	0.16112275	0.04067953
JW2322	P64540	yfcL	uncharacterized protein	0.25525606	0.03533044
JW5076	Q47272	ylcG	uncharacterized protein, DLI	0.09539412	0.02690246
JW5251	Q2EES0	ynfO	uncharacterized protein, Qir	0.00488334	0.80991838
JW1349	P0ACW0	ydaF	uncharacterized protein, Ra	-0.004724	0.96783373
JW0601	P77316	ybdR	uncharacterized zinc-type al	0.06375516	0.34284703
JW2250	P76472	yfbH	undecaprenyl phosphate-alç	0.01859983	0.66376992
JW5373	P76474	yfbJ	undecaprenyl phosphate-alç	-0.2217331	0.02714248
JW2252	Q47377	yfbW	undecaprenyl phosphate-alç	0.04710731	0.29876213
JW2248	P77757	yfbF	undecaprenyl phosphate-L-A	0.07005918	0.15459633
JW3029	P60932	bacA	undecaprenyl pyrophosphat	-0.0246505	0.40449054
JW5112	P75806	ybjG	undecaprenyl pyrophosphat	0.05150215	0.00241897
JW3461	P0A8S5	yhiO	universal stress (ethanol tol	-0.1399621	0.06771675
JW3462	P0AED0	uspA	universal stress global respc	-0.0416583	0.31292593
JW1884	P46888	yecG	universal stress protein	-0.2251006	0.12932718
JW0600	P39177	uspG	universal stress protein UP1	-0.0605897	0.01145461

JW2918	P67080	yggS	UPF0001 family protein, PLF	-0.0893892	0.03303598
JW3316	P45524	yheT	UPF0017 family putative hy	-0.0328535	0.52635599
JW5577	P27862	yigZ	UPF0029 family protein	-0.2134047	0.13719231
JW4177	P0AE45	ytfL	UPF0053 family inner meml	-0.0304835	0.47353484
JW2800	P67127	ygdQ	UPF0053 family inner meml	0.02166595	0.7478093
JW5415	P37908	yfjD	UPF0053 family inner meml	0.02990322	0.31895298
JW1229	P25743	yche	UPF0056 family inner meml	-0.0909339	0.0239785
JW3397	P67143	yhgN	UPF0056 family inner meml	-0.0495613	0.02939361
JW1522	P0AEY1	marC	UPF0056 family inner meml	-0.0185176	0.2948639
JW1574	P76169	ynfA	UPF0060 family inner meml	0.00111695	0.96437933
JW1696	P77649	ydiU	UPF0061 family protein	-0.0231574	0.23583013
JW1853	P0A8A0	yebC	UPF0082 family protein	0.01013467	0.79131367
JW1964	P0A8A2	yeeN	UPF0082 family protein	0.01100104	0.56745129
JW3117	P45465	yraN	UPF0102 family protein	-0.0173997	0.68719397
JW2971	P67244	yqhA	UPF0114 family putative inr	-0.035813	0.76128436
JW1678	P0AFS7	ydiK	UPF0118 family inner meml	0.00836239	0.80297276
JW5680	P0AGM0	yhhT	UPF0118 family putative tra	-0.0031721	0.2944921
JW2575	P33644	yfiH	UPF0124 family protein	-0.0301716	0.53146125
JW2599	P52119	yfjF	UPF0125 family protein	0.02021269	0.38430323
JW3621	P0AGM2	yicG	UPF0126 family inner meml	-0.0761269	0.12744365
JW0153	P0AFP0	yadS	UPF0126 family inner meml	-0.0261211	0.34846842
JW4206	P39332	yjgH	UPF0131 family protein	0.06030468	0.04983123
JW0850	P0A8C1	ybjQ	UPF0145 family protein	-0.0453585	1.42E-06
JW1896	P0AD05	yecA	UPF0149 family protein	-0.1662458	5.36E-09
JW5473	P0A8C4	ygfB	UPF0149 family protein	0.04833499	0.32138673
JW0282	P0AAL9	ykgJ	UPF0153 cysteine cluster pr	0.02087535	0.68439657
JW5361	P0AFT8	yeiW	UPF0153 cysteine cluster pr	0.03163718	0.39296184
JW5180	P0A8L5	ycgN	UPF0153 family cysteine clu	-0.0568728	0.10758928
JW0010	P75617	yaaW	UPF0174 family protein	0.02700976	0.51073977
JW0378	P0A8D3	yail	UPF0178 family protein	0.0490846	0.02415131
JW2292	P0A8D9	yfbV	UPF0208 family inner meml	-0.0079262	0.79043234
JW1221	P37052	yehJ	UPF0225 family protein	0.06906273	0.47652379
JW1773	P76235	yeaH	UPF0229 family protein	0.06411168	0.31998969
JW0115	P0A8E5	yacl	UPF0231 family protein	-0.0922466	0.01440404
JW5479	P52060	yggU	UPF0235 family protein	-0.0037815	0.87199693
JW0626	P0A8J4	ybeD	UPF0250 family protein	-0.2877419	0.03049848
JW0185	P0A8K5	yaeP	UPF0253 family protein	-0.0043121	0.83651556
JW5258	P67553	ynfC	UPF0257 family lipoprotein	0.03904711	0.12122521
JW1247	P21365	yciC	UPF0259 family inner meml	-0.0647952	0.00063323
JW1240	P0A8L7	yciU	UPF0263 family protein	-0.0301009	0.12654914
JW1989	P0A8M6	yeeX	UPF0265 family protein	0.09343848	0.00020989
JW1809	P67601	yobD	UPF0266 family inner meml	-0.1019443	0.04650516
JW2868	P67603	yqfB	UPF0267 family protein	-0.0911881	0.25826288
JW3317	P67624	yheU	UPF0270 family protein	0.00096714	0.97097793
JW0703	P75746	ybgL	UPF0271 family protein	0.00777427	0.77373392

JW1315	P0A8R7	ycjF	UPF0283 family inner mem	0.00926709	0.70691096
JW2129	P60632	yohJ	UPF0299 family inner mem	0.04543408	0.00208108
JW2291	P0A8W8	yfbU	UPF0304 family protein	0.11087248	0.0068382
JW3123	P67762	yhbP	UPF0306 family protein	-0.0127174	0.83120408
JW0947	P0A8X4	yccT	UPF0319 family protein	0.0407477	0.24602846
JW2145	P62723	yeiH	UPF0324 family inner mem	0.0634617	0.25327407
JW0159	P62768	yaeH	UPF0325 family protein	0.00367222	0.96422026
JW5339	P76402	yegP	UPF0339 family protein	0.04324027	0.15192497
JW2175	P0AD24	yejL	UPF0352 family protein	-0.0170363	0.25019677
JW3893	P32162	yiiS	UPF0381 family protein	0.01337831	0.71559307
JW2340	P0AD33	yfcZ	UPF0381 family protein	0.07622826	5.44E-07
JW2778	P0ADR2	ygdD	UPF0382 family inner mem	0.1703495	7.74E-05
JW5968	Q2EEU2	yjhX	UPF0386 family protein	-0.1471625	0.14746829
JW1995	P33015	yeeE	UPF0394 family inner mem	0.00377872	0.89028879
JW1914	P31064	yedE	UPF0394 family sulphur tra	0.09974338	0.01323941
JW1784	P64485	yeaQ	UPF0410 family protein	0.01509926	0.58900342
JW1184	P76011	ymgE	UPF0410 family putative inr	-0.0541134	0.24685451
JW0012	P28696	yaal	UPF0412 family protein	0.0006681	0.69162479
JW3737	P0ADN2	yifE	UPF0438 family protein	-0.0573111	0.46717935
JW1575	P76170	ynfB	UPF0482 family putative pe	0.05413341	0.26578074
JW1054	P29217	yceH	UPF0502 family protein	-0.0138933	0.20660104
JW3619	P23839	yicC	UPF0701 family protein	-0.1728769	0.00019844
JW0889	P75839	ycaP	UPF0702 family putative inr	-0.0616604	0.19273541
JW4142	P0AF80	yjfL	UPF0719 family inner mem	-0.0274815	0.32257604
JW1168	P0AB43	ycgL	UPF0745 family protein	0.01745638	0.70606812
JW1778	P0ACY6	yeaL	UPF0756 family putative inr	-0.032156	0.05379065
JW5643	P25531	yicR	UPF0758 family protein	-0.3016303	0.02072391
JW1857	P37348	yecE	UPF0759 family protein	-0.1413014	0.04320575
JW2482	P0AGM7	uraA	uracil permease	0.02508863	0.39856533
JW2483	P0A8F0	upp	uracil phosphoribosyltransfe	-0.0773424	0.23965997
JW2564	P12295	ung	uracil-DNA-glycosylase	0.02083157	0.43518705
JW5139	P75897	ycdL	ureidoacrylate amidohydroli	-0.0450989	0.02162076
JW0505	P77555	allD	ureidoglycolate dehydrogeni	0.0031522	0.81126091
JW0493	P77731	allA	ureidoglycolate lyase, releas	0.06185774	0.09815351
JW5470	Q46821	ygfU	uric acid permease	0.06037772	0.13037554
JW5372	P77690	yfbE	uridine 5'-(beta-1-threo-per	0.04038423	0.08402597
JW3808	P12758	udp	uridine phosphorylase	-0.007019	0.87513614
JW2051	P0A8F4	udk	uridine-cytidine kinase	-0.1350612	0.01750098
JW0162	P27249	glnD	uridylyltransferase	-0.0337698	0.40512961
JW3063	P0A8G3	uxaC	uronate isomerase	-0.0050522	0.883233
JW3961	P29680	hemE	uroporphyrinogen decarboxy	0.01455897	0.45711339
JW5514	P42597	ygjP	UTP pyrophosphatase	0.01956458	0.50344609
JW3661	P31453	yidP	UTRA domain-containing Gr	-0.0442802	0.36909753
JW1494	P76135	ydeO	UV-inducible global regulat	0.11640023	0.00013072
JW5652	P09053	avtA	valine-pyruvate aminotransf	-0.3646317	0.046278

JW1699	P06611	btuD	vitamin B12 ABC transporte	-0.0459388	0.25936849
JW0154	P37028	btuF	vitamin B12 ABC transporte	0.25099794	0.03015463
JW1701	P06609	btuC	vitamin B12 ABC transporte	-0.0406583	0.13825113
JW3938	P06129	btuB	vitamin B12/cobalamin oute	0.17657861	0.00322428
JW2058	P76396	yegL	VMA domain protein	-0.1319551	0.14025582
JW5350	P33352	yehP	VMA domain putative YehL	-0.009162	0.77831912
JW1242	P31069	kch	voltage-gated potassium ch	0.06304318	0.06519171
JW2265	P76481	yfbK	Von Willebrand factor doma	0.0035721	0.90306257
JW5131	P0AB65	yccX	weak acylphosphatase	-0.0156838	0.71917303
JW0570	P77213	ybdK	weak gamma-glutamyl:cyst	0.05087955	0.04183664
JW2413	P78271	yfeS	WGR domain protein	0.01821502	0.70904681
JW2382	P76524	ypdF	Xaa-Pro aminopeptidase	0.04308522	0.0630673
JW2835	Q46800	xdhB	xanthine dehydrogenase, FA	0.00903564	0.85252413
JW2836	Q46801	xdhC	xanthine dehydrogenase, Fe	0.08396021	0.25490611
JW5462	Q46799	xdhA	xanthine dehydrogenase, m	0.00419994	0.90335079
JW3629	P0AGM9	yicE	xanthine permease	-0.022824	0.56825784
JW2850	P67444	ygfO	xanthine permease	0.18786268	0.0630034
JW0228	P0A9M5	gpt	xanthine phosphoribosyltrar	0.01684647	0.35243001
JW2397	P45562	xapB	xanthosine transporter	0.00286437	0.90953655
JW2843	Q46808	yqeB	XdhC-CoxI family protein wi	-0.0868588	0.01138094
JW3541	P0ACI3	xylR	xylose divergent operon trar	0.00504823	0.79266577
JW3536	P09099	xylB	xylulokinase	-0.0218791	0.06668487
JW4157	P0AF86	yjfY	YhcN family protein, peripla	-0.4733131	0.00147492
JW5654	P11286	yiaB	YiaAB family inner membra	-0.5677757	0.00037122
JW3534	P0ADJ8	yiaA	YiaAB family inner membra	0.00273713	0.91264498
JW5644	P25666	htrL	YibB family protein, functio	0.0862142	0.25924589
JW5356	P0AD17	yohC	Yip1 family inner membran	-0.0942664	0.00952409
JW5729	P39267	yjcZ	YjcZ family protein; yhjH mc	-0.0548654	0.11078078
JW1847	P0A9X1	znuC	zinc ABC transporter ATPase	0.11790545	0.00573541
JW5831	P39172	znuA	zinc ABC transporter peripla	0.03343635	0.17456459
JW1848	P39832	znuB	zinc ABC transporter perme	0.02974726	0.31303246
JW1956	P76344	yodA	zinc and cadmium binding p	-0.1038161	0.03993711
JW0735	P75757	zitB	zinc efflux system	-0.0526005	0.00534137
JW3008	P0A8H3	ygiE	zinc transporter	0.00878134	0.29953724
JW4069	P0AFJ1	phnA	zinc-ribbon family protein	0.0453166	0.00251512
JW4299	P39385	yjiN	zinc-type alcohol dehydroge	0.13623636	7.05E-05
JW3434	P37617	zntA	zinc, cobalt and lead efflux s	0.02940976	0.50330753
JW2911	P39902	sprT	Zn-dependent metalloprote	-0.2664155	0.01378661
JW5546	P0AAA9	zraP	Zn-dependent periplasmic c	0.04428939	0.02203248
JW2161	P33030	yeiR	Zn-stimulated GTPase invol	-0.011034	0.6861454
JW3254	P0ACS5	zntR	zntA gene transcriptional ac	-0.0119539	0.55437656
JW5095	NA	ybfH	#N/A	-0.3784786	0.00627273
JW5420	NA	ypjM	#N/A	-0.3205746	0.00181882
JW3755	P0ADF3	rhoL	#N/A	-0.2994129	0.00062944
JW2221	NA	yfaS	#N/A	-0.2235009	0.0403942

JW3741	NA	ilvG	#N/A	-0.1615197	2.18E-05
JW0621	NA	ybeM	#N/A	-0.1488054	0.00235702
JW3780	P11291	yzcX	#N/A	-0.1279977	0.02043289
JW5461	Q46797	ygeQ	#N/A	-0.1064309	0.21563276
JW2335	NA	yfcU	#N/A	-0.0988256	0.00350814
JW5002	P0ACG4	hokC	#N/A	-0.0968138	0.00228013
JW5912	NA	yedN	#N/A	-0.0869305	0.2602113
JW1948	NA	yedS	#N/A	-0.0826768	0.06096537
JW5496	NA	yghY	#N/A	-0.0798377	0.00594524
JW3740	NA	ilvG	#N/A	-0.0789036	0.14181902
JW2012	NA	wbbL	#N/A	-0.0762169	5.94E-06
JW2631	NA	ygaR	#N/A	-0.0694752	0.08336419
JW5179	NA	ymgH	#N/A	-0.0689243	0.05802649
JW5916	NA	molR	#N/A	-0.0663597	0.08655126
JW1502	P77286	ydeU	#N/A	-0.0654193	0.09438152
JW1128	P75971	yfmH	#N/A	-0.0530676	0.01258481
JW3750	NA	yifN	#N/A	-0.0455623	0.39517263
JW3660	P31452	glvC	#N/A	-0.0451348	0.03620163
JW5278	NA	arpB	#N/A	-0.0432327	0.09390873
JW1413	NA	gapC	#N/A	-0.0393694	0.50635043
JW5904	NA	lomR	#N/A	-0.0382102	0.14844389
JW5325	NA	yeeL	#N/A	-0.037461	0.10610303
JW5619	NA	tnaB	#N/A	-0.034363	0.07102634
JW4233	Q9Z3A0	yjgW	#N/A	-0.034148	0.25649925
JW2016	P36667	wbbL	#N/A	-0.0201891	0.45636587
JW5176	NA	ycgH	#N/A	-0.013342	0.62580357
JW2074	NA	gatR	#N/A	-0.0110802	0.69933956
JW5802	NA	ydbA	#N/A	-0.0053656	0.73437938
JW5199	NA	yciX	#N/A	-0.0050486	0.86594738
JW5426	NA	yqaC	#N/A	-0.0022625	0.93070269
JW5340	NA	gatR	#N/A	-0.00219	0.94037693
JW5917	NA	rscC	#N/A	-0.0012572	0.95153078
JW5915	NA	molR	#N/A	-0.0008182	0.96740035
JW0616	NA	dcuC	#N/A	0.00084425	0.97619424
JW5961	NA	yncK	#N/A	0.00102054	0.0198216
JW2222	NA	yfaS	#N/A	0.00128856	0.97153324
JW0498	P75711	ybbV	#N/A	0.00156995	0.01613356
JW5198	NA	yciX	#N/A	0.00302397	0.94868101
JW0247	P75680	insO	#N/A	0.00325738	0.92394315
JW4234	NA	yjgX	#N/A	0.00692419	0.79283961
JW0613	NA	dcuC	#N/A	0.00722118	0.83107487
JW4065	P16683	phnE	#N/A	0.01001347	0.61970361
JW4302	P39387	yjiQ	#N/A	0.01168136	0.65079271
JW5893	Q2EEQ3	yahH	#N/A	0.01363284	0.46432071
JW5049	NA	ykiB	#N/A	0.01473213	0.5835341

JW1002	NA	ycdN	#N/A	0.01480856	0.60445895
JW5227	NA	yncK	#N/A	0.01590266	0.12705337
JW5424	P76613	ypjC	#N/A	0.01864745	0.13095186
JW1918	NA	yedN	#N/A	0.0230666	0.15912351
JW5257	NA	ynfP	#N/A	0.02399758	0.14436626
JW5237	NA	yncM	#N/A	0.02468308	0.42186964
JW2102	NA	molR	#N/A	0.02484575	0.45196289
JW5763	NA	yjgX	#N/A	0.02511711	0.02479763
JW1949	NA	yedS	#N/A	0.02904775	0.44370682
JW0508	NA	ylbE	#N/A	0.03219933	0.11450611
JW3184	NA	yhcE	#N/A	0.03228644	0.0714834
JW5428	NA	ygaY	#N/A	0.0324946	0.11437098
JW0507	NA	ylbE	#N/A	0.03299136	0.09758166
JW5937	NA	ysdC	#N/A	0.03472301	0.22885981
JW5141	NA	ycdN	#N/A	0.03594802	0.29266216
JW1402	NA	ydbA	#N/A	0.03729052	0.25522525
JW5001	P28697	htgA	#N/A	0.0404832	0.18229161
JW5203	NA	ymjB	#N/A	0.04055677	0.09700431
JW5764	NA	yjgX	#N/A	0.04114652	0.24370711
JW0258	Q79E92	ykgN	#N/A	0.05037227	0.12568727
JW2633	NA	yqaD	#N/A	0.05111612	0.0037298
JW0694	Q2EEQ8	ybfQ	#N/A	0.05310029	0.08555376
JW5319	NA	yedS	#N/A	0.05540347	0.09151304
JW5906	NA	gapC	#N/A	0.06057071	0.0173493
JW5954	NA	yjiV	#N/A	0.06157264	0.04717257
JW3457	P37629	yhiL	#N/A	0.06308541	0.29532279
JW1466	P76122	yddJ	#N/A	0.07434043	0.00751962
JW5814	NA	yaiF	#N/A	0.07516615	0.07901414
JW5051	NA	yaiU	#N/A	0.08697847	0.0001626
JW2824	NA	ygeL	#N/A	0.08753303	0.01638308
JW4182	P08339	yzfA	#N/A	0.09203686	0.15081629
JW1961	NA	yeeL	#N/A	0.09388039	0.00331594
JW1920	P76322	yedM	#N/A	0.09853064	0.01915679
JW5460	NA	ygeN	#N/A	0.10405377	0.00806673
JW5901	NA	ycgH	#N/A	0.10681531	0.00011425
JW5358	NA	yohH	#N/A	0.1485802	0.00604098
JW2621	NA	yfjV	#N/A	0.233575	0.01382785
JW1130	P75973	ymfJ	#N/A	0.34793924	0.03519036