## Discretely calibrated regulatory loops controlled by ppGpp partition gene induction across the 'feast to famine' gradient in Escherichia coli

Matthew F. Traxler<sup>§</sup>, Vineetha M. Zacharia, Stafford Marquardt, Sean M. Summers, Huyen-Tran Nquyen, S. Elizabeth Stark, and Tyrrell Conway\*

Advanced Center for Genome Technology, University of Oklahoma, Norman, OK 73019

 $Email: matthew \ traxler@hms.harvard.edu, Vineetha.Zacharia@UTSouthwestern.edu, staffordmarquardt@qmail.com, sean-summers@ouhsc.edu, cecelia-nquyen@ouhsc.edu, sestark@northwestern.edu \\$ 

\* Corresponding author: Tyrrell Conwa

Tyrrell Conway Department of Botany and Microbiology The University of Oklahoma Norman, OK 73019-0245 Voice: 405 325 1683 FAX: 405 325 3442 E-mail: tconway@ou.edu

## Supplemental Table 1: Venn Diagram Gene List

Venn 2.3 >2fold lower in ΔrelAspoT, ΔrpoS 116 genes

GENE	LOCUS TAG	GENE PRODUCT	FUNCTION	PROBESETS	WT	Irp	rpoS	crp	dksA	relA	re	IAspoT
dkgA	b3012	2,5-diketo-D-gluconate reductase A	orf: Unknown	K-12_b3012_dkgA_s_at	** '	2.062	1.357	0.679	2.854	0.099	-1.198	-1.479
rpsV	b1480	30S ribosomal subunit protein S22		K-12 b1480 rpsV s at		4.516	4.962	2.666	4.858	0.066	-1.723	-0.828
dacC	b0839	D-alanyl-D-alanine carboxypeptidase (penicillin-binding protein 6a)	enzyme; Murein sacculus, peptidoglycan	K-12 b0839 dacC s at		2.704	2,609	1.387	2.102	1.143	0.724	0.13
osmE	b1739	DNA-binding transcriptional activator	regulator; Global regulatory functions	K-12 b1739 osmE s at		3.273	3.143	0.736	2.589	-0.23	-0.353	-0.583
vhiE	b3512	DNA-binding transcriptional activator	orf: Unknown	K-12 b3512 yhiE s at		2.94	2.425	1.654	2.86	1.823	-0.115	-0.581
gadX	b3516	DNA-binding transcriptional dual regulator	putative regulator; Not classified	K-12 b3516 gadX at		2.318	2.317	1.214	1.845	1.013	0.065	-0.022
yehV	b2127	DNA-binding transcriptional regulator	putative regulator; Not classified -!- transcriptional regulator of curli			2.171	1.975	0.693	2.69	1.142	0.413	0.131
sufA	b1684	Fe-S cluster assembly protein	orf: Unknown	K-12 b1684 sufA s at		1.276	1.822	0.159	2.649	0.928	0.054	-0.129
dps	b0812	Fe-binding and storage protein	regulator; Global regulatory functions	K-12 b0812 dps s at		3.653	3.54	0.83	2.628	-0.073	-1.337	-0.5
yedU	b1967	Hsp31 molecular chaperone	orf; Unknown	K-12 b1967 yedU s at		4.143	4.08	2.913	3.663	1.876	1.347	1.638
cysQ	b4214	PAPS (adenosine 3'-phosphate 5'-phosphosulfate) 3'(2'),5'-bisphosph	phenotype; Central intermediary metabolism: Sulfur metabolism	K-12 b4214 cysQ s at		1.631	1.534	-0.266	-0.238	-0.472	-0.152	-0.275
rpoS	b2741	RNA polymerase, sigma S (sigma 38) factor	enzyme; Global regulatory functions -!- involved in the response to o	K-12 b2741 rpoS s at		2.752	2.798	-2.188	1.846	1.373	0.244	1.121
acnA	b1276	aconitate hydratase 1	enzyme; Energy metabolism, carbon: TCA cycle	K-12 b1276 acnA s at		2.167	2.14	1.165	1.621	0.96	-1.059	-0.066
astA	b1747	arginine succinyltransferase	orf; Unknown	CFT073_c2147_s_at		1.55	1.292	0.495	0.611	0.753	0.183	-0.131
bfr	b3336	bacterioferritin, iron storage and detoxification protein	carrier; Transport of small molecules: Cations	K-12_b3336_bfr_a_at		4.425	3.942	0.815	4.254	-0.205	1.557	1.44
sufD	b1681	component of SufBCD complex	orf; Unknown	K-12_b1681_sufD_s_at		1.237	1.297	0.033	1.507	0.625	-0.547	-0.187
sufB	b1683	component of SufBCD complex	orf; Unknown	K-12_b1683_sufB_s_at		1.794	1.952	-0.023	2.25	0.702	0.147	-0.109
sufC	b1682	component of SufBCD complex, ATP-binding component of ABC super	putative transport; Not classified	K-12_b1682_sufC_s_at		1.563	1.754	0.135	2.14	0.836	0.048	-0.012
ycaP	b0906	conserved inner membrane protein	orf; Unknown	K-12_b0906_ycaP_s_at		2.286	2.387	1.014	4.777	0.541	0.98	0.055
yeaQ	b1795	conserved inner membrane protein	orf; Unknown	K-12_b1795_yeaQ_s_at		3.716	3.492	1.061	3.01	0.994	0.807	-0.03
yqjE	b3099	conserved inner membrane protein	orf; Unknown	K-12_b3099_yqjE_s_at		3.682	2.924	1.059	2.156	0.626	1.034	0.56
psiF	b0384	conserved protein	phenotype; Central intermediary metabolism: Phosphorus compound			3.17	2.933	0.571	3.679	0.168	0.4	0.83
ybeL	b0643	conserved protein	phenotype; Not classified	K-12_b0643_ybeL_s_at		2.967	3.01	1.443	2.63	1.24	-0.837	-0.594
ybgA	b0707	conserved protein	orf; Unknown	K-12_b0707_ybgA_s_at		1.532	0.827	0.486	1.559	0.353	0.629	-0.347
yccT	b0964	conserved protein	orf; Unknown	K-12_b0964_yccT_s_at		1.512	1.582	0.498	1.157	1.064	0.879	0.378
ycgB	b1188	conserved protein	putative factor; Not classified	K-12_b1188_ycgB_s_at		4.447	5.094	0.926	2.493	0.965	0.489	-0.249
ydeI	b1536	conserved protein	orf; Unknown	K-12_b1536_ydeI_s_at		2.878	2.421	0.993	2.568	1.076	0.023	0.168
ynhG	b1678	conserved protein	orf; Unknown	K-12_b1678_ynhG_s_at		4.058	4.248	1.188	2.192	0.215	-0.164	-0.148
yeaH	b1784	conserved protein	orf; Unknown	K-12_b1784_yeaH_s_at		2.696	2.232	0.283	3.184	1.365	-0.435	-0.4
yedP	b1955	conserved protein	orf; Unknown	K-12_b1955_yedP_s_at		2.347	1.93	0.555	1.524	1.287	0.394	0.398
yegS	b2086	conserved protein	orf; Unknown	K-12_b2086_yegS_s_at		2.026	1.74	0.356	2.996	1.816	0.217	0.159
elaB	b2266	conserved protein	orf; Unknown	K-12_b2266_elaB_s_at		4.711	3.865	1.553	4.872	0.556	-0.245	-0.035
yfcZ	b2343	conserved protein	orf; Unknown	K-12_b2343_yfcZ_s_at		1.957	1.301	0.609	0.391	0.603	0.587	0.554
yqjC	b3097	conserved protein	orf; Unknown	K-12_b3097_yqjC_s_at		2.386	2.331	0.632	2.97	0.406	-0.482	0.244
yqjD	b3098	conserved protein	orf; Unknown	K-12_b3098_yqjD_s_at		3.284	3.195	1.099	2.504	-0.516	0.662	0.138
yqjK	b3100	conserved protein	orf; Unknown	K-12_b3100_yqjK_s_at		2.616	2.263	0.208	1.156	0.577	0.604	0.68
yhhA	b3448 b4107	conserved protein	orf; Unknown	K-12_b3448_yhhA_s_at		2.34 3.005	2.402 3.302	0.316 0.451	1.777 2.261	0.794 -0.083	-0.237 0.332	-0.231 -0.068
phnB		conserved protein	orf; Unknown	K-12_b4107_phnB_s_at		3.005	3.302	0.451	2.261	0.325	0.332	-0.068
yjdI yjhT	b4126 b4310	conserved protein	orf; Unknown	K-12_b4126_yjdI_s_at K-12_b4310_yjhT_s_at		2.875	3.809	1.567	2.343	0.325	0.144	-0.128 0.749
	b4310 b1783	conserved protein	orf; Unknown	K-12_04310_yjiii_s_at K-12_b1783_yeaG_s_at		4.633	4.144	0.579	3.793	2.312	-0.269	-0.55
yeaG cbpA	b1763 b1000	conserved protein with nucleoside triphosphate hydrolase domain curved DNA-binding protein. DnaJ homologue that functions as a co-	orf; Unknown	K-12_D1763_yeaG_S_at K-12_D1000_cbpA_s_at		1.759	1.16	0.579	0.335	0.103	-0.269	0.541
treF	b3519	cytoplasmic trehalase	enzyme; Degradation of small molecules: Carbon compounds	K-12_b1000_cbpA_s_at K-12_b3519_treF_s_at		1.436	1.568	0.062	1.487	0.585	-0.037	-0.338
ecnB	b4411	entericidin B membrane lipoprotein	enzyme, begradation of small molecules. Carbon compounds	K-12_b3313_crer_s_ac K-12_b4411_ecnB_s_at		3.398	3.49	0.244	3.907	0.305	1.291	1.674
fbaB	b2097	fructose-bisphosphate aldolase class I	orf: Unknown	K-12 b2097 fbaB s at		4.8	4.12	1.955	4.621	0.947	-0.457	-0.846
ybdK	b0581	gamma-glutamyl:cysteine ligase	orf: Unknown	K-12 b0581 ybdK s at		2.145	2.203	-0.016	2.284	0.9	0.369	-0.019
ggt	b3447	gamma-glutamyltranspeptidase	enzyme; Biosynthesis of cofactors, carriers: Thioredoxin, glutaredoxi			1.701	1.202	-0.162	2.328	0.609	0.099	-0.524
agp	b1002	glucose-1-phosphatase/inositol phosphatase	enzyme; Central intermediary metabolism: Pool, multipurpose conve			1.2	1.086	0.081	0.757	1.138	-0.145	-0.417
ugpB	b3453		transport; Transport of small molecules: Carbohydrates, organic acid			2.016	2.377	0.745	2.427	0.332	-0.76	-0.645
aidB	b4187	isovaleryl CoA dehydrogenase	putative enzyme; Not classified	K-12 b4187 aidB s at		1.648	1.371	0.2	1.531	0.959	0.391	0.012
osmB	b1283	lipoprotein	putative membrane; Osmotic adaptation	K-12 b1283 osmB s at		3,366	3.3	1.553	3.143	0.671	0.555	1.584
narU	b1469	nitrate/nitrite transporter	transport; Transport of small molecules: Anions	K-12 b1469 narU s at		1.426	0.863	0.276	1.429	0.701	0.721	-0.291
osmC	b1482	osmotically inducible, stress-inducible membrane protein	phenotype: Osmotic adaptation	K-12 b1482 osmC s at		4.519	4.311	2.846	3.913	0.983	-0.276	0.902
slp	b3506	outer membrane lipoprotein	membrane; Outer membrane constituents	K-12 b3506 slp s at		1.289	0.292	-0.032	-0.022	0.163	0.379	0.051
blc	b4149	outer membrane lipoprotein (lipocalin)	membrane; Macromolecule synthesis, modification: Lipoprotein	K-12_b4149_blc_s_at		2.441	2.644	-0.055	1.752	0.627	-0.283	-0.236
osmY	b4376	periplasmic protein	phenotype; Osmotic adaptation	K-12_b4376_osmY_s_at		4.39	5.016	-0.126	3.48	0.245	-0.564	0.816
treA	b1197	periplasmic trehalase	enzyme; Osmotic adaptation	K-12_b1197_treA_a_at		1.542	1.086	-0.161	1.621	0.465	-0.602	-0.753
ybeM	b0626	predicted C-N hydrolase superfamily, NAD(P)-binding amidase/nitrila	putative enzyme; Not classified	K-12_b0626_ybeM_s_at		1.353	1.342	0.127	0.122	0.247	0.71	0.295
yccU	b0965	predicted CoA-binding protein with NAD(P)-binding Rossmann-fold do	orf; Unknown	O157_ECs1049_s_at		1.78	1.622	0.199	-0.197	-2.385	-0.554	-0.194
ybhP	b0790	predicted DNase	orf; Unknown	K-12_b0790_ybhP_s_at		3.516	2.896	0.756	3.439	-0.381	0.457	-0.365
yqjG	b3102	predicted S-transferase	putative enzyme; Not classified	K-12_b3102_yqjG_s_at		2.536	2.396	0.386	2.619	0.713	0.215	-0.19

<sup>§</sup> Present address: Dept. of Microbiology and Molecular Genetics, Harvard Medical School, 200 Longwood Ave., Boston MA, 02115

yjdJ	b4127	predicted acyltransferase with acyl-CoA N-acyltransferase domain	orf: Unknown	K-12_b4127_yjdJ_s_at		4.053	3.979	2.933	3.829	1.085	0.658	0.277
yjgB	b4269	predicted alcohol dehydrogenase, Zn-dependent and NAD(P)-bindin	putative enzyme; Not classified	K-12_b4269_yjgB_s_at		1.11	1.017	-0.02	1.463	1.147	-0.29	-0.738
yhcO	b3239	predicted barnase inhibitor	orf; Unknown	K-12_b3239_yhcO_s_at		2.443	2.056	-0.128	1.474	0.232	0.607	-0.305
b3000	b3000	predicted dienlactone hydrolase (pseudogene)	orf; Unknown	K-12_b3000_s_at		2.777	2.547	1.237	3.2	0.978	1.093	-0.182
ydcK	b1428	predicted enzyme	orf; Unknown	K-12_b1428_ydcK_s_at		2.328	1.664	0.739	1.866	1.232	-0.117	-0.371
wrbA	b1004	predicted flavoprotein in Trp regulation	regulator; Amino acid biosynthesis: Tryptophan	K-12_b1004_wrbA_a_at		3.928	4.321	0.812	3.541	0.928	-0.549	-0.94
ybaS	b0485	predicted glutaminase	putative enzyme; Not classified	K-12_b0485_ybaS_s_at		1.561	0.848	-0.071	1.396	0.708	-0.387	-0.586
yfcG	b2302	predicted glutathione S-transferase	putative enzyme; Not classified	K-12_b2302_yfcG_s_at		2.337	2.399	0.423	3.207	0.696	0.195	-0.177
yghA	b3003	predicted glutathionylspermidine synthase, with NAD(P)-binding Ros		K-12_b3003_yghA_s_at		1.24	1.181	-0.174	1.613	1.063	0.067	-0.455
glgS	b3049	predicted glycogen synthesis protein	putative enzyme; Macromolecule synthesis, modification: Polysaccha	ır K-12_b3049_glgS_s_at		4.415	4.914	2.66	2.808	1.029	1.67	0.057
ycaC	b0897	predicted hydrolase	orf; Unknown	K-12_b0897_ycaC_s_at		2.975	2.323	0.3	2.817	0.918	0.07	-0.93
ysgA	b3830	predicted hydrolase	putative enzyme; Not classified	K-12_b3830_ysgA_s_at		1.548	1.34	-0.398	1.071	0.89	-0.745	-0.842
ychH	b1205	predicted inner membrane protein	orf; Unknown	K-12_b1205_ychH_s_at		2.459	2.686	0.28	1.09	0.762	0.232	-0.61
yohC	b2135	predicted inner membrane protein	orf; Unknown	K-12_b2135_yohC_s_at		5.076	4.571	2.116	3.627	1.962	1.407	0.157
yhbO	b3153	predicted intracellular protease	orf; Unknown	K-12_b3153_yhbO_s_at		2.108	1.625	-0.155	1.927	1.111	-0.316	-0.379
ybjP	b0865	predicted lipoprotein	putative enzyme; Not classified	K-12_b0865_ybjP_at		2.483	2.272	0.175	0.707	-0.642	-0.713	-0.714
ydcL	b1431	predicted lipoprotein	orf; Unknown	K-12_b1431_ydcL_s_at		2.327	2.507	0.533	1.901	-0.189	0.023	1.267
ybaY	b0453	predicted outer membrane lipoprotein	phenotype; Not classified	K-12_b0453_ybaY_s_at		3.132	2.687	0.024	1.641	0.316	0.154	0.102
yajO	b0419	predicted oxidoreductase, NAD(P)-binding	putative enzyme; Not classified	K-12_b0419_yaj0_s_at		1.662	2.089	0.193	2.137	-0.244	-0.095	-0.134
yahK	b0325	predicted oxidoreductase, Zn-dependent and NAD(P)-binding	putative enzyme; Not classified	K-12_b0325_yahK_s_at		2.849	2.555	1.372	3.256	0.004	-0.341	-0.437
yncB	b1449	predicted oxidoreductase, Zn-dependent and NAD(P)-binding	putative enzyme; Not classified	K-12_b1449_yncB_s_at		2.511	2.268	0.669	3.117	0.67	0.622	1.22
yniA	b1725	predicted phosphotransferase/kinase	orf; Unknown	K-12_b1725_yniA_s_at		2.97	2.981	1.727	2.378	0.395 -0.46	0.77 1.794	0.11
yahO	b0329 b0806	predicted protein	orf; Unknown	K-12_b0329_yah0_s_at		4.812	4.997 3.009	1.664 1.125	4.877	0.629	0.255	1.28 -0.081
ybiM yccJ	b1003	predicted protein predicted protein	orf; Unknown orf; Unknown	K-12_b0806_ybiM_s_at K-12_b1003_yccJ_s_at		2.308 4.418	5.182	1.125	3.122 4.007	1.005	0.255	-0.081 -0.594
yccJ msvB	b1003 b1051	predicted protein				4.418	5.182 4.093	0.857	4.007	0.45	-1.117	-0.594 -0.864
			phenotype; Protein, peptide secretion	K-12_b1051_msyB_s_at					3.015			
yciG	b1259 b1586	predicted protein	orf; Unknown orf: Unknown	K-12_b1259_yciG_s_at		2.423	2.401	0.064 0.452	2.458	1.421	-0.588 -1.214	-0.539 -0.448
ynfD	b1586 b1810	predicted protein	orf; Unknown	K-12_b1586_ynfD_s_at		2.04	2.491 3.765	1.841	3.352	-0.577 1.539	-1.214 0.722	-0.448 1.462
yoaC		predicted protein		K-12_b1810_yoaC_s_at								
yebV	b1836	predicted protein	orf; Unknown	K-12_b1836_yebV_s_at		3.831	3.223	0.436	2.424	1.92	-0.022	0.329
yodD	b1953	predicted protein	orf; Unknown	K-12_b1953_yodD_s_at		2.788	3.252	0.087	1.7	0.906	0.327	-0.141
yegP	b2080	predicted protein	orf; Unknown	K-12_b2080_yegP_s_at		4.256	3.781	0.496	3.928	1.089	-0.251	-0.25
yehE	b2112	predicted protein	orf; Unknown	K-12_b2112_yehE_a_at		1.7	1.243	0.356	1.631	0.225	0.596	0.383
b2659	b2659	predicted protein	orf; Unknown	K-12_b2659_at		1.048	1.292	-0.001	0.66	0.833	-0.17	-0.076
ygaU	b2665	predicted protein	orf; Unknown	K-12_b2665_ygaU_s_at		3.427	2.989	0.508	3.434	0.291	0.393	1.235
ygaM	b2672	predicted protein	orf; Unknown	CFT073_c3223_ygaM_s_at	t	3.221	2.817	-0.009	2.399	0.484	-0.302	-0.474
yhfG	b3362	predicted protein	orf; Unknown	K-12_b3362_yhfG_s_at		2.773	2.766	0.026	2.034	0.128	0.262	0.009
yjbJ_	b4045	predicted stress response protein	orf; Unknown	K-12_b4045_yjbJ_s_at		4.601	5.191	-0.026	3.495	0.334	0.842	1.44
yiaG	b3555	predicted transcriptional regulator	orf; Unknown	K-12_b3555_yiaG_s_at		4.68	4.799	0.153	5.188	-0.338	-0.923	-0.952
ybaT	b0486	predicted transporter	putative transport; Not classified	K-12_b0486_ybaT_s_at		1.586	0.686	0.488	1.217	1.028	0.893	0.02
yehZ	b2131	predicted transporter subunit: periplasmic-binding component of AB		K-12_b2131_yehZ_at		3.594	3.166	0.789	5.358	1.237	-0.12	0.393
yhiO	b3494	predicted universal stress (ethanol tolerance) protein B	orf; Unknown	K-12_b3494_yhiO_s_at		2.89	3.095	0.616	1.713	0.476	0.51	-0.145
poxB	b0871	pyruvate dehydrogenase (pyruvate oxidase), thiamin-dependent, FA		K-12_b0871_poxB_at		1.645	1.104	-0.445	1.362	1.113	-1.006	-0.859
qor	b4051	quinone oxidoreductase, NADPH-dependent	enzyme; Energy metabolism, carbon: Electron transport	K-12_b4051_qor_s_at		2.128	1.632	1.126	1.551	-0.103	-0.492	-0.904
bolA	b0435	regulator of penicillin binding proteins and beta lactamase transcript	ic putative regulator; Murein sacculus, peptidoglycan	K-12_b0435_bolA_s_at		3.239	4.214	1.313	2.267	0.782	0.677	0.314
ryjA	b4459	small RNA		K-12_b4459_ryjA_at		2.357	2.101	1.053	3.251	1.507	0.011	-0.288
fic	b3361	stationary-phase protein, cell division	phenotype; Cell division	K-12_b3361_fic_s_at		3.007	3.401	0.725	3.457	0.853	0.636	0.233
gabD	b2661	succinate-semialdehyde dehydrogenase I, NADP-dependent	enzyme; Central intermediary metabolism: Pool, multipurpose conve			2.323	1.739	0.315	1.084	0.765	-0.047	-0.498
astC	b1748	succinylornithine transaminase, PLP-dependent	enzyme; Amino acid biosynthesis: Arginine	K-12_b1748_astC_s_at		1.915	2.256	0.895	2.128	1.806	0.469	0.201
sodC	b1646	superoxide dismutase, Cu, Zn	enzyme; Detoxification	K-12_b1646_sodC_s_at		3.442	4.074	1.151	3.834	0.887	0.516	0.258
thrL	b0001	thr operon leader peptide	leader; Amino acid biosynthesis: Threonine	EDL933_Z0001_thrL_x_at		1.379	0.949	0.129	-0.833	-0.378	0.264	-0.23
tam	b1519	trans-aconitate methyltransferase	putative enzyme; Not classified	K-12_b1519_tam_s_at		1.657	1.723	0.482	1.844	0.701	-0.23	-0.406
talA	b2464	transaldolase A	enzyme; Central intermediary metabolism: Non-oxidative branch, pe			2.342	1.641	-0.309	3.36	0.338	-0.612	-1.294
otsB	b1897	trehalose-6-phosphate phosphatase, biosynthetic	enzyme; Osmotic adaptation	K-12_b1897_otsB_s_at		4.085	4.373	0.444	4.642	0.592	0.192	-0.153
otsA	b1896	trehalose-6-phosphate synthase	enzyme; Osmotic adaptation	K-12_b1896_otsA_s_at		3.421	2.818	0.231	2.606	0.659	-0.337	-0.036
Venn 3.1 >2fold lowe 11 genes GENE	er in ΔrelAspoT,	. ΔrpoS, Δlrp G GENE PRODUCT	FUNCTION	PROBESETS	WT	lrp	rpoS	crp	dk	sA rel	n rol	AspoT
gabT	b2662	4-aminobutyrate aminotransferase, PLP-dependent	enzyme: Central intermediary metabolism: Pool, multipurpose conve			2.736	1.322	0.661	2.972	sa rei 2.21	0.965	-0.39
hdeD	b2662 b3511	acid-resistance membrane protein	orf: Unknown	K-12 b3511 hdeD s at	-	1.23	0.141	0.001	0.735	-0.109	1.212	0.049
hdeB	b3509	acid-resistance protein	orf: Unknown	K-12_b3511_lideb_s_at K-12_b3509_hdeB_s_at		2.355	1.197	0.544	2.169	-0.109	-1.706	-2.22
gabP	b2663	gamma-aminobutyrate transporter	transport; Transport of small molecules: Carbohydrates, organic acid			1.656	0.491	0.453	1.693	0.657	0.757	-0.334
gadA	b3517	qlutamate decarboxylase A, PLP-dependent	enzyme: Central intermediary metabolism: Pool, multipurpose conve			1.417	0.333	0.433	2.096	-0.194	0.737	-0.354
gadB	b1493	glutamate decarboxylase A, PLP-dependent glutamate decarboxylase B, PLP-dependent	enzyme; Central intermediary metabolism: Pool, multipurpose conve enzyme; Central intermediary metabolism: Pool, multipurpose conve			2.039	0.333	0.697	3.186	0.341	-0.13	-0.354
katE	b1732	hydroperoxidase HPII(III) (catalase)	enzyme; Central Intermediary metabolism: Pool, multipurpose conve enzyme: Detoxification	K-12_b1493_gadb_s_at K-12_b1732_katE_s_at		2.039	0.512	0.697	2.583	1.33	-0.13	-0.127
xasA	b1492	predicted glutamate:gamma-aminobutyric acid antiporter	putative transport; Not classified	K-12_b1/32_katL_s_at K-12_b1492_xasA_s_at		2.577	1.354	1.309	1.779	1.033	0.642	-0.009
ygjG	b3073	putrescine:2-oxoglutaric acid aminotransferase, PLP-dependent	putative enzyme; Amino acid biosynthesis: Arginine	K-12_b3073_ygjG_s_at		4.137	1.001	0.454	3.628	0.202	0.474	0.166
hdeA		stress response protein acid-resistance protein	orf: Unknown	K-12_b3575_ygj0_s_at K-12_b3510_hdeA_s_at		1.362	0.34	-0.063	2.021	-1.532	-2.181	-3.399
							0.54					-0.847
tktB	b3510 b2465	transketolase 2, thiamin-binding	enzyme: Central intermediary metabolism: Non-oxidative branch, ne			2.782	1.748	0.292		0.855	-0.511	
tktB Venn 2.1 >2fold lowe 26 genes	b3510 b2465 er in ΔrelAspoT,	transketolase 2, thiamin-binding	enzyme; Central intermediary metabolism: Non-oxidative branch, pe			2.782	1.748	0.292	3.461	0.855	-0.511	
Venn 2.1 >2fold lowe 26 genes	b2465 er in ΔrelAspoT,	Δlrp		ท K-12_b2465_tktB_s_at	WT							NoneT.
Venn 2.1 >2fold lowe 26 genes GENE	b2465 er in ΔrelAspoT, LOCUS_TAG	Δirp G GENE_PRODUCT	FUNCTION	PROBESETS	WT	Irp	rpoS	crp	dk	sA rel	A rel.	AspoT
Venn 2.1 >2fold lowe 26 genes GENE leuA	b2465 er in ΔrelAspoT, LOCUS_TAG b0074	Δlrp G GENE_PRODUCT 2-isopropylmalate synthase	FUNCTION enzyme; Amino acid biosynthesis: Leucine	PROBESETS K-12_b0074_leuA_s_at	WT	lrp 4.727	rpoS 2.598	crp 4.952	dk 3.624	sA rel 0.6	م rel، 0.011	-0.162
Venn 2.1 >2fold lowe 26 genes GENE leuA leuB	b2465 er in ΔrelAspoT, LOCUS_TAG b0074 b0073	Δlrp  GENE_PRODUCT 2-isopropylmalate synthase 3-isopropylmalate dehydrogenase	FUNCTION enzyme; Amino acid biosynthesis: Leucine enzyme; Amino acid biosynthesis: Leucine	r K-12_b2465_tktB_s_at  PROBESETS  K-12_b0074_leuA_s_at  K-12_b0073_leuB_s_at	WT	lrp 4.727 3.39	rpoS 2.598 1.326	crp 4.952 3.715	dk 3.624 2.692	sA rel 0.6 0.875	4 rel. 0.011 -0.84	-0.162 -1.187
Venn 2.1 >2fold lowe 26 genes GENE leuA leuB leuD	b2465 er in ΔrelAspoT, LOCUS_TAG b0074 b0073 b0071	Δlrp  3 GENE_PRODUCT 2-isopropylmalate synthase 3-isopropylmalate idhydrogenase 3-isopropylmalate isomerase subunit	FUNCTION enzyme; Amino acid biosynthesis: Leucine enzyme; Amino acid biosynthesis: Leucine enzyme; Amino acid biosynthesis: Leucine	PROBESETS K-12_b0074_leuA_s_at K-12_b0073_leuB_s_at K-12_b0073_leuB_s_at K-12_b0071_leuD_s_at	WT	Irp 4.727 3.39 3.084	rpoS 2.598 1.326 0.596	crp 4.952 3.715 3.02	dk 3.624 2.692 1.306	sA rel. 0.6 0.875 0.074	A rel. 0.011 -0.84 -1.527	-0.162 -1.187 -1.679
Venn 2.1 >2fold lowe 26 genes GENE leuA leuB leuD leuC	b2465 er in ΔrelAspoT, LOCUS_TAG b0074 b0073 b0071 b0072	∆Irp  GENE_PRODUCT  2-isopropylmalate synthase 3-isopropylmalate dehydrogenase 3-isopropylmalate isomerase subunit 3-isopropylmalate isomerase subunit, dehydratase component	FUNCTION enzyme; Amino acid biosynthesis: Leucine	PROBESETS K-12_b0074_leuA_s_at K-12_b0073_leuB_s_at K-12_b0071_leuD_s_at K-12_b0071_leuC_s_at	WT	lrp 4.727 3.39 3.084 3.51	rpoS 2.598 1.326 0.596 1.084	crp 4.952 3.715 3.02 3.501	dk 3.624 2.692 1.306 2.279	sA rel. 0.6 0.875 0.074 -1.016	A rel. 0.011 -0.84 -1.527 -1.87	-0.162 -1.187 -1.679 -1.906
Venn 2.1 >2fold lowe 26 genes GENE leuA leuB leuD leuC amn	b2465 er in ΔrelAspoT,  LOCUS_TAG b0074 b0073 b0071 b0072 b1982	GENE_PRODUCT 2-isopropylmalate synthase 3-isopropylmalate dehydrogenase 3-isopropylmalate isomerase subunit 3-isopropylmalate isomerase subunit, dehydratase component AMP nucleosidase	FUNCTION enzyme; Amino acid biosynthesis: Leucine enzyme; Salvage of nucleosides and nucleotides	PROBESETS K-12_b0074_leuA_5_at K-12_b0073_leuB_5_at K-12_b0071_leuD_5_at K-12_b0072_leuC_5_at K-12_b0072_leuC_5_at	WT	lrp 4.727 3.39 3.084 3.51 1.235	rpoS 2.598 1.326 0.596 1.084 0.143	crp 4.952 3.715 3.02 3.501 1.366	dk 3.624 2.692 1.306 2.279 0.737	sA rel. 0.6 0.875 0.074 -1.016 -1.355	0.011 -0.84 -1.527 -1.87 -1.972	-0.162 -1.187 -1.679 -1.906 -2.65
Venn 2.1 >2fold lowe 26 genes GENE leuA leuB leuD leuC amn serA	b2465 er in ΔrelAspoT, LOCUS_TAG b0074 b0073 b0071 b0072 b1982 b2913	∆Irp  GENE_PRODUCT 2-isopropylmalate synthase 3-isopropylmalate dehydrogenase 3-isopropylmalate isomerase subunit 3-isopropylmalate isomerase subunit, dehydratase component AMP nucleosidase D-3-phosphoglycerate dehydrogenase	FUNCTION enzyme; Amino acid biosynthesis: Leucine enzyme; Salvage of nucleosides and nucleotides enzyme; Amino acid biosynthesis: Serine	PROBESETS K-12_b0074_leuA_s_at K-12_b0073_leuB_s_at K-12_b0073_leuB_s_at K-12_b0071_leuD_s_at K-12_b0071_leuC_s_at K-12_b0071_seuS_amn_s_st K-12_b1982_amn_s_st	WT	Irp 4.727 3.39 3.084 3.51 1.235 1.118	rpoS 2.598 1.326 0.596 1.084 0.143 -2.173	crp 4.952 3.715 3.02 3.501 1.366 1.205	dk 3.624 2.692 1.306 2.279 0.737 -0.065	sA rela 0.6 0.875 0.074 -1.016 -1.355 -2.685	0.011 -0.84 -1.527 -1.87 -1.972 -2.25	-0.162 -1.187 -1.679 -1.906 -2.65 -2.682
Venn 2.1 >2fold lowe 26 genes  GENE leuA leuB leuD leuC amn serA dadA	b2465 er in ΔrelAspoT, LOCUS_TAC b0074 b0073 b0071 b0072 b1982 b2913 b1189	GENE_PRODUCT 2-isopropylmalate synthase 3-isopropylmalate dehydrogenase 3-isopropylmalate isomerase subunit 3-isopropylmalate isomerase subunit 3-isopropylmalate isomerase subunit 3-isopropylmalate isomerase subunit dehydrotase component AMP nucleosidase D-3-phosphoglycerate dehydrogenase D-amino acid dehydrogenase	FUNCTION enzyme; Amino acid biosynthesis: Leucine enzyme; Ayavage of nucleosides and nucleotides enzyme; Amino acid biosynthesis: Serine enzyme; Degradation of small molecules: Amino acids	PROBESETS K-12_b0074_leuA_s_at K-12_b0074_leuA_s_at K-12_b0071_leuD_s_at K-12_b0071_leuD_s_at K-12_b0072_leuC_s_at K-12_b1072_leuC_s_at K-12_b182_amm_s_at K-12_b182_dadA_s_s_at	WT	lrp 4.727 3.39 3.084 3.51 1.235 1.118 2.779	rpoS 2.598 1.326 0.596 1.084 0.143 -2.173 0.422	crp 4.952 3.715 3.02 3.501 1.366 1.205 2.152	dk 3.624 2.692 1.306 2.279 0.737 -0.065 0.16	sA rel. 0.6 0.875 0.074 -1.016 -1.355 -2.685 -1.703	A rel 0.011 -0.84 -1.527 -1.87 -1.972 -2.25 -1.247	-0.162 -1.187 -1.679 -1.906 -2.65 -2.682 -1.58
Venn 2.1 > 2fold lowe 26 genes  GENE leuA leuB leuD leuC amn serA dadA add	b2465 er in ΔrelAspoT, LOCUS_TAG b0074 b0073 b0071 b0072 b1982 b2913 b1189 b1623	GENE_PRODUCT 2-isopropylmalate synthase 3-isopropylmalate dehydrogenase 3-isopropylmalate isomerase subunit 3-isopropylmalate isomerase subunit, dehydratase component AMP nucleosidase D-3-phosphoglycerate dehydrogenase D-amino acid dehydrogenase adenosine deaminase	FUNCTION enzyme; Amino acid biosynthesis: Leucine enzyme; Salvage of nucleosides and nucleotides enzyme; Salvage of nucleosides and nucleotides enzyme; Degradation of small molecules: Amino acids enzyme; Degradation of small molecules: Amino acids enzyme; Salvage of nucleosides and nucleotides	PROBESETS K-12_b0074_leuA_s_at K-12_b0073_leuB_s_at K-12_b0073_leuB_s_at K-12_b0071_leuD_s_at K-12_b0072_leuC_s_at K-12_b0173_serA_s_at K-12_b0173_serA_s_at K-12_b1982_amn_s_at K-12_b1981_aerA_s_at K-12_b1981_aerA_s_at K-12_b1981_aerA_s_at K-12_b1893_add_s_at	WT	Irp 4.727 3.39 3.084 3.51 1.235 1.118 2.779 2.386	rpoS 2.598 1.326 0.596 1.084 0.143 -2.173 0.422 1.188	4.952 3.715 3.02 3.501 1.366 1.205 2.152 2.477	dk 3.624 2.692 1.306 2.279 0.737 -0.065 0.16 0.422	sA rel. 0.6 0.875 0.074 -1.016 -1.355 -2.685 -1.703 -0.49	A rel. 0.011 -0.84 -1.527 -1.87 -1.972 -2.25 -1.247 -0.272	-0.162 -1.187 -1.679 -1.906 -2.65 -2.682 -1.58 -0.232
Venn 2.1 >2fold lowe 26 genes GENE leuA leuB leuC amn serA dadA add	b2465 er in ΔrelAspoT, LOCUS_TAC b0074 b0073 b0071 b0072 b1982 b2913 b1189 b1623 b1190	3 GENE_PRODUCT 2-isopropylmalate synthase 3-isopropylmalate isomerase subunit 3-isopropylmalate isomerase subunit 3-isopropylmalate isomerase subunit 3-isopropylmalate isomerase subunit 0-3-phosphoglycerate dehydrogenase 0-3-phosphoglycerate dehydrogenase 0-3-phosphoglycerate dehydrogenase adenosine deaminase alanine racemase 2, PLP-binding	FUNCTION enzyme; Amino acid biosynthesis: Leucine enzyme; Amino acid biosynthesis: Serine enzyme; Parino acid biosynthesis: Serine enzyme; Degradation of small molecules: Amino acids enzyme; Salvage of nucleosides and nucleotides enzyme; Salvage of nucleosides and nucleotides enzyme; Salvage of nucleosides and solutions of the salvage of solutions	PROBESETS K-12_b0074_leuA_s_at K-12_b0071_leuB_s_at K-12_b0071_leuB_s_at K-12_b0071_leuC_s_at K-12_b1092_arm_s_at K-12_b1982_arm_s_s_at K-12_b1982_arm_s_at K-12_b193_ada4_s_at K-12_b1623_add_s_at K-12_b11623_add_s_at K-12_b11633_add_s_at	WT	lrp 4.727 3.39 3.084 3.51 1.235 1.118 2.779 2.386 2.918	rpoS 2.598 1.326 0.596 1.084 0.143 -2.173 0.422 1.188 0.714	crp 4.952 3.715 3.02 3.501 1.366 1.205 2.152 2.477 2.64	dk 3.624 2.692 1.306 2.279 0.737 -0.065 0.16 0.422 1.096	sA rel. 0.6 0.875 0.074 -1.016 -1.355 -2.685 -1.703 -0.49	A rel. 0.011 -0.84 -1.527 -1.87 -1.972 -2.25 -1.247 -0.272	-0.162 -1.187 -1.679 -1.906 -2.65 -2.682 -1.58 -0.232 -1.344
Venn 2.1 > 2fold lowe 26 genes  GENE leuA leuB leuD leuC amn serA dadA add	b2465 er in ΔrelAspoT, LOCUS_TAG b0074 b0073 b0071 b0072 b1982 b2913 b1189 b1623	GENE_PRODUCT 2-isopropylmalate synthase 3-isopropylmalate dehydrogenase 3-isopropylmalate isomerase subunit 3-isopropylmalate isomerase subunit, dehydratase component AMP nucleosidase D-3-phosphoglycerate dehydrogenase D-amino acid dehydrogenase adenosine deaminase	FUNCTION enzyme; Amino acid biosynthesis: Leucine enzyme; Salvage of nucleosides and nucleotides enzyme; Salvage of nucleosides and nucleotides enzyme; Degradation of small molecules: Amino acids enzyme; Degradation of small molecules: Amino acids enzyme; Salvage of nucleosides and nucleotides	PROBESETS K-12_b0074_leuA_s_at K-12_b0073_leuB_s_at K-12_b0073_leuB_s_at K-12_b0071_leuD_s_at K-12_b0072_leuC_s_at K-12_b0173_serA_s_at K-12_b0173_serA_s_at K-12_b1982_amn_s_at K-12_b1981_aerA_s_at K-12_b1981_aerA_s_at K-12_b1981_aerA_s_at K-12_b1893_add_s_at	WT	Irp 4.727 3.39 3.084 3.51 1.235 1.118 2.779 2.386	rpoS 2.598 1.326 0.596 1.084 0.143 -2.173 0.422 1.188	4.952 3.715 3.02 3.501 1.366 1.205 2.152 2.477	dk 3.624 2.692 1.306 2.279 0.737 -0.065 0.16 0.422	sA rel. 0.6 0.875 0.074 -1.016 -1.355 -2.685 -1.703 -0.49	A rel. 0.011 -0.84 -1.527 -1.87 -1.972 -2.25 -1.247 -0.272	-0.162 -1.187 -1.679 -1.906 -2.65 -2.682 -1.58 -0.232

yjdA thrA maeB glgP glgA thrB aceA leuL fimA aceB rhtB yfbT yliD yliB yfiD rybA	b4109 b0002 b2463 b3428 b3429 b0003 b4015 b0075 b4314 b3824 b2293 00832 00830 b2579 b4416	conserved protein with nucleoside triphosphate hydrolase domain fused aspartokinase I -I - homoserine dehydrogenase I fused malic enzyme predicted oxidoreductase -I- predicted phosphot glycogen phosphorylase phomoserine kinase isoditrate lyase leu operon leader peptide major type I subunt firinbrin (pilin) malate synthase A neutral amino-acid effix system predicted hydrolase or phosphatase predicted peptide transporter subunit: membrane component of ABC predicted peptide transporter subunit: periplasmic-binding componer pyruvate formate lyase subunit small RNA	enzyme; Macromolecule synthesis, modification: Polysaccharides - (c enzyme; Macromolecule synthesis, modification: Polysaccharides - (c enzyme; Amino acid biosynthesis: Threonine -l - enzyme; Amino acid enzyme; Central intermediary metabolism: Glyoxylate bypass leader; Amino acid biosynthesis: Leucine structural component; Surface structures enzyme; Central intermediary metabolism: Glyoxylate bypass orf; Unknown putative enzyme; Not classified putative transport; Not classified	K-12, b2463, maeB, at K-12, b3429, glgP, s, at K-12, b3429, glgA, s, at K-12, b0003, thrB, s, at K-12, b0075, leat, s, at K-12, b0075, leat, s, at K-12, b4014, aceB, s, at K-12, b4314, fimA, s, at K-12, b34354, yiGK, s, at K-12, b0832, yiID, s, at K-12, b0832, yiID, s, at K-12, b0832, yiB, s, at		1.321 1.248 1.389 1.598 1.928 1.1 1.309 1.684 2.738 1.59 1.027 2.033 1.452 3.55 1.864 2.448	0.277 -0.289 -0.002 0.575 0.726 -1.199 -0.548 -0.611 -2.818 -0.33 -0.029 1 0.087 2.546 0.812	2.015 1.082 0.892 1.254 1.855 1.003 1.152 1.62 2.937 1.687 1.758 1.645 1.348 3.587 1.962	-0.494 -0.466 -0.658 0.597 -0.24 -0.279 -0.144 -0.243 -0.431 0.781 0.781 0.785 0.507 1.789 0.668 -0.067	-0.047 -1.071 -0.471 -0.353 -0.057 -0.975 -2.929 -1.808 2.395 -1.858 0.325 0.771 2.148 0.865 1.456	-0.272 -0.101 0.843 -0.949 -0.369 -0.317 -1.298 -0.831 -0.2 -1.736 -0.633 -0.045 0.455 0.145 -0.591 0.706	-0.476 -0.464 0.005 -1.526 -1.155 -0.673 -1.885 -1.935 -0.651 -1.618 -0.484 -0.368 -0.366 -1.219 0.846
Venn 1.1 >2fold lov 2 genes	ver in Δlrp											
GENE ydcF ydjN	LOCUS_TAG b1414 b1729	GENE_PRODUCT conserved protein predicted transporter	FUNCTION orf; Unknown putative enzyme; Not classified	PROBESETS K-12_b1414_ydcF_s_at K-12_b1729_ydjN_s_at	WT	lrp 1.002 4.235	rpoS -0.117 2.957	crp 1.148 3.957	dksA -0.688 0.887	relA 0.005 3.058	rel 0.263 3.601	0.868 4.331
Venn 1.2 >2fold lov 6 genes	ver in ΔrpoS											
GENE adhP ybaA yqaE yaiA yqjF hnr	LOCUS_TAG b1478 b0456 b2666 b0389 b3101 b1235	GENE_PRODUCT alcohol dehydrogenase, 1-propanol preferring conserved protein predicted membrane protein predicted protein predicted quinol oxidase subunit response regulator of RpoS	FUNCTION enzyme; Energy metabolism, carbon: Anaerobic respiration orf; Unknown orf; Unknown orf; Unknown orf; Unknown orf; Unknown regulator; Basic proteins - synthesis, modification	PROBESETS K-12_b1478_adhP_s_at K-12_b0456_ybaA_s_at K-12_b2666_yqaE_s_at K-12_b3101_yqiF_s_at K-12_b3101_yqiF_s_at K-12_b1235_hnr_s_at	WT	1.507 1.507 1.994 2.306 1.079 1.847	rpoS 1.497 1.134 1.407 2.505 0.825 1.59	0.465 0.362 0.16 0.191 -0.037 0.715	dksA 2.433 1.534 0.6 1.058 1.168 2.072	relA 1.319 1.131 0.237 -0.415 1.542 0.097	rel 0.291 0.685 1.195 0.991 1.116 0.854	1.214 1.368 1.05 1.836 0.914 1.145
Venn 1.3 >2fold lov 212 gene	ver in ΔrelAspoT											
GENE	LOCUS TAG	GENE_PRODUCT	FUNCTION	PROBESETS	WT	lrp	rpoS	crp	dksA	relA	rel	IAspoT
cysH	b2762	3'-phosphoadenosine 5'-phosphosulfate reductase	enzyme; Central intermediary metabolism: Sulfur metabolism	K-12_b2762_cysH_s_at		5.638	5.594	5.355	3.987	3.787	2.261	2.092
aroD aroG	b1693 b0754	3-dehydroquinate dehydratase 3-deoxy-D-arabino-heptulosonate-7-phosphate synthase, phenylalar	enzyme; Amino acid biosynthesis: Chorismate	K-12_b1693_aroD_s_at K-12_b0754_aroG_s_at		2.053 1.319	1.687 0.763	1.887	1.069	0.006	-0.574 -0.379	-1.17 -0.479
ydcE	b1461	4-oxalocrotonate tautomerase	orf; Unknown	K-12_b1461_ydcE_s_at		1.715	1.247	1.881	0.699	0.538	0.221	0.465
pfkB vbhE	b1723 b0767	6-phosphofructokinase II 6-phosphogluconolactonase	enzyme; Energy metabolism, carbon: Glycolysis orf: Not classified	K-12_b1723_pfkB_s_at		2.728 1.223	2.755 0.934	2.685 0.316	2.38 0.281	1.099 -0.63	0.533 -1.177	0.748 -1.378
ssrS	b2911	6S regulatory RNA	RNA; Ribosomal and stable RNAs -!- modulates promoter use via inte	K-12_b0767_ybhE_s_at K-12_b2911_ssrS_s_at		1.544	1.204	1.007	0.281	-0.63	-0.167	0.131
hdhA	b1619	7-alpha-hydroxysteroid dehydrogenase, NAD-dependent	enzyme; Central intermediary metabolism: Pool, multipurpose conve	r K-12_b1619_hdhA_s_at		2.722	2.491	2.294	2.001	1.282	-0.781	-0.394
clpA vffO	b0882 b2446	ATPase and specificity subunit of ClpA-ClpP ATP-dependent serine pr CPZ-55 prophage; predicted protein	enzyme; Degradation of proteins, peptides, glyco	K-12_b0882_clpA_s_at K-12_b2446_vffO_at		2.802 1.028	2.793 1.093	2.787 0.641	1.847	0.939	-0.425 -0.283	-0.209 -0.275
b2449	b2449	CPZ-55 prophage; predicted protein	orf; Unknown	K-12_b2440_yno_at K-12_b2449_at		1.541	1.35	1.576	1.117	0.257	-0.283	-0.166
yedO	b1919	D-cysteine desulfhydrase, PLP-dependent	putative enzyme; Not classified	K-12_b1919_yedO_a_at		2.239	2.123	1.832	0.889	0.904	0.312	0.402
dld sbmC	b2133 b2009	D-lactate dehydrogenase, FAD-binding, NADH independent DNA gyrase inhibitor	enzyme; Energy metabolism, carbon: Aerobic respiration orf; Unknown function	K-12_b2133_dld_s_at K-12_b2009_sbmC_s_at		1.255 2.574	0.579 2.659	1.267 2.045	0.796 2.818	-0.826 1.014	-1.786 0.451	-1.797 1.049
fucR	b2805	DNA-binding transcriptional activator	regulator; Degradation of small molecules: Carbon compounds	K-12_b2805_fucR_s_at		1.563	1.274	1.744	0.815	0.537	0.016	-0.443
csgD cbl	b1040 b1987	DNA-binding transcriptional activator in two-component regulatory sy DNA-binding transcriptional activator of cysteine biosynthesis	y putative regulator; Not classified regulator: Amino acid biosynthesis: Cysteine	K-12_b1040_csgD_s_at K-12_b1987_cbl_s_at		2.93 2.53	2.945 2.595	3.327 2.021	2.247 1.299	0.63 1.894	0.614 0.688	0.585 0.089
iciA	b2916	DNA-binding transcriptional activator, replication initiation inhibitor	regulator; DNA - replication, repair, restriction/modification	K-12_b2916_iciA_s_at		1.041	1.126	1.148	0.269	-0.617	-0.819	-1.408
crp folE	b3357 b2153	DNA-binding transcriptional dual regulator GTP cyclohydrolase I	regulator; Global regulatory functions enzyme; Biosynthesis of cofactors, carriers: Folic acid	K-12_b3357_crp_s_at K-12_b2153_folE_s_at		1.291 1.049	1.51 0.862	1.248 1.07	-5.177 0.535	-0.442 -1.282	-0.115 -1.864	-0.293 -0.584
ybiK	b0828	L-asparaginase	orf; Not classified	K-12_b0828_ybiK_s_at		3.514	3.813	3.701	3.089	2.089	1.652	1.108
fucU	b2804	L-fucose mutarotase	phenotype; Degradation of small molecules: Carbon compounds	K-12_b2804_fucU_s_at		2.303	2.213	2.351	1.299	0.442	-0.031	0.231
sdaA celA	b1814 b1738	L-serine deaminase I N,N'-diacetylchitobiose-specific enzyme IIB component of PTS	enzyme; Degradation of small molecules: Amino acids enzyme; Transport of small molecules: Carbohydrates, organic acids,	K-12_b1814_sdaA_s_at K-12_b1738_celA_s_at		1.375 2.699	1.82 2.384	0.904 2.698	0.777 1.894	0.767 1.561	-1.031 1.243	-0.414 1.299
ampD	b0110	N-acetyl-anhydromuranmyl-L-alanine amidase	regulator; Not classified	K-12_b0110_ampD_s_at		1.37	1.695	1.689	0.594	-0.665	0.169	-1.077
nemA nadE	b1650 b1740	N-ethylmaleimide reductase, FMN-linked NAD synthetase, NH3/glutamine-dependent	enzyme; Central intermediary metabolism: Pool, multipurpose conve enzyme; Biosynthesis of cofactors, carriers: Pyridine nucleotide	r K-12_b1650_nemA_s_at K-12_b1740_nadE_s_at		1.078 1.018	0.58 0.584	0.883 1.324	0.85 0.465	0.921 -0.667	-0.377 -2.137	-0.295 -1.587
acpD	b1412	NADH-azoreductase, FMN-dependent	enzyme; Fatty acid and phosphatidic acid biosynthesis	K-12_b1412_acpD_s_at		1.726	1.849	2.088	0.102	0.018	-0.902	-0.759
ilvG argE	b4488 b3957	acetolactate synthase II, large subunit (pseudogene) acetylornithine deacetylase	enzyme; Amino acid biosynthesis: Isoleucine, Valine enzyme; Amino acid biosynthesis: Arginine	K-12_b4488_ilvG_s_at K-12_b3957_argE_s_at		4.511 1.307	5.26 1.171	4.624 1.226	3.891 0.792	2.614	2.801 -1.119	2.503 -1.223
asr	b1597	acid shock-inducible periplasmic protein	phenotype; Not classified	K-12_b1597_asr_s_at		1.215	1.872	0.896	1.606	1.396	-0.615	-0.293
fadE	b0221 b2750	acyl coenzyme A dehydrogenase	putative enzyme; Not classified	K-12_b0221_fadE_at		1.735 4.154	1.195	1.268	1.207 2.541	0.714	1.405	0.467 1.217
cysC asd	b2/50 b3433	adenosine 5'-phosphosulfate kinase aspartate-semialdehyde dehydrogenase, NAD(P)-binding	enzyme; Central intermediary metabolism: Sulfur metabolism enzyme; Amino acid biosynthesis: Lysine	K-12_b2750_cysC_s_at K-12_b3433_asd_s_at		4.154 1.204	3.243 0.875	3.839 1.614	0.402	2.74 -1.196	1.279 -1.933	1.21/ -2.576
ushA	b0480	bifunctional UDP-sugar hydrolase and 5'-nucleotidase	enzyme; Central intermediary metabolism: Sugar-nucleotide biosyntl	K-12_b0480_ushA_s_at		1.054	0.731	0.898	1.063	0.666	-0.299	-0.605
ilvE cstA	b3770 b0598	branched-chain amino-acid aminotransferase carbon starvation protein	enzyme; Amino acid biosynthesis: Isoleucine, Valine phenotype; Global regulatory functions	K-12_b3770_ilvE_s_at K-12_b0598_cstA_s_at		3.008 1.505	3.338 1.592	3.201 1.71	0.488 1.195	-0.033 0.885	1.339	0.726 0.171
ybhO	b0789	cardiolipin synthase 2	orf; Not classified	K-12_b0789_ybhO_s_at		1.465	1.378	0.48	2.309	1.658	-0.577	-0.894
yfiA cspD	b2597 b0880	cold shock protein associated with 30S ribosomal subunit cold shock protein homolog	putative regulator; Not classified phenotype: Not classified	K-12_b2597_yfiA_s_at K-12_b0880_cspD_s_at		2.195 3.875	1.757 3.916	1.979 4.055	0.788 1.766	0.785 1.727	0.07 0.427	-0.531 0.431
ybgE	b0735	conserved inner membrane protein	orf; Unknown	K-12_b0735_ybgE_s_at		1.294	0.632	0.809	0.149	0.031	0.464	0.105
yedI yeb1	b1958 b2141	conserved inner membrane protein	orf; Unknown orf: Unknown	K-12_b1958_yedI_s_at		1.434 1.231	1.777 0.653	1.008 1.457	1.105	0.171 0.837	0.293 1.055	0.383 0.058
yohJ ygbE	b2141 b2749	conserved inner membrane protein conserved inner membrane protein	putative enzyme; Not classified	K-12_b2141_yohJ_s_at K-12_b2749_ygbE_s_at		1.231	1.852	2.159	1.561 1.549	0.837	1.161	0.058
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ydgC	b1607	conserved inner membrane protein associated with alginate biosynthe	orf; Unknown	K-12_b1607_ydgC_s_at	2.211	2.025	2.625	1.576	1.231	0.961	1.025
ybgI	b0710 b1908	conserved metal-binding protein conserved metal-binding protein	orf; Unknown orf; Unknown	K-12_b0710_ybgI_s_at K-12_b1908_yecA_s_at	1.089 2.184	1.134 2.559	1.375 2.853	0.673 2.121	-0.24 0.185	-0.267 0.508	-0.937 0.96
yecA	b1908 b0163				2.184 1.87	1.47	1.647	1.133	0.185	-0.44	
yaeH		conserved protein		K-12_b0163_yaeH_s_at							-0.348
ylbA	b0515	conserved protein	orf; Unknown	K-12_b0515_ylbA_s_at	1.341	1.28	1.454	0.31	-0.43	-0.927	-0.634
ybiI	b0803 b0836		orf; Unknown	K-12_b0803_ybiI_s_at	1.163 4.304	1.263	0.245 4.131	0.975 2.805	0.395 1.87	-0.139 0.251	-0.368 -0.113
yliH		conserved protein	putative factor; Not classified	K-12_b0836_yliH_s_at							
ybjI	b0844	conserved protein		K-12_b0844_ybjI_s_at	1.415	0.959	1.882	0.773	0.616	0.25	-0.06
ycbK	b0926		orf; Unknown	K-12_b0926_ycbK_s_at	1.567	1.666	1.923	1.96	-0.321	0.722	0.15
yceH	b1067	conserved protein	orf; Unknown	K-12_b1067_yceH_s_at	1.647	1.209	1.564	0.492	0.897	0.354	-0.403
ycfP	b1108			K-12_b1108_ycfP_s_at	1.586	1.753	1.179	1.721	-0.706	-0.167	-0.189
yciF	b1258	conserved protein	putative structure; Not classified	K-12_b1258_yciF_s_at	1.175	1.13	0.237	1.954	1.215	-0.002	-0.044
ydhQ	b1664	conserved protein	putative enzyme; Not classified	K-12_b1664_ydhQ_s_at	1.615	1.69	1.249	1.374	0.505	-0.591	0.021
yeaO	b1792	conserved protein		K-12_b1792_yeaO_s_at	1.579	1.694	1.131	-0.229	-0.235	-0.836	-0.32
yeeX	b2007	conserved protein	phenotype; Not classified	K-12_b2007_yeeX_s_at	1.367	1.449	1.376	0.535	0.311	-0.874	0.025
yfbU	b2294	conserved protein	orf; Unknown	K-12_b2294_yfbU_s_at	1.525	1.064	1.079	-0.253	-1.93	-0.81	0.003
yggE	b2922	conserved protein	phenotype; Not classified	K-12_b2922_yggE_s_at	1.12	0.572	0.6	1.942	-0.603	-0.637	-0.103
smg	b3284	conserved protein	orf; Unknown	K-12_b3284_smg_s_at	1.198	1.426	1.247	0.722	-0.096	0.014	0.198
yihD	b3858		orf; Unknown	K-12_b3858_yihD_s_at	1.074	0.737	1.393	0.924	-0.033	-1.034	-1.077
yiiS	b3922		orf; Unknown	K-12_b3922_yiiS_s_at	2.483	2.736	2.645	2.749	1.88	0.829	0.152
yjeI	b4144	conserved protein	orf; Unknown	K-12_b4144_yjeI_s_at	1.089	0.949	1.266	-0.01	0.122	0.398	-0.52
yjfO	b4189	conserved protein	orf; Unknown	K-12_b4189_yjfO_s_at	1.579	1.901	0.785	1.357	1.232	0.406	0.461
yaeP	b4406	conserved protein		K-12_b4406_yaeP_s_at	2.228	2.044	2.196	1.435	0.974	-0.232	0.021
erfK	b1990	conserved protein with NAD(P)-binding Rossmann-fold domain		K-12_b1990_erfK_s_at	2.006	2.279	1.343	2.189	1.115	1.06	0.955
phoH	b1020	conserved protein with nucleoside triphosphate hydrolase domain	regulator; Central intermediary metabolism: Phosphorus compounds		4.143	4.418	4.164	2.271	1.347	0.024	0.617
csgA	b1042	cryptic curlin major subunit	regulator; Surface structures	K-12_b1042_csgA_at	3.245	2.999	3.543	1.847	-0.177	0.972	0.549
csgB	b1041	curlin nucleator protein, minor subunit in curli complex	structural component; Surface structures	K-12_b1041_csgB_s_at	1.417	1.514	1.736	1.606	0.236	0.435	0.012
cfa	b1661	cyclopropane fatty acyl phospholipid synthase (unsaturated-phosphol	enzyme; Fatty acid and phosphatidic acid biosynthesis	K-12_b1661_cfa_s_at	2.865	2.382	2.527	1.312	0.08	-0.014	0.991
cysK	b2414	cysteine synthase A, O-acetylserine sulfhydrolase A subunit	enzyme; Amino acid biosynthesis: Cysteine	K-12_b2414_cysK_s_at	3.913	3.79	3.622	2.643	2.089	3.113	2.796
cysM	b2421	cysteine synthase B (O-acetylserine sulfhydrolase B)	enzyme; Amino acid biosynthesis: Cysteine	K-12 b2421 cysM s at	2.914	2.701	3.09	3.3	1.383	1.741	1.329
fliY	b1920	cystine transporter subunit -!- periplasmic-binding component of ABC	putative transport: Not classified	K-12_b1920_fliY_s_at	2.737	2.491	2.292	1.224	1.269	0.283	0.149
cydA	b0733		enzyme; Energy metabolism, carbon: Electron transport	K-12_b0733_cydA_s_at	1.041	0.779	1.131	-0.269	-0.716	-0.672	-0.568
cydB	b0734	cytochrome d terminal oxidase, subunit II	enzyme: Energy metabolism, carbon: Electron transport	K-12 b0734 cydB s at	1.618	1.694	1.631	0.341	0.129	-0.206	0.37
nlpA	b3661	cytoplasmic membrane lipoprotein-28	membrane; Macromolecule synthesis, modification: Lipoprotein	K-12_b3661_nlpA_at	3.5	3.38	2.995	0.854	0.93	2.193	0.891
ilvD	b3771		enzyme; Amino acid biosynthesis: Isoleucine, Valine	K-12 b3771 ilvD s at	3,483	3,512	3.329	1.73	0.076	1.607	1.354
vmfI	b1143		orf: Unknown	K-12 b1143 vmfI at	1.681	1.044	1.785	-0.017	-0.243	-0.819	-0.451
focA	b0904		putative transport; Degradation of small molecules: Carbon compoun		1.432	1.659	0.91	0.54	-0.023	-0.263	-0.669
putA	b1014	fused DNA-binding transcriptional regulator -!- proline dehydrogenase		K-12_b1014_putA_s_at	1.912	1.27	1.543	1.355	0.286	-0.092	-0.367
yfcX	h2341	fused enoyl-CoA hydratase and epimerase and isomerase -!- 3-hydro:		K-12_b2341_yfcX_s_at	1.386	1.11	1.163	2.226	1.751	-0.525	-0.548
fruA	b2167	fused fructose-specific PTS enzymes: IIBcomponent -!- IIC componer		K-12 b2167 fruA s at	1.218	1.249	1.35	1.745	1.796	0.623	0.06
trpC	b1262	fused indole-3-qlycerolphosphate synthetase -!- N-(5-phosphoribosyl		K-12_b1262_trpC_s_at	1.198	1.636	1.53	1.622	0.205	-0.679	-0.402
yliA	b0829	fused predicted peptide transport subunits of ABC superfamily: ATP-b		K-12_b0829_yliA_s_at	3.064	2.831	3.151	1.893	1.835	0.035	0.868
glgC	h3430	glucose-1-phosphate adenvivitransferase	enzyme; Macromolecule synthesis, modification: Polysaccharides - (co	K 12_00025_yllA_3_dc	2.02	1.03	2.085	0.474	0.363	-1.72	-1.685
gltI	b0655	qlutamate and aspartate transporter subunit -!- periplasmic-binding of	putative transport. Not electified	K-12_b0655_gltI_s_at	1.181	0.954	1.216	-0.157	-0.403	-1.193	-0.501
gdhA	b1761		enzyme; Amino acid biosynthesis: Glutamate	K-12_b0033_git1_s_at K-12_b1761_gdhA_s_at	1.299	0.82	1.188	-0.137	-0.403	0.075	-0.175
guna	b1/61		carrier; Biosynthesis of cofactors, carriers: Thioredoxin, glutaredoxin,		1.756	1.178	1.100	0.733	-1.336	-1.491	-0.175
grxB	b1635				2.709	2.448	2.684	1.082		0.158	1.155
gst ilvL	b3766	glutathionine S-transferase ilvG operon leader peptide	enzyme; Biosynthesis of cofactors, carriers: Thioredoxin, qlutaredoxir leader; Amino acid biosynthesis: Isoleucine, Valine	K-12_b1635_gst_s_at K-12_b3766_ilvL_s_at	1.338	2.448	1.478	0.579	0.113 0.169	0.625	-0.974
yccA ilvC	b0970 b3774	inner membrane protein	putative transport; Not classified	K-12_b0970_yccA_s_at	2.298 1.208	1.682	2.27 1.699	-0.026 0.158	0.407 0.158	0.713 -0.085	1.298
		ketol-acid reductoisomerase, NAD(P)-binding		K-12_b3774_ilvC_s_at							
argT	b2310	lysine/arqinine/ornithine transporter subunit -!- periplasmic-binding o		K-12_b2310_argT_s_at	1.323	0.512	1.225	0.879	0.285	0.32	0.264
glcB_	b2976		enzyme; Central intermediary metabolism: Glyoxylate bypass	K-12_b2976_glcB_a_at	1.069	0.76	0.886	1.555	0.601	-0.56	-0.664
yggB	b2924	mechanosensitive channel	putative transport; Not classified	K-12_b2924_yggB_s_at	2.961	2.052	2.306	3.045	1.147	0.143	0.737
msrA	b4219	methionine sulfoxide reductase A	enzyme; Proteins - translation and modification	K-12_b4219_msrA_s_at	1.952	2.164	1.791	0.99	0.449	-0.609	-1.181
moaB	b0782		enzyme; Biosynthesis of cofactors, carriers: Molybdopterin	K-12_b0782_moaB_s_at	1.17	0.245	1.352	-0.585	-0.706	-0.847	-0.929
tesA	b0494	multifunctional acyl-CoA thioesterase I and protease I and lysophosph		K-12_b0494_tesA_s_at	1.353	1.301	1.614	-0.131	-0.013	-0.152	-0.661
ycjI	b1326	murein peptide amidase A	putative enzyme; Not classified	K-12_b1326_ycjI_s_at	1.187	1.138	1.34	1.327	0.255	0.27	-0.256
napA	b2206	nitrate reductase, periplasmic, large subunit	putative enzyme; Energy metabolism, carbon: Anaerobic respiration		1.028	0.591	1.379	1.249	2.334	0.134	-0.479
napB	b2203	nitrate reductase, small, cytochrome C550 subunit, periplasmic		K-12_b2203_napB_s_at	1.076	0.732	1.453	0.77	1.014	0.146	-0.153
nupG	b2964	nucleoside transporter	transport; Transport of small molecules: Nucleosides, purines, pyrimi	K-12_b2964_nupG_s_at	1.026	0.602	0.877	0.954	0.134	-0.164	-0.404
csgG	b1037	outer membrane lipoprotein	structural component; Surface structures	K-12_b1037_csgG_s_at	1.978	1.712	2.169	1.437	0.068	-0.115	0.386
slyB	b1641	outer membrane lipoprotein	putative membrane; Not classified	K-12_b1641_slyB_s_at	1.009	1.055	0.662	0.15	-0.325	-0.075	-0.098
pepT	b1127	peptidase T		K-12_b1127_pepT_s_at	2.445	2.134	1.632	1.879	0.72	0.324	-0.734
pgsA	b1912	phosphatidylglycerophosphate synthetase	enzyme; Macromolecule synthesis, modification: Phospholipids	K-12_b1912_pgsA_s_at	1.109	0.286	1.173	-0.629	0.338	0.603	-0.143
ppsA	b1702	phosphoenolpyruvate synthase	enzyme; Central intermediary metabolism: Gluconeogenesis	K-12_b1702_ppsA_s_at	1.418	0.706	1.646	-0.507	-1.518	-1.974	-1.286
csgE	b1039	predicted transport protein	structural component; Surface structures	K-12_b1039_csgE_s_at	1.882	1.574	2.648	2.318	0.344	0.302	-0.148
yjgR	b4263	predicted ATPase	orf; Unknown	K-12_b4263_yjgR_s_at	1.072	0.876	0.303	1.644	0.653	-0.168	-0.12
yafV	b0219	predicted C-N hydrolase family amidase, NAD(P)-binding	putative enzyme; Not classified	K-12_b0219_yafV_s_at	1.104	1.518	0.641	1.004	0.818	-0.048	-0.204
yeaT	b1799	predicted DNA-binding transcriptional regulator	putative regulator; Not classified	K-12_b1799_yeaT_s_at	1.718	1.156	1.197	1.608	0.657	0.181	-0.246
yghU	b2989	predicted S-transferase	orf; Unknown	K-12_b2989_yghU_s_at	1.692	0.96	1.528	2.435	0.758	-0.159	-0.792
yhhY	b3441	predicted acetyltransferase	orf; Unknown	K-12_b3441_yhhY_at	1.318	1.962	1.438	0.494	-0.447	0.132	-0.914
yccX	b0968	predicted acylphosphatase	orf; Unknown	K-12_b0968_yccX_s_at	2.247	2.521	2.007	2.319	0.728	0.128	-0.428
yncA	b1448	predicted acyltransferase with acyl-CoA N-acyltransferase domain	putative transport; Drug/analog sensitivity	K-12_b1448_yncA_s_at	1.541	1.163	1.537	1.166	0.384	-0.171	-0.679
elaA	b2267		orf; Unknown	K-12_b2267_elaA_s_at	1.134	1.087	1.509	1.729	-0.996	0.157	-0.169
yneI	b1525	predicted aldehyde dehydrogenase	putative enzyme; Not classified	K-12_b1525_yneI_s_at	1.37	1.114	1.538	0.887	0.744	-0.314	-0.357
ycbB	b0925	predicted carboxypeptidase	putative enzyme; Not classified	K-12 b0925 ycbB s at	1.686	1.831	0.87	0.909	0.217	0.112	0.36
ytfB	b4206	predicted cell envelope opacity-associated protein		K-12_b4206_ytfB_s_at	1.442	1.939	1.591	1.207	0.864	-0.243	0.04
ybiC	b0801	predicted dehydrogenase	putative enzyme; Not classified	K-12_b0801_ybiC_s_at	1.7	0.803	1.929	0.833	0.272	0.329	0.029
yddV	b1490	predicted diquanylate cyclase	orf: Unknown	K-12_b1490_yddV_s_at	1.289	1.005	0.494	0.597	0.207	-0.167	0.061
yciI	b1251			K-12_b1251_yciI_s_at	1.859	1.209	1.855	0.138	0.31	-0.939	-1.375
yfcF	b2301	predicted enzyme	orf: Unknown	K-12_b2301_yfcF_s_at	1.326	0.693	0.355	1.105	0.694	0.419	-0.307
vbaJ	b0711	predicted enzyme predicted enzyme subunit	putative enzyme: Not classified	K-12_b0711_ybgJ_s_at	1.089	0.874	1.151	0.231	-0.31	-0.381	-0.816
ybgK	b0711 b0712	predicted enzyme subunit		K-12_b0711_ybgS_s_at K-12_b0712_ybgK_s_at	1.11	1.396	1.022	0.196	-1.495	-0.328	-1.017
yeiG	b2154	predicted esterase	orf: Not classified	K-12_b2154_yeiG_s_at	1.187	0.538	1.24	0.035	-0.242	0.048	-0.564
yliJ	b0838	predicted esterase predicted glutathione S-transferase	putative enzyme; Not classified	K-12_b2134_yeld_s_at K-12 b0838 yliJ s at	2.538	2.088	2.469	1.551	0.279	-0.633	-0.805
vibF	b3592	predicted glutathione S-transferase	putative enzyme; Not classified putative enzyme; Not classified	K-12_00636_yiiJ_s_at K-12_b3592_vibF_s_at	1.623	1.067	0.838	0.399	-0.375	0.385	-0.862
btuE	b1710	predicted glutathione peroxidase	transport; Transport of small molecules: Other	K-12_b3392_ylor_s_at K-12_b1710_btuE_s_at	1.012	0.597	0.061	1.799	-0.373	-0.993	-0.445
b2999	b2999	predicted hydrolase (pseudogene)	orf: Unknown	K-12_b1710_btue_s_at K-12_b2999_s_at	1.012	0.597	0.061	1.799	0.123	-0.104	-0.445
ybhL	b0786			K-12_b2999_s_at K-12_b0786_ybhL_s_at	1.05	1.228	0.181	0.395	0.123	0.429	0.014
YULL	20700	predicted affici membrane protein	on, onmoni	12_00/00_y011L_5_dt	1.3/3	1.220	0.041	0.555	0.00	0.727	0.014

ymgE	b1195	predicted inner membrane protein	orf; Unknown	K-12_b1195_ymgE_s_at	1.213	1.412	0.384	2.983	1.033	0.536	0.092
ydiK	b1688	predicted inner membrane protein	orf; Unknown	K-12_b1688_ydiK_s_at	2.098	2.261	1.865	0.738	1.533	0.516	0.716
yfdC	b2347	predicted inner membrane protein	putative transport; Not classified	K-12_b2347_yfdC_s_at	1.07	0.91	0.441	2.69	0.51	0.175	-0.06
yphA	b2543	predicted inner membrane protein	orf; Unknown	K-12_b2543_yphA_s_at	1.312	1.017	0.396	1.49	0.869	1.018	-0.166
b2670	b2670	predicted inner membrane protein	orf; Unknown	CFT073_c3221_ygaW_s_at	2.408	2.31	2.821	1.941	0.512	0.378	0.301
yhaH	b3103	predicted inner membrane protein	putative carrier; Not classified	K-12_b3103_yhaH_s_at	1.365	1.506	0.467	1.156	0.262	0.048	-0.213
ycgM	b1180	predicted isomerase/hydrolase	putative enzyme; Not classified	K-12_b1180_ycgM_s_at	2.825	2.588	2.962	1.056	1.206	0.882	1.245
yciW	b1287	predicted oxidoreductase	putative enzyme; Not classified	K-12_b1287_yciW_s_at	2.69	2.145	2.712	1.757	1.423	0.669	0.53
ydjA	b1765	predicted oxidoreductase	orf; Unknown	K-12_b1765_ydjA_s_at	1.167	1.263	1.598	0.499	0.63	0.196	-0.256
mviM	b1068	predicted oxidoreductase with NAD(P)-binding Rossmann-fold domain	putative factor; Not classified	K-12_b1068_mviM_s_at	1.448	1.518	1.365	0.987	1.072	-0.477	-0.162
tas	b2834	predicted oxidoreductase, NADP(H)-dependent aldo-keto reductase	orf; Unknown	K-12_b2834_tas_s_at	1.303	1.355	1.302	1.637	0.792	-0.654	0.133
yhdH	b3253	predicted oxidoreductase, Zn-dependent and NAD(P)-binding	putative enzyme; Not classified	K-12_b3253_yhdH_s_at	1.322	1.262	0.957	1.393	-0.625	-0.895	-1.649
yqfA	b2899	predicted oxidoreductase, inner membrane subunit	putative enzyme; Not classified	K-12_b2899_yqfA_s_at	2.808	2.807	2.986	2.881	1.466	1.685	1.309
ydgD	b1598	predicted peptidase	orf; Unknown	O157_ECs2304_s_at	1.644	1.674	0.762	2.131	0.883	-0.137	0.34
tldD	b3244	predicted peptidase	phenotype; Not classified	K-12 b3244 tldD s at	1.026	1.349	0.605	0.922	-0.232	-0.674	-0.246
yliC	b0831	predicted peptide transporter subunit: membrane component of ABC	putative transport; Not classified	K-12 b0831 yliC s at	2.779	1.928	2.864	1.516	1.869	0.826	0.336
yjbA	b4030	predicted phosphate starvation inducible protein	orf; Unknown	K-12_b4030_yjbA_s_at	4.062	4.9	4.068	1.407	1.787	1.391	0.122
yaiB	b0382	predicted protein	orf: Unknown	K-12_b0382_yaiB_s_at	3.421	3.49	3.736	3.186	2.396	1.263	1.146
vbeH	b0625	predicted protein	orf: Unknown	K-12 b0625 vbeH s at	2.041	1.888	1.276	2.202	1.213	1.305	0.473
ybfA	b0699	predicted protein	orf: Unknown	K-12_b0699_ybfA_s_at	2,492	2.397	2.71	1.768	1.377	0.381	0.612
yceF	b1087	predicted protein	orf; Unknown	K-12_b1087_yceF_s_at	2.548	2.17	2.301	1.446	1.134	0.815	0.672
ycfL	b1104	predicted protein	orf; Unknown	K-12 b1104 ycfL s at	1.17	0.9	0.908	0.158	-1.147	-0.86	-0.554
ycqJ	b1177	predicted protein	orf: Unknown	K-12 b1177 ycqJ s at	1.119	1.153	1.442	1.048	-0.125	-0.244	-0.283
ydiH	b1685	predicted protein	orf: Unknown	K-12_b1685_ydiH_s_at	1.677	1.879	2.254	1.576	-0.281	-0.721	-0.031
ydiZ	b1724	predicted protein	orf; Unknown	K-12_b1724_ydiZ_s_at	4.776	4.9	3.946	5.859	1.574	0.152	0.572
yodC	b1957	predicted protein	orf; Unknown	K-12 b1957 yodC s at	2.974	3.684	2.184	4.524	1.086	1.337	0.766
yfqG	b2504	predicted protein	orf: Unknown	K-12_b2504_yfgG_s_at	1.052	0.887	0.947	-0.043	-1.267	0.226	-0.505
yfiL	b2602	predicted protein	orf: Unknown	K-12_b2602_yfiL_s_at	1.188	1.535	0.451	2.277	0.446	0.09	-0.51
ygeA	b2840	predicted racemase	putative transport; Drug/analog sensitivity	K-12_b2840_ygeA_s_at	1.135	1.775	1.401	1.912	0.723	0.38	-0.145
yedY	b1971	predicted reductase	putative enzyme; Not classified	K-12_b2640_ygeA_s_at K-12_b1971_yedY_s_at	1.676	1.383	0.993	1.628	0.884	0.508	0.436
	b2381				1.008	1.018	0.993	1.026	0.182	-0.288	
ypdB	b4135	predicted response regulator in two-component system withYpdA	putative regulator; Not classified orf: Unknown	K-12_b2381_ypdB_s_at	1.008	1.018	1.172	1.658	-0.029	-0.288	-0.712 -1.47
yjdC		predicted transcriptional regulator		K-12_b4135_yjdC_s_at							
ybhK	b0780 b0800	predicted transferase with NAD(P)-binding Rossmann-fold domain	putative structure; Not classified	K-12_b0780_ybhK_s_at	1.288	1.521 2.251	1.273	0.36	0.514 -0.756	0.601	0.103
ybiB		predicted transferase/phosphorylase	putative enzyme; Not classified	K-12_b0800_ybiB_s_at				0.66		-0.369	0.08
csgF	b1038	predicted transport protein	structural component; Surface structures	K-12_b1038_csgF_s_at	3.039	2.964	3.488	2.646	0.282	0.518	0.787
yhjE_	b3523	predicted transporter	putative transport; Not classified	K-12_b3523_yhjE_s_at	1.646	0.96	1.464	0.422	-0.053	1.073	-0.739
yecC	b1917	predicted transporter subunit: ATP-binding component of ABC superfi		K-12_b1917_yecC_s_at	2.068	1.602	1.603	0.438	0.632	0.412	0.606
yecS	b1918	predicted transporter subunit: membrane component of ABC superface		K-12_b1918_yecS_s_at	2.466	1.704	1.995	0.292	0.428	0.519	0.722
yagT	b0286	predicted xanthine dehydrogenase, 2Fe-2S subunit	putative enzyme; Not classified	K-12_b0286_yagT_s_at	1.18	1.732	0.57	2.277	1.054	0.116	-0.137
yfdZ	b2379	prediected aminotransferase, PLP-dependent	putative enzyme; Not classified	K-12_b2379_yfdZ_s_at	1.812	2.146	1.533	1.065	0.52	0.105	-0.194
ycfF	b1103	purine nucleoside phosphoramidase	orf; Unknown	K-12_b1103_ycfF_s_at	1.491	0.828	0.872	0.487	-1.114	-0.941	-0.239
potF	b0854	putrescine transporter subunit: periplasmic-binding component of AB		K-12_b0854_potF_s_at	1.295	0.539	0.51	1.365	-0.737	-1.84	-2.301
pdxJ	b2564	pyridoxine 5'-phosphate synthase	enzyme; Biosynthesis of cofactors, carriers: Pyridoxine	K-12_b2564_pdxJ_s_at	1.448	0.813	1.625	0.973	-0.171	-0.657	-0.258
pykA	b1854	pyruvate kinase II	enzyme; Energy metabolism, carbon: Glycolysis	K-12 b1854 pykA s at	1.395	1.122	1.005	0.316	0.815	-1.348	-1.082
ygiN	b3029	quinol monooxygenase	orf; Unknown	K-12 b3029 ygiN s at	1.085	0.713	1.359	0.238	-0.314	-0.56	-0.557
yljA	b0881	regulatory protein for ClpA substrate specificity	orf; Unknown	K-12_b0881_yljA_s_at	1.704	2.005	1.842	1.828	0.141	-0.498	-0.975
rydB	b4430	regulatory sRNA	,	K-12 b4430 rydB at	1.188	2.034	1.683	2.425	1.39	-0.019	-0.133
csrC	b4457	regulatory sRNA		K-12 b4457 csrC at	2.796	3.483	2.756	2.347	-0.237	-1.214	-1.437
ribC	b1662	riboflavin synthase, alpha subunit	enzyme: Biosynthesis of cofactors, carriers: Riboflavin	K-12_b1662_ribC_s_at	1.139	0.837	0.967	-0.152	0.38	-0.433	-0.174
rimJ	b1066	ribosomal-protein-S5-alanine N-acetyltransferase	enzyme; Ribosomes - maturation and modification	K-12_b1066_rimJ_s_at	1.372	1.938	1.256	0.802	-0.182	-1.219	-0.617
rmf	b0953	ribosome modulation factor	factor; Ribosomes - maturation and modification	LT2_STM1066_rmf_s_at	5.376	5.3	5.489	5.034	2.327	-0.877	-0.588
sufS	b1680	selenocysteine Ivase, PLP-dependent	orf: Unknown	K-12_b1680_sufS_s_at	1.481	1.602	0.678	2.14	0.54	0.416	-0.031
	b3234				1.291	1.461	1.171		0.45		-0.416
degQ	b4432	serine endoprotease, periplasmic small RNA	enzyme; Degradation of proteins, peptides, glyco	K-12_b3234_degQ_s_at				1.96 0.12		-0.44 -0.134	
ryeA						4 272					
				K-12_b4432_ryeA_at	1.765	1.273	2.656		0.646		-0.882
tke1	b4441	small RNA		K-12_b4441_tke1_at	1.117	1.273 0.701	2.656 0.872	1.269	-0.835	-1.555	-1.079
ygjU	b4441 b3089	small RNA sodium:serine/threonine symporter	putative transport; Not classified	K-12_b4441_tke1_at K-12_b3089_ygjU_s_at	1.117 1.49	1.273 0.701 0.855	2.656 0.872 1.389	1.269 1.152	-0.835 -1.188	-1.555 0.136	-1.079 -0.076
ygjU csiE	b4441 b3089 b2535	small RNA sodium:serine/threonine symporter stationary phase inducible protein	orf; Unknown	K-12_b4441_tke1_at K-12_b3089_ygjU_s_at K-12_b2535_csiE_s_at	1.117 1.49 1.053	1.273 0.701 0.855 1.732	2.656 0.872 1.389 0.342	1.269 1.152 1.181	-0.835 -1.188 1.596	-1.555 0.136 0.246	-1.079 -0.076 -0.331
ygjU csiE rsd	b4441 b3089 b2535 b3995	small RNA sodium:serine/threonine symporter stationary phase inducible protein stationary phase protein, binds sigma 70 RNA polymerase subunit	orf; Unknown putative regulator; Not classified	K-12_b4441_tke1_at K-12_b3089_ygjU_s_at K-12_b2535_csiE_s_at K-12_b3995_rsd_s_at	1.117 1.49 1.053 1.735	1.273 0.701 0.855 1.732 1.89	2.656 0.872 1.389 0.342 1.939	1.269 1.152 1.181 0.626	-0.835 -1.188 1.596 -1.427	-1.555 0.136 0.246 -0.841	-1.079 -0.076 -0.331 -1.044
ygjU csiE rsd ydaA	b4441 b3089 b2535 b3995 b1333	small RNA sodium:serine/threonine symporter stationary phase inducible protein stationary phase protein, binds sigma 70 RNA polymerase subunit stress-induced protein	orf; Unknown putative regulator; Not classified orf; Unknown	K-12_b4441_tke1_at K-12_b3089_ygjU_s_at K-12_b2535_csiE_s_at K-12_b3995_rsd_s_at K-12_b1333_ydaA_s_at	1.117 1.49 1.053 1.735 3.464	1.273 0.701 0.855 1.732 1.89 3.606	2.656 0.872 1.389 0.342 1.939 3.536	1.269 1.152 1.181 0.626 2.864	-0.835 -1.188 1.596 -1.427 1.574	-1.555 0.136 0.246 -0.841 0.606	-1.079 -0.076 -0.331 -1.044 1.034
ygjU csiE rsd ydaA yiiT	b4441 b3089 b2535 b3995 b1333 b3923	small RNA sodium:serine/threonine symporter stationary phase inducible protein stationary phase protein, binds sigma 70 RNA polymerase subunit stress-induced protein stress-induced protein stress-induced protein	orf; Unknown putative regulator; Not classified orf; Unknown putative regulator; Not classified	K-12_b4441_tke1_at K-12_b3089_ygjU_s_at K-12_b2535_csiE_s_at K-12_b3995_rsd_s_at K-12_b1333_ydaA_s_at K-12_b3923_yiiT_s_at	1.117 1.49 1.053 1.735 3.464 2.87	1.273 0.701 0.855 1.732 1.89 3.606 3.043	2.656 0.872 1.389 0.342 1.939 3.536 2.883	1.269 1.152 1.181 0.626 2.864 0.979	-0.835 -1.188 1.596 -1.427	-1.555 0.136 0.246 -0.841 0.606 0.17	-1.079 -0.076 -0.331 -1.044 1.034 0.668
ygjU csiE rsd ydaA yiiT ynaF	b4441 b3089 b2535 b3995 b1333 b3923 b1376	small RNA sodium:serine/threonine symporter stationary phase inducible protein stationary phase protein, binds sigma 70 RNA polymerase subunit stress-induced protein stress-induced protein stress-induced protein stress-induced protein stress-induced protein	orf; Unknown putative regulator; Not classified orf; Unknown putative regulator; Not classified putative structure; Not classified	K-12_b4441_tke1_at K-12_b3089_ygjU_s_at K-12_b2535_csiE_s_at K-12_b3995_rsd_s_at K-12_b1333_ydaA_s_at K-12_b3923_yiiT_s_at K-12_b1376_ynaF_s_at	1.117 1.49 1.053 1.735 3.464 2.87 2.911	1.273 0.701 0.855 1.732 1.89 3.606 3.043 3.085	2.656 0.872 1.389 0.342 1.939 3.536 2.883 2.021	1.269 1.152 1.181 0.626 2.864 0.979 1.47	-0.835 -1.188 1.596 -1.427 1.574 1.442	-1.555 0.136 0.246 -0.841 0.606 0.17 1.282	-1.079 -0.076 -0.331 -1.044 1.034 0.668 1.152
ygjU csiE rsd ydaA yiiT ynaF cysN	b4441 b3089 b2535 b3995 b1333 b3923 b1376 b2751	small RNA sodium:serine/threonine symporter stationary phase inducible protein stationary phase protein, binds sigma 70 RNA polymerase subunit stress-induced protein stress-induced pr	orf, Unknown putative regulator; Not classified orf, Unknown putative regulator; Not classified putative regulator; Not classified putative structure; Not classified enzyme; Central intermediary metabolism: Sulfur metabolism	K-12_b4441_tke1_at K-12_b3089_vgjU_s_at K-12_b5253_csiE_s_at K-12_b3995_rsd_s_at K-12_b333_ydaA_s_at K-12_b333_ydiA_s_at K-12_b3323_yiIT_s_at K-12_b375_vgiAs_at	1.117 1.49 1.053 1.735 3.464 2.87 2.911 6.392	1.273 0.701 0.855 1.732 1.89 3.606 3.043 3.085 5.69	2.656 0.872 1.389 0.342 1.939 3.536 2.883 2.021 5.901	1.269 1.152 1.181 0.626 2.864 0.979 1.47 3.994	-0.835 -1.188 1.596 -1.427 1.574 1.442 1	-1.555 0.136 0.246 -0.841 0.606 0.17 1.282 3.303	-1.079 -0.076 -0.331 -1.044 1.034 0.668 1.152 2.948
ygjU csiE rsd ydaA yiiT ynaF cysN cysD	b4441 b3089 b2535 b3995 b1333 b3923 b1376 b2751 b2752	small RNA sodium:serine/threonine symporter stationary phase inducible protein stationary phase protein, binds sigma 70 RNA polymerase subunit stress-induced protein stress-induced protein stress-induced protein, ATP-binding protein sulfate adenylytransferase, subunit 1 sulfate adenylytransferase, subunit 2	orf, Unknown putative regulator; Not classified orf; Unknown putative regulator; Not classified putative regulator; Not classified putative structure; Not classified enzyme; Central intermediary metabolism: Sulfur metabolism enzyme; Central intermediary metabolism: Sulfur metabolism	K-12_b4441_tke1_at K-12_b3089_vgiU_s_at K-12_b2039_csiE_s_at K-12_b3995_csiE_s_at K-12_b3933_vjda_s_at K-12_b3933_vjda_s_at K-12_b3933_vjda_s_at K-12_b3736_vjaaF_s_at K-12_b2751_cysiN_at K-12_b2752_cysiN_at	1.117 1.49 1.053 1.735 3.464 2.87 2.911 6.392 6.739	1.273 0.701 0.855 1.732 1.89 3.606 3.043 3.085 5.69 6.841	2.656 0.872 1.389 0.342 1.939 3.536 2.883 2.021 5.901 6.479	1.269 1.152 1.181 0.626 2.864 0.979 1.47 3.994 5.492	-0.835 -1.188 1.596 -1.427 1.574 1.442 1 4.288 4.318	-1.555 0.136 0.246 -0.841 0.606 0.17 1.282 3.303 4.379	-1.079 -0.076 -0.331 -1.044 1.034 0.668 1.152 2.948 3.545
ygjU csiE rsd ydaA yiiT ynaF cysN cysD cysA	b4441 b3089 b2535 b3995 b1333 b3923 b1376 b2751 b2752 b2422	small RNA sodium:serine/threonine symporter stationary phase inducible protein stationary phase protein, binds sigma 70 RNA polymerase subunit stress-induced protein stress-induced protein stress-induced protein, ATP-binding protein sulfate ademylytransferase, subunit 1 sulfate ademylytransferase, subunit 1 sulfate ademylytransferase, subunit 1- sulfate more protein at the subunit 1- sulfate more protein subunit 1- sulfate throughtate transporter subunit 1- sulfate/thiosulfate transporter subunit 1- sulfate ademylfate ademylfate transporter subunit 1- sulfate ademylfate transporter subunit 1-	orf, Unknown putative regulator; Not classified orf, Unknown putative regulator; Not classified putative structure; Not classified putative structure; Not classified enzyme; Central intermediary metabolism: Sulfur metabolism enzyme; Central intermediary metabolism: Sulfur metabolism transport, Transport of small molecules: Anion molecules:	K-12_b4441_tkel_at K-12_b3089_vgjlU_s_at K-12_b5253_csiE_s_at K-12_b3995_rsiS_s_at K-12_b3933_viriS_s_at K-12_b333_ydaA_s_at K-12_b1376_ynaF_s_at K-12_b12751_cysN_at K-12_b2752_cysD_s_at K-12_b2722_cysD_s_at K-12_b2722_cysA_s_at	1.117 1.49 1.053 1.735 3.464 2.87 2.911 6.392 6.739 4.784	1.273 0.701 0.855 1.732 1.89 3.606 3.043 3.085 5.69 6.841 4.231	2.656 0.872 1.389 0.342 1.939 3.536 2.883 2.021 5.901 6.479 4.435	1.269 1.152 1.181 0.626 2.864 0.979 1.47 3.994 5.492 3.971	-0.835 -1.188 1.596 -1.427 1.574 1.442 1 4.288 4.318 3.152	-1.555 0.136 0.246 -0.841 0.606 0.17 1.282 3.303 4.379 3.11	-1.079 -0.076 -0.331 -1.044 1.034 0.668 1.152 2.948 3.545 3.218
ygjU csiE rsd ydaA yiiT ynaF cysN cysD cysA cysW	b4441 b3089 b2535 b3995 b1333 b3923 b1376 b2751 b2752 b2422 b2423	small RNA sodium:serine/threonine symporter stationary phase inducible protein stationary phase protein, binds sigma 70 RNA polymerase subunit stress-induced protein stress-induced protein stress-induced protein, ATP-binding protein sulfate adenylytransferase, subunit 1 sulfate adenylytransferase, subunit 2 sulfate adenylytransferase, subunit 1 sulfate valengulfate transporter subunit -I- ATP-binding component of A sulfate/thiosulfate transporter subunit -I- membrane component of A	orf; Unknown putative regulator; Not classified orf; Unknown putative regulator; Not classified putative regulator; Not classified putative structure; Not classified putative structure; Not classified enzyme; Central intermediary metabolism: Sulfur metabolism enzyme; Central intermediary metabolism: Sulfur metabolism transport; Transport of small molecules: Anions	K-12 b4441 tke1 at K-12 b3089 ygiU s, at K-12 b2535 csiE s, at K-12 b3995 rsd s at K-12 b3995 rsd s at K-12 b3933 ydaA s_at K-12 b3923 yiii s, at K-12 b375 ynaF s_at K-12 b2751 cysN at K-12 b2752 cysD s_at K-12 b2422 cysA s_at K-12 b2423 cysW x_at	1.117 1.49 1.053 1.735 3.464 2.87 2.911 6.392 6.739 4.784 4.951	1.273 0.701 0.855 1.732 1.89 3.606 3.043 3.085 5.69 6.841 4.231 4.883	2.656 0.872 1.389 0.342 1.939 3.536 2.883 2.021 5.901 6.479 4.435 4.897	1.269 1.152 1.181 0.626 2.864 0.979 1.47 3.994 5.492 3.971 4.027	-0.835 -1.188 1.596 -1.427 1.574 1.442 1 4.288 4.318 3.152 3.165	-1.555 0.136 0.246 -0.841 0.606 0.17 1.282 3.303 4.379 3.11 3.545	-1.079 -0.076 -0.331 -1.044 1.034 0.668 1.152 2.948 3.545 3.218 3.739
ygjU csiE rsd ydaA yiiT ynaF cysN cysD cysA cysW cysU	b4441 b3089 b2535 b3995 b1333 b3923 b1376 b2751 b2752 b2422 b2423 b2424	small RNA sodium:serine/threonine symporter stationary phase inducible protein stationary phase protein, binds sigma 70 RNA polymerase subunit stress-induced protein stress-induced protein stress-induced protein stress-induced protein sulfate adenylyltransferase, subunit 1 sulfate adenylyltransferase, subunit 2 sulfate/thiosulfate transporter subunit -!- ATP-binding component of sulfate/thiosulfate transporter subunit -!- membrane component of A sulfate/thiosulfate transporter subunit -!- membrane component of A sulfate/thiosulfate transporter subunit -!- membrane component of A	orf, Unknown putative regulator; Not classified orf, Unknown putative regulator; Not classified putative structure; Not classified putative structure; Not classified putative structure; Not classified enzyme; Central intermediary metabolism: Sulfur metabolism enzyme; Central intermediary metabolism: Sulfur metabolism transport, Transport of small molecules: Anions Itransport; Transport of small molecules: Anions	K-12_b4441_tke1_at K-12_b3089_vgjU_s_at K-12_b2535_csiE_s_at K-12_b3995_csiE_s_at K-12_b3935_vsiS_s_at K-12_b333_ydaA_s_at K-12_b3923_yiiT_s_at K-12_b375_vsiS_sat K-12_b2751_cysN_at K-12_b2752_cysD_s_at K-12_b2422_cysA_s_at K-12_b2422_cysM_x_at K-12_b2424_cysU_s_at	1.117 1.49 1.053 1.735 3.464 2.87 2.911 6.392 6.739 4.784 4.951 4.773	1.273 0.701 0.855 1.732 1.89 3.606 3.043 3.085 5.69 6.841 4.231 4.883 4.93	2.656 0.872 1.389 0.342 1.939 3.536 2.883 2.021 5.901 6.479 4.435 4.897 4.652	1.269 1.152 1.181 0.626 2.864 0.979 1.47 3.994 5.492 3.971 4.027 3.575	-0.835 -1.188 1.596 -1.427 1.574 1.442 1 4.288 4.318 3.152 3.165 2.781	-1.555 0.136 0.246 -0.841 0.606 0.17 1.282 3.303 4.379 3.11 3.545 3.409	-1.079 -0.076 -0.331 -1.044 1.034 0.668 1.152 2.948 3.545 3.218 3.739 3.296
ygjU csiE rsd ydaA yiiT ynaF cysN cysD cysA cysW cysU cysU cysJ	b4441 b3089 b2535 b3995 b1333 b3923 b1376 b2751 b2752 b2422 b2423 b2424 b2764	small RNA sodium:serine/threonine symporter stationary phase inducible protein stationary phase inducible protein stationary phase protein, binds sigma 70 RNA polymerase subunit stress-induced protein stress-induced protein, ATP-binding protein sulfate adenylytransferase, subunit 1 sulfate adenylytransferase, subunit 2 sulfate/thiosulfate transporter subunit -I- ATP-binding component of A sulfate/thiosulfate transporter subunit -I- membrane component of A sulfate refuserase, alpha subunit, flavoprotein	orf, Unknown putative regulator; Not classified orf, Unknown putative regulator; Not classified putative regulator; Not classified putative structure; Not classified enzyme; Central intermediary metabolism: Sulfur metabolism transport; Transport of small molecules: Anions Itransport; Transport of small molecules: Anions Itransport; Transport of small molecules: Anions enzyme; Central intermediary metabolism: Sulfur metabolism enzyme; Central intermediary metabolism: Sulfur metabolism	K-12 b4441 tke1 at K-12 b3089 ygiU s. at K-12 b2535 cslE s. at K-12 b1335 cslE s. at K-12 b1333 ydaA s. at K-12 b1333 ydaA s. at K-12 b1337 ynaF s. at K-12 b2751 cysN at K-12 b2752 cysD s. at K-12 b2422 cysA s. at K-12 b2423 cysW x. at K-12 b2426 cysU s. at K-12 b2426 cysU s. at K-12 b2426 cysU s. at	1.117 1.49 1.053 1.735 3.464 2.87 2.911 6.392 6.739 4.784 4.951 4.773 5.858	1.273 0.701 0.855 1.732 1.89 3.606 3.043 3.085 5.69 6.841 4.231 4.883 4.93 5.983	2.656 0.872 1.389 0.342 1.939 3.536 2.883 2.021 5.901 6.479 4.435 4.897 4.652 5.657	1.269 1.152 1.181 0.626 2.864 0.979 1.47 3.994 5.492 3.971 4.027 3.575 4.928	-0.835 -1.188 1.596 -1.427 1.574 1.442 1 4.288 4.318 3.152 3.165 2.781	-1.555 0.136 0.246 -0.841 0.606 0.17 1.282 3.303 4.379 3.11 3.545 3.409	-1.079 -0.076 -0.331 -1.044 1.034 0.668 1.152 2.948 3.545 3.218 3.739 3.296 3.114
ygjU csiE rsd ydaA yiiT ynaF cysN cysN cysA cysW cysU cysU cysJ cysI	b4441 b3089 b2535 b3995 b1333 b3923 b1376 b2751 b2752 b2422 b2423 b2424 b2764	small RNA sodium:serine/threonine symporter stationary phase inducible protein stationary phase protein, binds sigma 70 RNA polymerase subunit stress-induced protein stress-induced protein stress-induced protein stress-induced protein sulfate adenylyltransferase, subunit 1 sulfate adenylyltransferase, subunit 1 sulfate deflylyltransferase, subunit 1 sulfate (Thiosulfate transporter subunit -!- ATP-binding component of a sulfate/thiosulfate transporter subunit -!- membrane component of A sulfate/thiosulfate transporter subunit -!- membrane component of A sulfate/thiosulfate transporter subunit -!- membrane component of A sulfate reductase, alpha subunit, flavoprotein sulfite reductase, beta subunit, MAD(P)-binding, heme-binding	orf, Unknown putative regulator; Not classified orf, Unknown putative regulator; Not classified putative structure; Not classified putative structure; Not classified putative structure; Not classified enzyme; Central intermediary metabolism: Sulfur metabolism enzyme; Central intermediary metabolism: Sulfur metabolism transport; Transport of small molecules: Anions Itransport; Transport of small molecules: Anions Itransport; Transport of small molecules: Anions enzyme; Central intermediary metabolism: Sulfur metabolism enzyme; Central intermediary metabolism: Sulfur metabolism enzyme; Central intermediary metabolism: Sulfur metabolism	K-12 b4441 tkel_at K-12 b3089 ygjU_s_at K-12 b2535_csiE_s_at K-12 b2535_csiE_s_at K-12 b1333_ydba_s_at K-12 b1333_ydba_s_at K-12 b1376_ynaF_s_at K-12_b1376_ynaF_s_at K-12_b2751_cysh_at K-12_b2751_cysh_s_at K-12_b2422_cysh_s_at K-12_b2422_cysh_s_at K-12_b2424_cysU_s_at K-12_b2424_cysU_s_at K-12_b2764_cysl_s_at K-12_b2763_cysl_s_at K-12_b2763_cysl_s_at	1.117 1.49 1.053 1.735 3.464 2.87 2.911 6.392 6.739 4.784 4.951 4.773 5.858 5.38	1.273 0.701 0.855 1.732 1.89 3.606 3.043 3.085 5.69 6.841 4.231 4.883 4.93 5.983 5.063	2.656 0.872 1.389 0.342 1.939 3.536 2.883 2.021 5.901 6.479 4.435 4.897 4.652 5.657	1.269 1.152 1.181 0.626 2.864 0.979 1.47 3.994 5.492 3.971 4.027 3.575 4.928 3.314	-0.835 -1.188 1.596 -1.427 1.574 1.442 1 4.288 4.318 3.152 3.165 2.781 4.51 3.5	-1.555 0.136 0.246 -0.841 0.606 0.17 1.282 3.303 4.379 3.11 3.545 3.409 3.402 2.073	-1.079 -0.076 -0.331 -1.044 1.034 0.668 1.152 2.948 3.545 3.218 3.739 3.296 3.114 2.189
ygjU csiE rsd ydaA yiiT ynaF cysN cysD cysA cysW cysU cysU cysJ cysJ garR	b4441 b3089 b2535 b3995 b1333 b1376 b2751 b2752 b2422 b2423 b2424 b2764 b2763 b3125	small RNA sodium:serine/threonine symporter stationary phase inducible protein stationary phase protein, binds sigma 70 RNA polymerase subunit stress-induced protein stress-induced protein stress-induced protein, ATP-binding protein sulfate adenylytransferase, subunit 1 sulfate adenylytransferase, subunit 2 sulfate denylytransferase, subunit 1- sulfate tansporter subunit -1- ATP-binding component of a sulfate/thiosulfate transporter subunit -1- membrane component of A sulfate/thiosulfate transporter subunit -1- membrane component of A sulfate/thiosulfate transporter subunit -1- membrane component of a sulfate reductase, apiha subunit, flavoprotein sulfite reductase.	orf, Unknown putative regulator; Not classified orf, Unknown putative regulator; Not classified putative structure; Not classified putative structure; Not classified enzyme; Central intermediary metabolism: Sulfur metabolism enzyme; Central intermediary metabolism: Sulfur metabolism transport; Transport of small molecules: Anions Itransport; Transport of small molecules: Anions Itransport; Transport of small molecules: Anions enzyme; Central intermediary metabolism: Sulfur metabolism enzyme; Central intermediary metabolism: Sulfur metabolism putative enzyme; Not classified	K-12 b4441 tke1 at K-12 b3089 ygiU s. at K-12 b2535 csiE s. at K-12 b1935 csiE s. at K-12 b1939 yrid s. at K-12 b1933 yrid s. at K-12 b1933 yrid s. at K-12 b1936 yrid s. at K-12 b1936 yrid s. at K-12 b2751 cysD s. at K-12 b2752 cysD s. at K-12 b2422 cysM x. at K-12 b2423 cysW x. at K-12 b2426 cysU s. at K-12 b2426 cysU s. at K-12 b2764 cysJ s. at K-12 b2763 cysI s. at K-12 b2763 cysI s. at	1.117 1.49 1.053 1.735 3.464 2.87 2.911 6.392 6.739 4.784 4.951 4.773 5.858 5.38	1.273 0.701 0.855 1.732 1.89 3.606 3.043 3.085 5.69 6.841 4.231 4.883 4.93 5.983 5.063 0.893	2.656 0.872 1.389 0.342 1.939 3.536 2.883 2.021 5.901 6.479 4.435 4.897 4.652 5.657 4.949 1.023	1.269 1.152 1.181 0.626 2.864 0.979 1.47 3.994 5.492 3.971 4.027 3.575 4.928 3.314 2.362	-0.835 -1.188 1.596 -1.427 1.574 1.442 1 4.288 4.318 3.152 3.165 2.781 4.51 3.5	-1.555 0.136 0.246 -0.841 0.606 0.17 1.282 3.303 4.379 3.11 3.545 3.402 2.073 0.632	-1.079 -0.076 -0.331 -1.044 1.034 0.668 1.152 2.948 3.545 3.218 3.739 3.296 3.114 2.189 -0.125
ygjU csiE rsd ydaA yiiT ynaF cysN cysD cysA cysW cysU cysJ cysI garR tauB	b4441 b3089 b2535 b3995 b1333 b3923 b1376 b2751 b2752 b2422 b2423 b2424 b2764 b2763 b3125 b0366	small RNA sodium:serine/threonine symporter stationary phase inducible protein stationary phase protein, binds sigma 70 RNA polymerase subunit stress-induced protein stress-induced protein stress-induced protein stress-induced protein sulfate adenylytransferase, subunit 1 sulfate adenylytransferase, subunit 1 sulfate adenylytransferase, subunit 1 sulfate/thiosulfate transporter subunit -I- ATP-binding component of A sulfate/thiosulfate transporter subunit -I- membrane component of A sulfate/thiosulfate transporter subunit, reperting the subunit of the sulfate/thiosulfate transporter subunit -I- membrane component of A sulfite reductase, plab subunit, flavoprotein sulfite reductase, beta subunit, NAD(P)-binding, heme-binding tartronate semialdehyde reductase	orf, Unknown putative regulator; Not classified orf, Unknown putative regulator; Not classified putative structure; Not classified putative structure; Not classified putative structure; Not classified enzyme; Central intermediary metabolism: Sulfur metabolism enzyme; Central intermediary metabolism: Sulfur metabolism transport; Transport of small molecules: Anions Itransport; Transport of small molecules: Anions enzyme; Central intermediary metabolism: Sulfur metabolism enzyme; Central intermediary metabolism: Sulfur metabolism putative enzyme; Not classified it ransport of small molecules: Amino acids, amines	K-12 b4441 tke1 at K-12 b3089 ygiU s. at K-12 b2535 csiE s. at K-12 b2935 csiE s. at K-12 b3995 rsd s. at K-12 b3932 yiiT s. at K-12 b1376 ynaF s. at K-12 b1376 ynaF s. at K-12 b2751 cysh. at K-12 b2752 cysD s. at K-12 b2422 cysA s. at K-12 b2424 cysU s. at K-12 b2424 cysU s. at K-12 b2763 cysI s. at K-12 b2763 cysI s. at K-12 b2763 cysI s. at K-12 b3763 cysI s. at K-12 b3766 fauB s. at	1.117 1.49 1.053 1.735 3.464 2.87 2.911 6.392 6.739 4.784 4.951 4.773 5.858 5.38 1.253 1.197	1.273 0.701 0.855 1.732 1.89 3.606 3.043 3.085 5.69 6.841 4.231 4.883 4.93 5.983 5.063 0.893	2.656 0.872 1.389 0.342 1.939 3.536 2.883 2.021 5.901 6.479 4.435 4.897 4.652 5.657 4.949 1.023 1.257	1.269 1.152 1.181 0.626 2.864 0.979 1.47 3.994 5.492 3.971 4.027 3.575 4.928 3.314 2.362 1.359	-0.835 -1.188 1.596 -1.427 1.574 1.442 1 4.288 4.318 3.152 3.165 2.781 4.51 3.5	-1.555 0.136 0.246 -0.841 0.606 0.17 1.282 3.303 4.379 3.11 3.545 3.409 2.073 0.632 0.632	-1.079 -0.076 -0.331 -1.044 1.034 -0.668 1.152 2.948 3.545 3.218 3.739 3.296 3.114 2.189 -0.125
ygjU csiE rsd ydaA yiiT ynaF cysN cysD cysA cysW cysU cysJ garR tauB cysP	b4441 b3089 b2535 b3995 b1333 b3923 b1376 b2751 b2752 b2422 b2423 b2424 b2764 b2763 b3125 b0366 b2425	small RNA sodium:serine/threonine symporter stationary phase inducible protein stationary phase inducible protein stationary phase protein, binds sigma 70 RNA polymerase subunit stress-induced protein stress-induced protein stress-induced protein stress-induced protein sulfate adenylytransferase, subunit 1 sulfate adenylytransferase, subunit 1 sulfate adenylytransferase, subunit 2 sulfate/thiosulfate transporter subunit 1-I- ATP-binding component of A sulfate/thiosulfate transporter subunit -I- membrane component of A sulfate/thiosulfate transporter subunit -I- membrane component of A sulfate/thiosulfate transporter subunit -I- membrane component of A sulfate reductase, apiha subunit, flavoprotein sulfite reductase, apih	orf, Unknown putative regulator; Not classified orf, Unknown putative regulator; Not classified putative structure; Not classified putative structure; Not classified enzyme; Central intermediary metabolism: Sulfur metabolism enzyme; Central intermediary metabolism: Sulfur metabolism transport; Transport of small molecules: Anions Itransport; Transport of small molecules: Anions Itransport; Transport of small molecules: Anions enzyme; Central intermediary metabolism: Sulfur metabolism enzyme; Central intermediary metabolism: Sulfur metabolism putative enzyme; Not classified itransport; Transport of small molecules: Anion adds, amines Itransport; Transport of small molecules: Anions	K-12 b4441 tkel at K-12 b3089 ygiU s, at K-12 b2535 csiE s, at K-12 b2935 csiE s, at K-12 b1935 csiE s, at K-12 b1932 yiii S at K-12 b1973 yiii S at K-12 b1976 ynaf s, at K-12 b1976 ynaf s, at K-12 b2752 cysD s, at K-12 b2422 cysA s, at K-12 b2422 cysA s, at K-12 b2426 cysU s, at K-12 b2426 cysU s, at K-12 b2766 cysJ s, at K-12 b2763 cysI s, at K-12 b3763 cysI s, at K-12 b3763 cysI s, at K-12 b3765 cysI s, at K-12 b3765 cysI s, at K-12 b3766 tsuB s, at K-12 b3766 tsuB s, at K-12 b3766 tsuB s, at	1.117 1.49 1.053 1.735 3.464 2.87 2.911 6.392 6.799 4.784 4.951 4.773 5.858 5.38 1.197 5.822	1.273 0.701 0.855 1.732 1.89 3.606 3.043 3.085 5.69 6.841 4.231 4.883 4.93 5.983 5.063 0.893 1.178 6.303	2.656 0.872 1.389 0.342 1.939 3.536 2.883 2.021 5.901 6.479 4.435 4.897 4.652 5.657 4.949 1.023 1.257 5.38	1.269 1.152 1.181 0.626 2.864 0.979 1.47 3.994 5.492 3.971 4.027 3.575 4.928 3.314 2.362 1.359 3.442	-0.835 -1.188 1.596 -1.427 1.574 1.442 1 4.288 4.318 3.152 3.165 2.781 4.51 3.5 1.07 1.528 3.666	-1.555 0.136 0.246 -0.841 0.606 0.17 1.282 3.303 4.379 3.11 3.545 3.409 3.402 2.073 0.632 0.601 3.514	-1.079 -0.076 -0.331 -1.044 1.034 0.668 1.152 2.948 3.545 3.218 3.739 3.296 3.114 2.189 -0.125 0.172
ygjl csiE rsd Ada Ada ydda Ayda AydiT ynaF cysD cysD cysU cysU cysU garR tauB cysP jivA	b4441 b3089 b2535 b3995 b1333 b3923 b1376 b2751 b2752 b2422 b2423 b2424 b2764 b2764 b2763 b3125 b0366 b2425 b3772	small RNA sodium:serine/threonine symporter stationary phase inducible protein stationary phase protein, binds sigma 70 RNA polymerase subunit stress-induced protein stress-induced protein stress-induced protein stress-induced protein stress-induced protein sulfate adenylytransferase, subunit 1 sulfate adenylytransferase, subunit 1 sulfate adenylytransferase, subunit 2 sulfate/thiosulfate transporter subunit -I- ATP-binding component of A sulfate/thiosulfate transporter subunit -I- membrane component of A sulfate reductase, alpha subunit, flavoprotein sulfite reductase, beta subunit, NAD(P)-binding, heme-binding tartronate semialdehyde reductase taurine transporter subunit -I- ATP-binding component of ABC superf thiosulfate transporter subunit -I- arp-pinding component of ABC superf thiosulfate transporter subunit -I- periplasmic-binding component of	orf, Unknown putative regulator; Not classified orf, Unknown putative regulator; Not classified putative structure; Not classified putative structure; Not classified putative structure; Not classified enzyme; Central intermediary metabolism: Sulfur metabolism transport; Transport of small molecules: Anions Itransport; Transport of small molecules: Anions Itransport; Transport of small molecules: Anions enzyme; Central intermediary metabolism: Sulfur metabolism enzyme; Central intermediary metabolism: Sulfur metabolism putative enzyme; Not classified transport of small molecules: Anion acids, amines Itransport; Transport of small molecules: Anions enzyme; Post no acid biosynthesis: Soleculer, Valine	K-12 b4441 tkel_at K-12 b3089 ygiU_s_at K-12 b2535_csiE_s_at K-12 b2535_csiE_s_at K-12 b395_fsid_s_at K-12 b3935_fsid_s_at K-12 b3932_yiii_s_at K-12 b3923_yiii_s_at K-12 b375_cysh_at K-12 b375_cysh_s_at K-12 b275_cysh_s_at K-12 b2422_cysh_s_at K-12 b2422_cysh_s_at K-12 b2424_cysU_s_at K-12 b2424_cysU_s_at K-12 b2764_cysl_s_at K-12 b3763_cysl_s_at K-12 b3763_cysl_s_at K-12 b3165_garR_s_at K-12 b3165_garR_s_s_at K-12 b3165_garR_s_s_at K-12 b3165_garR_s_s_at K-12 b3177_gilyA_s_s_at	1.117 1.49 1.053 1.735 3.464 2.87 2.911 6.392 6.739 4.784 4.951 4.773 5.858 5.38 1.253 1.197 5.822	1.273 0.701 0.855 1.732 1.89 3.606 3.043 3.085 6.841 4.231 4.883 4.93 5.983 5.063 0.893 1.178 6.303 2.882	2.656 0.872 1.389 0.342 1.939 3.536 2.883 2.021 5.901 6.479 4.435 4.897 4.652 5.657 4.949 1.023 1.257 5.38	1.269 1.152 1.181 0.626 2.864 0.979 1.47 3.994 5.492 3.971 4.027 3.575 4.928 3.314 2.362 1.359 3.442 1.347	-0.835 -1.188 1.596 -1.427 1.574 1.442 1 4.288 4.318 3.165 2.781 4.51 3.5 1.07 1.528 3.666 0.825	-1.555 0.136 0.246 -0.841 0.606 0.17 1.282 3.303 4.379 3.111 3.545 3.409 3.409 2.073 0.632 0.601 3.514	-1.079 -0.076 -0.331 -1.044 1.034 0.668 1.152 2.948 3.545 3.218 3.739 3.296 3.114 2.189 -0.125 0.172 3.701
ygjU csiE rsd ydaA yiiT ynaF cysN cysD cysA cysW cysU cysJ garR tauB cysP	b4441 b3089 b2535 b3995 b1333 b3923 b1376 b2751 b2752 b2422 b2423 b2424 b2764 b2763 b3125 b0366 b2425 b345 b345 b345 b345 b345 b345 b345 b34	small RNA sodium:serine/threonine symporter stationary phase inducible protein stationary phase inducible protein stationary phase protein, binds sigma 70 RNA polymerase subunit stress-induced protein stress-induced protein stress-induced protein stress-induced protein sulfate adenylytransferase, subunit 1 sulfate adenylytransferase, subunit 1 sulfate adenylytransferase, subunit 2 sulfate/thiosulfate transporter subunit 1-I- ATP-binding component of A sulfate/thiosulfate transporter subunit -I- membrane component of A sulfate/thiosulfate transporter subunit -I- membrane component of A sulfate/thiosulfate transporter subunit -I- membrane component of A sulfate reductase, apiha subunit, flavoprotein sulfite reductase, apih	orf, Unknown putative regulator; Not classified orf, Unknown putative regulator; Not classified putative structure; Not classified putative structure; Not classified enzyme; Central intermediary metabolism: Sulfur metabolism enzyme; Central intermediary metabolism: Sulfur metabolism transport; Transport of small molecules: Anions Itransport; Transport of small molecules: Anions Itransport; Transport of small molecules: Anions enzyme; Central intermediary metabolism: Sulfur metabolism enzyme; Central intermediary metabolism: Sulfur metabolism putative enzyme; Not classified itransport; Transport of small molecules: Anion adds, amines Itransport; Transport of small molecules: Anions	K-12 b4441 tke1 at K-12 b3089 ygiU s, at K-12 b2535 csiE s, at K-12 b1935 csiE s, at K-12 b1935 csiE s, at K-12 b1937 yill s at K-12 b1973 yill s at K-12 b1976 ynaf s, at K-12 b1976 ynaf s, at K-12 b2751 cysD s, at K-12 b2752 cysD s, at K-12 b2422 cysW x, at K-12 b2421 cysU s, at K-12 b246 cysU s, at K-12 b2764 cysI s, at K-12 b2764 cysI s, at K-12 b2763 cysI s, at K-12 b2765 cysI s, at K-12 b3765 cysI s, at K-12 b3765 cysI s, at K-12 b3765 cysI s, at K-12 b3767 cysI s, at K-12 b3787 s, at K-12 b3888 csiB s, at	1.117 1.49 1.053 1.735 3.464 2.87 2.911 6.392 6.799 4.784 4.951 4.773 5.858 5.38 1.197 5.822	1.273 0.701 0.855 1.732 1.89 3.606 3.043 3.085 5.69 6.841 4.231 4.883 4.93 5.983 5.063 0.893 1.178 6.303	2.656 0.872 1.389 0.342 1.939 3.536 2.021 5.901 6.479 4.435 4.897 4.652 5.657 4.949 1.023 1.257 5.38 3.259 0.442	1.269 1.152 1.181 0.626 2.864 0.979 1.47 3.994 5.492 3.971 4.027 3.575 4.928 3.314 2.362 1.359 3.442 1.347 0.257	-0.835 -1.188 1.596 -1.427 1.574 1.442 1 4.288 4.318 3.152 3.165 2.781 4.51 3.5 1.07 1.528 3.666 0.825 0.885	-1.555 0.136 0.246 -0.841 0.606 0.17 1.282 3.303 4.379 3.11 3.545 3.402 2.073 0.632 0.601 3.514 1.05	-1.079 -0.076 -0.331 -1.044 1.034 0.668 1.152 2.948 3.545 3.218 3.739 3.296 3.114 2.189 -0.125 0.172
ygjl csiE rsd ydaA ydiaA yiiT ynaF cysN cysD cysD cysU cysU cysI garR tauB cysP iivA deoA trpA	b4441 b3089 b2535 b3995 b1333 b13923 b1376 b2751 b2752 b2423 b2424 b2764 b2763 b3125 b0366 b2425 b3772 b4382 b1260	small RNA sodium:serine/threonine symporter stationary phase inducible protein stationary phase protein, binds sigma 70 RNA polymerase subunit stress-induced protein stress-induced protein stress-induced protein, ATP-binding protein sulfate adenylytransferase, subunit 1 sulfate adenylytransferase, subunit 1 sulfate adenylytransferase, subunit 1 sulfate adenylytransferase, subunit 1 ATP-binding component of a sulfate/thiosulfate transporter subunit -1- membrane component of a sulfate/thiosulfate transporter subunit -1- at -1- sulfate reductase, plaha subunit, flavoprotein sulfate reductase, beta subunit, flavoprotein sulfate reductase, beta subunit, flavoprotein taurine transporter subunit -1- aTP-binding component of ABC superf thiosulfate transporter subunit -1- a TP-binding component of threonine deaminase thymidine phosphorylase tryptophan synthase, alpha subunit	orf, Unknown putative regulator; Not classified orf, Unknown putative regulator; Not classified putative structure; Not classified putative structure; Not classified putative structure; Not classified putative structure; Not classified enzyme; Central intermediary metabolism: Sulfur metabolism transport; Gransport of small molecules: Anions Itransport; Transport of small molecules: Anions Itransport; Transport of small molecules: Anions enzyme; Central intermediary metabolism: Sulfur metabolism enzyme; Central intermediary metabolism: Sulfur metabolism putative enzyme; Not classified transport; Transport of small molecules: Anions acids, amines Itransport; Transport of small molecules: Anions enzyme; Parion acid biosynthesis: Isolecules, Valine enzyme; Salvage of nucleosides and nucleotides enzyme; Salvage of nucleosides and nucleotides enzyme; Salvage of nucleosides and nucleotides enzyme; Anion acid biosynthesis: Tryptophan	K-12 b4441 tkel_at K-12 b3089 ygiU_s_at K-12 b2535_csiE_s_at K-12 b2535_csiE_s_at K-12 b3935_rsiG_s_at K-12 b3935_rsiG_s_at K-12 b3932_yiIT_s_at K-12 b375_cysh_at K-12 b375_cysh_s_at K-12 b2752_cysh_s_at K-12 b2422_cysh_s_at K-12 b2422_cysh_s_at K-12 b2424_cysU_s_at K-12 b2424_cysU_s_at K-12 b2764_cysl_s_at K-12 b3125_garR_s_at K-12 b3435_deoA_s_at K-12 b3432_deoA_s_at K-12 b3432_deoA_s_at	1.117 1.49 1.053 1.735 3.464 2.87 2.911 6.392 6.739 4.784 4.951 4.773 5.858 5.38 1.253 1.153 7.5822 3.372 1.309	1.273 0.701 0.855 1.732 1.89 3.606 3.043 3.085 5.69 6.841 4.281 4.93 5.983 5.063 0.893 1.178 6.303 2.882 0.523	2.656 0.872 1.389 0.342 1.939 3.536 2.883 2.021 5.901 6.479 4.435 4.897 4.652 5.657 4.949 1.023 1.257 5.38 3.259 0.442 2.092	1.269 1.152 1.181 0.626 2.864 0.979 1.47 3.994 4.027 3.575 4.928 3.314 2.362 1.359 3.442 1.347 0.253	-0.835 -1.188 1.596 -1.427 1.574 1.442 4.318 4.318 3.152 3.165 2.781 4.51 3.5 1.07 1.528 3.666 0.825 0.085	-1.555 0.136 0.246 -0.841 0.606 0.17 1.282 3.303 4.379 3.11 3.545 3.409 2.073 0.632 0.601 3.514 1.05 -0.704 -0.805	-1.079 -0.076 -0.331 -1.044 1.034 0.668 1.152 2.948 3.545 3.218 3.739 3.296 3.114 2.189 -0.172 3.701 0.777 -0.774
ygil csiE rsd ydaA yiiT ynaF cysN cysD cysA cysW cysU cysJ cysJ garR tauB cysP ilvA deoA	b4441 b3089 b2535 b3995 b1333 b3923 b1376 b2751 b2752 b2422 b2423 b2424 b2764 b2763 b3125 b0366 b2425 b345 b345 b345 b345 b345 b345 b345 b34	small RNA sodium:serine/threonine symporter stationary phase inducible protein stationary phase protein, binds sigma 70 RNA polymerase subunit stress-induced protein sulfate ademylytransferase, subunit 1 sulfate ademylytransferase, subunit 1 sulfate (Phiosulfate transporter subunit -1- ATP-binding component of a sulfate/thiosulfate transporter subunit -1- membrane component of A sulfate/thiosulfate transporter subunit -1- membrane component of A sulfate/thiosulfate transporter subunit -1- membrane component of A sulfate reductase, apiha subunit, flavoprotein sulfite reductase, plate subunit -1- pripiading component of ABC super flosulfate transporter subunit -1- periplasmic-binding component of threonine deaminase thymdine phosphorylase	orf, Unknown putative regulator; Not classified orf, Unknown putative regulator; Not classified putative structure; Not classified putative structure; Not classified putative structure; Not classified putative structure; Not classified enzyme; Central intermediary metabolism: Sulfur metabolism enzyme; Central intermediary metabolism: Sulfur metabolism transport; Transport of small molecules: Anions transport; Transport of small molecules: Anions transport; Transport of small molecules: Anions enzyme; Central intermediary metabolism: Sulfur metabolism enzyme; Central intermediary metabolism: Sulfur metabolism transport; Transport of small molecules: Anion acids, amines transport, Transport of small molecules: Anion enzyme; Anion acid biosynthesis: Isoleucine, Valine enzyme; Anion acids and nucleotides	K-12 b4441 tke1 at K-12 b3089 ygiU s, at K-12 b2535 csiE s, at K-12 b1935 csiE s, at K-12 b1935 csiE s, at K-12 b1937 yill s at K-12 b1973 yill s at K-12 b1976 ynaf s, at K-12 b1976 ynaf s, at K-12 b2751 cysD s, at K-12 b2752 cysD s, at K-12 b2422 cysW x, at K-12 b2421 cysU s, at K-12 b246 cysU s, at K-12 b2764 cysI s, at K-12 b2764 cysI s, at K-12 b2763 cysI s, at K-12 b2765 cysI s, at K-12 b3765 cysI s, at K-12 b3765 cysI s, at K-12 b3765 cysI s, at K-12 b3767 cysI s, at K-12 b3787 s, at K-12 b3888 csiB s, at	1.117 1.49 1.053 1.735 3.464 2.87 2.911 6.392 6.739 4.784 4.951 4.773 5.858 1.253 1.197 5.822 3.372 1.309	1.273 0.701 0.855 1.732 1.89 3.606 3.043 3.085 5.69 6.841 4.231 4.883 4.93 5.983 5.063 0.893 1.178 6.303 2.882 0.523 1.7	2.656 0.872 1.389 0.342 1.939 3.536 2.021 5.901 6.479 4.435 4.897 4.652 5.657 4.949 1.023 1.257 5.38 3.259 0.442	1.269 1.152 1.181 0.626 2.864 0.979 1.47 3.994 5.492 3.971 4.027 3.575 4.928 3.314 2.362 1.347 0.257 1.083 0.23	-0.835 -1.188 1.596 -1.427 1.574 1.442 1 4.288 4.318 3.152 3.165 2.781 4.51 3.5 1.07 1.528 3.666 0.825 0.885	-1.555 0.136 0.246 -0.841 0.606 0.17 1.282 3.303 4.379 3.11 3.545 3.402 2.073 0.632 0.601 3.514 1.05	-1.079 -0.076 -0.331 -1.044 1.034 0.668 1.152 2.948 3.545 3.218 3.739 3.296 3.114 2.189 -0.125 0.172 3.701 0.77
ygjl U csiE rsd ydaA yliT ynaF cysh Cysh CysD cysA cysU cysJ garR tauB cysP ilvA deoA trpA trpB	b4441 b3089 b2535 b3995 b1333 b13923 b1376 b2751 b2752 b2423 b2424 b2764 b2763 b3125 b0366 b2425 b3772 b4382 b1260	small RNA sodium:serine/threonine symporter stationary phase inducible protein stationary phase protein, binds sigma 70 RNA polymerase subunit stress-induced protein stress-induced protein stress-induced protein, ATP-binding protein sulfate ademylytransferase, subunit 1 sulfate ademylytransferase, subunit 1 sulfate ademylytransferase, subunit 1-! ATP-binding component of sulfate/thiosulfate transporter subunit -!- membrane component of A sulfate/thiosulfate transporter subunit -!- brinding component of ABC super fithiosulfate transporter subunit -!- periplasmic-binding component of threonine deaminase thymidine phosphorylase tryptophan synthase, alpha subunit tryptophan synthase, alpha subunit	orf, Unknown putative regulator; Not classified orf, Unknown putative regulator; Not classified putative structure; Not classified putative structure; Not classified putative structure; Not classified putative structure; Not classified enzyme; Central intermediary metabolism: Sulfur metabolism enzyme; Central intermediary metabolism: Sulfur metabolism transport; Transport of small molecules: Anions transport; Transport of small molecules: Anions transport; Transport of small molecules: Anions enzyme; Central intermediary metabolism: Sulfur metabolism enzyme; Central intermediary metabolism: Sulfur metabolism enzyme; Central intermediary metabolism: Sulfur metabolism transport; Transport of small molecules: Anion acids, anines transport, Transport of small molecules: Anion enzyme; Anino acid biosynthesis: Inyptophan enzyme; Anino acid biosynthesis: Tryptophan	K-12 b4441 tkel at K-12 b3089 ygiU s at K-12 b2035 csiE s at K-12 b2935 csiE s at K-12 b1939 csid s at K-12 b1939 csid s at K-12 b1939 yill s at K-12 b1975 lcysN at K-12 b1975 lcysN at K-12 b2752 cysD s at K-12 b2423 cysW x at K-12 b2423 cysW x at K-12 b2424 cysU s at K-12 b2426 cysU s at K-12 b2764 cysI s at K-12 b2764 cysI s at K-12 b2764 cysI s at K-12 b2765 cysI s at K-12 b2785 cysP s at K-12 b2782 cysP s at K-12 b2760 trpA s at K-12 b1260 trpA s at	1.117 1.49 1.053 1.735 3.464 2.87 2.911 6.392 6.739 4.784 4.951 4.773 5.858 5.38 1.253 1.197 5.822 3.372 1.309 1.82	1.273 0.701 0.855 1.732 1.89 3.606 3.043 3.085 5.69 6.841 4.281 4.93 5.983 5.063 0.893 1.178 6.303 2.882 0.523	2.656 0.872 1.389 0.342 1.939 3.536 2.883 2.021 5.901 6.479 4.435 4.897 4.652 5.657 4.949 1.023 1.257 5.38 3.259 0.442 2.092	1.269 1.152 1.181 0.626 2.864 0.979 1.47 3.994 4.027 3.575 4.928 3.314 2.362 1.359 3.442 1.347 0.253	-0.835 -1.188 1.596 -1.427 1.574 1.442 4.318 4.318 3.152 3.165 2.781 4.51 3.5 1.07 1.528 3.666 0.825 0.085	-1.555 0.136 0.246 -0.841 0.606 0.17 1.282 3.303 4.379 3.11 3.545 3.409 2.073 0.632 0.601 3.514 1.05 -0.704 -0.805	-1.079 -0.076 -0.331 -1.044 1.034 0.668 1.152 2.948 3.545 3.218 3.739 3.296 3.114 2.189 -0.172 3.701 0.777 -0.774
ygjl csiE rsd ydaA ydiaA yiiT ynaF cysN cysD cysD cysU cysU cysI garR tauB cysP iivA deoA trpA	b4441 b3089 b2535 b3995 b1333 b3923 b1376 b2751 b2752 b2422 b2423 b2424 b2764 b2763 b3125 b0366 b2425 b3772 b4382 b1260 b1261	small RNA sodium:serine/threonine symporter stationary phase inducible protein stationary phase protein, binds sigma 70 RNA polymerase subunit stress-induced protein stress-induced protein stress-induced protein, ATP-binding protein sulfate adenylytransferase, subunit 1 sulfate adenylytransferase, subunit 1 sulfate adenylytransferase, subunit 1 sulfate adenylytransferase, subunit 1 ATP-binding component of a sulfate/thiosulfate transporter subunit -1- membrane component of a sulfate/thiosulfate transporter subunit -1- at -1- sulfate reductase, plaha subunit, flavoprotein sulfate reductase, beta subunit, flavoprotein sulfate reductase, beta subunit, flavoprotein taurine transporter subunit -1- aTP-binding component of ABC superf thiosulfate transporter subunit -1- a TP-binding component of threonine deaminase thymidine phosphorylase tryptophan synthase, alpha subunit	orf, Unknown putative regulator; Not classified orf, Unknown putative regulator; Not classified putative structure; Not classified putative structure; Not classified putative structure; Not classified putative structure; Not classified enzyme; Central intermediary metabolism: Sulfur metabolism transport; Gransport of small molecules: Anions Itransport; Transport of small molecules: Anions Itransport; Transport of small molecules: Anions enzyme; Central intermediary metabolism: Sulfur metabolism enzyme; Central intermediary metabolism: Sulfur metabolism putative enzyme; Not classified transport; Transport of small molecules: Anions acids, amines Itransport; Transport of small molecules: Anions enzyme; Parion acid biosynthesis: Isolecules, Valine enzyme; Salvage of nucleosides and nucleotides enzyme; Salvage of nucleosides and nucleotides enzyme; Salvage of nucleosides and nucleotides enzyme; Anion acid biosynthesis: Tryptophan	K-12 b4441 tkel. at K-12 b3089 ygiU s. at K-12 b2535 csiE s. at K-12 b2935 csiE s. at K-12 b3995 rsd s. at K-12 b3939 rsd s. at K-12 b3932 yill s. at K-12 b3932 yill s. at K-12 b3751 cysN. at K-12 b3751 cysN. at K-12 b2752 cysD s. at K-12 b2742 cysD s. at K-12 b2422 cysW x. at K-12 b2424 cysU s. at K-12 b2424 cysU s. at K-12 b2763 cysI s. at K-12 b3125 garR s. at K-12 b3126 [crpR s. at K-12 b3456 [crpR s. at K-12 b3450 [crpR s. at	1.117 1.49 1.053 1.735 3.464 2.87 2.911 6.392 6.739 4.784 4.951 4.773 5.858 5.38 1.253 1.153 7.5822 3.372 1.309	1.273 0.701 0.855 1.732 1.89 3.606 3.043 3.085 5.69 6.841 4.231 4.883 4.93 5.983 5.063 0.893 1.178 6.303 2.882 0.523 1.7	2.656 0.872 1.389 0.342 1.939 3.536 2.021 5.901 6.479 4.435 4.897 4.652 5.657 4.949 1.023 1.257 5.38 3.252 2.092 1.538	1.269 1.152 1.181 0.626 2.864 0.979 1.47 3.994 5.492 3.971 4.027 3.575 4.928 3.314 2.362 1.347 0.257 1.083 0.23	-0.835 -1.188 1.596 -1.427 1.574 1.442 1 4.288 4.318 3.152 3.165 2.781 4.51 3.5 1.07 1.528 3.666 0.825 0.085 -0.31	-1.555 0.136 0.246 -0.841 0.606 0.17 1.282 3.303 4.379 3.11 3.545 3.409 3.402 2.073 0.632 0.601 3.514 1.05 -0.704 -0.805 -0.901	-1.079 -0.076 -0.331 -1.044 -1.034 -0.668 1.152 2.948 3.545 3.218 3.296 3.114 2.189 -0.125 0.172 3.701 0.77 -0.714 -1.094 -1.173
ygil csiE rsd ydaA yliT ynaF cysN cysD cysD cysU cysU cysU cysU cysI garR tauB cysP ilvA deoA trpB uspA udp	b4441 b3089 b2535 b3995 b1333 b13376 b2751 b2752 b2423 b2424 b2764 b2763 b3125 b0366 b2475 b3423 b2424 b2764 b2763 b3125 b0366 b2475 b3482 b1260 b1261 b3495	small RNA sodium:serine/threonine symporter stationary phase inducible protein stationary phase protein, binds sigma 70 RNA polymerase subunit stress-induced protein stress-induced protein stress-induced protein, ATP-binding protein sulfate adenylytransferase, subunit 1 sulfate adenylytransferase, subunit 1 sulfate adenylytransferase, subunit 2 sulfate/thiosulfate transporter subunit -1- ATP-binding component of A sulfate/thiosulfate transporter subunit -1- membrane component of A sulfate reductase, alpha subunit, flavoprotein sulfite reductase, alpha subunit -1- ATP-binding component of ABC superf thiosulfate transporter subunit -1- ATP-binding component of subunit -1- periplasmic-binding component of threonine deaminase thymidine phosphorylase tryptophan synthase, alpha subunit tryptophan synthase, beta subunit tryptophan synthase, beta subunit universal stress global response regulator	orf, Unknown putative regulator; Not classified orf, Unknown putative regulator; Not classified putative structure; Not classified putative structure; Not classified putative structure; Not classified putative structure; Not classified enzyme; Central intermediary metabolism: Sulfur metabolism transport; Carnaport of small molecules: Anions Itransport; Transport of small molecules: Anions Itransport; Transport of small molecules: Anions enzyme; Central intermediary metabolism: Sulfur metabolism enzyme; Central interpative special sulfur metabolism enzyme; Amino acid biosynthesis: Toptophan enzyme; Amino acid biosynthesis: Tryptophan enzyme; Amino acid biosynthesis: Tryptophan putative regulator; Adaptations, atypical conditions enzyme; Siniogae of nucleosides and nucleotides	K-12 b4441 tkel at K-12 b3089 ygiU s at K-12 b2035 csiE s at K-12 b2935 csiE s at K-12 b1939 csid s at K-12 b1939 csid s at K-12 b1932 yill s at K-12 b1975 lcysN at K-12 b1975 lcysN at K-12 b2752 cysD s at K-12 b2423 cysW x at K-12 b2423 cysW x s K-12 b2424 cysU s at K-12 b2426 cysU s at K-12 b2764 cysI s at K-12 b2764 cysI s at K-12 b2764 cysI s at K-12 b2765 cysI s at K-12 b2785 cysP s at K-12 b2782 cysP s at K-12 b2760 cysI s at K-12 b2761 cysI s as K-12 b2761 cysI s at	1.117 1.49 1.053 1.755 3.464 2.87 2.911 6.392 6.739 4.784 4.951 4.773 5.858 5.38 1.253 1.197 5.822 3.372 1.309 1.82	1.273 0.701 0.855 1.732 1.89 3.606 3.043 3.085 5.69 6.841 4.231 4.833 4.93 5.983 5.963 0.893 1.178 6.303 2.882 0.523 1.7 1.45	2.656 0.872 1.389 0.342 1.399 3.536 2.883 2.021 5.901 6.479 4.435 4.897 4.652 4.994 1.023 1.257 5.38 3.259 0.442 2.092 1.257 5.38	1.269 1.151 1.61 1.626 2.864 0.979 1.47 3.994 5.492 3.971 4.027 3.575 4.928 3.314 2.362 1.359 3.344 2.362 1.359 3.442 1.347 0.257 1.083 0.23 -2.398	-0.835 -1.188 1.596 -1.427 1.574 1.442 1.428 4.318 3.152 3.165 2.781 4.51 3.5 1.07 1.528 3.666 0.825 0.085 -0.31 -0.241 -3.661	-1.555 0.136 0.246 -0.841 0.606 0.17 1.282 3.303 4.379 3.11 3.545 3.409 2.073 0.601 3.514 1.05 -0.704 -0.805 -0.901	-1.079 -0.076 -0.331 -1.044 1.034 0.668 1.152 2.948 3.545 3.218 3.739 3.296 3.114 2.189 -0.172 3.701 0.77 -0.714 -1.094 -1.173 -0.757
ygjlU cslE rsd ydaA yilT ynaF cysN cysD cysA cysW cysU cysJ garR tauB cysP livA deoA trpA trpB uspA udp ybgR	b4441 b3089 b2535 b3995 b1333 b1376 b2751 b2752 b2422 b2423 b2424 b2764 b2763 b3125 b0366 b2425 b33772 b4382 b1260 b1261 b3495 b3831 b0752	small RNA sodium:serine/threonine symporter stationary phase inducible protein stationary phase protein, binds sigma 70 RNA polymerase subunit stress-induced protein stress-induced protein stress-induced protein, ATP-binding protein sulfate adenylytransferase, subunit 1 sulfate adenylytransferase, subunit 2 sulfate/thiosulfate transporter subunit -I- ATP-binding component of a sulfate/thiosulfate transporter subunit -I- membrane component of A sulfate/thiosulfate transporter subunit -I- periplamic phase tarronate semiladelyde reductase taurine transporter subunit -I- ATP-binding component of ABC superf thiosulfate transporter subunit -I- ATP-binding component of threonine deaminase thymidine phosphorylase thymidine phosphorylase line efflux system	orf, Unknown putative regulator; Not classified orf, Unknown putative regulator; Not classified putative structure; Not classified putative structure; Not classified putative structure; Not classified putative structure; Not classified enzyme; Central intermediary metabolism: Sulfur metabolism transport, Transport of small molecules: Anions Itransport; Transport of small molecules: Anions Itransport; Transport of small molecules: Anions enzyme; Central intermediary metabolism: Sulfur metabolism enzyme; Central intermediary metabolism: Sulfur metabolism putative enzyme; Not classified transport; Transport of small molecules: Anions enzyme; Transport of small molecules: Anions enzyme; Salvage of nucleosides and nucleotides enzyme; Salvage of nucleosides and nucleotides enzyme; Anino acid biosynthesis: Tryptophan enzyme; Anino acid biosynthesis: Tryptophan putative regulator; Adaptations, atypical conditions enzyme; Salvage of nucleosides and nucleotides putative transport; Not classified	K-12 b4441 tke1 at K-12 b3089 ygiU s at K-12 b2535 csiE s at K-12 b2935 csiE s at K-12 b3995 rsd s at K-12 b3935 rsd s at K-12 b3932 yill s at K-12 b3932 yill s at K-12 b3975 lcysN at K-12 b3751 cysN at K-12 b2751 cysN s at K-12 b2742 cysM s at K-12 b2422 cysM s at K-12 b2424 cysU s at K-12 b2424 cysU s at K-12 b2763 cysI s at K-12 b3125 garR s at K-12 b3495 cspM s at K-12 b3495 cspM s at K-12 b3495 sat	1.117 1.49 1.053 1.735 3.464 2.87 2.911 6.392 6.739 4.784 4.951 4.773 5.858 5.38 1.253 1.197 5.822 3.372 1.309 1.207 2.068	1.273 0.701 0.855 1.732 1.89 3.606 3.043 3.085 5.69 6.841 4.231 4.893 5.063 0.893 5.063 0.893 1.178 6.303 0.893 1.178 1.296 0.355 0.355 0.35	2.656 0.872 1.389 0.342 1.939 3.536 2.883 2.021 5.901 6.479 4.435 4.652 5.657 5.657 5.27 5.27 5.27 5.27 5.27 5.27 5.27 5.	1.269 1.152 1.181 0.626 2.864 0.979 1.47 3.994 5.492 3.971 4.027 3.575 4.928 3.314 2.362 1.359 1.347 0.257 1.083 0.23 -2.398 0.305 0.793	-0.835 -1.188 1.596 -1.427 1.574 1.442 1 4.288 4.318 3.155 2.781 4.51 3.5 1.07 1.528 3.666 0.825 0.825 0.081 -3.681 0.067	-1.555 0.136 0.246 -0.841 0.606 0.17 1.282 3.303 4.379 3.11 3.545 3.402 2.073 0.632 0.632 0.601 3.514 1.05 -0.703 0.632 0.632 0.601 0.17 0.05 0.17 0.05 0.17 0.05 0.17 0.05 0.17 0.05 0.17 0.05 0.05 0.05 0.05 0.05 0.05 0.05 0.0	-1.079 -0.076 -0.331 -1.044 1.034 0.668 1.152 2.948 3.545 3.218 3.739 3.296 3.114 2.189 -0.125 0.172 3.701 0.77 -0.714 -1.094 -1.173 -0.757 -0.944 -0.04
ygil csiE rsd ydaA yliT ynaF cysN cysD cysD cysU cysU cysU cysU cysI garR tauB cysP ilvA deoA trpB uspA udp	b4441 b3089 b2535 b3995 b1393 b1333 b1376 b2751 b2752 b2422 b2423 b2424 b2764 b2763 b3125 b0366 b2425 b3772 b4382 b1260 b1261 b3495 b3831	small RNA sodium:serine/threonine symporter stationary phase inducible protein stationary phase protein, binds sigma 70 RNA polymerase subunit stress:-induced protein stress:-induced protein stress:-induced protein stress:-induced protein stress:-induced protein, ATP-binding protein sulfate adenylyltransferase, subunit 1 sulfate adenylyltransferase, subunit 1 sulfate/thiosulfate transporter subunit -!- ATP-binding component of a sulfate/thiosulfate transporter subunit -!- membrane component of A sulfate/thiosulfate transporter subunit -!- aTP-binding surfter reductase, plans subunit, flavoprotein sulfate reductase, plans subunit trytophan synthase, alpha subunit trytophan synthase, alpha subunit trytophan synthase, alpha subunit trytophan synthase, beta subunit universal stress global response regulator urridine phosphorylase	orf, Unknown putative regulator; Not classified orf, Unknown putative regulator; Not classified putative structure; Not classified putative structure; Not classified putative structure; Not classified putative structure; Not classified enzyme; Central intermediary metabolism: Sulfur metabolism transport; Carnaport of small molecules: Anions Itransport; Transport of small molecules: Anions Itransport; Transport of small molecules: Anions enzyme; Central intermediary metabolism: Sulfur metabolism enzyme; Central interpative special sulfur metabolism enzyme; Amino acid biosynthesis: Toptophan enzyme; Amino acid biosynthesis: Tryptophan enzyme; Amino acid biosynthesis: Tryptophan putative regulator; Adaptations, atypical conditions enzyme; Siniogae of nucleosides and nucleotides	K-12 b4441 tkel at K-12 b3089 ygiU s at K-12 b2035 csiE s at K-12 b2935 csiE s at K-12 b19395 rsd s at K-12 b19395 rsd s at K-12 b19392 yill s at K-12 b1975 cysh s at K-12 b1975 cysh s at K-12 b2751 cysh s at K-12 b2752 cysh s at K-12 b2722 cysh s at K-12 b2422 cysh s at K-12 b2422 cysh s at K-12 b2423 cysh s at K-12 b2764 cysl s at K-12 b2764 cysl s at K-12 b2764 cysl s at K-12 b2762 cysl s at K-12 b2762 cysl s at K-12 b2762 cysl s at K-12 b2782 cysh s at K-12 b2761 cysl s at K-12 b2761 cysh s at K-12 b2781 cysh s at K-12 b2781 cysh s at K-12 b3791 cysh s at	1.117 1.49 1.053 1.735 3.464 2.87 2.911 6.392 6.739 4.784 4.951 5.88 5.38 1.253 1.197 5.822 3.372 1.399 1.82 1.189	1.273 0.701 0.855 1.732 3.606 3.043 3.043 3.043 5.69 6.841 4.231 4.883 4.93 5.983 5.983 5.063 0.893 1.178 6.303 2.882 1.75 1.75 1.75 1.75 1.75 1.75 1.75 1.75	2.656 0.872 1.389 0.342 1.939 3.536 2.021 6.479 4.435 4.897 4.652 5.657 4.949 1.023 1.257 5.38 3.259 1.253 0.442 2.092 1.523 0.995 0.442 0.442 0.443 0.442 0.443 0.442 0.443 0.443 0.442 0.443 0	1.269 1.152 1.181 0.626 2.864 0.979 1.47 3.994 5.492 3.971 4.027 4.027 4.027 4.027 4.025 1.359 3.442 1.359 3.442 1.359 3.442 1.359 3.429 1.357 1.083 0.237 0.237 0.239 0.305	-0.835 -1.188 1.596 -1.427 1.574 1.472 1.424 4.218 4.318 3.152 3.165 2.781 4.51 3.5 1.07 1.528 3.666 0.825 0.085 -0.31 -0.241 -3.681 0.067	-1.555 0.136 0.246 -0.841 0.606 0.17 1.282 3.303 4.379 3.11 3.545 3.409 3.402 2.073 0.632 0.601 3.514 1.05 -0.704 -0.805 -0.994 -0.063	-1.079 -0.076 -0.331 -1.044 -1.034 0.668 1.152 2.948 3.545 3.218 3.739 3.296 3.114 2.189 -0.125 0.172 3.701 0.77 -0.714 -1.094 -1.173 -0.757 -0.944
ygjlU cslE rsd ydaA yilT ynaF cysN cysD cysA cysW cysU cysJ garR tauB cysP livA deoA trpA trpB uspA udp ybgR	b4441 b3089 b2535 b3995 b1333 b1376 b2751 b2752 b2422 b2423 b2424 b2764 b2763 b3125 b0366 b2425 b3426 b1261 b3495 b3831 b0752	small RNA sodium:serine/threonine symporter stationary phase inducible protein stationary phase protein, binds sigma 70 RNA polymerase subunit stress-induced protein stress-induced protein stress-induced protein, ATP-binding protein sulfate adenylytransferase, subunit 1 sulfate adenylytransferase, subunit 2 sulfate/thiosulfate transporter subunit -I- ATP-binding component of a sulfate/thiosulfate transporter subunit -I- membrane component of A sulfate/thiosulfate transporter subunit -I- periplamic phase tarronate semiladelyde reductase taurine transporter subunit -I- ATP-binding component of ABC superf thiosulfate transporter subunit -I- ATP-binding component of threonine deaminase thymidine phosphorylase thymidine phosphorylase line efflux system	orf, Unknown putative regulator; Not classified orf, Unknown putative regulator; Not classified putative structure; Not classified putative structure; Not classified putative structure; Not classified putative structure; Not classified enzyme; Central intermediary metabolism: Sulfur metabolism transport, Transport of small molecules: Anions Itransport; Transport of small molecules: Anions Itransport; Transport of small molecules: Anions enzyme; Central intermediary metabolism: Sulfur metabolism enzyme; Central intermediary metabolism: Sulfur metabolism putative enzyme; Not classified transport; Transport of small molecules: Anions enzyme; Transport of small molecules: Anions enzyme; Salvage of nucleosides and nucleotides enzyme; Salvage of nucleosides and nucleotides enzyme; Anino acid biosynthesis: Tryptophan enzyme; Anino acid biosynthesis: Tryptophan putative regulator; Adaptations, atypical conditions enzyme; Salvage of nucleosides and nucleotides putative transport; Not classified	K-12 b4441 tke1 at K-12 b3089 ygiU s at K-12 b2535 csiE s at K-12 b2935 csiE s at K-12 b3995 rsd s at K-12 b3935 rsd s at K-12 b3932 yill s at K-12 b3932 yill s at K-12 b3975 lcysN at K-12 b3751 cysN at K-12 b2751 cysN s at K-12 b2742 cysM s at K-12 b2422 cysM s at K-12 b2424 cysU s at K-12 b2424 cysU s at K-12 b2763 cysI s at K-12 b3125 garR s at K-12 b3495 cspM s at K-12 b3495 cspM s at K-12 b3495 sat	1.117 1.49 1.053 1.735 3.464 2.87 2.911 6.392 6.739 4.784 4.951 4.773 5.858 5.38 1.253 1.197 5.822 3.372 1.309 1.207 2.068	1.273 0.701 0.855 1.732 1.89 3.606 3.043 3.085 5.69 6.841 4.231 4.893 5.063 0.893 5.063 0.893 1.178 6.303 0.893 1.178 1.296 0.355 0.355 0.35	2.656 0.872 1.389 0.342 1.939 3.536 2.883 2.021 5.901 6.479 4.435 4.652 5.657 5.657 5.27 5.27 5.27 5.27 5.27 5.27 5.27 5.	1.269 1.152 1.181 0.626 2.864 0.979 1.47 3.994 5.492 3.971 4.027 3.575 4.928 3.314 2.362 1.359 1.347 0.257 1.083 0.23 -2.398 0.305 0.793	-0.835 -1.188 1.596 -1.427 1.574 1.442 1 4.288 4.318 3.155 2.781 4.51 3.5 1.07 1.528 3.666 0.825 0.825 0.081 -3.681 0.067	-1.555 0.136 0.246 -0.841 0.606 0.17 1.282 3.303 4.379 3.11 3.545 3.402 2.073 0.632 0.632 0.601 3.514 1.05 -0.703 0.632 0.632 0.601 0.17 0.05 0.17 0.05 0.17 0.05 0.17 0.05 0.17 0.05 0.17 0.05 0.05 0.05 0.05 0.05 0.05 0.05 0.0	-1.079 -0.076 -0.331 -1.044 1.034 0.668 1.152 2.948 3.545 3.218 3.739 3.296 3.114 2.189 -0.125 0.172 3.701 0.77 -0.714 -1.094 -1.173 -0.757 -0.944 -0.04
ygjIU csIE rsd ydaA yiIT ynaF cysN cysN cysD cysA cysW cysU cysI garR tauB cysP livA deoA trpA trpB uspA udp ybgR ygiE  Venn: Unaffe	b4441 b3089 b2535 b3995 b1333 b13736 b2751 b27752 b2422 b2423 b2424 b2764 b2763 b3125 b0366 b2425 b3772 b4382 b1260 b1261 b3495 b3831 b0752 b3040	small RNA sodium:serine/threonine symporter stationary phase inducible protein stationary phase protein, binds sigma 70 RNA polymerase subunit stress-induced protein stress-induced protein stress-induced protein, ATP-binding protein sulfate adenylytransferase, subunit 1 sulfate adenylytransferase, subunit 2 sulfate/thiosulfate transporter subunit -I- ATP-binding component of a sulfate/thiosulfate transporter subunit -I- membrane component of A sulfate/thiosulfate transporter subunit -I- periplamic phase tarronate semiladelyde reductase taurine transporter subunit -I- ATP-binding component of ABC superf thiosulfate transporter subunit -I- ATP-binding component of threonine deaminase thymidine phosphorylase thymidine phosphorylase line efflux system	orf, Unknown putative regulator; Not classified orf, Unknown putative regulator; Not classified putative structure; Not classified putative structure; Not classified putative structure; Not classified putative structure; Not classified enzyme; Central intermediary metabolism: Sulfur metabolism transport, Transport of small molecules: Anions Itransport; Transport of small molecules: Anions Itransport; Transport of small molecules: Anions enzyme; Central intermediary metabolism: Sulfur metabolism enzyme; Central intermediary metabolism: Sulfur metabolism putative enzyme; Not classified transport; Transport of small molecules: Anions enzyme; Transport of small molecules: Anions enzyme; Salvage of nucleosides and nucleotides enzyme; Salvage of nucleosides and nucleotides enzyme; Anino acid biosynthesis: Tryptophan enzyme; Anino acid biosynthesis: Tryptophan putative regulator; Adaptations, atypical conditions enzyme; Salvage of nucleosides and nucleotides putative transport; Not classified	K-12 b4441 tke1 at K-12 b3089 ygiU s at K-12 b2535 csiE s at K-12 b2935 csiE s at K-12 b3995 rsd s at K-12 b3935 rsd s at K-12 b3932 yill s at K-12 b3932 yill s at K-12 b3975 lcysN at K-12 b3751 cysN at K-12 b2751 cysN s at K-12 b2742 cysM s at K-12 b2422 cysM s at K-12 b2424 cysU s at K-12 b2424 cysU s at K-12 b2763 cysI s at K-12 b3125 garR s at K-12 b3495 cspM s at K-12 b3495 cspM s at K-12 b3495 sat	1.117 1.49 1.053 1.735 3.464 2.87 2.911 6.392 6.739 4.784 4.951 4.773 5.858 5.38 1.253 1.197 5.822 3.372 1.309 1.207 2.068	1.273 0.701 0.855 1.732 1.89 3.606 3.043 3.085 5.69 6.841 4.231 4.893 5.063 0.893 5.063 0.893 1.178 6.303 0.893 1.178 1.296 0.355 0.355 0.35	2.656 0.872 1.389 0.342 1.939 3.536 2.883 2.021 5.901 6.479 4.435 4.652 5.657 5.657 5.27 5.27 5.27 5.27 5.27 5.27 5.27 5.	1.269 1.152 1.181 0.626 2.864 0.979 1.47 3.994 5.492 3.971 4.027 3.575 4.928 3.314 2.362 1.359 1.347 0.257 1.083 0.23 -2.398 0.305 0.793	-0.835 -1.188 1.596 -1.427 1.574 1.442 1 4.288 4.318 3.155 2.781 4.51 3.5 1.07 1.528 3.666 0.825 0.825 0.081 -3.681 0.067	-1.555 0.136 0.246 -0.841 0.606 0.17 1.282 3.303 4.379 3.11 3.545 3.402 2.073 0.632 0.632 0.601 3.514 1.05 -0.703 0.632 0.632 0.601 0.17 0.05 0.17 0.05 0.17 0.05 0.17 0.05 0.17 0.05 0.17 0.05 0.05 0.05 0.05 0.05 0.05 0.05 0.0	-1.079 -0.076 -0.331 -1.044 1.034 0.668 1.152 2.948 3.545 3.218 3.739 3.296 3.114 2.189 -0.125 0.172 3.701 0.77 -0.714 -1.094 -1.173 -0.757 -0.944 -0.04
ygil csiE rsd ydaA yliT ard ydaA yliT ynaF cysN cysD cysA cysU cysJ cysJ garR tauB cysP ibvA deoA trpA trpB uspA ygiE	b4441 b3089 b2535 b3995 b1333 b13736 b2751 b27752 b2422 b2423 b2424 b2764 b2763 b3125 b0366 b2425 b3772 b4382 b1260 b1261 b3495 b3831 b0752 b3040	small RNA sodium:serine/threonine symporter stationary phase inducible protein stationary phase protein, binds sigma 70 RNA polymerase subunit stress-induced protein stress-induced protein stress-induced protein, ATP-binding protein sulfate adenylytransferase, subunit 1 sulfate adenylytransferase, subunit 2 sulfate/thiosulfate transporter subunit -I- ATP-binding component of a sulfate/thiosulfate transporter subunit -I- membrane component of A sulfate/thiosulfate transporter subunit -I- periplamic phase tarronate semiladelyde reductase taurine transporter subunit -I- ATP-binding component of ABC superf thiosulfate transporter subunit -I- ATP-binding component of threonine deaminase thymidine phosphorylase thymidine phosphorylase line efflux system	orf, Unknown putative regulator; Not classified orf, Unknown putative regulator; Not classified putative structure; Not classified putative structure; Not classified putative structure; Not classified putative structure; Not classified enzyme; Central intermediary metabolism: Sulfur metabolism transport, Transport of small molecules: Anions Itransport; Transport of small molecules: Anions Itransport; Transport of small molecules: Anions enzyme; Central intermediary metabolism: Sulfur metabolism enzyme; Central intermediary metabolism: Sulfur metabolism putative enzyme; Not classified transport; Transport of small molecules: Anions enzyme; Transport of small molecules: Anions enzyme; Salvage of nucleosides and nucleotides enzyme; Salvage of nucleosides and nucleotides enzyme; Anino acid biosynthesis: Tryptophan enzyme; Anino acid biosynthesis: Tryptophan putative regulator; Adaptations, atypical conditions enzyme; Salvage of nucleosides and nucleotides putative transport; Not classified	K-12 b4441 tke1 at K-12 b3089 ygiU s at K-12 b2535 csiE s at K-12 b2935 csiE s at K-12 b3995 rsd s at K-12 b3935 rsd s at K-12 b3932 yill s at K-12 b3932 yill s at K-12 b3975 lcysN at K-12 b3751 cysN at K-12 b2751 cysN s at K-12 b2742 cysM s at K-12 b2422 cysM s at K-12 b2424 cysU s at K-12 b2424 cysU s at K-12 b2763 cysI s at K-12 b3125 garR s at K-12 b3495 cspM s at K-12 b3495 cspM s at K-12 b3495 sat	1.117 1.49 1.053 1.735 3.464 2.87 2.911 6.392 6.739 4.784 4.951 4.773 5.858 5.38 1.253 1.197 5.822 3.372 1.309 1.207 2.068	1.273 0.701 0.855 1.732 1.89 3.606 3.043 3.085 5.69 6.841 4.231 4.893 5.063 0.893 5.063 0.893 1.178 6.303 0.893 1.178 1.296 0.355 0.355 0.35	2.656 0.872 1.389 0.342 1.939 3.536 2.883 2.021 5.901 6.479 4.435 4.652 5.657 5.657 5.27 5.27 5.27 5.27 5.27 5.27 5.27 5.	1.269 1.152 1.181 0.626 2.864 0.979 1.47 3.994 5.492 3.971 4.027 3.575 4.928 3.314 2.362 1.359 1.347 0.257 1.083 0.23 -2.398 0.305 0.793	-0.835 -1.188 1.596 -1.427 1.574 1.442 1 4.288 4.318 3.155 2.781 4.51 3.5 1.07 1.528 3.666 0.825 0.825 0.081 -3.681 0.067	-1.555 0.136 0.246 -0.841 0.606 0.17 1.282 3.303 4.379 3.11 3.545 3.402 2.073 0.632 0.632 0.601 3.514 1.05 -0.703 0.632 0.632 0.601 0.17 0.05 0.17 0.05 0.17 0.05 0.17 0.05 0.17 0.05 0.17 0.05 0.05 0.05 0.05 0.05 0.05 0.05 0.0	-1.079 -0.076 -0.331 -1.044 1.034 0.668 1.152 2.948 3.545 3.218 3.739 3.296 3.114 2.189 -0.125 0.172 3.701 0.77 -0.714 -1.094 -1.173 -0.757 -0.944 -0.04
ygjlU cslE rsd ydaA yilT ynaF cysN cysN cysD cysA cysW cysU cysJ garR tauB topA deoA trpA tupB uspA udp ybgR ygiE  Venn: Unafft 121 genes	b4441 b3089 b2535 b3995 b1333 b1376 b2751 b27752 b2422 b2423 b2424 b2764 b2763 b3125 b0366 b2425 b3426 b1261 b3495 b3831 b0752 b3040	small RNA sodium:serine/threonine symporter stationary phase inducible protein stationary phase protein, binds sigma 70 RNA polymerase subunit stress-induced protein stress-induced protein stress-induced protein stress-induced protein, ATP-binding protein sulfate adenylytransferase, subunit 1 sulfate adenylytransferase, subunit 2 sulfate (thiosulfate transporter subunit -1- ATP-binding component of A sulfate/thiosulfate transporter subunit -1- membrane component of A sulfate/thiosulfate transporter subunit -1- pripate component of A sulfate reductase, plans bubunit, flavoprotein sulfite reductase, plans bubunit -1- ATP-binding component of ABC superf thiosulfate transporter subunit -1- priplasmic-binding component of threonine deaminase thymidine phosphorylase tryptophan synthase, alpha subunit tryptophan synthase, beta subunit universal stress global response regulator undine phosphorylase zinc efflux system zinc transporter	orf, Unknown putative regulator; Not classified orf, Unknown putative regulator; Not classified putative structure; Not classified putative structure; Not classified putative structure; Not classified putative structure; Not classified enzyme; Central intermediary metabolism: Sulfur metabolism transport; Transport of small molecules: Anions Itransport; Transport of small molecules: Anions Itransport; Transport of small molecules: Anions enzyme; Central intermediary metabolism: Sulfur metabolism enzyme; Central intermediary metabolism: Sulfur metabolism putative enzyme; Not classified transport; Transport of small molecules: Anions enzyme; Post of small molecules: Anions enzyme; Salvage of nucleosides and nucleotides enzyme; Salvage of nucleosides and nucleotides enzyme; Amino acid biosynthesis: Tryptophan enzyme; Amino acid biosynthesis: Tryptophan putative regulator; Adaptations, atypical conditions enzyme; Salvage of nucleosides and nucleotides putative transport; Not classified orf; Unknown	K-12 b4441 tkel. at K-12 b3089 ygjU s. at K-12 b2535 csiE s. at K-12 b3995 rsd s. at K-12 b3995 rsd s. at K-12 b3939 rsd s. at K-12 b3932 yill s. at K-12 b3932 yill s. at K-12 b3751 cysh. at K-12 b3751 cysh. at K-12 b2752 cysh s. at K-12 b2742 cysh s. at K-12 b2424 cysl s. at K-12 b2424 cysl s. at K-12 b2424 cysl s. at K-12 b2763 cysl s. at K-12 b3125 garR s. at K-12 b3495 (sab s. at K-12 b3495 usph s. at K-12 b3831 udp s. at K-12 b3831 udp s. at K-12 b3040 ygiE s. at	1.117 1.49 1.053 1.735 3.464 2.911 6.392 6.739 4.784 4.951 4.773 5.858 5.38 1.253 1.197 5.822 3.372 1.309 1.82 1.189 1.379 1.207 2.068 2.132	1.273 0.701 0.855 1.732 1.89 3.606 3.043 3.085 5.69 6.841 4.231 4.231 4.231 4.883 4.93 5.963 0.893 5.983 5.983 5.983 1.178 6.303 1.178 6.303 1.178 6.303 1.178 6.303 1.179 1.296 0.355 1.296	2.656 0.872 1.389 0.342 1.939 3.536 2.883 2.021 5.901 6.479 4.435 4.897 4.652 5.657 4.949 1.023 3.259 0.442 1.257 5.057 0.492 1.257 0.492 1.257 0.492 1.257 0.492 1.257 0.492 1.257 0.492 1.258 0.492 1.257 1.257	1.269 1.152 1.181 0.626 2.864 0.979 1.47 3.994 4.027 3.575 4.922 3.314 2.362 1.359 3.344 2.362 1.359 3.442 1.347 0.257 1.083 0.23 0.23 0.23 0.23 0.23 0.23 0.23 0.2	-0.835 -1.188 1.596 -1.427 1.574 1.574 1.442 1 4.288 4.318 3.155 2.781 4.51 3.55 2.781 4.51 3.566 0.825 0.085 -0.31 -0.241 -0.241 -0.482 0.061	-1.555 0.136 0.246 -0.841 0.606 0.17 1.282 3.303 3.311 3.545 3.409 3.402 2.073 0.632 0.601 3.514 1.05 -0.709 0.083	-1.079 -0.076 -0.331 -1.044 1.034 0.668 1.152 2.948 3.545 3.218 3.545 3.218 3.14 2.189 -0.125 0.172 3.701 0.77 -0.714 -1.094 -1.173 -0.757 -0.944 -0.04 0.534
ygiU csiE rsd ydaA yiiT ynaF cysN cysD cysA cysW cysU cysI garR tauB cysP iivA deoA trpA trpB uspA ydgE Venn: Unaffn 121 genes GENE	b4441 b3089 b2535 b3995 b1333 b3993 b1376 b2751 b2752 b2422 b2423 b2424 b2764 b2763 b3125 b0366 b2425 b3772 b4382 b1260 b1261 b3495 b3831 b0752 b3040 fected	small RNA sodium:serine/threonine symporter stationary phase inducible protein stationary phase protein, binds sigma 70 RNA polymerase subunit strass:-induced protein sulfate adenyl/transferase, subunit 1 sulfate adenyl/transferase, subunit 2 sulfate/thiosulfate transporter subunit -!- ATP-binding component of a sulfate/thiosulfate transporter subunit -!- membrane component of A sulfate/thiosulfate transporter subunit -!- membrane component of A sulfate/thiosulfate transporter subunit -!- membrane component of A sulfate/thiosulfate transporter subunit -!- pripinding component of ABC super thiosulfate transporter subunit -!- periplasmic-binding component of threonine deaminase tryptophan synthase, alpha subunit tuniversal stress global response regulator uridine phosphorylase zinc efflux system zinc transporter	orf; Unknown putative regulator; Not classified orf; Unknown putative regulator; Not classified putative structure; Not classified putative structure; Not classified putative structure; Not classified enzyme; Central intermediary metabolism: Sulfur metabolism enzyme; Central intermediary metabolism: Sulfur metabolism transport; Transport of small molecules: Anions Itransport; Transport of small molecules: Anions enzyme; Central intermediary metabolism: Sulfur metabolism enzyme; Anion acid biosynthesis: Anions enzyme; Anion acid biosynthesis: Interpolphan enzyme; Anion acid biosynthesis: Tryptophan enzyme; Anion acid biosynthesis: Tryptophan putative regulator; Adaptations, atypical conditions enzyme; Silvage of nucleosides and nucleotides putative transport; Not classified orf; Unknown	K-12 b4441 tkel at K-12 b3089 ygiU s at K-12 b2035 csiE s at K-12 b2935 csiE s at K-12 b3995 rsd s at K-12 b3995 rsd s at K-12 b3995 rsd s at K-12 b3932 yill s at K-12 b3751 cysN at K-12 b3751 cysN at K-12 b2751 cysN s K-12 b2422 cysW s at K-12 b2422 cysW s at K-12 b2422 cysW s at K-12 b2424 cysU s at K-12 b2424 cysU s at K-12 b2424 cysU s at K-12 b2425 cysW s at K-12 b2764 cysJ s at K-12 b2765 cysJ s at K-12 b3772 livN s s K-12 b3772 livN s s K-12 b3772 livN s s K-12 b3782 dsoA s at K-12 b3832 dsoA s at K-12 b3831 udp s at K-12 b3831 udp s at CFT073 c0827 s at	1.117 1.49 1.053 1.735 3.464 2.87 2.911 6.392 6.739 4.784 4.951 4.773 5.858 5.88 5.88 1.253 1.197 5.822 3.372 1.189 1.379 1.207 2.068 2.132	1.273 0.701 0.855 1.732 1.89 3.606 3.043 3.085 5.69 6.841 4.231 4.83 5.063 0.893 1.178 6.303 2.882 0.523 1.7 1.45 1.296 0.355 2.447 2.132	2.656 0.872 1.389 0.342 1.939 3.536 2.883 2.021 5.901 6.479 4.435 4.897 4.652 5.657 4.949 1.023 1.257 5.38 3.259 0.442 2.092 1.523 0.995 0.613 1.802 2.005	1.269 1.152 1.181 0.626 2.864 0.979 1.47 3.994 5.492 3.971 4.928 3.3142 2.362 1.359 1.025 1.025 0.793 0.801	-0.835 -1.188 1.596 -1.427 1.574 1.472 1 4.288 4.318 3.152 2.781 4.51 3.165 2.781 4.51 3.566 0.825 0.085 -0.31 0.067 0.482 0.061	-1.555 0.136 0.246 -0.841 -0.606 0.17 1.282 3.303 3.303 3.379 3.11 3.545 3.409 2.073 3.652 0.651 1.070 -0.901 -0.994 -0.063 0.709 0.296	-1.079 -0.076 -0.331 -1.044 -1.034 0.668 1.152 2.948 3.545 3.218 3.739 3.296 3.114 2.189 -0.125 0.172 0.777 -0.714 -1.094 -1.173 -0.757 -0.9444 -0.04
ygjIU csIE rsd ydaA yiIT ynaF cysN cysN cysD cysA cysW cysU cysJ cysI garR tauB trpA deoA trpA trpB uspA udp ybgR ygiE  Venn: Unaff 121 genes  GENE cysH	b4441 b3089 b2535 b3995 b1333 b1376 b2751 b2752 b2422 b2423 b2424 b2764 b2763 b3125 b30366 b2425 b3366 b2425 b3366 b2425 b3364 b2763 b31261 b3495 b3831 b0752 b3040 crected	small RNA sodium:serine/threonine symporter stationary phase inducible protein stationary phase protein, binds sigma 70 RNA polymerase subunit stress:-induced protein sulfate adenylytransferase, subunit 2 sulfate/thiosulfate transporter subunit -1- membrane component of A sulfate/thiosulfate transporter subunit -1- membrane component of A sulfate/thiosulfate transporter subunit -1- membrane component of A sulfate reductase, elapha subunit, RaD(P)-binding, heme-binding tartronate semialdehyde reductase taurine transporter subunit -1- ATP-binding component of ABC superf thiosulfate transporter subunit -1- ATP-binding component of ABC superf thiosulfate transporter subunit -1- ATP-binding component of ABC superf thiosulfate transporter subunit -1- ATP-binding component of ABC superf thiosulfate transporter subunit -1- and the superf thiosulfate transporter subunit -1- universal stress global response regulator uniden phosphorylase tryptophan synthase, alpha subunit tryptophan synthase,	orf, Unknown putative regulator; Not classified orf, Unknown putative regulator; Not classified putative structure; Not classified putative structure; Not classified putative structure; Not classified putative structure; Not classified enzyme; Central intermediary metabolism: Sulfur metabolism transport; Transport of small molecules: Anions Itransport; Transport of small molecules: Anions enzyme; Central intermediary metabolism: Sulfur metabolism enzyme; Central intermediary metabolism: Sulfur metabolism putative enzyme; Not classified transport; Transport of small molecules: Anions enzyme; Post classified transport; Transport of small molecules: Anions enzyme; Salvage of nucleosides and nucleotides enzyme; Anino acid biosynthesis: Isopleucine, Valine enzyme; Anino acid biosynthesis: Tryptophan enzyme; Anino acid biosynthesis: Tryptophan putative regulator; Adaptations, atypical conditions enzyme; Salvage of nucleosides and nucleotides putative transport; Not classified orf; Unknown	K-12 b4441 tkel_at K-12 b3089 ygjU_s_at K-12 b2535_csiE_s_at K-12 b2535_csiE_s_at K-12 b3935_rsiG_s_at K-12 b3935_rsiG_s_at K-12 b3935_yriG_s_at K-12 b3935_yriG_s_at K-12 b3751_cysN_at K-12 b3751_cysN_at K-12 b2752_cysD_s_at K-12 b2422_cysM_x_at K-12 b2424_cysU_s_at K-12 b2424_cysU_s_at K-12 b2424_cysU_s_at K-12 b2763_cysI_s_at K-12 b3125_garR_s_at K-12 b3125_garR_s_at K-12 b3125_garR_s_at K-12 b3125_garR_s_at K-12 b3125_garR_s_at K-12 b3495_cspS_s_at K-12 b3495_uspS_s_at	1.117 1.49 1.053 1.735 3.464 2.87 2.911 6.392 6.739 4.784 4.951 4.773 5.858 1.253 1.197 5.822 3.372 1.309 1.82 1.189 1.379 1.207 2.068 2.132	1.273 0.701 0.855 1.732 1.89 3.606 3.043 3.085 5.69 6.841 4.231 4.883 4.93 5.963 0.893 1.178 6.303 1.178 6.303 1.178 6.303 1.296 0.355 1.296 1.2	2.656 0.872 1.389 0.342 1.939 3.536 2.883 2.021 5.901 6.479 4.435 4.897 4.652 5.657 4.549 1.023 3.259 0.449 1.023 1.257 0.95 0.95 0.95 0.95 0.95 0.95	1.269 1.152 1.181 0.626 2.864 0.979 1.47 3.994 5.492 3.971 4.027 3.575 4.928 3.314 2.362 1.359 3.442 1.362 1.362 1.37 0.257 1.083 0.23 -2.398 0.305 0.793 0.801	-0.835 -1.188 1.596 -1.427 1.574 1.472 1.428 4.318 4.318 3.152 3.165 2.781 4.51 3.55 1.07 1.528 3.666 0.825 0.085 0.085 0.031 0.042 0.061	-1.555 0.136 0.246 0.136 0.246 0.841 0.606 0.17 1.282 3.303 4.379 3.411 3.545 3.409 3.402 2.073 0.662 0.601 3.514 1.05 0.709 0.296	-1.079 -0.076 -0.331 -1.044 -1.034 -0.668 -1.152 -2.948 -3.545 -3.218 -3.739 -3.296 -3.114 -2.189 -0.125 -0.172 -3.701 -0.77 -0.714 -1.094 -1.173 -0.757 -0.944 -0.04 -0.534
ygiU csiE rsd ydaA yiiT ynaF cysN cysU cysJ cysI garR tauB cysP iivA deoA trpA trpB uspA udp ybgR ygiE  Venn: Unaffr 121 genes  GENE cysH aroD	b4441 b3089 b2535 b3995 b1333 b3993 b1376 b2751 b2752 b2422 b2423 b2424 b2764 b2763 b3125 b0366 b2425 b3772 b4382 b1260 b1261 b3495 b3831 b0752 b3040 fected	small RNA sodium:serine/threonine symporter stationary phase inducible protein stationary phase protein, binds sigma 70 RNA polymerase subunit strass:-induced protein strass-induced protein	orf, Unknown putative regulator; Not classified orf, Unknown putative regulator; Not classified orf, Unknown putative regulator; Not classified putative structure; Not classified putative structure; Not classified enzyme; Central intermediary metabolism: Sulfur metabolism enzyme; Central intermediary metabolism: Sulfur metabolism transport; Transport of small molecules: Anions Itransport; Transport of small molecules: Anions enzyme; Central intermediary metabolism: Sulfur metabolism enzyme; Anion acid song the sulfur metabolism enzyme; Anion acid biosynthesis: Inspotucies: Anions enzyme; Anion acid biosynthesis: Tryptophan enzyme; Anion acid biosynthesis: Tryptophan putative regulator; Adaptations, atypical conditions enzyme; Sulfur metabolism enzyme; Sulfur metabolism putative transport; Not classified orf; Unknown  FUNCTION enzyme; Central intermediary metabolism: Sulfur metabolism enzyme; Central intermediary	K-12 b4441 tkel at K-12 b3089 ygiU s at K-12 b2035 csiE s at K-12 b2935 csiE s at K-12 b3995 rsd s at K-12 b3995 rsd s at K-12 b3995 rsd s at K-12 b3932 yill s at K-12 b3751 cysN at K-12 b3751 cysN at K-12 b2751 cysN s at K-12 b2422 cysW s at K-12 b2422 cysW s at K-12 b2422 cysW s at K-12 b2424 cysU s at K-12 b2424 cysU s at K-12 b2424 cysU s at K-12 b2425 cysW s at K-12 b2426 cysJ s at K-12 b2766 cysJ s at K-12 b3772 livN s s at K-12 b3772 livN s s at K-12 b3782 cysP s at K-12 b3832 deoA s at K-12 b3832 deoA s at K-12 b3831 udp s at CFT073 c0827 s at K-12 b3940 ygiE s at K-12 b3960 rysU s at	1.117 1.49 1.053 1.735 3.464 2.87 2.911 6.392 6.739 4.784 4.951 4.773 5.858 5.85 1.253 1.197 5.822 3.372 1.189 1.379 1.207 2.068 2.132	1.273 0.701 0.855 1.732 1.89 3.606 3.043 3.085 5.69 6.841 4.231 4.93 5.963 5.063 0.893 1.178 6.303 2.882 0.523 1.7 1.45 1.296 0.355 2.447 2.132	2.656 0.872 1.389 0.342 1.939 3.536 2.883 2.021 5.901 6.479 4.435 4.897 4.652 5.657 4.949 1.023 1.257 5.38 3.259 0.442 2.092 1.523 0.995 0.613 1.802 2.005	1.269 1.152 1.181 0.626 2.864 0.979 1.47 3.994 5.492 3.971 4.027 3.575 4.928 3.3142 1.342 1.342 1.342 1.342 1.349 0.257 1.083 0.235 0.793 0.801	-0.835 -1.188 1.596 -1.427 1.574 1.474 1.421 1 4.288 4.318 3.152 2.781 4.51 3.165 2.781 4.51 3.166 0.825 0.085 -0.31 0.067 0.482 0.061	-1.555 0.136 0.246 -0.841 -0.606 0.17 1.282 -0.303 -0.303 -0.303 -0.303 -0.303 -0.303 -0.503 -0.503 -0.503 -0.504 -0.805 -0.704 -0.705 -0.704 -0.705 -0.704 -0.705	-1.079 -0.076 -0.331 -1.044 -1.034 0.668 1.152 2.948 3.218 3.739 3.296 3.214 2.189 -0.125 0.172 0.771 -0.714 -1.094 -1.173 -0.757 -0.9444 -0.04 0.534
ygjlU cslE rsd ydaA yilT ynaF cysN cysN cysD cysA cysW cysU cysJ garR tauB trpA deoA trpA trpB udp ybgR ygiE  Venn: Unaff 121 genes  GENE cysH aroD aroG	b4441 b3089 b2535 b3995 b1333 b1376 b2751 b2752 b2422 b2423 b2424 b2764 b2763 b3125 b0366 b2425 b3772 b4382 b1260 b1261 b3495 b3831 b0752 b3040 crected	small RNA sodium:serine/threonine symporter stationary phase inducible protein stationary phase inducible protein stationary phase inducible protein stationary phase protein, binds sigma 70 RNA polymerase subunit stress-induced protein stress-induced protein stress-induced protein, ATP-binding protein sulfate adenylytransferase, subunit 1 sulfate adenylytransferase, subunit 2 sulfate/thiosulfate transporter subunit -1- ATP-binding component of A sulfate/thiosulfate transporter subunit -1- membrane component of A sulfate/thiosulfate transporter subunit -1- pripinding component of ABC superf thiosulfate transporter subunit -1- ATP-binding component of ABC superf thiosulfate transporter subunit -1- priplasmic-binding component of threonine deaminase tryptophan synthase, alpha subunit tryptophan synthase, alpha subunit tryptophan synthase, alpha subunit tryptophan synthase, alpha subunit turitorial stress global response regulator uridine phosphorylase zinc efflux system zinc transporter  GENE_PRODUCT 3'-phosphoadenosine 5'-phosphosulfate reductase 3-dehydroquinate dehydratase 3-dehydroquinate dehydratase	orf, Unknown putative regulator; Not classified orf, Unknown putative regulator; Not classified putative structure; Not classified enzyme; Central intermediary metabolism: Sulfur metabolism transport; Transport of small molecules: Anions Itransport; Transport of small molecules: Anions enzyme; Central intermediary metabolism: Sulfur metabolism enzyme; Central intermediary metabolism: Sulfur metabolism putative enzyme; Not classified transport; Transport of small molecules: Anions enzyme; Salvage of nucleosides and nucleotides enzyme; Anino acid biosynthesis: Isopleucine, Valine enzyme; Anino acid biosynthesis: Iryntophan enzyme; Anino acid biosynthesis: Tryntophan putative regulator; Adaptations, atypical conditions enzyme; Salvage of nucleosides and nucleotides putative transport; Not classified orf; Unknown  FUNCTION enzyme; Central intermediary metabolism: Sulfur metabolism enzyme; Anino acid biosynthesis: Chorismate lenzyme; Anino acid biosynthesis: Chorismate	K-12 b4441 tkel_at K-12 b3089 ygjU_s_at K-12 b2535_csiE_s_at K-12 b2535_csiE_s_at K-12 b3935_rsid_s_at K-12 b3935_rsid_s_at K-12 b3935_rsid_s_at K-12 b3935_yiiT_s_at K-12 b3751_cysN_at K-12 b3751_cysN_at K-12 b2751_cysN_s_at K-12 b2742_cysN_s_at K-12 b2422_cysN_s_at K-12 b2424_cysU_s_at K-12 b2424_cysU_s_at K-12 b2764_cysJ_s_at K-12 b2763_cysJ_s_at K-12 b3125_garR_s_at K-12 b3125_garR_s_at K-12 b3125_garR_s_at K-12 b3125_garR_s_at K-12 b3495_cspN_s_at K-12 b3495_uspN_s_at K-12 b3695_uspN_s_at	1.117 1.49 1.053 1.735 3.464 2.937 2.911 6.392 4.784 4.951 4.773 5.858 5.38 1.253 1.197 5.822 3.372 1.309 1.82 1.189 1.379 1.207 2.068 2.132	1.273 0.701 0.855 1.732 1.89 3.606 3.043 3.085 5.69 6.841 4.231 4.93 5.983 5.063 0.893 5.063 0.893 1.178 6.303 1.178 6.303 1.296 0.355 1.296 1.2	2.656 0.872 1.389 0.342 1.939 3.536 2.883 2.021 5.901 6.479 4.435 4.897 4.652 5.657 4.949 1.023 1.257 5.358 0.449 1.023 1.257 5.657 0.492 1.023 1.257 5.657 0.492 1.023 1.257 5.657	1.269 1.152 1.181 0.626 2.864 0.979 1.47 3.994 5.492 3.971 4.027 3.575 4.928 3.314 2.362 1.359 3.442 1.362 1.37 0.257 1.083 0.23 0.23 0.801	-0.835 -1.188 1.596 -1.427 1.574 1.427 1.574 1.428 4.318 3.152 3.165 2.781 4.51 3.55 1.07 1.528 3.666 0.825 0.085 0.085 0.085 0.045 0.061	-1.555 0.136 0.246 0.136 0.246 0.841 0.606 0.17 1.282 3.303 4.379 3.11 3.545 3.409 3.402 2.073 0.632 0.601 3.514 1.05 0.709 0.296	-1.079 -0.076 -0.331 -1.044 1.034 0.686 1.152 2.948 3.545 3.218 3.545 3.218 3.144 2.189 -0.125 0.172 3.701 0.77 -0.714 -1.094 -1.173 -0.757 -0.944 -0.04 0.534
ygiU csiE rsd ydaA yiiT ynaF cysN cysU cysJ cysI garR tauB cysP iivA deoA trpA trpB uspA udp ybgR ygiE  Venn: Unaffr 121 genes  GENE cysH aroD	b4441 b3089 b2535 b3995 b1333 b3993 b1376 b2751 b2752 b2422 b2423 b2424 b2764 b2763 b3125 b0366 b2425 b3772 b4382 b1260 b1261 b3495 b3831 b0752 b3040 fected	small RNA sodium:serine/threonine symporter stationary phase inducible protein stationary phase protein, binds sigma 70 RNA polymerase subunit strass:-induced protein strass-induced protein	orf, Unknown putative regulator; Not classified orf, Unknown putative regulator; Not classified orf, Unknown putative regulator; Not classified putative structure; Not classified putative structure; Not classified enzyme; Central intermediary metabolism: Sulfur metabolism enzyme; Central intermediary metabolism: Sulfur metabolism transport; Transport of small molecules: Anions Itransport; Transport of small molecules: Anions enzyme; Central intermediary metabolism: Sulfur metabolism enzyme; Anion acid song the sulfur metabolism enzyme; Anion acid biosynthesis: Inspotucies: Anions enzyme; Anion acid biosynthesis: Tryptophan enzyme; Anion acid biosynthesis: Tryptophan putative regulator; Adaptations, atypical conditions enzyme; Sulfur metabolism enzyme; Sulfur metabolism putative transport; Not classified orf; Unknown  FUNCTION enzyme; Central intermediary metabolism: Sulfur metabolism enzyme; Central intermediary	K-12 b4441 tkel at K-12 b3089 ygiU s at K-12 b2035 csiE s at K-12 b2935 csiE s at K-12 b3995 rsd s at K-12 b3995 rsd s at K-12 b3995 rsd s at K-12 b3932 yill s at K-12 b3751 cysN at K-12 b3751 cysN at K-12 b2751 cysN s at K-12 b2422 cysW s at K-12 b2422 cysW s at K-12 b2422 cysW s at K-12 b2424 cysU s at K-12 b2424 cysU s at K-12 b2424 cysU s at K-12 b2425 cysW s at K-12 b2426 cysJ s at K-12 b2766 cysJ s at K-12 b3772 livN s s at K-12 b3772 livN s s at K-12 b3782 cysP s at K-12 b3832 deoA s at K-12 b3832 deoA s at K-12 b3831 udp s at CFT073 c0827 s at K-12 b3940 ygiE s at K-12 b3960 rysU s at	1.117 1.49 1.053 1.735 3.464 2.87 2.911 6.392 6.739 4.784 4.951 4.773 5.858 5.85 1.253 1.197 5.822 3.372 1.189 1.379 1.207 2.068 2.132	1.273 0.701 0.855 1.732 1.89 3.606 3.043 3.085 5.69 6.841 4.231 4.93 5.963 5.063 0.893 1.178 6.303 2.882 0.523 1.7 1.45 1.296 0.355 2.447 2.132	2.656 0.872 1.389 0.342 1.939 3.536 2.883 2.021 5.901 6.479 4.435 4.897 4.652 5.657 4.949 1.023 1.257 5.38 3.259 0.442 2.092 1.523 0.995 0.613 1.802 2.005	1.269 1.152 1.181 0.626 2.864 0.979 1.47 3.994 5.492 3.971 4.027 3.575 4.928 3.3142 1.342 1.342 1.342 1.342 1.349 0.257 1.083 0.235 0.793 0.801	-0.835 -1.188 1.596 -1.427 1.574 1.474 1.421 1 4.288 4.318 3.152 2.781 4.51 3.165 2.781 4.51 3.166 0.825 0.085 -0.31 0.067 0.482 0.061	-1.555 0.136 0.246 -0.841 -0.606 0.17 1.282 -0.303 -0.303 -0.303 -0.303 -0.303 -0.303 -0.503 -0.503 -0.503 -0.504 -0.805 -0.704 -0.705 -0.704 -0.705 -0.704 -0.705	-1.079 -0.076 -0.331 -1.044 -1.034 0.668 1.152 2.948 3.218 3.739 3.296 3.214 2.189 -0.125 0.172 0.771 -0.714 -1.094 -1.173 -0.757 -0.9444 -0.04 0.534

pfkB	b1723	6-phosphofructokinase II	enzyme; Energy metabolism, carbon: Glycolysis	K-12_b1723_pfkB_s_at	2.728	2.755	2.685	2.38	1.099	0.533	0.748
ybhE	b0767		orf; Not classified	K-12_b0767_ybhE_s_at	1.223	0.934	0.316	0.281	-0.63	-1.177	-1.378
ssrS	b2911		RNA; Ribosomal and stable RNAs -!- modulates promoter use via inte		1.544	1.204	1.007	0.906	-0.857	-0.167	0.131
hdhA	b1619		enzyme; Central intermediary metabolism: Pool, multipurpose conve		2.722	2.491	2.294	2.001	1.282	-0.781	-0.394
clpA	b0882	ATPase and specificity subunit of ClpA-ClpP ATP-dependent serine pro	enzyme; Degradation of proteins, peptides, glyco	K-12_b0882_clpA_s_at	2.802	2.793	2.787	1.847	0.939	-0.425	-0.209
yffO	b2446		orf; Unknown	K-12_b2446_yffO_at	1.028	1.093	0.641	1.267	0.922	-0.283	-0.275
b2449	b2449		orf; Unknown	K-12_b2449_at	1.541	1.35	1.576	1.117	0.257	-0.123	-0.166
yedO	b1919	D-cysteine desulfhydrase, PLP-dependent	putative enzyme; Not classified	K-12 b1919 yedO a at	2.239	2.123	1.832	0.889	0.904	0.312	0.402
dld	b2133	D-lactate dehydrogenase, FAD-binding, NADH independent	enzyme; Energy metabolism, carbon: Aerobic respiration	K-12_b2133_dld_s_at	1.255	0.579	1.267	0.796	-0.826	-1.786	-1.797
sbmC	b2009		orf: Unknown function	K-12 b2009 sbmC s at	2.574	2.659	2.045	2.818	1.014	0.451	1.049
fucR	b2805		regulator; Degradation of small molecules: Carbon compounds	K-12_b2805_fucR_s_at	1.563	1.274	1.744	0.815	0.537	0.016	-0.443
	b1040	DNA-binding transcriptional activator in two-component regulatory sy		K-12_02003_IUCK_S_at	2.93	2.945	3.327	2.247	0.63	0.614	0.585
csgD				K-12_b1040_csgD_s_at							
cbl	b1987	DNA-binding transcriptional activator of cysteine biosynthesis	regulator; Amino acid biosynthesis: Cysteine	K-12_b1987_cbl_s_at	2.53	2.595	2.021	1.299	1.894	0.688	0.089
iciA	b2916	DNA-binding transcriptional activator, replication initiation inhibitor	regulator; DNA - replication, repair, restriction/modification	K-12_b2916_iciA_s_at	1.041	1.126	1.148	0.269	-0.617	-0.819	-1.408
crp	b3357	DNA-binding transcriptional dual regulator	regulator; Global regulatory functions	K-12 b3357 crp s at	1.291	1.51	1.248	-5.177	-0.442	-0.115	-0.293
folE	b2153		enzyme; Biosynthesis of cofactors, carriers: Folic acid	K-12 b2153 folE s at	1.049	0.862	1.07	0.535	-1.282	-1.864	-0.584
ybiK	b0828	L-asparaginase	orf; Not classified	K-12_b0828_ybiK_s_at	3.514	3.813	3.701	3.089	2.089	1.652	1.108
			orr, Not classified		3.314	3.013	3.701				1.100
fucU	b2804		phenotype; Degradation of small molecules: Carbon compounds	K-12_b2804_fucU_s_at	2.303	2.213	2.351	1.299	0.442	-0.031	0.231
sdaA	b1814		enzyme; Degradation of small molecules: Amino acids	K-12_b1814_sdaA_s_at	1.375	1.82	0.904	0.777	0.767	-1.031	-0.414
celA	b1738		enzyme; Transport of small molecules: Carbohydrates, organic acids,	, K-12_b1738_celA_s_at	2.699	2.384	2.698	1.894	1.561	1.243	1.299
ampD	b0110	N-acetyl-anhydromuranmyl-L-alanine amidase	regulator; Not classified	K-12 b0110 ampD s at	1.37	1.695	1.689	0.594	-0.665	0.169	-1.077
nemA	b1650	N-ethylmaleimide reductase, FMN-linked	enzyme; Central intermediary metabolism: Pool, multipurpose conve	r K-12 b1650 nemA s at	1.078	0.58	0.883	0.85	0.921	-0.377	-0.295
nadE	b1740	NAD synthetase, NH3/glutamine-dependent	enzyme; Biosynthesis of cofactors, carriers: Pyridine nucleotide	K-12 b1740 nadE s at	1.018	0.584	1.324	0.465	-0.667	-2.137	-1.587
acpD	h1412		enzyme; Fatty acid and phosphatidic acid biosynthesis	K-12 b1412 acpD s at	1.726	1.849	2.088	0.102	0.018	-0.902	-0.759
	b4488										
ilvG			enzyme; Amino acid biosynthesis: Isoleucine, Valine	K-12_b4488_ilvG_s_at	4.511	5.26	4.624	3.891	2.614	2.801	2.503
argE	b3957		enzyme; Amino acid biosynthesis: Arginine	K-12_b3957_argE_s_at	1.307	1.171	1.226	0.792	-0.596	-1.119	-1.223
asr	b1597	acid shock-inducible periplasmic protein	phenotype; Not classified	K-12_b1597_asr_s_at	1.215	1.872	0.896	1.606	1.396	-0.615	-0.293
fadE	b0221	acyl coenzyme A dehydrogenase	putative enzyme; Not classified	K-12 b0221 fadE at	1.735	1.195	1.268	1.207	0.714	1.405	0.467
cysC	b2750	adenosine 5'-phosphosulfate kinase	enzyme; Central intermediary metabolism: Sulfur metabolism	K-12_b2750_cysC_s_at	4.154	3.243	3.839	2.541	2.74	1.279	1.217
asd	b3433		enzyme; Amino acid biosynthesis: Lysine	K-12_b3433_asd_s_at	1.204	0.875	1.614	0.402	-1.196	-1.933	-2.576
ushA	b0480	aspartate-semialdenyde denydrogenase, NAD(r)-binding	enzyme: Central intermediary metabolism: Sugar-nucleotide biosyntl		1.054	0.731	0.898	1.063	0.666	-0.299	-0.605
ilvE	b3770		enzyme; Amino acid biosynthesis: Isoleucine, Valine	K-12_b3770_ilvE_s_at	3.008	3.338	3.201	0.488	-0.033	1.339	0.726
cstA	b0598	carbon starvation protein	phenotype; Global regulatory functions	K-12_b0598_cstA_s_at	1.505	1.592	1.71	1.195	0.885	1.027	0.171
ybhO	b0789	cardiolipin synthase 2	orf: Not classified	K-12 b0789 ybhO s at	1.465	1.378	0.48	2.309	1.658	-0.577	-0.894
yfiA	h2597	cold shock protein associated with 30S ribosomal subunit	putative regulator; Not classified	K-12_b2597_yfiA_s_at	2.195	1.757	1.979	0.788	0.785	0.07	-0.531
cspD	b0880	cold shock protein homolog	phenotype; Not classified	K-12 b0880 cspD s at	3.875	3.916	4.055	1.766	1.727	0.427	0.431
ybgE	b0735	conserved inner membrane protein	orf; Unknown	K-12_b0735_ybgE_s_at	1.294	0.632	0.809	0.149	0.031	0.464	0.105
yedI	b1958		orf; Unknown	K-12_b1958_yedI_s_at	1.434	1.777	1.008	1.105	0.171	0.293	0.383
yohJ	b2141	conserved inner membrane protein	orf; Unknown	K-12_b2141_yohJ_s_at	1.231	0.653	1.457	1.561	0.837	1.055	0.058
ygbE	b2749	conserved inner membrane protein	putative enzyme; Not classified	K-12 b2749 yqbE s at	1.989	1.852	2.159	1.549	0.587	1.161	0.39
ydgC	b1607	conserved inner membrane protein associated with alginate biosynthe	orf: Unknown	K-12_b1607_ydgC_s_at	2.211	2.025	2.625	1.576	1.231	0.961	1.025
ybqI	b0710	conserved metal-binding protein	orf; Unknown	K-12 b0710 vbgI s at	1.089	1.134	1.375	0.673	-0.24	-0.267	-0.937
	b1908		orf: Unknown		2.184	2.559	2.853	2.121	0.185	0.508	0.96
yecA				K-12_b1908_yecA_s_at							
yaeH	b0163		putative structure; Not classified	K-12_b0163_yaeH_s_at	1.87	1.47	1.647	1.133	0.975	-0.44	-0.348
ylbA	b0515		orf; Unknown	K-12_b0515_ylbA_s_at	1.341	1.28	1.454	0.31	-0.43	-0.927	-0.634
ybiI	b0803	conserved protein	orf; Unknown	K-12_b0803_ybiI_s_at	1.163	1.263	0.245	0.975	0.395	-0.139	-0.368
yliH	b0836	conserved protein	putative factor; Not classified	K-12 b0836 yliH s at	4.304	4.011	4.131	2.805	1.87	0.251	-0.113
ybjI	b0844		orf: Unknown	K-12_b0844_ybjI_s_at	1.415	0.959	1.882	0.773	0.616	0.25	-0.06
ycbK	b0926		orf: Unknown	K-12_b0926_ycbK_s_at	1.567	1.666	1.923	1.96	-0.321	0.722	0.15
ycok											
yceH	b1067		orf; Unknown	K-12_b1067_yceH_s_at	1.647	1.209	1.564	0.492	0.897	0.354	-0.403
ycfP	b1108		orf; Unknown	K-12_b1108_ycfP_s_at	1.586	1.753	1.179	1.721	-0.706	-0.167	-0.189
yciF	b1258	conserved protein	putative structure; Not classified	K-12_b1258_yciF_s_at	1.175	1.13	0.237	1.954	1.215	-0.002	-0.044
ydhQ	b1664		putative enzyme; Not classified	K-12_b1664_ydhQ_s_at	1.615	1.69	1.249	1.374	0.505	-0.591	0.021
yeaO	b1792		orf: Unknown	K-12 b1792 yeaO s at	1.579	1.694	1.131	-0.229	-0.235	-0.836	-0.32
yeeX	b2007		phenotype; Not classified	K-12_b2007_yeeX_s_at	1.367	1.449	1.376	0.535	0.311	-0.874	0.025
yeek			orf: Unknown					0.353			
yfbU	b2294			K-12_b2294_yfbU_s_at	1.525	1.064	1.079	-0.253	-1.93	-0.81	0.003
yggE	b2922	conserved protein	phenotype; Not classified	K-12_b2922_yggE_s_at	1.12	0.572	0.6	1.942	-0.603	-0.637	-0.103
smg	b3284		orf; Unknown	K-12_b3284_smg_s_at	1.198	1.426	1.247	0.722	-0.096	0.014	0.198
yihD	b3858	conserved protein	orf; Unknown	K-12_b3858_yihD_s_at	1.074	0.737	1.393	0.924	-0.033	-1.034	-1.077
yiiS	b3922		orf: Unknown	K-12_b3922_yiiS_s_at	2.483	2.736	2.645	2.749	1.88	0.829	0.152
yjeI	b4144	conserved protein	orf: Unknown	K-12_b4144_yjeI_s_at	1.089	0.949	1.266	-0.01	0.122	0.398	-0.52
yjfO	b4189		orf: Unknown	K-12_b4189_yjfO_s_at	1.579	1.901	0.785	1.357	1.232	0.406	0.461
	h4406	conserved protein	on, onknown		2.228	2.044	2.196	1.435	0.974	-0.232	0.021
yaeP			orf; Unknown	K-12_b4406_yaeP_s_at						1.00	
erfK	b1990			K-12_b1990_erfK_s_at	2.006	2.279	1.343	2.189	1.115	1.06	0.955
phoH	b1020		regulator; Central intermediary metabolism: Phosphorus compounds		4.143	4.418	4.164	2.271	1.347	0.024	0.617
csgA	b1042		regulator; Surface structures	K-12_b1042_csgA_at	3.245	2.999	3.543	1.847	-0.177	0.972	0.549
csgB	b1041		structural component; Surface structures	K-12_b1041_csgB_s_at	1.417	1.514	1.736	1.606	0.236	0.435	0.012
cfa	b1661	cyclopropane fatty acyl phospholipid synthase (unsaturated-phosphol	enzyme; Fatty acid and phosphatidic acid biosynthesis	K-12_b1661_cfa_s_at	2.865	2.382	2.527	1.312	0.08	-0.014	0.991
cvsK	b2414		enzyme: Amino acid biosynthesis: Cysteine	K-12 b2414 cvsK s at	3.913	3.79	3.622	2.643	2.089	3.113	2.796
cysM	h2421		enzyme; Amino acid biosynthesis: Cysteine	K-12 b2421 cysM s at	2.914	2.701	3.09	3.3	1.383	1.741	1.329
fliY	b1920	cystine transporter subunit -!- periplasmic-binding component of ABC		K-12_b1920_fliY_s_at	2.737	2.491	2.292	1.224	1.269	0.283	0.149
	b1920 b0733					0.779					0.149
cydA		cytochrome d terminal oxidase, subunit I	enzyme; Energy metabolism, carbon: Electron transport	K-12_b0733_cydA_s_at	1.041		1.131	-0.269	-0.716	-0.672	-0.568
cydB	b0734		enzyme; Energy metabolism, carbon: Electron transport	K-12_b0734_cydB_s_at	1.618	1.694	1.631	0.341	0.129	-0.206	0.37
nlpA	b3661		membrane; Macromolecule synthesis, modification: Lipoprotein	K-12_b3661_nlpA_at	3.5	3.38	2.995	0.854	0.93	2.193	0.891
ilvD	b3771	dihydroxyacid dehydratase	enzyme; Amino acid biosynthesis: Isoleucine, Valine	K-12_b3771_ilvD_s_at	3.483	3.512	3.329	1.73	0.076	1.607	1.354
ymfI	b1143		orf; Unknown	K-12_b1143_ymfI_at	1.681	1.044	1.785	-0.017	-0.243	-0.819	-0.451
focA	b0904		putative transport: Degradation of small molecules: Carbon compour		1.432	1.659	0.91	0.54	-0.023	-0.263	-0.669
putA	b1014	fused DNA-binding transcriptional regulator -!- proline dehydrogenase		K-12_b0904_locA_s_at K-12_b1014_putA_s_at	1.912	1.039	1.543	1.355	0.286	-0.203	-0.367
		fused about CoA budgatage and enterprise and enterp	putative enzyme. Not classified								
yfcX	b2341	fused enoyl-CoA hydratase and epimerase and isomerase -!- 3-hydro:		K-12_b2341_yfcX_s_at	1.386	1.11	1.163	2.226	1.751	-0.525	-0.548
fruA	b2167	fused fructose-specific PTS enzymes: IIBcomponent -!- IIC componer		K-12_b2167_fruA_s_at	1.218	1.249	1.35	1.745	1.796	0.623	0.06
trpC	b1262	fused indole-3-glycerolphosphate synthetase -!- N-(5-phosphoribosyl		K-12_b1262_trpC_s_at	1.198	1.636	1.53	1.622	0.205	-0.679	-0.402
yliA	b0829	fused predicted peptide transport subunits of ABC superfamily: ATP-b	putative transport; Not classified	K-12_b0829_yliA_s_at	3.064	2.831	3.151	1.893	1.835	0.035	0.868
glgC	b3430			K-12_b3430_glgC_s_at	2.02	1.03	2.085	0.474	0.363	-1.72	-1.685
gltI	b0655	glutamate and aspartate transporter subunit -!- periplasmic-binding c		K-12_b0655 gltI s at	1.181	0.954	1.216	-0.157	-0.403	-1.193	-0.501
gdhA	b1761		enzyme: Amino acid biosynthesis: Glutamate	K-12_00033_git1_s_at K-12_b1761_qdhA_s_at	1.299	0.934	1.188	-0.137	-0.403	0.075	-0.301
						1.178	1.188	-0.988 0.733			-0.175 -1.284
grxB	b1064	glutaredoxin 2 (Grx2)	carrier; Biosynthesis of cofactors, carriers: Thioredoxin, glutaredoxin	, N-12_DIU04_grXB_S_at	1.756				-1.336	-1.491	
gst	b1635	glutathionine S-transferase	enzyme; Biosynthesis of cofactors, carriers: Thioredoxin, glutaredoxi	r K-12_b1635_gst_s_at	2.709	2.448	2.684	1.082	0.113	0.158	1.155
ilvL	b3766		leader; Amino acid biosynthesis: Isoleucine, Valine	K-12_b3766_ilvL_s_at	1.338	2.041	1.478	0.579	0.169	0.625	-0.974
yccA	b0970	inner membrane protein	putative transport; Not classified	K-12_b0970_yccA_s_at	2.298	1.682	2.27	-0.026	0.407	0.713	1.298

ilvC	b3774	ketol-acid reductoisomerase, NAD(P)-binding	enzyme; Amino acid biosynthesis: Isoleucine, Valine	K-12_b3774_ilvC_s_at	1.208	0.576	1.699	0.158	0.158	-0.085	-0.393
argT	b2310	lysine/arqinine/ornithine transporter subunit -!- periplasmic-binding of	transport; Transport of small molecules: Amino acids, amines	K-12_b2310_argT_s_at	1.323	0.512	1.225	0.879	0.285	0.32	0.264
glcB	b2976	malate synthase G	enzyme; Central intermediary metabolism: Glyoxylate bypass	K-12_b2976_glcB_a_at	1.069	0.76	0.886	1.555	0.601	-0.56	-0.664
yggB	b2924		putative transport; Not classified	K-12_b2924_yggB_s_at	2.961	2.052	2.306	3.045	1.147	0.143	0.737
msrA	b4219	methionine sulfoxide reductase A		K-12_b4219_msrA_s_at	1.952	2.164	1.791	0.99	0.449	-0.609	-1.181
moaB	b0782			K-12_b0782_moaB_s_at	1.17	0.245	1.352	-0.585	-0.706	-0.847	-0.929
tesA	b0494	multifunctional acyl-CoA thioesterase I and protease I and lysophospl	enzyme; Fatty acid and phosphatidic acid biosynthesis	K-12_b0494_tesA_s_at	1.353	1.301	1.614	-0.131	-0.013	-0.152	-0.661
ycjI	b1326	murein peptide amidase A		K-12_b1326_ycjI_s_at	1.187	1.138	1.34	1.327	0.255	0.27	-0.256
napA	b2206	nitrate reductase, periplasmic, large subunit	putative enzyme; Energy metabolism, carbon: Anaerobic respiration	K-12_b2206_napA_s_at	1.028	0.591	1.379	1.249	2.334	0.134	-0.479
napB	b2203			K-12 b2203 napB s at	1.076	0.732	1.453	0.77	1.014	0.146	-0.153
nupG	b2964		transport; Transport of small molecules: Nucleosides, purines, pyrimin	K-12 b2964 nupG s at	1.026	0.602	0.877	0.954	0.134	-0.164	-0.404
csqG	b1037			K-12_b1037_csgG_s_at	1.978	1.712	2.169	1.437	0.068	-0.115	0.386
slyB	b1641			K-12_b1641_slyB_s_at	1.009	1.055	0.662	0.15	-0.325	-0.075	-0.098
pepT	h1127			K-12 b1127 pepT s at	2.445	2.134	1.632	1.879	0.72	0.324	-0.734
pgsA	b1912	phosphatidylglycerophosphate synthetase		K-12_b1912_pgsA_s_at	1.109	0.286	1.173	-0.629	0.338	0.603	-0.143
	b1702				1.418	0.706	1.646	-0.507	-1.518	-1.974	-1.286
ppsA		phosphoenolpyruvate synthase		K-12_b1702_ppsA_s_at							
csgE	b1039			K-12_b1039_csgE_s_at	1.882	1.574	2.648	2.318	0.344	0.302	-0.148
yjgR	b4263			K-12_b4263_yjgR_s_at	1.072	0.876	0.303	1.644	0.653	-0.168	-0.12
yafV	b0219			K-12_b0219_yafV_s_at	1.104	1.518	0.641	1.004	0.818	-0.048	-0.204
yeaT	b1799	predicted DNA-binding transcriptional regulator	putative regulator; Not classified	K-12_b1799_yeaT_s_at	1.718	1.156	1.197	1.608	0.657	0.181	-0.246
yghU	b2989		orf; Unknown	K-12_b2989_yghU_s_at	1.692	0.96	1.528	2.435	0.758	-0.159	-0.792
yhhY	b3441	predicted acetyltransferase	orf; Unknown	K-12_b3441_yhhY_at	1.318	1.962	1.438	0.494	-0.447	0.132	-0.914
yccX	b0968	predicted acylphosphatase	orf: Unknown	K-12_b0968_yccX_s_at	2.247	2.521	2.007	2.319	0.728	0.128	-0.428
vncA	b1448			K-12 b1448 vncA s at	1.541	1.163	1.537	1.166	0.384	-0.171	-0.679
elaA	b2267			K-12_b2267_elaA_s_at	1.134	1.087	1.509	1.729	-0.996	0.157	-0.169
	b1525			K-12_b1525_yneI_s_at	1.134	1.114	1.538	0.887	0.744	-0.314	-0.357
yneI											
ycbB	b0925			K-12_b0925_ycbB_s_at	1.686	1.831	0.87	0.909	0.217	0.112	0.36
ytfB	b4206			K-12_b4206_ytfB_s_at	1.442	1.939	1.591	1.207	0.864	-0.243	0.04
ybiC	b0801			K-12_b0801_ybiC_s_at	1.7	0.803	1.929	0.833	0.272	0.329	0.029
yddV	b1490			K-12_b1490_yddV_s_at	1.289	1.005	0.494	0.597	0.207	-0.167	0.061
yciI	b1251	predicted enzyme	orf; Unknown	K-12 b1251 yciI s at	1.859	1.209	1.855	0.138	0.31	-0.939	-1.375
yfcF	b2301	predicted enzyme	orf; Unknown	K-12_b2301_yfcF_s_at	1.326	0.693	0.355	1.105	0.694	0.419	-0.307
ybgJ	b0711			K-12_b0711_ybgJ_s_at	1.089	0.874	1.151	0.231	-0.31	-0.381	-0.816
ybgK	b0712			K-12_b0712_ybgK_s_at	1.11	1.396	1.022	0.196	-1.495	-0.328	-1.017
yeiG	b2154			K-12_b2154_yeiG_s_at	1.187	0.538	1.24	0.035	-0.242	0.048	-0.564
yliJ	b0838	predicted esterase predicted glutathione S-transferase		K-12_02134_yeld_5_at	2.538	2.088	2.469	1.551	0.279	-0.633	-0.805
	b3592			K-12_b0838_yliJ_s_at		1.067		0.399		0.385	-0.862
yibF				K-12_b3592_yibF_s_at	1.623		0.838		-0.375		
btuE	b1710			K-12_b1710_btuE_s_at	1.012	0.597	0.061	1.799	-0.379	-0.993	-0.445
b2999	b2999			K-12_b2999_s_at	1.05	0.98	0.181	1.246	0.123	-0.104	-0.078
ybhL	b0786	predicted inner membrane protein	orf; Unknown	K-12_b0786_ybhL_s_at	1.373	1.228	0.841	0.395	0.06	0.429	0.014
ymgE	b1195	predicted inner membrane protein	orf; Unknown	K-12 b1195 ymgE s at	1.213	1.412	0.384	2.983	1.033	0.536	0.092
ydiK	b1688	predicted inner membrane protein	orf: Unknown	K-12_b1688_ydiK_s_at	2.098	2.261	1.865	0.738	1.533	0.516	0.716
yfdC	b2347	predicted inner membrane protein		K-12_b2347_yfdC_s_at	1.07	0.91	0.441	2.69	0.51	0.175	-0.06
vphA	b2543			K-12_b2543_yphA_s_at	1.312	1.017	0.396	1.49	0.869	1.018	-0.166
b2670	b2670			CFT073_c3221_ygaW_s_at	2,408	2.31	2.821	1.941	0.512	0.378	0.301
vhaH	b3103		putative carrier; Not classified	K-12 b3103 yhaH s at	1.365	1.506	0.467	1.156	0.262	0.048	-0.213
ycgM	b1180			K-12_b1180_ycgM_s_at	2.825	2.588	2.962	1.056	1.206	0.882	1.245
yciW	b1287			K-12_b1287_yciW_s_at	2.69	2.145	2.712	1.757	1.423	0.669	0.53
ydjA	b1765		orf; Unknown	K-12_b1765_ydjA_s_at	1.167	1.263	1.598	0.499	0.63	0.196	-0.256
mviM	b1068	predicted oxidoreductase with NAD(P)-binding Rossmann-fold domain	putative factor; Not classified	K-12_b1068_mviM_s_at	1.448	1.518	1.365	0.987	1.072	-0.477	-0.162
tas	b2834	predicted oxidoreductase, NADP(H)-dependent aldo-keto reductase	orf; Unknown	K-12_b2834_tas_s_at	1.303	1.355	1.302	1.637	0.792	-0.654	0.133
yhdH	b3253	predicted oxidoreductase, Zn-dependent and NAD(P)-binding	putative enzyme; Not classified	K-12_b3253_yhdH_s_at	1.322	1.262	0.957	1.393	-0.625	-0.895	-1.649
yqfA	b2899	predicted oxidoreductase, inner membrane subunit	putative enzyme; Not classified	K-12_b2899_yqfA_s_at	2.808	2.807	2.986	2.881	1.466	1.685	1.309
ydqD	b1598			O157 ECs2304 s at	1.644	1.674	0.762	2.131	0.883	-0.137	0.34
tldD	h3244	predicted peptidase		K-12 b3244 tldD s at	1.026	1.349	0.605	0.922	-0.232	-0.674	-0.246
yliC	b0831	predicted peptide transporter subunit: membrane component of ABC		K-12_b0831_yliC_s_at	2.779	1.928	2.864	1.516	1.869	0.826	0.336
	b4030						4.068				
yjbA	b0382			K-12_b4030_yjbA_s_at	4.062 3.421	4.9 3.49	3.736	1.407 3.186	1.787 2.396	1.391	0.122
yaiB				K-12_b0382_yaiB_s_at							
ybeH	b0625			K-12_b0625_ybeH_s_at	2.041	1.888	1.276	2.202	1.213	1.305	0.473
ybfA	b0699		orf; Unknown	K-12_b0699_ybfA_s_at	2.492	2.397	2.71	1.768	1.377	0.381	0.612
yceF	b1087			K-12_b1087_yceF_s_at	2.548	2.17	2.301	1.446	1.134	0.815	0.672
ycfL	b1104			K-12_b1104_ycfL_s_at	1.17	0.9	0.908	0.158	-1.147	-0.86	-0.554
ycgJ	b1177			K-12_b1177_ycgJ_s_at	1.119	1.153	1.442	1.048	-0.125	-0.244	-0.283
ydiH	b1685			K-12_b1685_ydiH_s_at	1.677	1.879	2.254	1.576	-0.281	-0.721	-0.031
ydiZ	b1724			K-12_b1724_ydiZ_s_at	4.776	4.9	3.946	5.859	1.574	0.152	0.572
yodC	b1957	predicted protein	orf; Unknown	K-12_b1957_yodC_s_at	2.974	3.684	2.184	4.524	1.086	1.337	0.766
yfgG	b2504			K-12_b2504_yfgG_s_at	1.052	0.887	0.947	-0.043	-1.267	0.226	-0.505
vfiL	b2602			K-12 b2602 vfiL s at	1.188	1.535	0.451	2,277	0.446	0.09	-0.51
ygeA	b2840	predicted racemase		K-12_b2840_ygeA_s_at	1.135	1.775	1.401	1.912	0.723	0.38	-0.145
yedY	b1971	predicted reductase		K-12_b1971_yedY_s_at	1.676	1.383	0.993	1.628	0.884	0.508	0.436
ypdB	b2381		putative enzyme; Not classified	K-12_b1971_yed1_s_at K-12_b2381_ypdB_s_at	1.008	1.018	0.659	1.076	0.884	-0.288	-0.712
	b2381 b4135				1.008	1.018	1.172	1.076	-0.182	-0.288 -0.988	-0./12 -1.47
yjdC	b4135 b0780			K-12_b4135_yjdC_s_at							
ybhK			putative structure; Not classified	K-12_b0780_ybhK_s_at	1.288	1.521	1.273	0.36	0.514	0.601	0.103
ybiB	b0800	predicted transferase/phosphorylase		K-12_b0800_ybiB_s_at	2.033	2.251	1.765	0.66	-0.756	-0.369	0.08
csgF	b1038			K-12_b1038_csgF_s_at	3.039	2.964	3.488	2.646	0.282	0.518	0.787
yhjE	b3523		putative transport; Not classified	K-12_b3523_yhjE_s_at	1.646	0.96	1.464	0.422	-0.053	1.073	-0.739
yecC	b1917	predicted transporter subunit: ATP-binding component of ABC superfa	putative transport; Not classified	K-12_b1917_yecC_s_at	2.068	1.602	1.603	0.438	0.632	0.412	0.606
yecS	b1918	predicted transporter subunit: membrane component of ABC superfar	putative transport; Not classified	K-12_b1918_yecS_s_at	2.466	1.704	1.995	0.292	0.428	0.519	0.722
yagT	b0286	predicted xanthine dehydrogenase, 2Fe-2S subunit	putative enzyme; Not classified	K-12_b0286_yagT_s_at	1.18	1.732	0.57	2.277	1.054	0.116	-0.137
yfdZ	b2379			K-12_b2379_yfdZ_s_at	1.812	2.146	1.533	1.065	0.52	0.105	-0.194
ycfF	b1103			K-12_b1103_ycfF_s_at	1.491	0.828	0.872	0.487	-1.114	-0.941	-0.239
potF	b0854	putrescine transporter subunit: periplasmic-binding component of AB		K-12_b1105_ycn_s_at K-12_b0854_potF_s_at	1.295	0.539	0.51	1.365	-0.737	-1.84	-2.301
	b2564	pyridoxine 5'-phosphate synthase		K-12_b0554_pdxJ_s_at	1.448	0.813	1.625	0.973	-0.737	-0.657	-0.258
pdx3	b1854						1.625	0.973	0.815		
pykA			enzyme; Energy metabolism, carbon: Glycolysis	K-12_b1854_pykA_s_at	1.395	1.122				-1.348	-1.082
ygiN	b3029		orf; Unknown	K-12_b3029_ygiN_s_at	1.085	0.713	1.359	0.238	-0.314	-0.56	-0.557
yljA	b0881	regulatory protein for ClpA substrate specificity	orf; Unknown	K-12_b0881_yljA_s_at	1.704	2.005	1.842	1.828	0.141	-0.498	-0.975
rydB	b4430	regulatory sRNA		K-12_b4430_rydB_at	1.188	2.034	1.683	2.425	1.39	-0.019	-0.133
csrC	b4457	regulatory sRNA		K-12_b4457_csrC_at	2.796	3.483	2.756	2.347	-0.237	-1.214	-1.437
ribC	b1662	riboflavin synthase, alpha subunit	enzyme; Biosynthesis of cofactors, carriers: Riboflavin	K-12_b1662_ribC_s_at	1.139	0.837	0.967	-0.152	0.38	-0.433	-0.174

rimJ rmf susfS degQ ryeA tke1 ygjU csiE rsd ydaA ydaA ydaA ydaA ydaA cysN cysD cysD cysD cysD cysD tsiB tsiB tsiB tsiB trpA trpA trpB trpB tybgR tybgR	b1066 b0953 b1680 b3234 b4441 b3089 b4432 b4441 b3089 b2535 b1376 b2752 b2422 b2423 b2424 b2764 b2764 b2764 b2764 b2765 b3125	ribosomal-protein-S5-alanine N-acetyltransferase ribosome modulation factor selenocysteine lyase, PLP-dependent serine endoprotease, periplasmic small RNA small RNA sodium: serine/threonine symporter stationary phase inducible protein stationary phase protein, binds sigma 70 RNA polymerase subunit stress-induced protein suifate adenylyltransferase, subunit 2 suifate/thiosulfate transporter subunit -1- membrane component of suifate/thiosulfate transporter subunit -1- membrane component of auffite reductase, plans subunit, NAD(P)-binding, heme-binding tartronate semialdehyde reductase taurine transporter subunit -1- ATP-binding component of ABC supert thiosulfate transporter subunit -1- Periplasmic-binding component of threonine deaminase thymidine phosphorylase tryptophan synthase, alpha subunit tryptophan synthase, beta subunit universal stress global response regulator unidne phosphorylase zinc efflux system zinc transporter	I transport; Transport of small molecules: Anions I transport; Transport of small molecules: Anions enzyme; Central intermediary metabolism: Sulfur metabolism enzyme; Central intermediary metabolism: Sulfur metabolism putative enzyme; Not classified i transport; Transport of small molecules: Amino acids, amines	K-12_b1066_rimJ_s_at LT2_STM1066_rimI_s_at K-12_b1680_sufS_s_at K-12_b4080_sufS_s_at K-12_b4382_ryeA_at K-12_b4382_ryeA_at K-12_b4382_ryeA_at K-12_b4382_ryeA_at K-12_b4382_ryeA_at K-12_b535_csiE_s_at K-12_b535_csiE_s_at K-12_b535_rsiS_s_at K-12_b535_rsiS_s_at K-12_b535_rsiS_s_at K-12_b535_rsiS_s_at K-12_b535_ryeA_s_at K-12_b535_ryeA_s_at K-12_b535_ryeA_s_at K-12_b535_ryeA_s_at K-12_b535_ryeA_s_at K-12_b536_ryeA_s_at		1.372 5.376 1.481 1.291 1.765 1.117 1.49 1.053 3.464 2.87 2.91 2.87 2.912 6.392 6.392 6.392 6.393 5.538 1.253 1.197 5.38 1.253 1.197 5.38 1.253 1.197 5.38 1.197 5.38 1.198 1.199 1.	1.938 5.3 1.602 1.461 1.273 0.701 1.89 3.606 3.043 3.085 5.69 6.841 4.833 4.93 5.983 5.983 5.983 5.983 6.303 2.882 0.523 1.178 1.178 1.282 0.523 1.178 1.295 0.355 2.447 1.296	1.256 5.489 1.171 1.389 0.342 2.685 0.872 2.883 2.021 6.479 1.435 4.897 4.435 4.897 1.257 5.38 3.259 1.257 5.38 3.259 0.442 2.053 0.442 2.053 0.613 1.605	0.802 5.034 1.96 0.12 1.22 1.181 0.626 2.864 0.979 1.47 5.492 3.494 5.492 3.494 4.027	-0.182 2.327 0.54 0.45 0.646 -0.835 -1.188 1.596 -1.427 1.574 1.442 1 4.288 4.318 3.165 2.781 4.51 3.165 2.781 4.51 3.666 0.825 0.085 -0.31 -0.241 3.681 0.067 0.482	-1.219 -0.877 0.416 -0.44 -0.134 -1.555 0.136 0.246 -0.841 0.606 0.17 1.282 3.303 4.379 3.111 3.545 3.409 2.073 0.632 0.601 3.514 1.05 -0.704 -0.805 -0.901 -0.904 0.063	-0.617 -0.588 -0.031 -0.416 -0.882 -1.079 -0.076 -0.331 -1.044 -1.034 -1.034 -1.054
Venn: Other >2fold higher 17 genes	· in ΔrelAspoT o	only										
GENE cycA umuD narP relB hokD relE rnr ygiT yniB yeeE ykiA ycbW yceP ycfR ydcD ydhR yeiG	LOCUS_TAG b4208 b1183 b2193 b1564 b1562 b1563 b4179 b3021 b1726 b2013 b0392 b0946 b1060 b1112 b1457 b1667 b2181	GENE_PRODUCT D-alanine/D-serine/glycine transporter D-Alanine/D-serine/glycine transporter DNA polymerase V, subunit D DNA-binding response regulator in two-component regulatory system Olin prophage; bifunctional antitoxin of the RelE-RelB toxin-antitoxin Qlin prophage; toxin of the RelE-RelB toxin-antitoxin system exoribonuclease R, RNase R predicted DNA-binding transcriptional regulator predicted inner membrane protein predicted protein		PROBESETS K-12, b4208_cycA_s_at K-12, b1183_umuD_s_at K-12, b2193_narP_s_at K-12, b1564_relB_at K-12, b1564_relB_at K-12, b1565_relE_at K-12, b1563_relE_at K-12, b3021_ygiT_at K-12, b3021_ygiT_at K-12, b3021_ygiT_at K-12, b3021_ygiT_s_at K-12, b3021_ygiT_s_at K-12, b3021_ygiT_s_at K-12, b3021_ygiT_s_at K-12, b3030_yeiR_s_at K-12, b3030_yeiR_s_at K-12, b3030_yeiR_s_at K-12, b1030_yeiR_s_at K-12, b1112_ycfR_s_at 0157_ECs0244_s_at K-12, b1667_ydiR_s_at	WT	Irp 1.001 1.045 1.113 1.765 3.075 2.26 1.526 2.04 1.014 3.937 1.126 1.262 2.229 1.872 1.307 1.228	rpoS 0.602 0.646 1.4 2.748 3.327 2.457 2.232 2.656 1.043 4.277 1.926 1.086 3.153 2.281 1.644 0.927 0.652	1.003 0.587 1.127 2.101 3.168 2.169 1.358 2.324 1.069 3.607 0.297 1.46 1.617 1.899 1.91	dksA 0.334 0.639 1.848 2.46 1.799 1.388 -0.343 2.032 0.489 2.205 0.145 0.576 0.394 1.866 2.362 -0.064 0.553	relA 0.716 0.356 1.365 0.879 1.502 1.714 0.617 2.178 0.56 3.813 0.046 1.08 0.705 1.406 0.376 0.658 1.406	rel. 1.621 0.896 2.108 3.314 3.514 2.616 2.556 4.01 1.487 5.553 1.023 1.43 2.44 2.779 2.337 1.395	2.03 2.462 2.304 3.25 4.238 3.312 2.666 4.399 2.237 5.332 2.302 2.434 3.238 3.358 2.816 2.683 2.45
> 2fold higher 5 genes GENE ybcM		GENE_PRODUCT DIP12 prophage; predicted DNA-binding transcriptional regulator	FUNCTION putative regulator; Not classified	PROBESETS K-12_b0546_ybcM_at	WT	lrp 2.187	rpoS 3.33	crp 2.28	dksA 1.743	relA 1.033	rel. 0.608	AspoT 1.729
ydiV dinJ yabQ ybiJ	b1707 b0226 b0057 b0802	conserved protein predicted antitoxin of YafQ-DinJ toxin-antitoxin system predicted protein predicted protein	orf; Unknown phenotype; Not classified orf; Unknown orf; Unknown	K-12_b1707_ydiV_s_at K-12_b0226_dinJ_s_at K-12_b0057_yabQ_at K-12_b0802_ybiJ_s_at		1.327 1.732 1.325 2.026	2.358 2.874 2.469 3.311	1.847 2.2 1.984 2.394	0.985 2.836 0.855 0.563	0.565 0.566 0.282 0.75	0.589 2.265 0.69 0.444	1.44 1.94 0.774 1.055
Venn: Other >2fold lower 6 genes	in ∆relAspoT, h	nigher in Δlrp										
GENE ilvM ygiW ycgZ ymgA ymgC yhjX	LOCUS_TAG b3769 b3024 b1164 b1165 b1167 b3547	GENE_PRODUCT acetolactate synthase II, small subunit conserved protein predicted protein predicted protein predicted protein predicted protein predicted protein	FUNCTION enzyme; Amino acid biosynthesis: Isoleucine, Valine orf; Unknown orf; Unknown orf; Unknown orf; Unknown orf; Unknown orf; Unknown putative transport; Drug/analog sensitivity	PROBESETS K-12_b3769_livM_s_at K-12_b3024_ygiW_s_at K-12_b1064_ycgZ_x_at K-12_b1165_ymgA_at K-12_b1167_ymgC_at K-12_b3547_yhjX_s_at	WT	lrp 4.628 1.616 3.687 4.631 1.795 1.758	rpoS 5.766 3.051 5.257 5.881 3.145 4.818	5.117 1.149 3.247 4.132 0.84 1.045	dksA 3.981 3.242 5.104 6.089 1.014 -0.036	relA 2.399 0.776 0.404 0.765 0.349 2.251	76.3.505 -0.118 1.355 1.302 0.374 -0.088	2.379 0.152 1.694 1.666 0.195 -0.788
Venn: Other >2fold higher 1 gene	· in both ∆relAs	spoT and Δlrp										
GENE ygiU	LOCUS_TAG b3022	GENE_PRODUCT predicted cyanide hydratase	FUNCTION orf; Unknown	PROBESETS K-12_b3022_ygiU_at	WT	lrp 2.184	rpoS 3.299	crp 2.196	dksA 0.93	relA 1.13	rel. 4.031	AspoT 4.616
Venn: Other >2fold higher 1 gene	in ΔrelAspoT,	Δlrp, and ΔrpoS										
GENE	LOCUS_TAG	GENE_PRODUCT	FUNCTION	PROBESETS	WT	Irp	rpoS	crp	dksA	relA	rela	AspoT

ynaE	b1375	Rac prophage; predicted DNA-binding transcriptional regulator	orf; Unknown	K-12_b1544_ydfK_s_at		2.002	3.048	3.187	2.278	0.257	1.765	3.666
	Venn: Chter > -2fold higher in ΔτροS, lower in ΔτelAspoT and Δlrp 2 genes											
GENE fimC fimI	LOCUS_TAG b4316 b4315	GENE_PRODUCT chaperone, periplasmic fimbrial protein involved in type 1 pilus biosynthesis	FUNCTION factor; Surface structures structural component; Surface structures	PROBESETS K-12_b4316_fimC_s_at K-12_b4315_fimI_s_at	WT	lrp 1.472 1.725	rpoS -1.821 -2.317	crp 2.844 2.745	dksA 0.645 0.482	relA 2.626 2.398	relA 0.643 0.455	AspoT 0.258 -0.04
Venn: Othe >2fold high 1 gene	r ier in Δlrp, lowe	r in ΔrpoS										
GENE yhiP	LOCUS_TAG b3496	G GENE_PRODUCT predicted transporter	FUNCTION putative transport; Not classified	PROBESETS K-12_b3496_yhiP_s_at	WT	lrp 1.337	rpoS 2.657	crp 0.176	dksA 0.422	relA 0.7	rel <i>l</i> 1.599	AspoT 1.952
Venn: Othe >2fold high 3 genes		r in ΔrpoS, lower in ΔrelAspoT										
GENE ybgS ymgB yjfY	LOCUS_TAG b0753 b1166 b4199	GENE_PRODUCT conserved protein predicted protein predicted protein	FUNCTION putative regulator; Not classified orf; Unknown orf; Unknown	PROBESETS K-12_b0753_ybgS_s_at K-12_b1166_ymgB_x_at K-12_b4199_yjfY_s_at	WT	2.62 4.66 2.466	rpoS 3.658 5.928 3.675	crp 0.948 3.6 0.712	dksA 1.505 3.806 4.135	relA 1.086 0.341 1.213	rel <i>A</i> -0.52 0.339 0.267	AspoT -0.407 1.523 0.053
	Venn: Other >2fold higher in ΔrelAspoT, lower in ΔrpoS 2 genes											
GENE yebF yjgH	LOCUS_TAG b1847 b4248	GENE_PRODUCT predicted protein predicted mRNA endoribonuclease	FUNCTION orf; Unknown orf; Unknown	PROBESETS K-12_b1847_yebF_s_at K-12_b4248_yjgH_s_at	WT	lrp 2.024 1.751	rpoS 1.654 1.429	crp 0.259 0.284	dksA 1.017 1.47	relA -0.122 -0.181	rel <i>l</i> 1.975 0.497	AspoT 3.857 5.955