Supplementary Figure Legends

Fig. S1. Alignment of the AbcR sRNAs from *Agrobacterium tumefaciens* C58 and *Brucella abortus* 2308

The nucleotide sequence of AbcR1 and AbcR2 from *Brucella abortus* 2308 and *Agrobacterium tumefaciens* C58 were aligned using the AlignX® software from Vector NTI® (Invitrogen). Identical nucleotides between the two sRNAs are shown as the consensus sequence in bold font.

A. Alignment of AbcR1 sRNAs

B. Alignment of AbcR2 sRNAs

Fig. S2. Northern blot analysis of AbcR sRNAs from different *Brucella* species

Total RNA isolated from cultures of *B. abortus* 2308, *B. suis* 1330, and *B. melitensis* 16M was separated on denaturing polyacrylamide gels. Following transfer to a membrane, a single probe designed to detect either AbcR1 or AbcR2 were used in the northern blot analyses. Detection of 5S rRNA was also performed as a loading control.

Fig. S3. Folding predictions of the AbcR1 and AbcR2 secondary structures

Secondary structure predictions of the AbcR sRNAs from *Brucella abortus* 2308 were determined using mfold (http://mfold.rna.albany.edu/?q=mfold).

Fig. S4. Hfq binding to AbcR1 and AbcR2

Electrophoretic mobility shift assays (EMSAs) were employed to test the binding between of Hfq to the AbcR sRNAs, and methods described previously were used for these experiments (Caswell et al., 2012). The AbcR1 and AbcR2 sRNAs were transcribed in vitro and radiolabeled by [α-^{32}P]UTP incorporation, and EMSAs were performed using the labeled in vitro transcribed sRNAs and purified recombinant *Brucella abortus* Hfq. Increasing concentrations of rHfq were incubated with the labeled RNA probe, and the binding reactions were resolved in 5% native polyacrylamide gels and visualized by autoradiography.

Fig. S5. Schematic of putative interacting motif between the AbcR sRNAs and target mRNAs in *B. abortus* 2308.

The numbers in parentheses depict the nucleotide position of the motif within the AbcR sRNAs, and similarly, the distance from the putative binding motif to the start codon is shown for the mRNAs.

Fig. S6. Proteomic analysis of *B. abortus* 2308 and the *B. abortus abcR1 abcR2* double mutant strains

iTRAQ analysis was performed as described in the Experimental procedures. The value for a given protein represents the fold difference in the level of that protein between the two indicated strains. For example, values in the “*abcR*/WT-1” column depict protein levels in the *abcR1 abcR2* double mutant strain compared to protein levels in the parental strain 2308.

Figure S1

A

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Agrobacterium AbcR1   AGUUGAUGCACACGGUGGCUUUUCCUCCCAGUUCCACCGCAUCAGCUGUU
Brucella AbcR1        -------ACUUACCGUUGUGCCUCCUCCCAUUGCGCACGG-UAAG-UGUU
  Consensus                   C  AC GU G    UCCUCCCA U C   CG  U AG UGUU

Agrobacterium AbcR1   CCCCUCUGGAGGUUUUUGACCUUCACACUUAAAGGGCCCUG--GAUCUAU
Brucella AbcR1        CCCCUCUGGAGGUUUGCCCAAGUGGCACCUUCAUAACUUGGCCGGACUUC
  Consensus           CCCCUCUGGAGGUUU       U  CAC U  A   C   G  G  CU

Agrobacterium AbcR1   CCGGCGGCCCUCUUUUUUU
Brucella AbcR1        CCAGUCCGGCUCUUUUUUU          Identity = 53.8%
  Consensus           CC G     CUCUUUUUUU
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B

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Agrobacterium AbcR2   ---------CUGUCACGCUUGCCCACGGCACGCGACAGC----UGUUCCC
Brucella AbcR2        AUCUCAGUGCUGCGUUUCCUCCUCCCAUUUUGCGCAGGCUGAGUGUUCCC
  Consensus                    CUG     C U C C C     GCG   GC    UGUUCCC

Agrobacterium AbcR2   CUCUGGAGGUUU-------UG--ACCUUCAAACUUGUCAGGCCGCGGAGC
Brucella AbcR2        CUCUGGAGGUUUGCCUCAAUGGCACCUUCAAAAUUCAAAAGCCG----GA
  Consensus           CUCUGGAGGUUU       UG  ACCUUCAAA UU   A GCCG    G

Agrobacterium AbcR2   AAUCCAGCGGCCUUCUUUUUUU
Brucella AbcR2        CGUUUGUCUGGCUUUUUUUUU-       Identity = 51.2%
  Consensus             U    C G CUU UUUUU
```

Figure S2

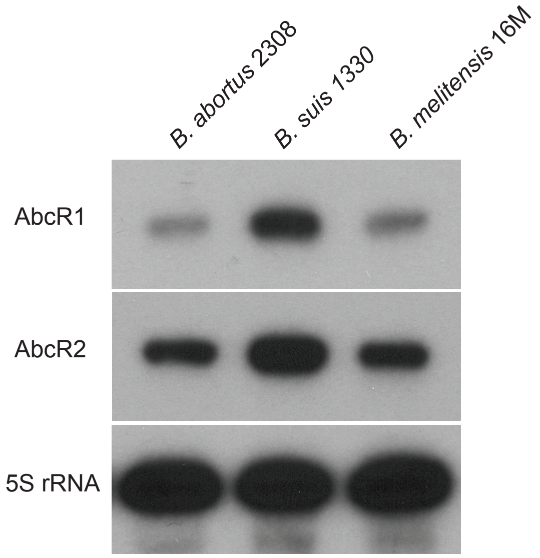
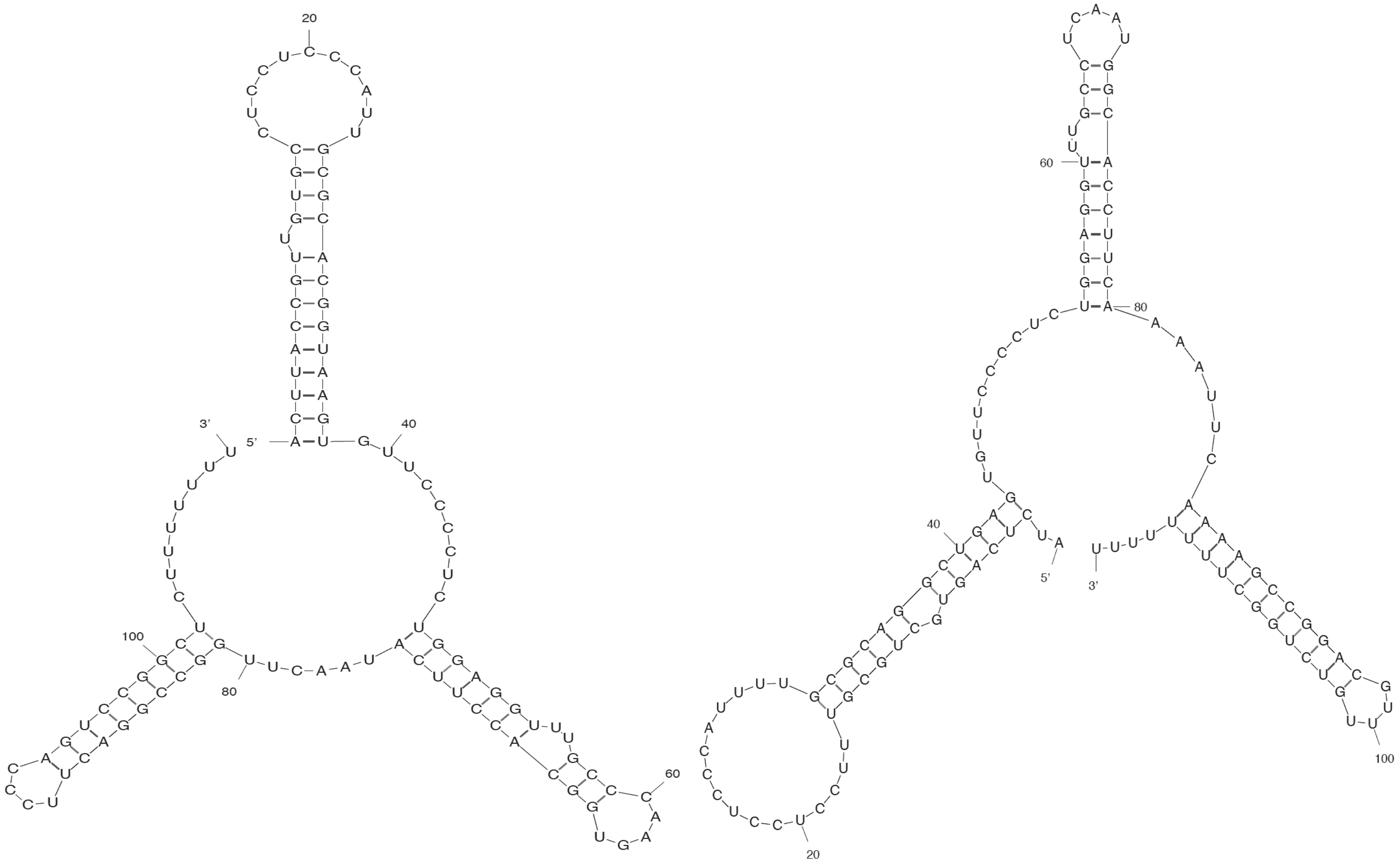

B. abortus 2308
B. suis 1330
B. melitensis 16M
AbcR1
AbcR2
5S rRNA

Figure S3



AbcR1
$\Delta G=-43.40$ kcal/mol

AbcR2
$\Delta G=-43.60$ kcal/mol

Figure S4

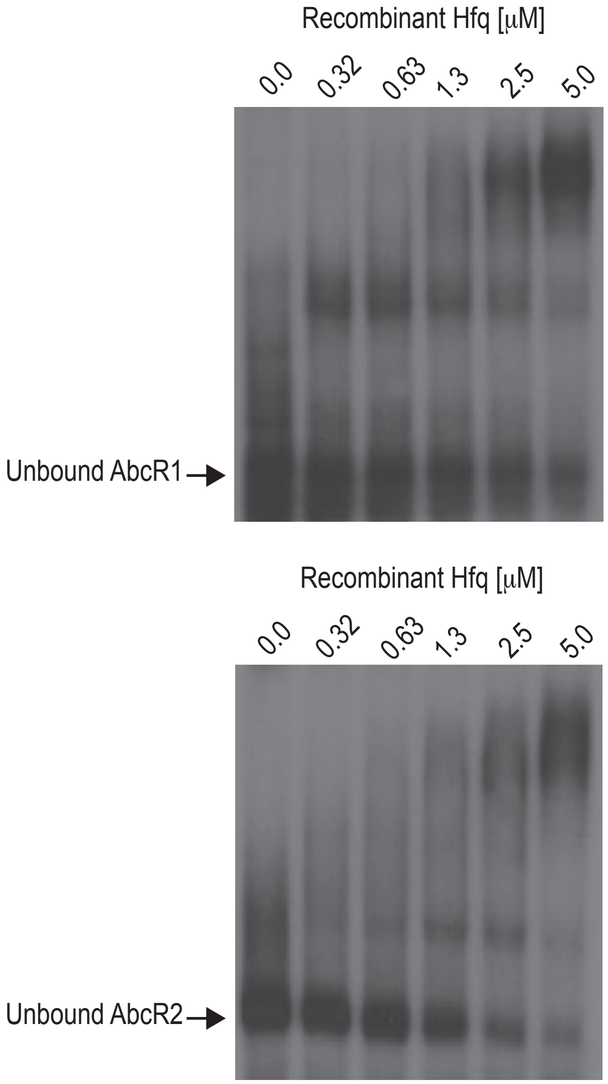

Recombinant Hfq [μM]
0.0
0.32
0.63
1.3
2.5
5.0
Unbound AbcR1
Recombinant Hfq [μM]
0.0
0.32
0.63
1.3
2.5
5.0
Unbound AbcR2

Figure S5

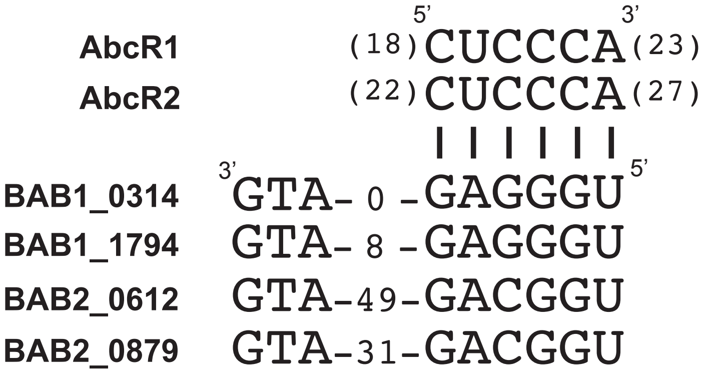

AbcR1
5'
3'
(18)CUCCCA(23)
AbcR2
(22)CUCCCA(27)
BAB1_0314
3'
GTA-0-GAGGGU
5'
BAB1_1794
GTA-8-GAGGGU
BAB2_0612
GTA-49-GACGGU
BAB2_0879
GTA-31-GACGGU

Figure S6 Proteomic analysis of *B. abortus* 2308 and the *B. abortus abcR1 abcR2* double mutant strains

Accession #	Name	BAB number	abcR/WT-1	abcR/WT-2	WT/WT	abcR/abcR
gi|82700075	DNA-directed RNA polymerase subunit beta'	BAB1_1263	1.0357	1.0305	0.9956	1.0004
gi|83269127	chaperonin GroEL	BAB2_0189	1.109	1.0669	0.9467	0.9831
gi|82700076	DNA-directed RNA polymerase subunit beta	BAB1_1264	1.0087	1.0265	0.9991	0.9808
gi|82700876	molecular chaperone DnaK	BAB1_2129	1.0564	1.0474	0.995	1.0037
gi|82700083	elongation factor Tu	BAB1_1271	0.9799	1.0024	0.9948	0.9719
gi|82700597	NAD-glutamate dehydrogenase	BAB1_1827	1.1603	1.1623	1.0062	1.0046
gi|82700638	chaperonin ClpA/B	BAB1_1868	1.0928	1.0673	0.9808	1.0033
gi|82700689	alpha-ketoglutarate decarboxylase	BAB1_1923	1.0184	1.0333	1.0078	0.9925
gi|82700070	elongation factor G	BAB1_1258	1.0541	1.0465	0.9873	0.9931
gi|82699012	aconitate hydratase	BAB1_0090	1.0533	1.0518	1.0158	1.0175
gi|82700911	translation initiation factor IF-2	BAB1_2165	1.0018	1.0496	1.0483	0.9999
gi|82700915	polynucleotide phosphorylase/polyadenylase	BAB1_2169	1.0392	1.0328	0.9806	0.986
gi|82699768	trigger factor	BAB1_0917	1.0253	0.9831	0.975	1.0161
gi|82700579	F0F1 ATP synthase subunit beta	BAB1_1807	0.9775	0.9948	1.0105	0.9915
gi|82700692	malate dehydrogenase	BAB1_1927	0.9741	0.9994	1.0212	0.9948
gi|82699993	surface antigen (D15)	BAB1_1176	1.02	1.0237	0.9917	0.9875
gi|82698954	30S ribosomal protein S1	BAB1_0025	1.0443	1.0375	0.9889	0.9948
gi|82700691	succinyl-CoA synthetase subunit beta	BAB1_1926	0.9822	0.958	0.9908	1.0154
gi|83269417	bifunctional proline dehydrogenase	BAB2_0518	1.4853	1.5006	1.017	1.0061
gi|82700581	F0F1 ATP synthase subunit alpha	BAB1_1809	1.0066	1.0048	0.973	0.9744
gi|82700516	transketolase	BAB1_1740	1.0235	0.9817	0.9944	1.0357
gi|82699578	leucyl aminopeptidase	BAB1_0710	1.0029	1.0125	1.0051	0.9951
gi|82698997	argininosuccinate synthase	BAB1_0071	1.0431	1.0298	0.9838	0.9952
gi|82700690	succinyl-CoA synthetase subunit alpha	BAB1_1925	1.0209	0.9921	0.983	1.0105
gi|82699528	hypothetical protein BAB1_0660	BAB1_0660	0.8552	0.8618	0.9474	0.9394
gi|82700709	preprotein translocase subunit SecA	BAB1_1946	0.9886	0.987	0.9946	0.9957
gi|82699892	ribonucleotide-diphosphate reductase subunit alpha	BAB1_1063	1.1122	1.1493	1.0369	1.0014
gi|83269363	glucose-6-phosphate 1-dehydrogenase	BAB2_0460	0.9705	0.9479	0.9748	0.9979
gi|82700033	isocitrate dehydrogenase	BAB1_1221	0.9184	0.9495	1.0277	0.9934
gi|82699685	NADH dehydrogenase subunit G	BAB1_0828	1.0562	1.0741	0.9895	0.9725
gi|82699815	valyl-tRNA synthetase	BAB1_0966	0.9717	0.9921	0.9978	0.9766
gi|82700300	carbamoyl phosphate synthase large subunit	BAB1_1508	1.0974	1.0521	0.9975	1.0391
gi|82700000	elongation factor Ts	BAB1_1183	1.076	0.9873	0.9821	1.0744
gi|82699405	pyruvate phosphate dikinase	BAB1_0525	0.9888	0.998	1.013	1.0036
gi|82699705	30S ribosomal protein S4	BAB1_0851	0.9084	0.9641	1.0385	0.9768
gi|82699987	type II citrate synthase	BAB1_1170	0.9958	1.0286	1.0149	0.9813
gi|82699949	chaperonin ClpA/B	BAB1_1130	1.0805	1.1015	0.9872	0.9678
gi|82700567	Leu/Ile/Val-binding family protein	BAB1_1794	6.1752	5.7498	0.9338	1
gi|82700043	DNA-directed RNA polymerase subunit alpha	BAB1_1231	1.0319	1.0514	0.9997	0.9808
gi|82700688	dihydrolipoamide acetyltransferase	BAB1_1922	0.9902	0.9968	1.0127	1.006

gi|82700535	pyruvate kinase	BAB1_1761	0.9846	0.9977	1.0195	1.0057
gi|82699210	glucose-6-phosphate isomerase	BAB1_0316	0.9085	0.952	1.029	0.9816
gi|82700001	30S ribosomal protein S2	BAB1_1184	1.0305	1.0226	0.996	1.0033
gi|83269857	phosphoglyceromutase	BAB2_1013	1.0749	1.017	0.9471	1.0012
gi|83269434	copper/Zinc superoxide dismutase	BAB2_0535	0.9258	0.8915	0.9699	1.0072
gi|162002872	2-isopropylmalate synthase	BAB1_1583	0.9895	0.9369	0.9328	0.9842
gi|82699634	aspartyl-tRNA synthetase	BAB1_0775	1.0887	1.0262	0.9831	1.0483
gi|83269582	solute-binding family 5 protein	BAB2_0699	2.3464	2.1712	0.9242	0.9986
gi|83269060	6-phosphogluconate dehydrogenase	BAB2_0109	0.9634	0.9612	0.9931	0.9947
gi|82698981	phosphoglucomutase	BAB1_0055	1.0853	1.0832	1.0049	1.0069
gi|82700896	DNA starvation/stationary phase protection protein Dps	BAB1_2150	0.9682	0.9302	0.9726	1.0125
gi|82700007	chaperonin ClpA/B	BAB1_1191	1.0275	1.0315	1.0206	1.0178
gi|82700587	leucyl-tRNA synthetase	BAB1_1815	0.9516	0.9918	1.0361	0.9927
gi|82700242	cell division protein FtsZ	BAB1_1444	0.9251	1.052	1.0994	0.9689
gi|82699682	NADH dehydrogenase subunit D	BAB1_0825	1.0301	1.0063	0.9812	1.0044
gi|82699040	hypothetical protein BAB1_0118	BAB1_0118	1.0386	0.9781	0.9568	1.0159
gi|83269309	N-6 adenine-specific DNA methylase	BAB2_0397	0.9753	1.0244	1.0477	0.9972
gi|82700615	tail specific protease	BAB1_1845	1.0045	1.0145	0.9994	0.9891
gi|82700064	50S ribosomal protein L2	BAB1_1252	1.0377	1.0177	0.9917	1.01
gi|82699319	glycyl-tRNA synthetase subunit beta	BAB1_0433	0.9372	0.9464	1.0053	0.9944
gi|83269116	aldo/keto reductase	BAB2_0177	1.1	1.0184	0.9366	1.011
gi|82699747	arginyl-tRNA synthetase	BAB1_0896	1.0109	1.0073	1.0014	1.0048
gi|82699711	phosphoribosylformylglycinamidine synthase II	BAB1_0857	1.0318	0.9824	0.9813	1.0302
gi|82700909	transcription elongation factor NusA	BAB1_2163	0.9864	1.0004	1.0052	0.991
gi|82700383	substrate-binding region of ABC-type glycine betaine transport system	BAB1_1593	1.4082	1.3366	0.9564	1.006
gi|82700055	50S ribosomal protein L5	BAB1_1243	0.9542	1.0018	1.034	0.9854
gi|82700707	PpiC-type peptidyl-prolyl cis-trans isomerase	BAB1_1944	1.0229	0.9681	0.9876	1.0407
gi|82699672	O-acetylhomoserine aminocarboxypropyltransferase	BAB1_0813	1.029	0.9487	0.9275	1.0047
gi|83269277	elongation factor G	BAB2_0361	1.0738	1.0675	1.0127	1.0184
gi|82700343	50S ribosomal protein L25/general stress protein Ctc	BAB1_1551	1.0321	1.0067	1.0193	1.0434
gi|82699086	GrpE protein	BAB1_0170	1.0777	1.0176	0.9835	1.04
gi|82699425	Short-chain dehydrogenase	BAB1_0545	0.9706	0.9902	0.999	0.9783
gi|82700684	dihydrolipoamide dehydrogenase	BAB1_1918	1.1111	1.0706	0.9562	0.9897
gi|82700158	calcium-binding EF-hand	BAB1_1355	0.8286	0.8497	0.9988	0.9735
gi|82699781	ribonuclease E and G	BAB1_0930	1.0229	1.0117	1	1.0106
gi|82699950	ATP-dependent protease ATP-binding subunit	BAB1_1131	1.0079	1.035	1.014	0.9864
gi|82699363	50S ribosomal protein L9	BAB1_0477	0.9943	1.0087	0.9958	0.9812
gi|82700669	succinate dehydrogenase flavoprotein subunit	BAB1_1901	0.9683	1.0076	1.0291	0.9879
gi|82700035	alanyl-tRNA synthetase	BAB1_1223	1.0868	0.977	0.9376	1.0409
gi|83269444	solute-binding family 1 protein	BAB2_0547	0.8859	0.8561	0.9263	0.9575
gi|82699769	aspartyl/glutamyl-tRNA amidotransferase subunit B	BAB1_0918	1.011	0.9896	0.9782	0.9977
gi|82700850	S-adenosyl-L-homocysteine hydrolase	BAB1_2099	1.0342	1.0074	0.9679	0.9923
gi|82700282	choloylglycine hydrolase	BAB1_1488	0.945	0.9172	0.9627	0.99

gi|83269216	dihydroxy-acid dehydratase	BAB2_0294	1.1336	1.1507	1.0229	1.0073
gi|82700077	50S ribosomal protein L7/L12	BAB1_1265	1.2614	1.1004	0.9465	1.0758
gi|82700517	glyceraldehyde 3-phosphate dehydrogenase	BAB1_1741	0.9994	0.9708	0.9574	0.9844
gi|83269274	peptidase M3:neutral zinc metallopeptidases	BAB2_0358	1.1773	1.0571	0.9043	1.0052
gi|82700195	aminotransferase, class I and II	BAB1_1397	0.9585	0.9438	0.9501	0.9644
gi|82700604	ATP/GTP-binding motif-containing protein	BAB1_1834	0.8886	0.9809	1.0751	0.9738
gi|82699972	enolase	BAB1_1155	1.0038	0.9914	0.9941	1.0071
gi|82699966	dihydrolipoamide dehydrogenase	BAB1_1149	1.1172	1.0922	1.001	1.023
gi|82699503	serine protease family protein	BAB1_0635	0.9613	0.865	0.9212	1.026
gi|82700306	aspartate aminotransferase	BAB1_1514	0.8587	0.8506	0.9827	0.9909
gi|82700061	30S ribosomal protein S3	BAB1_1249	0.9686	1.0313	1.0399	0.9764
gi|82699940	DNA gyrase subunit A	BAB1_1121	0.9972	1.0441	1.0267	0.9801
gi|82699257	saccharopine dehydrogenase	BAB1_0364	0.8817	0.9202	1.0162	0.9739
gi|82699956	chaperonin clpA/B	BAB1_1138	0.9458	0.9804	1.0138	0.9781
gi|83269281	fructose-1,6-bisphosphate aldolase	BAB2_0365	1.091	1.0838	0.9943	0.9996
gi|83269414	glycine dehydrogenase	BAB2_0515	1.2031	1.2301	1.0007	0.9782
gi|82700564	pyruvate carboxylase	BAB1_1791	1.0364	1.0325	0.9947	0.9972
gi|82699636	DNA topoisomerase IV subunit A	BAB1_0777	0.9253	0.9982	1.0561	0.9783
gi|83269128	co-chaperonin GroES	BAB2_0190	0.9969	0.9651	1.0007	1.0356
gi|83269714	inositol-5-monophosphate dehydrogenase	BAB2_0851	1.0882	1.0359	0.9849	1.0337
gi|82700079	50S ribosomal protein L1	BAB1_1267	1.0563	1.0173	0.9566	0.992
gi|82700752	inorganic pyrophosphatase	BAB1_1993	0.9519	0.9564	1.0163	1.0109
gi|82700071	30S ribosomal protein S7	BAB1_1259	1.0309	1.0393	0.9811	0.9723
gi|82699030	cyclic beta 1-2 glucan synthetase	BAB1_0108	0.9927	0.9967	1.0281	1.024
gi|82699915	threonyl-tRNA synthetase	BAB1_1093	1.1054	0.9887	0.9677	1.0825
gi|82699048	zinc-containing alcohol dehydrogenase	BAB1_0128	1.001	1.021	1.0061	0.9861
gi|83269132	isoleucyl-tRNA synthetase	BAB2_0194	1.0184	1.0509	1.0178	0.9852
gi|82699684	NADH dehydrogenase I subunit F	BAB1_0827	1.0583	1.0609	0.9957	0.9925
gi|82699967	branched-chain alpha-keto acid dehydrogenase subunit E2	BAB1_1150	1.1724	1.1293	1.0002	1.0377
gi|82700819	transcription termination factor Rho	BAB1_2065	0.978	1.0202	1.0368	0.9926
gi|82699968	pyruvate dehydrogenase subunit beta	BAB1_1151	1.12	1.1239	0.9726	0.9684
gi|82699861	hypothetical protein BAB1_1029	BAB1_1029	1.0655	0.9564	0.9509	1.06
gi|82700272	putative ABC transporter ATP-binding protein	BAB1_1474	1.0502	1.0147	0.9812	1.0161
gi|82700674	50S ribosomal protein L19	BAB1_1906	0.9928	1.0091	1.0145	0.9977
gi|82699465	esterase/lipase/thioesterase	BAB1_0593	1.0548	0.9885	0.9839	1.0495
gi|82700197	ketol-acid reductoisomerase	BAB1_1399	0.9063	0.9202	0.9852	0.9688
gi|82699794	tyrosyl-tRNA synthetase	BAB1_0943	0.9617	0.9164	0.9475	0.9935
gi|82700844	response regulator receiver:transcriptional regulatory protein	BAB1_2092	0.9418	0.9859	0.992	0.9465
gi|82699539	DNA-directed RNA polymerase subunit omega	BAB1_0671	1.0298	0.9825	0.9616	1.0045
gi|82700931	enoyl-CoA hydratase	BAB1_2185	0.9916	1.0008	1.0126	1.0038
gi|82699699	prolyl-tRNA synthetase	BAB1_0842	1.0022	0.9789	0.9778	1.0005
gi|82700425	periplasmic binding protein/LacI transcriptional regulator	BAB1_1648	1.0128	0.9966	0.9905	1.0039
gi|82699722	adenylosuccinate lyase	BAB1_0868	0.9703	1.0131	1.0202	0.9767

gi|162002882	aminotransferase	BAB2_0572	1.0934	1.0145	0.9255	0.9964
gi|82699806	ATP-dependent helicase	BAB1_0955	1.2236	1.003	0.9559	1.1904
gi|82699225	bifunctional N-succinyldiaminopimelate-aminotransferase	BAB1_0331	1.0436	1.0507	1.0086	1.001
gi|82700554	hypothetical protein BAB1_1781	BAB1_1781	0.9932	1.0231	1.0214	0.9913
gi|82700067	50S ribosomal protein L3	BAB1_1255	0.9855	1.0527	1.022	0.956
gi|82700448	two-component response regulator	BAB1_1671	1.1461	1.0313	0.9411	1.0445
gi|82699590	OmpA-like transmembrane domain-containing protein	BAB1_0722	1.3127	1.0254	0.9488	1.2131
gi|82700292	RNA polymerase sigma factor RpoD	BAB1_1498	1.0411	1.0081	0.9961	1.0277
gi|82699105	aminotransferase	BAB1_0191	0.9329	0.9246	0.9692	0.9777
gi|82700050	30S ribosomal protein S5	BAB1_1238	1.0072	1.0049	0.982	0.9837
gi|83269530	aspartyl/glutamyl-tRNA amidotransferase subunit A	BAB2_0646	1.0137	1.0052	0.9653	0.9726
gi|82700213	Band 7 protein	BAB1_1415	1.0012	1.0084	0.9927	0.9849
gi|82700081	transcription antitermination protein NusG	BAB1_1269	1.0273	1.0021	0.9746	0.999
gi|83269705	bifunctional GMP synthase/glutamine amidotransferase protein	BAB2_0842	0.9546	0.9784	1.0058	0.9802
gi|82699986	glutamyl-tRNA synthetase	BAB1_1169	1.0847	1.0529	0.9732	1.0025
gi|82699372	3-oxoacyl-(acyl carrier protein) synthase II	BAB1_0486	1.1527	1.0266	0.9516	1.0678
gi|83269293	periplasmic binding protein/LacI transcriptional regulator	BAB2_0377	0.8519	0.7984	0.9319	0.9935
gi|82699575	organic solvent tolerance protein	BAB1_0707	1.1402	0.954	0.8519	1.0178
gi|82700214	Band 7 protein:stomatin	BAB1_1416	1.0403	0.977	0.953	1.0141
gi|82700585	putative translaldolase	BAB1_1813	1.0274	1.0074	0.967	0.9857
gi|82699775	acetyl-CoA carboxylase biotin carboxylase subunit	BAB1_0924	0.9486	0.9731	1	0.9744
gi|82700645	3-demethylubiquinone-9 3-methyltransferase	BAB1_1875	1.004	0.9635	0.9833	1.0228
gi|82700705	bifunctional ornithine acetyltransferase	BAB1_1942	1.1072	1.0058	0.9309	1.0236
gi|82699018	dihydroxy-acid dehydratase	BAB1_0096	1.0209	1.0457	1.0323	1.0068
gi|82700471	adenylosuccinate synthetase	BAB1_1695	1.0077	0.9694	0.9712	1.0086
gi|82699716	phosphoribosylaminoimidazole-succinocarboxamide synthase	BAB1_0862	1.0448	1.0019	0.9543	0.9943
gi|82699119	aldehyde dehydrogenase	BAB1_0211	1.0585	1.0915	1.0004	0.9693
gi|82699044	DNA gyrase subunit B	BAB1_0122	0.9404	1.0044	1.0458	0.9785
gi|82700668	succinate dehydrogenase iron-sulfur subunit	BAB1_1900	1.0226	0.9832	0.9514	0.988
gi|82700596	bifunctional phosphoribosylaminoimidazolecarboxamide formyltransferase	BAB1_1824	1.0536	1.0307	1.0139	1.0364
gi|83269442	riboflavin synthase subunit beta	BAB2_0545	0.9897	0.9816	1.0046	1.0122
gi|82699744	hypothetical protein BAB1_0893	BAB1_0893	1.1735	1.1059	0.9588	1.0164
gi|82700479	peptidase M41	BAB1_1703	1.1028	1.0432	0.9386	0.991
gi|82700860	acetyl-CoA carboxylase subunit beta	BAB1_2109	1.0116	0.9795	0.9382	0.9691
gi|83269836	2,3,4,5-tetrahydropyridine-2-carboxylate N-succinyltransferase	BAB2_0991	1.0531	1.0127	0.947	0.9841
gi|82700053	30S ribosomal protein S8	BAB1_1241	0.9839	0.9868	1.0045	1.0011
gi|82700066	50S ribosomal protein L4	BAB1_1254	0.9751	1.0064	0.9955	0.9635
gi|82700052	50S ribosomal protein L6	BAB1_1240	0.9391	1.0018	1.0652	0.9957
gi|82700147	bifunctional preprotein translocase subunit SecD/SecF	BAB1_1344	0.9801	1.0261	1.0264	0.9704
gi|83269740	solute-binding family 1 protein	BAB2_0879	5.5857	5.2005	0.9725	1.015
gi|82699646	serine hydroxymethyltransferase	BAB1_0787	0.9587	0.9987	1.0172	0.9761
gi|82700045	30S ribosomal protein S13	BAB1_1233	1.0532	1.0392	0.9862	0.9992
gi|82700177	urease subunit alpha	BAB1_1378	0.9913	0.9502	0.9875	1.0302

gi|83269520	DNA topoisomerase I	BAB2_0636	1.0444	1.0031	0.9959	1.0367
gi|83269549	hypothetical protein BAB2_0665	BAB2_0665	1.1958	1.1404	0.9548	1.0011
gi|83269821	solute-binding family 5 protein	BAB2_0974	1.6392	1.5769	0.974	1.0107
gi|82700580	F0F1 ATP synthase subunit gamma	BAB1_1808	0.9861	1.0233	1.0314	0.9942
gi|82700644	aspartate kinase	BAB1_1874	1.035	1.0209	0.9697	0.9824
gi|82700206	acetolactate synthase 3 catalytic subunit	BAB1_1408	0.8976	0.9179	1.0313	1.0074
gi|82700103	aminotransferase	BAB1_1294	1.0171	1.0935	1.0371	0.9643
gi|82699974	CTP synthetase	BAB1_1157	0.9778	1.0328	1.0466	0.9902
gi|82699466	transcriptional regulatory protein MucR	BAB1_0594	0.887	0.9804	1.0361	0.9364
gi|82699937	peptidyl-prolyl cis-trans isomerase, cyclophilin type	BAB1_1118	1.0489	1.0881	1.0126	0.9746
gi|82700582	F0F1 ATP synthase subunit delta	BAB1_1810	1.0475	0.9905	0.9738	1.0295
gi|82699863	aminoacyl-tRNA synthetase, class I:DAHP synthetase, classII	BAB1_1031	1	0.9478	0.9973	1.0512
gi|82699583	nucleoside diphosphate kinase	BAB1_0715	0.8805	0.959	1.085	0.9944
gi|82699846	methionyl-tRNA synthetase	BAB1_1014	0.9754	1.0009	1.0081	0.9821
gi|82700731	electron transfer flavoprotein subunit beta	BAB1_1972	1.0484	0.9856	0.9243	0.9838
gi|83269436	solute-binding family 1 protein	BAB2_0539	1.1445	1.2274	0.9891	0.9222
gi|82700078	50S ribosomal protein L10	BAB1_1266	1.0083	1.001	0.9732	0.98
gi|82699366	30S ribosomal protein S6	BAB1_0480	1.1425	1.0488	0.9752	1.0624
gi|82699385	Alkyl hydroperoxide reductase/ Thiol specific antioxidant/ Mal allergen	BAB1_0504	0.9901	0.9948	0.992	0.9876
gi|83269064	solute-binding family 1 protein	BAB2_0113	1.9141	1.7258	0.9396	1.0388
gi|82700827	preprotein translocase subunit SecB	BAB1_2073	1.0043	1.0686	1.0188	0.9577
gi|82699402	DSBA oxidoreductase:twin-arginine translocation pathway signal	BAB1_0521	1.0251	0.9295	0.9182	1.0121
gi|83269024	UTP-glucose-1-phosphate uridylyltransferase:nucleotidyl transferase	BAB2_0070	0.9686	1.0011	1.0139	0.9804
gi|82699211	arginine/ornithine transport operon protein aot	BAB1_0317	1.0308	1.0031	1.0338	1.0675
gi|82699639	delta-aminolevulinic acid dehydratase	BAB1_0780	1.0534	1.023	0.9654	0.9936
gi|83269846	NADH-ubiquinone oxidoreductase 39 kd subunit	BAB2_1002	1.0513	1.0127	0.9482	0.9847
gi|82700324	cold shock DNA-binding domain-containing protein	BAB1_1532	0.9458	0.9168	0.9822	1.0126
gi|82700642	peptide chain release factor 1	BAB1_1872	0.9866	1.0601	0.9973	0.9275
gi|82699978	triosephosphate isomerase	BAB1_1161	0.922	1.0189	1.0583	0.9577
gi|82699669	30S ribosomal protein S9	BAB1_0810	0.9322	0.9875	1.0472	0.9874
gi|82699260	invasion protein B	BAB1_0368	1.0621	1.0567	0.9315	0.9366
gi|82700643	PEP-utilizing protein	BAB1_1873	1.0088	0.9436	0.9931	1.0608
gi|83269759	nitrate reductase alpha subunit	BAB2_0904	0.9289	1.0015	1.0729	0.9934
gi|82699001	hypothetical protein BAB1_0075	BAB1_0075	1.02	1.0094	0.9665	0.9758
gi|82699286	hypothetical protein BAB1_0400	BAB1_0400	1.0576	1.015	0.9689	1.0085
gi|82700080	50S ribosomal protein L11	BAB1_1268	1.0144	0.9989	0.9817	0.9963
gi|82699633	3'-5' exonuclease	BAB1_0774	0.968	0.9717	1.025	1.0204
gi|82699133	substrate-binding region of ABC-type glycine betaine transport system	BAB1_0226	1.0415	0.8909	0.8905	1.0413
gi|82699221	hypothetical protein BAB1_0327	BAB1_0327	0.9769	0.9597	1.01	1.0272
gi|82699238	alpha/beta fold hydrolase	BAB1_0344	1.0558	1.0562	1.0363	1.0354
gi|82699316	TPR repeat-containing protein	BAB1_0430	1.1214	0.9755	0.9148	1.0505
gi|83269528	metal-dependent hydrolase	BAB2_0644	1.0387	0.9408	0.9284	1.0246
gi|82699875	hypothetical protein BAB1_1043	BAB1_1043	0.9932	0.994	0.9821	0.9805

gi|82699868	malic enzyme	BAB1_1036	1.0057	1.0133	1.0273	1.0184
gi|82699463	manganese and iron superoxide dismutase	BAB1_0591	1.1352	1.0329	0.8866	0.9747
gi|82699556	dihydroorotase	BAB1_0688	0.9431	0.932	1.017	1.0293
gi|82699979	peptidyl-prolyl cis-trans isomerase D	BAB1_1162	1.0098	0.954	0.9496	1.0042
gi|83269822	3-ketoacyl-(acyl-carrier-protein) reductase	BAB2_0975	1.2022	1.2485	1.0233	0.9841
gi|82700518	phosphoglycerate kinase	BAB1_1742	1.0372	1.0472	1.0078	0.9983
gi|82699739	nicotinate-nucleotide--dimethylbenzimidazole phosphoribosyltransferase	BAB1_0886	0.9773	0.9772	0.9892	0.9884
gi|82699333	enoyl-(acyl carrier protein) reductase	BAB1_0447	0.9693	1.0094	0.9965	0.9572
gi|82699683	NADH dehydrogenase subunit E	BAB1_0826	1.0071	0.9641	0.9849	1.0298
gi|82699800	ABC transporter ATPase	BAB1_0949	1.063	1.0571	0.9824	0.9874
gi|82699681	NADH dehydrogenase subunit C	BAB1_0824	1.015	1.008	0.992	0.9983
gi|83269265	aspartate-semialdehyde dehydrogenase	BAB2_0349	1.0079	1.0558	1.0518	1.0041
gi|82700882	glutathione synthetase	BAB1_2135	0.9696	0.9726	1.0148	1.0107
gi|82699597	hypothetical protein BAB1_0729	BAB1_0729	0.9916	0.9383	0.9935	1.049
gi|83269350	lysyl-tRNA synthetase	BAB2_0447	0.9596	1.0118	1.0504	0.9947
gi|83269431	alkylhydroperoxidase	BAB2_0532	0.9139	0.9602	1.0346	0.984
gi|82700046	adenylate kinase	BAB1_1234	1.1437	1.0576	0.9721	1.0524
gi|82700834	ATP-dependent protease ATP-binding subunit	BAB1_2080	1.0574	1.0031	0.9462	0.997
gi|83269345	sugar transporter family protein	BAB2_0442	0.9814	0.9467	0.998	1.0342
gi|82699904	thiosulfate sulfurtransferase:rhodanese-like	BAB1_1075	0.9167	0.9741	1.046	0.9834
gi|83269034	peptidase M3:neutral zinc metallopeptidases, zinc-binding region	BAB2_0080	0.9923	0.9772	0.9709	0.9848
gi|83269583	solute-binding family 5 protein	BAB2_0700	1.8119	1.7648	0.9362	0.9645
gi|82700239	TPR repeat-containing protein	BAB1_1441	1.0952	1.0393	1.0054	1.0537
gi|82699369	3-ketoacyl-(acyl-carrier-protein) reductase	BAB1_0483	0.9754	1.0105	0.9986	0.9637
gi|82699855	glutamine synthetase class-I	BAB1_1023	1.0069	1.0261	1.0087	0.9891
gi|82700877	cytochrome c heme-binding domain-containing protein	BAB1_2130	1.1635	1.0804	0.9562	1.0289
gi|82699783	glycosyl transferase family 51 protein	BAB1_0932	0.9045	0.9813	1.0473	0.9636
gi|82699969	dehydrogenase, E1 component:mitochondrial substrate carrier	BAB1_1152	1.2136	1.1593	0.9658	1.0098
gi|82700808	hypothetical protein BAB1_2054	BAB1_2054	1.0486	1.0894	0.9979	0.9579
gi|82699208	putative oxidoreductase	BAB1_0314	7.7003	7.2893	1.1762	1.0517
gi|82700048	50S ribosomal protein L15	BAB1_1236	0.9119	0.9819	1.0408	0.9662
gi|83269741	hypothetical protein BAB2_0880	BAB2_0880	1.1215	0.9895	0.9088	1.0316
gi|83269699	putative phosphoketolase	BAB2_0836	1.0805	0.9473	0.9157	1.043
gi|82700666	2-octaprenyl-6-methoxyphenyl hydroxylase	BAB1_1898	0.9262	0.953	1.0605	1.0298
gi|82699548	signal peptidase S26A:Signal peptidase	BAB1_0680	0.996	0.9437	0.9364	0.9886
gi|82700655	porphobilinogen deaminase	BAB1_1887	1.0071	0.9769	1.012	1.0421
gi|82699670	50S ribosomal protein L13	BAB1_0811	0.9772	1.0526	1.042	0.9665
gi|83269499	glutamate-binding protein	BAB2_0612	8.6175	8.4049	1.0435	1.0205
gi|83269346	acetyl-CoA acetyltransferase	BAB2_0443	0.9458	0.9473	1.0007	1
gi|82700217	hypothetical protein BAB1_1419	BAB1_1419	1.1009	0.9962	0.919	1.0122
gi|83269559	Ferritin:bacterioferritin	BAB2_0675	0.8245	0.9126	1.0326	0.9318
gi|82700906	S-adenosylmethionine synthetase	BAB1_2160	0.9693	1.0494	1.0649	0.9835
gi|83269586	ABC transporter ATPase	BAB2_0703	1.3633	1.2726	0.9299	0.9957

gi|83269259	thioredoxin domain-containing protein	BAB2_0343	1.2074	1.1412	0.9699	1.0246
gi|82699574	peptidyl-prolyl cis-trans isomerase, putative	BAB1_0706	0.9611	1.0009	1.024	0.9818
gi|82699948	histone-like DNA-binding protein	BAB1_1129	1.0953	1.1424	1.0392	0.9966
gi|83269545	transcription repair coupling factor	BAB2_0661	0.9826	1.0207	1.0278	0.9886
gi|82699391	threonine synthase	BAB1_0510	1.0499	1.0299	0.9292	0.9469
gi|82700485	translocation protein TolB	BAB1_1709	1.0482	0.9624	0.8981	0.978
gi|83269533	DNA topoisomerase IV subunit B	BAB2_0649	0.9611	1.0079	1.0232	0.9755
gi|83269845	GTP-binding protein LepA	BAB2_1001	1.0061	1.005	1.0139	1.0139
gi|83269790	periplasmic binding protein/LacI transcriptional regulator	BAB2_0938	0.782	0.7409	0.9212	0.971
gi|82699187	UDP-N-acetylglucosamine 1-carboxyvinyltransferase	BAB1_0287	1.0498	1.0458	0.9662	0.9685
gi|83269661	D-3-phosphoglycerate dehydrogenase	BAB2_0783	1.0364	0.9559	0.977	1.0569
gi|82700469	basic-leucine zipper (bZIP) transcription factor	BAB1_1693	0.8827	0.9697	1.0553	0.961
gi|82699936	peptidyl-prolyl cis-trans isomerase	BAB1_1117	1.0418	0.9731	0.9638	1.034
gi|82699300	F0F1 ATP synthase subunit B	BAB1_0414	1.0119	1.0054	1.0131	1.0199
gi|83269246	aldehyde dehydrogenase	BAB2_0327	1.383	1.3782	1.0275	1.033
gi|82700345	translation-associated GTPase	BAB1_1553	1.0666	1.0352	0.9728	1.0019
gi|82699230	2'-deoxycytidine 5'-triphosphate deaminase	BAB1_0336	0.9189	0.9517	1.0334	0.9962
gi|82700730	antifreeze protein, type I:electron transfer flavoprotein, alpha subunit	BAB1_1971	0.9705	0.9728	0.9878	0.9844
gi|82699368	malonyl CoA-acyl carrier protein transacylase	BAB1_0482	0.9813	0.9835	0.9894	0.9866
gi|83269868	protein kinase:ABC1 protein	BAB2_1025	0.9549	1.0243	1.0438	0.9738
gi|82700813	ParB-like nuclease:ParB-like partition protein	BAB1_2059	1.0116	1.0188	0.9392	0.9317
gi|83269479	Renal dipeptidase	BAB2_0586	0.9576	0.9949	1.0191	0.9809
gi|83269412	glycine cleavage system aminomethyltransferase T	BAB2_0513	1.1077	1.1297	1.0388	1.0169
gi|82700747	histidinol-phosphate aminotransferase	BAB1_1988	0.8789	0.8948	0.9998	0.9818
gi|82699608	hypothetical protein BAB1_0740	BAB1_0740	0.9817	1.017	0.9972	0.962
gi|82698934	DNA polymerase III subunit beta	BAB1_0002	1.1071	0.9491	0.961	1.1221
gi|82700908	hypothetical protein BAB1_2162	BAB1_2162	0.9931	0.9922	0.9703	0.9703
gi|82700673	isopropylmalate isomerase large subunit	BAB1_1905	1.1344	1.0237	0.9904	1.0966
gi|82699725	glucose/ribitol dehydrogenase	BAB1_0871	0.9515	0.9899	1.0159	0.9759
gi|82700109	methionine aminopeptidase	BAB1_1300	1.1168	1.0009	0.9465	1.0555
gi|82699717	hypothetical protein BAB1_0863	BAB1_0863	1.0524	0.9579	0.9481	1.0405
gi|82699644	peptidoglycan binding domain-containing protein	BAB1_0785	0.9785	1.1328	1.1196	0.9668
gi|82700602	30S ribosomal protein S16	BAB1_1832	1.1017	1.0286	0.9235	0.9881
gi|82700358	coproporphyrinogen III oxidase	BAB1_1566	0.887	0.9853	1.0524	0.9456
gi|82698965	cytochrome c heme-binding site:cytochrome c	BAB1_0036	1.1092	0.9236	0.9316	1.12
gi|83269287	glycerol-3-phosphate dehydrogenase	BAB2_0371	0.8821	0.9084	1.0324	1.0017
gi|82699834	glycosyl transferase, group 1	BAB1_1000	1.0903	1.0314	0.9277	0.9796
gi|82700729	3-hydroxybutyryl-CoA dehydrogenase	BAB1_1970	1.0282	0.978	0.9536	1.002
gi|83269478	solute-binding family 1 protein	BAB2_0585	1.1416	1.0884	0.9962	1.044
gi|82700376	anthranilate synthase	BAB1_1586	0.9736	0.9433	0.9973	1.028
gi|82700315	transcription elongation factor GreA	BAB1_1523	0.999	0.9109	0.9148	1.0027
gi|82699315	polyprenyl synthetase	BAB1_0429	0.9857	0.9699	0.9841	1
gi|82699821	fumarate lyase:Fe-S type hydro-lyase tartrate	BAB1_0977	1.3168	1.2508	0.9731	1.0236

gi|82700789	acetyl-CoA carboxylase carboxyltransferase subunit alpha	BAB1_2033	0.9783	0.9981	0.9981	0.9777
gi|82700607	carbonic anhydrase	BAB1_1837	0.9835	0.9796	0.996	0.9995
gi|82699599	phosphoribosylaminoimidazole synthetase	BAB1_0731	1.0814	1.0156	1.0371	1.1054
gi|82700235	M24 family metallopeptidase	BAB1_1437	1.0729	0.9225	0.879	1.0211
gi|82699951	ATP-dependent Clp protease proteolytic subunit	BAB1_1132	1.0436	1.0167	0.9821	1.008
gi|82700063	30S ribosomal protein S19	BAB1_1251	1.0405	1.089	1.0275	0.9808
gi|83269221	D-amino acid aminotransferase	BAB2_0301	0.9987	0.9864	1.0427	1.055
gi|83269379	glutamate--cysteine ligase, plant	BAB2_0476	0.9067	0.9765	1.0351	0.9608
gi|83269813	dihydrodipicolinate synthetase	BAB2_0961	1.0652	1.1624	1.0631	0.9746
gi|82700874	phenylalanyl-tRNA synthetase subunit beta	BAB1_2127	0.9788	0.9908	1.0029	0.9906
gi|82699812	Outer membrane efflux protein	BAB1_0963	1.1442	1.085	0.9657	1.0173
gi|82700871	50S ribosomal protein L20	BAB1_2124	1.0353	0.9986	0.9701	1.005
gi|82699998	ribosome recycling factor	BAB1_1181	0.9983	1.0324	0.9704	0.9375
gi|83269731	hypothetical protein BAB2_0868	BAB2_0868	1.017	0.9665	0.9858	1.0368
gi|82699755	seryl-tRNA synthetase	BAB1_0904	1.0011	1.0013	1.008	1.0066
gi|82700672	GCN5-related N-acetyltransferase	BAB1_1904	0.9128	0.9489	0.9762	0.9395
gi|82700042	50S ribosomal protein L17	BAB1_1230	1.0337	1.0524	1.0514	1.0319
gi|82700473	D-3-phosphoglycerate dehydrogenase	BAB1_1697	0.9099	0.9439	1.0081	0.9715
gi|82699461	ErfK/YbiS/YcfS/YnhG:twin-arginine translocation pathway signal	BAB1_0589	1.0064	0.9591	0.9633	1.01
gi|82700591	acetyl-CoA synthetase	BAB1_1819	0.7863	0.8698	1.092	0.9861
gi|82700873	phenylalanyl-tRNA synthetase subunit alpha	BAB1_2126	1.0011	1.0436	1.0034	0.9622
gi|82700062	50S ribosomal protein L22	BAB1_1250	1.0513	1.0071	0.9747	1.0185
gi|83269869	ubiquinone/menaquinone biosynthesis methyltransferase	BAB2_1026	1.0134	0.9953	1.0161	1.0332
gi|82700414	solute-binding family 1 protein	BAB1_1628	1.1883	1.1187	0.9539	1.0121
gi|83269711	catalase	BAB2_0848	0.9351	0.9884	1.031	0.9752
gi|83269542	D-fructose-6-phosphate amidotransferase	BAB2_0658	0.9817	1.0314	1.1018	1.0482
gi|82699792	Alkyl hydroperoxide reductase	BAB1_0941	0.9956	1.012	1.0324	1.0185
gi|82700341	ribose-phosphate pyrophosphokinase	BAB1_1549	1.0672	1.0092	0.9645	1.0191
gi|82700920	3-hydroxydecanoyl-(acyl carrier protein) dehydratase	BAB1_2174	1.0783	1.0107	0.9314	0.9934
gi|82698937	pyridine nucleotide-disulphide oxidoreductase	BAB1_0005	0.9456	1.0053	1.0516	0.989
gi|83269812	malate/L-lactate dehydrogenase	BAB2_0960	1.0113	1.0579	0.9972	0.9518
gi|82700198	transcriptional regulator TetR	BAB1_1400	0.86	0.829	0.9749	1.0106
gi|83269609	cytochrome bd ubiquinol oxidase, subunit I	BAB2_0728	0.9384	0.9578	0.9914	0.9716
gi|82700606	lytic murein transglycosylase, putative	BAB1_1836	0.9608	1.2043	1.095	0.873
gi|82699317	glycyl-tRNA synthetase subunit alpha	BAB1_0431	0.891	0.96	1.0621	0.9857
gi|83269307	DEAD/DEAH box helicase:helicase	BAB2_0395	0.9805	0.9668	0.9922	1.0085
gi|82699299	F0F1 ATP synthase subunit B'	BAB1_0413	1.0297	0.9888	0.9501	0.9889
gi|82700432	aldehyde dehydrogenase	BAB1_1655	1.0641	1.0176	0.9837	1.0278
gi|82699649	riboflavin synthase subunit alpha	BAB1_0790	0.9873	0.9746	0.991	1.0029
gi|82699226	ornithine carbamoyltransferase	BAB1_0332	0.9995	1.0136	1.0491	1.0355
gi|82699066	SAM dependent methyltransferase, putative	BAB1_0150	0.9831	1.0007	1.0116	0.9928
gi|82699906	Acetyl-CoA hydrolase/transferase	BAB1_1077	1.227	1.0672	0.9141	1.0501
gi|82700056	50S ribosomal protein L24	BAB1_1244	1.2044	1.0121	0.946	1.1214

gi|82700863	tryptophan synthase subunit beta	BAB1_2112	1.045	1.0386	1.0236	1.0289
gi|82700658	YciI-like protein	BAB1_1890	1.0448	1.0812	1.0028	0.9686
gi|82700475	phosphoserine aminotransferase	BAB1_1699	0.9178	0.9629	1.0026	0.9555
gi|82699780	1-aminocyclopropane-1-carboxylate synthase:aminotransferase	BAB1_0929	1.0296	0.9927	0.9427	0.9769
gi|82699776	acetyl-CoA carboxylase biotin carboxyl carrier protein subunit	BAB1_0925	1.0062	1.0141	0.9862	0.9769
gi|82699057	nitrogen-fixing NifU, C-terminal	BAB1_0139	0.9873	0.9855	0.969	0.9696
gi|83269856	dihydrodipicolinate reductase	BAB2_1012	1.037	0.9545	0.9392	1.0215
gi|83269142	hypothetical protein BAB2_0207	BAB2_0207	0.9552	0.9428	1.0156	1.0279
gi|82700478	phosphoglucomutase/phosphomannomutase	BAB1_1702	1.0919	1.0071	1.0286	1.1142
gi|82700446	PAS domain-containing protein	BAB1_1669	0.9497	0.9615	1.0415	1.0281
gi|82700404	DegT/DnrJ/EryC1/StrS aminotransferase	BAB1_1616	1.1061	1.0823	0.9567	0.9781
gi|82700044	30S ribosomal protein S11	BAB1_1232	1.1289	1.0277	0.9246	1.0185
gi|82699992	UDP-3-O-[3-hydroxymyristoyl] glucosamine N-acyltransferase	BAB1_1175	0.9514	0.9871	1.0238	0.9859
gi|162002881	uracil phosphoribosyltransferase	BAB2_1027	0.9265	0.9654	1.0578	1.0147
gi|82700402	response regulator receiver:transcriptional regulatory protein	BAB1_1614	1.05	1.0251	0.9674	0.9884
gi|82700179	urease accessory protein UreG	BAB1_1381	1.132	1.0104	0.9865	1.1056
gi|82699833	glycosyltransferase	BAB1_0999	0.9853	1.0261	0.9958	0.9555
gi|82700036	recombinase A	BAB1_1224	0.9961	0.9748	0.9692	0.9898
gi|83268979	Leu/Ile/Val-binding family protein	BAB2_0023	0.9275	0.8566	0.9118	0.9885
gi|83269231	D-amino acid dehydrogenase small subunit	BAB2_0311	1.0529	1.0894	0.9974	0.9631
gi|82700205	acetolactate synthase 3 regulatory subunit	BAB1_1407	0.9663	0.9724	1.0266	1.0192
gi|83269878	aldehyde dehydrogenase	BAB2_1035	1.7454	1.8269	1.0584	1.0102
gi|82699749	glycoside hydrolase family protein	BAB1_0898	1.0689	0.985	0.9479	1.0275
gi|83269007	glutamate synthase glutamate synthase amidotransferase subunit	BAB2_0053	0.9732	0.965	1.0032	1.011
gi|83269262	3-isopropylmalate dehydrogenase	BAB2_0346	1.0689	1.0451	0.9992	1.0213
gi|82700310	pyridine nucleotide-disulphide oxidoreductase class-II	BAB1_1518	0.9815	1.0559	1.0469	0.972
gi|83269347	fatty oxidation complex alpha subunit	BAB2_0444	0.9192	0.9612	1.0206	0.9752
gi|83269831	putative inner membrane protein translocase component YidC	BAB2_0986	1.0441	1.0058	0.908	0.942
gi|82699341	3,4-dihydroxy-2-butanone 4-phosphate synthase	BAB1_0455	0.975	1.0021	1.0004	0.9729
gi|83269732	secretion protein HlyD	BAB2_0869	1.125	0.9877	1.0117	1.1531
gi|82699659	MerR family regulatory protein	BAB1_0800	1.0693	0.9662	0.9537	1.0544
gi|82700628	50S ribosomal protein L21	BAB1_1858	1.0357	0.9526	0.9536	1.0358
gi|83269744	ATPase	BAB2_0883	1.0582	1.0503	0.976	0.9831
gi|82699565	cysteinyl-tRNA synthetase	BAB1_0697	0.8517	1.0096	1.106	0.9328
gi|83269718	phosphoglucomutase/phosphomannomutase	BAB2_0855	0.9044	1.0686	1.1448	0.9666
gi|82700556	acetyl-CoA acetyltransferase	BAB1_1783	1.0302	1.021	1.0181	1.0264
gi|82699332	heat shock protein DnaJ	BAB1_0446	1.1325	1.0501	0.9459	1.0177
gi|82700072	30S ribosomal protein S12	BAB1_1260	1.1165	1.0658	0.9463	0.9911
gi|82700247	UDP-N-acetylmuramate--L-alanine ligase	BAB1_1449	0.9424	1.0299	1.0694	0.9795
gi|82699727	3-oxoacyl-(acyl carrier protein) synthase II	BAB1_0873	1.0022	1.0762	1.1125	1.0326
gi|82699311	Clp protease:peptidase U7:Na+/H+ antiporter NhaA	BAB1_0425	0.9643	0.9749	0.9941	0.9825
gi|82699888	hypothetical protein BAB1_1058	BAB1_1058	0.9469	1.0611	1.1168	0.9951
gi|83269703	membrane antigen, putative	BAB2_0840	0.9496	0.9243	1.0022	1.0322

gi|162002879	tryptophanyl-tRNA synthetase	BAB1_0141	0.9308	1.0455	1.1332	1.011
gi|82699373	hypothetical protein BAB1_0487	BAB1_0487	0.9331	1.1552	1.1074	0.8945
gi|82699866	glutamyl-tRNA synthetase	BAB1_1034	1.1775	1.0625	0.9375	1.0399
gi|83269251	NADH:flavin oxidoreductase/NADH oxidase	BAB2_0335	1.0844	1.0027	0.9229	0.9972
gi|83269430	Alkyl hydroperoxide reductase	BAB2_0531	0.9496	0.9322	0.98	0.9978
gi|83269725	acid-resistance protein	BAB2_0862	0.9779	0.9333	0.9719	1.0177
gi|82700525	hypothetical protein BAB1_1749	BAB1_1749	0.9815	1.0367	1.0435	0.9875
gi|82699667	N-acetyl-gamma-glutamyl-phosphate reductase	BAB1_0808	0.9087	0.9213	1.0615	1.0453
gi|82700313	AsnC family regulatory protein	BAB1_1521	0.9651	1.0265	1.0431	0.9795
gi|82700058	30S ribosomal protein S17	BAB1_1246	1.1185	1.1375	1.0491	1.0331
gi|82698951	hypothetical protein BAB1_0022	BAB1_0022	1.015	0.9792	0.9579	0.9937
gi|82700853	ATP/GTP-binding protein	BAB1_2102	0.9624	0.9591	1.0208	1.0233
gi|82700505	hypothetical protein BAB1_1729	BAB1_1729	1.0471	1.0396	1.0088	1.0152
gi|82700824	shikimate 5-dehydrogenase	BAB1_2070	0.9971	0.964	1.002	1.0359
gi|83269005	low-specificity threonine aldolase	BAB2_0051	1.0065	1.0138	1.0164	1.0079
gi|82699947	excinuclease ABC subunit A	BAB1_1128	1.1162	1.0315	0.9888	1.0691
gi|82700028	tetracycline resistance protein TetB	BAB1_1216	1.2141	1.1548	0.9718	1.0226
gi|82700895	metalloprotease (M29)	BAB1_2149	0.9888	0.9696	0.9589	0.9773
gi|82700821	uroporphyrinogen decarboxylase	BAB1_2067	1.0317	1.006	1.0319	1.0574
gi|82700858	thioredoxin domain-containing protein	BAB1_2107	1.3659	1.1685	0.9076	1.0591
gi|82698938	ABC transporter ATPase	BAB1_0006	1.014	0.9621	0.9367	0.9865
gi|82698972	hypothetical protein BAB1_0046	BAB1_0046	0.8783	0.9089	1.0211	0.986
gi|82700504	50S ribosomal protein L31	BAB1_1728	1.0425	1.0308	1.0054	1.0167
gi|82699243	5-aminolevulinate synthase	BAB1_0349	1.4373	1.5532	1.0266	0.9499
gi|83269283	triosephosphate isomerase	BAB2_0367	1.0018	1.0113	0.9972	0.9873
gi|82700805	hypothetical protein BAB1_2051	BAB1_2051	1.0114	1.0375	1.0873	1.0587
gi|82700452	DNA gyrase, subunit B	BAB1_1675	0.9495	0.9483	0.9902	0.9908
gi|82698960	DNA polymerase III subunits gamma and tau	BAB1_0031	1.0021	0.9957	1.0071	1.0131
gi|82700772	50S ribosomal protein L28	BAB1_2016	1.0534	1.0668	0.9791	0.9663
gi|83269271	ATP/GTP-binding motif-containing protein	BAB2_0355	0.8632	0.928	1.1253	1.0458
gi|82699135	glutamate dehydrogenase	BAB1_0228	0.9227	0.9721	1.0375	0.9818
gi|83269837	succinyl-diaminopimelate desuccinylase	BAB2_0993	1.0129	0.9646	0.9789	1.0273
gi|82700922	NLPA lipoprotein	BAB1_2176	0.9452	1.2162	1.1184	0.8686
gi|82700418	7-alpha-hydroxysteroid dehydrogenase	BAB1_1634	0.9714	0.9887	1.0139	0.9952
gi|82699784	peptide chain release factor 2	BAB1_0933	0.9532	0.9858	1.0104	0.9758
gi|83269197	YaeC family lipoprotein	BAB2_0275	1.0392	0.972	0.999	1.0674
gi|82700498	elongation factor P	BAB1_1722	1.0121	1.0055	0.9649	0.9704
gi|83269225	histidine ammonia-lyase	BAB2_0305	0.9937	1.028	1.0558	1.0201
gi|83269835	hypothetical protein BAB2_0990	BAB2_0990	0.8997	0.958	1.0135	0.9516
gi|83269739	spermidine/putrescine ABC transporter ATP-binding protein	BAB2_0878	3.1369	3.091	1.0282	1.0195
gi|82699266	polysaccharide deacetylase	BAB1_0375	1.2311	1.2092	1.0096	1.0249
gi|82699728	acyl carrier protein	BAB1_0874	1.0662	0.8927	0.8322	0.9928
gi|83269866	elongation factor Tu	BAB2_1023	0.9805	1.023	1.0499	1.0062

gi|82699902	cysteine synthase A	BAB1_1073	1.0333	1.0297	0.9849	0.9876
gi|82700868	translation initiation factor IF-3	BAB1_2121	1.003	1.0426	1.0808	1.039
gi|82699515	AMP nucleosidase	BAB1_0647	0.9548	0.9215	0.9734	1.0075
gi|83269944	putative integral membrane protein	BAB2_1108	1.0407	0.9741	1.02	1.0896
gi|83269695	GntR family regulatory protein	BAB2_0832	0.7629	0.7457	1.0236	1.0452
gi|82700537	N-formylglutamate amidohydrolase	BAB1_1763	0.9915	0.9377	0.9734	1.0309
gi|82700483	outer membrane protein MotY	BAB1_1707	1.0262	0.9753	0.9875	1.0399
gi|82700330	response regulator receiver:transcriptional regulatory protein	BAB1_1538	0.9739	0.9185	0.9148	0.9691
gi|82700060	50S ribosomal protein L16	BAB1_1248	1.0769	1.0588	0.9411	0.9554
gi|82699390	insulinase-like peptidase	BAB1_0509	1.0046	0.955	0.9976	1.0463
gi|83269853	methylglyoxal synthase	BAB2_1009	1.0476	0.9623	0.9297	1.0115
gi|83269253	arginase:arginase/agmatinase/formiminoglutamase	BAB2_0337	1.0404	1.0051	0.9989	1.0332
gi|83269211	acetolactate synthase 2 catalytic subunit	BAB2_0289	1.0517	1.0795	1.0746	1.0455
gi|82700748	cyclohexadienyl dehydrogenase	BAB1_1989	0.8336	0.8547	1.0492	1.0231
gi|82700401	hypothetical protein BAB1_1613	BAB1_1613	0.946	1.0227	1.0299	0.9521
gi|82700283	hypothetical protein BAB1_1489	BAB1_1489	0.7386	1.0341	1.1756	0.8389
gi|82699799	cysteine desulfurase activator complex subunit SufB	BAB1_0948	1.1323	1.1047	0.9412	0.9641
gi|82699534	dihydrodipicolinate synthase	BAB1_0666	0.9525	1.0688	1.0594	0.9436
gi|82699420	Formyl transferase, N-terminal	BAB1_0540	1.0904	1.0435	0.9524	0.9944
gi|82699076	phosphoenolpyruvate-dependent sugar phosphotransferase system	BAB1_0160	1.0683	1.0718	0.9786	0.9722
gi|82699054	response regulator receiver:helix-turn-helix, Fis-type	BAB1_0136	1.0982	1.2494	1.0548	0.9265
gi|83269991	ParB-like nuclease:ParB-like partition protein	BAB2_1164	0.989	0.9486	0.9714	1.0118
gi|83269214	sugar transporter	BAB2_0292	1.0694	1.1342	1.0245	0.9652
gi|82700350	cytochrome b/b6, N-terminal:cytochrome b/b6, C-terminal	BAB1_1558	1.0888	0.923	0.9309	1.0966
gi|82699847	TatD-related deoxyribonuclease	BAB1_1015	0.9534	0.9878	1.0317	0.9962
gi|82699726	3-oxoacyl-(acyl carrier protein) synthase II	BAB1_0872	0.9654	0.9537	1.0166	1.0288
gi|82699422	ABC transporter ATPase	BAB1_0542	1.0325	1.0206	0.9604	0.9708
gi|82699216	secretion protein HlyD	BAB1_0322	0.9071	0.9376	1.0348	1.0002
gi|82699207	dihydropyrimidine dehydrogenase	BAB1_0313	4.8148	4.5204	0.982	1.0065
gi|82699182	translation initiation factor IF-1	BAB1_0282	0.983	0.9922	0.9699	0.9592
gi|82700111	hypothetical protein BAB1_1302	BAB1_1302	0.7212	0.6982	1.0443	1.078
gi|82699862	glutathione reductase	BAB1_1030	0.9515	0.9999	1.0619	1.0099
gi|82700305	glutathione S-transferase	BAB1_1513	0.9473	0.9357	0.9498	0.9583
gi|83269362	6-phosphogluconolactonase	BAB2_0459	0.9664	0.9861	0.9943	0.9728
gi|82700004	glycerophosphoryl diester phosphodiesterase	BAB1_1188	0.945	0.9632	0.9981	0.978
gi|82699856	nitrogen regulatory protein P-II:P-II protein urydylation site	BAB1_1024	1.0065	0.9777	0.9663	0.9934
gi|82699424	DegT/DnrJ/EryC1/StrS aminotransferase	BAB1_0544	0.9537	0.9996	1.0407	0.9924
gi|82700106	hypothetical protein BAB1_1297	BAB1_1297	1.1034	1.0029	0.9756	1.0726
gi|82699913	nitroreductase family protein	BAB1_1091	0.9116	0.9148	0.9982	0.9942
gi|82699653	SmpA/OmlA	BAB1_0794	0.9819	0.973	0.9887	0.9952
gi|82700065	50S ribosomal protein L23	BAB1_1253	1.0677	1.0187	0.9545	1
gi|83269394	extracellular solute-binding protein	BAB2_0491	4.66	4.3517	0.9417	1.0116
gi|83269984	Leu/Ile/Val-binding family protein	BAB2_1153	1.0848	0.9674	0.8976	1.0056

gi|82700740	sodium:dicarboxylate symporter	BAB1_1981	1.172	1.1216	0.9082	0.9473
gi|82700098	glyoxalase/bleomycin resistance protein/dioxygenase	BAB1_1286	0.93	1.0448	1.0904	0.9699
gi|83269235	FMN-dependent alpha-hydroxy acid dehydrogenase	BAB2_0315	0.9992	0.9296	0.9639	1.0348
gi|82699932	hypothetical protein BAB1_1113	BAB1_1113	0.9788	0.9944	1.0096	0.9933
gi|83269867	bifunctional phosphopantothenoylcysteine decarboxylase	BAB2_1024	0.973	1.0432	1.0151	0.9462
gi|82700238	DNA repair protein RecN	BAB1_1440	0.8977	0.9597	1.0587	0.9896
gi|82699851	RNA-binding S4	BAB1_1019	1.0572	0.9877	0.9442	1.0095
gi|83269217	2-keto-3-deoxy-galactonokinase	BAB2_0295	1.0125	1.0567	1.0118	0.9691
gi|83269215	oxidoreductase, N-terminal:oxidoreductase, C-terminal	BAB2_0293	1.1612	1.1621	1.0013	1.0007
gi|82699328	phosphoribosylamine--glycine ligase	BAB1_0442	0.9619	0.9211	0.995	1.0382
gi|82699043	ATP-dependent helicase	BAB1_0121	0.9306	0.8916	0.9899	1.0323
gi|83269158	glutathione S-transferase	BAB2_0230	1.0781	1.0819	0.9701	0.966
gi|82700652	hypothetical protein BAB1_1884	BAB1_1884	1.1315	0.9676	0.8878	1.0376
gi|82699537	hypothetical protein BAB1_0669	BAB1_0669	0.883	0.9721	1.1162	1.0151
gi|83269684	zinc-containing alcohol dehydrogenase	BAB2_0821	0.8933	0.9604	1.0551	0.9805
gi|82699072	ABC transporter ATPase	BAB1_0156	0.949	0.9964	1.0027	0.9543
gi|82699340	chorismate synthase	BAB1_0454	0.902	0.9845	1.0499	0.9607
gi|83269459	periplasmic binding protein	BAB2_0564	1.0292	0.879	0.8942	1.0469
gi|82700550	transcription factor CarD	BAB1_1777	0.8409	0.9953	1.1266	0.9513
gi|82699038	outer membrane protein, putative	BAB1_0116	1.2915	1.0259	0.9088	1.1433
gi|82699655	hypothetical protein BAB1_0796	BAB1_0796	1.0105	0.9902	1.021	1.0406
gi|82699591	aminoacyl-tRNA synthetase, class I	BAB1_0723	1.0141	0.9983	0.9948	1.0113
gi|83269185	RecA DNA recombination protein:alanine dehydrogenase	BAB2_0261	1.2146	1.1534	0.9561	1.0031
gi|82698936	molybdopterin biosynthesis protein MoeB	BAB1_0004	0.8803	1.0114	1.1094	0.9657
gi|82699509	membrane alanine aminopeptidase:neutral zinc metallopeptidase	BAB1_0641	0.9316	0.9692	1.0843	1.0418
gi|83269218	2-dehydro-3-deoxy-6-phosphogalactonate aldolase	BAB2_0296	1.1082	1.052	0.9743	1.0259
gi|83269541	nucleotidyl transferase	BAB2_0657	0.9068	1.0519	1.1031	0.9499
gi|83269089	AP endonuclease	BAB2_0144	0.8734	0.9422	1.042	0.9643
gi|82699973	2-dehydro-3-deoxyphosphooctonate aldolase	BAB1_1156	1.1176	0.9937	0.8794	0.9895
gi|83269760	cytochrome c heme-binding site:4Fe-4S ferredoxin	BAB2_0905	0.863	0.9365	1.1319	1.0424
gi|82700154	sulfate-/thiosulfate-binding protein	BAB1_1351	1.1485	1.0707	1.0072	1.0777
gi|82700139	3-hydroxyisobutyrate dehydrogenase	BAB1_1334	1.2692	1.1209	1.0104	1.1473
gi|83269427	oxidoreductase, N-terminal:oxidoreductase	BAB2_0528	0.9992	1.1082	1.1127	1.0019
gi|83269196	ABC transporter ATPase	BAB2_0274	0.9743	0.9887	1.0292	1.0134
gi|82699928	acyl-CoA dehydrogenase	BAB1_1109	1.0094	1.0628	1.0219	0.9699
gi|82700463	deoxyuridine 5'-triphosphate nucleotidohydrolase	BAB1_1687	0.9793	1.0095	1.0134	0.9823
gi|82700653	hypothetical protein BAB1_1885	BAB1_1885	1.073	0.9666	0.9147	1.0157
gi|82700102	homoserine dehydrogenase	BAB1_1293	1.1447	1.051	0.918	0.9996
gi|82700253	UDP-N-acetylmuramoylalanyl-D-glutamate--2,6-diaminopimelate ligase	BAB1_1455	1.1615	0.9878	0.8569	1.0076
gi|83269854	glucokinase	BAB2_1010	0.9152	0.9209	1.0087	1.003
gi|83269131	bifunctional riboflavin kinase/FMN adenylyltransferase	BAB2_0193	1.0087	1.0652	1.0128	0.9589
gi|82700792	cobalamin synthesis protein P47K	BAB1_2036	0.8937	0.962	1.026	0.9527
gi|82700647	nitrilase/cyanide hydratase/apolipoprotein N-acyltransferase	BAB1_1878	0.724	0.9367	1.5449	1.1781

gi|82700503	uridine kinase	BAB1_1727	0.9366	0.9578	1.0265	1.0028
gi|82699306	hypothetical protein BAB1_0420	BAB1_0420				
gi|82699348	1-deoxy-D-xylulose-5-phosphate synthase	BAB1_0462	0.8581	0.9992	1.061	0.9107
gi|82699540	amino acid-binding ACT domain-containing protein	BAB1_0672	0.8988	0.8979	1.0632	1.0636
gi|82700190	hypothetical protein BAB1_1392	BAB1_1392	0.9734	0.9354	0.9958	1.0364
gi|82699905	GCN5-related N-acetyltransferase	BAB1_1076	1.0084	0.9028	0.9934	1.109
gi|82699709	glutaredoxin:glutaredoxin-related protein	BAB1_0855	1.0883	1.0784	0.9632	0.9717
gi|82699279	cytochrome c heme-binding site:cytochrome C oxidase	BAB1_0391	1.1689	1	0.9819	1.1474
gi|82700400	hypothetical protein BAB1_1612	BAB1_1612	1.1908	0.9952	0.8449	1.0102
gi|82699899	TrpR binding protein WrbA	BAB1_1070	1.1007	0.97	0.9444	1.071
gi|82699459	hypothetical protein BAB1_0587	BAB1_0587	1.2342	1.0772	0.9231	1.057
gi|82700918	enoyl-(acyl carrier protein) reductase	BAB1_2172	1.0261	1.0568	0.9779	0.949
gi|82700743	diaminopimelate decarboxylase	BAB1_1984	0.9312	1.05	1.0748	0.9519
gi|83269133	hypothetical protein BAB2_0195	BAB2_0195	0.8565	0.8981	1.0736	1.0232
gi|82698933	chromosomal replication initiation protein	BAB1_0001	1.181	0.9593	1.0152	1.2531
gi|82700189	hypothetical protein BAB1_1391	BAB1_1391	0.9242	0.9531	1.0464	1.0132
gi|83269539	hypothetical protein BAB2_0655	BAB2_0655	0.859	1.0887	1.2292	0.9689
gi|82700912	ribosome-binding factor A	BAB1_2166	0.933	0.9188	0.9947	1.0069
gi|83269461	aldehyde dehydrogenase	BAB2_0566	1.2896	1.186	0.9376	1.0195
gi|82700617	hypothetical protein BAB1_1847	BAB1_1847	0.9401	1.0288	1.0728	0.9794
gi|82700068	30S ribosomal protein S10	BAB1_1256	1.1617	1.0513	1.0024	1.106
gi|82699797	esterase/lipase/thioesterase, active site	BAB1_0946	1.11	1.0481	1.0079	1.0659
gi|82699513	aromatic-ring hydroxylase	BAB1_0645	0.9592	0.9779	0.9507	0.9319
gi|82699358	amidophosphoribosyltransferase	BAB1_0472	0.9403	1.0045	1.0867	1.0166
gi|82699185	histidinol dehydrogenase	BAB1_0285	1.0242	0.9885	0.9513	0.9852
gi|83269562	iron-responsive transcriptional regulator	BAB2_0678	1.1098	1.0565	0.9491	0.9961
gi|83269124	fumarate hydratase	BAB2_0186	1.0237	0.973	0.9849	1.0357
gi|82700867	esterase/lipase/thioesterase, active site:Alpha/beta hydrolase	BAB1_2120	0.9959	1.0218	1.0886	1.0609
gi|82700395	tRNA (5-methylaminomethyl-2-thiouridylate)-methyltransferase	BAB1_1607	1.0687	1.0238	1.0564	1.1041
gi|82699496	response regulator receiver	BAB1_0628	0.9835	0.995	1.0699	1.0569
gi|82699088	ribonuclease PH	BAB1_0172	0.9825	1.0942	1.0396	0.9333
gi|83269833	acetylglutamate kinase	BAB2_0988	0.9826	0.9758	0.9794	0.9864
gi|83269548	solute-binding family 5 protein	BAB2_0664	1.0742	1.0232	0.9135	0.9582
gi|83269359	pyrroline-5-carboxylate reductase	BAB2_0456	0.9973	0.9289	0.9559	1.025
gi|83269269	isopropylmalate isomerase small subunit	BAB2_0353	0.9724	0.9731	1.013	1.0111
gi|82700861	tryptophan synthase subunit alpha	BAB1_2110	1.1207	1.092	1.0674	1.0941
gi|82700526	glucose/ribitol dehydrogenase	BAB1_1750	0.9656	0.9616	0.973	0.9764
gi|82700495	thiamine-phosphate pyrophosphorylase	BAB1_1719	1.171	1.0099	0.8725	1.0109
gi|82700427	ABC transporter ATPase	BAB1_1650	0.9362	0.9709	1.0409	1.0029
gi|82699976	ErfK/YbiS/YcfS/YnhG	BAB1_1159	0.9162	1.1829	1.1403	0.8831
gi|82699760	hypothetical protein BAB1_0909	BAB1_0909	1.0654	0.9634	0.887	0.9799
gi|82699623	cystathionine beta-lyase	BAB1_0760	1.0891	1.1301	0.9912	0.9546
gi|83269597	transketolase, central region:transketolase, C terminal	BAB2_0714	1.0607	0.9837	0.9136	0.9845

gi|83269351	hypothetical protein BAB2_0448	BAB2_0448	0.9784	0.9942	0.9827	0.9666
gi|82700836	imidazoleglycerol-phosphate dehydratase	BAB1_2082	0.9311	0.9059	0.999	1.0262
gi|82700578	F0F1 ATP synthase subunit epsilon	BAB1_1806	0.9871	0.9987	0.947	0.9354
gi|82700501	hypothetical protein BAB1_1725	BAB1_1725	0.9588	0.968	1.0726	1.0619
gi|82700453	hypothetical protein BAB1_1676	BAB1_1676	1.0807	0.8915	0.8421	1.0206
gi|82700128	hypothetical protein BAB1_1322	BAB1_1322	0.9826	1.0137	1.0521	1.0194
gi|82699695	glyoxalase/bleomycin resistance protein/dioxygenase	BAB1_0838	1.0391	0.9665	0.9928	1.0664
gi|82699525	histidinol-phosphate aminotransferase	BAB1_0657	0.8086	0.9022	1.1288	1.011
gi|82699471	hypothetical protein BAB1_0599	BAB1_0599	0.946	0.9712	1.0441	1.016
gi|82699458	Mg2+ transporter protein, CorA-like	BAB1_0583	1.15	0.9719	0.9611	1.1367
gi|82699229	O-succinylhomoserine sulfhydrylase	BAB1_0335	1.023	0.9234	0.9473	1.0502
gi|82699186	hypothetical protein BAB1_0286	BAB1_0286	1.072	1.0132	0.9454	0.9995
gi|82699635	hypothetical protein BAB1_0776	BAB1_0776	0.9747	1.0259	1.0599	1.0062
gi|82700741	argininosuccinate lyase	BAB1_1982	1.0272	0.9858	1.0369	1.0804
gi|82700496	Sel1 repeat-containing protein	BAB1_1720	1.0915	1.0893	0.9862	0.9866
gi|82700351	Rieske iron-sulphur domain-containing protein	BAB1_1559	1.0392	1.0687	1.0184	0.9897
gi|82699326	acyl-CoA dehydrogenase	BAB1_0440	1.0228	0.9672	0.9554	1.0096
gi|83269242	sugar isomerase (SIS)	BAB2_0323	0.9293	0.9547	1.0564	1.0268
gi|82699691	NADH dehydrogenase subunit M	BAB1_0834	0.9548	0.9929	1.0573	1.0164
gi|83269401	glycine betaine ABC transporter ATP-binding protein	BAB2_0502	1.2761	1.082	0.9254	1.0915
gi|82700779	chaperonin ClpA/B	BAB1_2023	0.9397	0.9708	1.0026	0.9698
gi|82700338	hypothetical protein BAB1_1546	BAB1_1546	0.9851	1.016	1.0443	1.0119
gi|83269204	Leu/Ile/Val-binding family protein	BAB2_0282	1.3554	1.1354	0.8395	1.0029
gi|82699748	antifreeze protein, type I	BAB1_0897	1.0931	1.0623	0.9842	1.0124
gi|82698942	solute-binding family 5 protein	BAB1_0010	1.0499	0.922	0.8698	0.9897
gi|83269140	modulator of DNA gyrase	BAB2_0205	0.9663	0.9331	0.9918	1.0249
gi|82700765	response regulator receiver:transcriptional regulatory protein	BAB1_2006	1.0234	0.9675	0.9899	1.0466
gi|82700914	30S ribosomal protein S15	BAB1_2168	1.0883	1.0196	0.9453	1.0076
gi|82700057	50S ribosomal protein L14	BAB1_1245	0.9892	1.1021	1.0728	0.9622
gi|82699504	response regulator receiver:transcriptional regulatory protein	BAB1_0636	1.0782	0.8681	0.8442	1.0473
gi|83269172	cobalamin synthesis protein P47K	BAB2_0246	1.1269	1.0716	0.9892	1.0394
gi|82700424	short chain dehydrogenase	BAB1_1647	1.1563	1.0039	0.8795	1.0127
gi|82698959	hypothetical protein BAB1_0030	BAB1_0030	1.2086	1.2097	0.9408	0.9473
gi|82699321	FAD linked oxidase	BAB1_0435	1.2158	1.1952	1.0063	1.0233
gi|82700781	heat shock protein DnaJ	BAB1_2025	0.9885	1.0778	1.0294	0.9446
gi|82700054	30S ribosomal protein S14	BAB1_1242	1.0287	1.0822	0.9663	0.9167
gi|82699607	ETC complex I subunit region	BAB1_0739	1.1495	1.0766	0.9837	1.0497
gi|82699710	hypothetical protein BAB1_0856	BAB1_0856	1.0854	0.9065	0.8622	1.0333
gi|82700047	preprotein translocase subunit SecY	BAB1_1235	0.9188	0.9367	0.9733	0.9542
gi|83269171	ATP/GTP-binding motif-containing protein	BAB2_0245	1.075	1.1395	1.033	0.9739
gi|83269023	peptidoglycan binding domain-containing protein	BAB2_0069	0.9368	1.1418	1.1434	0.9372
gi|82699388	PAS domain-containing protein	BAB1_0507	1.122	1.0229	1.037	1.1353
gi|83269136	high mobility group proteins HMG-I and HMG-Y	BAB2_0198	0.9549	0.9784	0.9661	0.9423

gi|82700296	carbamoyl phosphate synthase small subunit	BAB1_1502	1.0333	1.0394	0.9586	0.9523
gi|82700551	7Fe ferredoxin	BAB1_1778	1.0973	0.9771	0.8798	0.9873
gi|82700919	3-oxoacyl-(acyl carrier protein) synthase I	BAB1_2173	1.1151	1.1684	1.0174	0.9703
gi|83269120	ATP phosphoribosyltransferase regulatory subunit	BAB2_0182	0.9179	0.9305	1.0811	1.0661
gi|82699981	indole-3-glycerol-phosphate synthase	BAB1_1164	0.9166	1.0923	1.1134	0.9325
gi|82699377	hypothetical protein BAB1_0491	BAB1_0491	0.7966	0.9568	1.1416	0.949
gi|82700335	hypothetical protein BAB1_1543	BAB1_1543	0.9378	0.9695	0.9881	0.9549
gi|82700059	50S ribosomal protein L29	BAB1_1247	1.1851	1.0908	0.9939	1.0794
gi|82699330	pyridoxamine 5'-phosphate oxidase	BAB1_0444	1.1092	0.9908	0.9813	1.097
gi|82700304	cold shock DNA-binding domain-containing protein	BAB1_1512	1.0989	0.9399	0.8984	1.0495
gi|82700811	ABC transporter ATPase	BAB1_2057	0.9764	1.0711	1.0478	0.9556
gi|82700926	NLP/P60	BAB1_2180	0.9616	0.9945	1.0935	1.0563
gi|82700237	NAD-dependent DNA ligase LigA	BAB1_1439	0.9334	1.0185	1.1541	1.0576
gi|83269547	DSBA oxidoreductase	BAB2_0663	0.9098	1.1109	1.0751	0.8794
gi|82699953	RNA-binding protein Hfq	BAB1_1134	0.937	0.9267	0.9046	0.9144
gi|83269119	histidyl-tRNA synthetase	BAB2_0181	0.9156	0.9357	1.0117	0.9892
gi|82699701	ABC transporter ATPase	BAB1_0844	1.0229	0.9418	0.9528	1.034
gi|82699629	salicylate hydroxylase	BAB1_0770	0.9513	0.9928	1.0416	0.998
gi|82700627	50S ribosomal protein L27	BAB1_1857	0.9616	1.1652	1.186	0.9781
gi|82699910	NAD binding site:NAD-dependent epimerase/dehydratase	BAB1_1088	0.9962	1.0405	1.136	1.0851
gi|82700440	malate synthase G	BAB1_1663	0.5954	0.8977	1.5749	1.0432
gi|82700762	hypothetical protein BAB1_2003	BAB1_2003	0.9947	0.9873	0.9638	0.9714
gi|82699964	lipoyl synthase	BAB1_1147	1.0533	1.104	1.0473	0.9959
gi|83269506	hypothetical protein BAB2_0620	BAB2_0620	1.29	1.2386	1.0005	1.039
gi|82700839	1-(5-phosphoribosyl)-5-[(5-phosphoribosylamino)methylideneamino]	BAB1_2085	1.0132	0.9668	0.948	0.9922
gi|82699205	allantoate amidohydrolase	BAB1_0310	9.6518	11.4809	1.3422	1.0955
gi|82699256	carboxynorspermidine decarboxylase	BAB1_0363	1.0821	1.0095	0.9159	0.9811
gi|82699991	(3R)-hydroxymyristoyl-ACP dehydratase	BAB1_1174	0.9864	0.9693	0.9613	0.9771
gi|82700101	fructose 1,6-bisphosphatase II	BAB1_1292	1.0173	1.0328	1.0118	0.9959
gi|82700442	RNA polymerase factor sigma-32	BAB1_1665	1.0224	0.9772	1.0504	1.1003
gi|82699451	betaine aldehyde dehydrogenase	BAB1_0576	1.2133	1.2411	1.0171	0.993
gi|82699657	3-oxoacyl-(acyl carrier protein) synthase III	BAB1_0798	1.1314	1.0151	0.9186	1.0232
gi|82699223	Pollen allergen Poa pIX/Phl pVI, C-terminal	BAB1_0329	0.9163	1.1496	1.1838	0.943
gi|82699042	DNA polymerase I	BAB1_0120	1.0074	0.944	0.956	1.0198
gi|83269223	urocanate hydratase	BAB2_0303	1.2057	1.2162	0.9625	0.9538
gi|82699068	integration host factor subunit beta	BAB1_0152	0.9512	1.0005	1.0258	0.9747
gi|82700360	polynucleotide adenylyltransferase	BAB1_1570	1.0115	1.0263	1.0527	1.0367
gi|83269585	binding-protein dependent transport system inner membrane protein	BAB2_0702	1.3316	1.272	0.9988	1.0448
gi|82700728	glucose/ribitol dehydrogenase	BAB1_1968	1.0294	0.9942	0.9987	1.0325
gi|82700421	OmpA-like transmembrane domain-containing protein	BAB1_1639	1.1024	0.6811	0.854	1.3808
gi|82700049	50S ribosomal protein L30	BAB1_1237	1.1761	1.1842	0.9776	0.9711
gi|82699656	putative glycerol-3-phosphate acyltransferase PlsX	BAB1_0797	0.9226	1.052	1.134	0.9941
gi|82699142	solute-binding family 1 protein	BAB1_0238	0.8921	0.8505	0.9347	0.9791

gi|82700745	phosphoribosyltransferase:hypoxanthine phosphoribosyl transferase	BAB1_1986	0.8278	1.0247	1.1526	0.9305
gi|82700159	RbsD or FucU transport	BAB1_1356	1.0934	0.9704	0.912	1.0272
gi|82699365	30S ribosomal protein S18	BAB1_0479	1.1044	1.0143	0.9374	1.02
gi|82699460	ATP/GTP-binding motif-containing protein	BAB1_0588	0.9474	1.0421	1.0791	0.9821
gi|82700756	ABC transporter ATPase	BAB1_1997	0.95	0.9637	1.0493	1.0359
gi|82699291	GTP-binding protein EngA	BAB1_0405	0.8933	0.9477	1.0491	0.9883
gi|83269374	glutamine synthetase catalytic domain	BAB2_0471	1.0022	1.0178	1.0182	1.0024
gi|82700900	hypothetical protein BAB1_2154	BAB1_2154	0.9581	0.9913	1.0525	1.0166
gi|82700610	aldehyde dehydrogenase	BAB1_1840	0.9038	1.1169	1.1531	0.933
gi|83269203	ABC transporter ATPase	BAB2_0281	0.9983	0.9552	1.0287	1.0743
gi|83269086	putative aldolase	BAB2_0141	0.746	0.8298	1.0356	0.9354
gi|83269404	immunoreactive 14 kDa protein BA14k	BAB2_0505	1.1089	1.0838	0.9475	0.9688
gi|82698971	surface antigen (D15)	BAB1_0038	0.928	0.8978	0.9638	0.9956
gi|82698967	copper center Cu(A):cytochrome o ubiquinol oxidase subunit II	BAB1_0038	0.8622	1.1883	1.2189	0.8837
gi|162002873	uridylate kinase	BAB1_1182	1.2138	1.2683	1.0237	0.979
gi|83269454	hydantoinase/oxoprolinase:hydantoinase B/oxoprolinase	BAB2_0559	1.0212	1.0318	1.0107	0.9988
gi|82700221	hypothetical protein BAB1_1423	BAB1_1423	0.9513	0.9929	0.9321	0.8905
gi|82699102	B12-dependent methionine synthase	BAB1_0188	0.9875	1.0113	1.0256	1.0004
gi|82700593	heat shock protein HtpX	BAB1_1821	1.0753	1.1641	1.032	0.9526
gi|82700038	outer membrane protein MotY	BAB1_1226	1.1956	1.0361	0.9052	1.0427
gi|83269138	patatin	BAB2_0203	0.9965	0.8659	0.8696	1.0012
gi|82700913	tRNA pseudouridine synthase B	BAB1_2167	1.0174	0.9876	1.0451	1.0753
gi|82700634	hypothetical protein BAB1_1864	BAB1_1864	0.8858	0.9325	1.0193	0.9656
gi|82699688	NADH dehydrogenase subunit J	BAB1_0831	0.9942	1.0221	0.9568	0.9303
gi|82700225	Alpha-isopropylmalate/homocitrate synthase:AsmA	BAB1_1427	0.8935	0.959	1.0779	1.0033
gi|83269008	glutamate synthase subunit beta	BAB2_0054	0.951	0.8866	0.9848	1.0557
gi|83269885	branched-chain alpha-keto acid dehydrogenase subunit E2	BAB2_1042	0.9757	0.9512	0.9385	0.9622
gi|83269865	phospholipase D/transphosphatidylase	BAB2_1021	0.8759	0.9899	1.0657	0.942
gi|82699195	urease subunit gamma	BAB1_0298	1.1193	1.1045	1.0014	1.0136
gi|82699212	thiol (cysteine) protease	BAB1_0318	1.0105	0.987	0.9945	1.0169
gi|82700499	inositol phosphatase/fructose-1,6-bisphosphatase	BAB1_1723	1.0262	0.9933	0.9216	0.9522
gi|82700025	hypothetical protein BAB1_1213	BAB1_1213	0.9524	0.9481	0.9586	0.9623
gi|82700405	oxidoreductase, N-terminal:oxidoreductase, C-terminal	BAB1_1617	1.0972	1.0591	0.9893	1.0242
gi|82699029	ABC transporter ATPase	BAB1_0107	1.0577	0.9477	0.9892	1.1034
gi|82699872	hypothetical protein BAB1_1040	BAB1_1040	1.0644	0.9371	0.8476	0.9622
gi|82699024	formate/nitrite transporter	BAB1_0102	0.8896	0.8766	0.976	0.99
gi|83269849	glutathione S-transferase	BAB2_1005	1.2516	0.8368	0.7148	1.0684
gi|83269450	Ppx/GppA phosphatase	BAB2_0555	0.9486	0.8925	1.0463	1.1102
gi|83269190	MaoC-like dehydratase	BAB2_0266	1.0038	0.9787	1.02	1.0458
gi|83269176	transcriptional regulator LacI	BAB2_0250	1.0186	1.0074	0.9764	0.9868
gi|82700486	hypothetical protein BAB1_1710	BAB1_1710	1.1011	0.9045	0.8424	1.0247
gi|82700117	hypothetical protein BAB1_1308	BAB1_1308	1.0029	1.0451	1.0682	1.0244
gi|82699084	ribokinase:carbohydrate kinase, PfkB	BAB1_0168	1.2075	1.0252	0.882	1.0376

gi|82699065	tRNA/rRNA methyltransferase (SpoU)	BAB1_0149	0.9385	0.925	1.0258	1.0397
gi|82700006	histidine triad (HIT) protein	BAB1_1190	0.96	1.1235	0.9861	0.842
gi|82698989	hypothetical protein BAB1_0063	BAB1_0063	0.9915	1.0047	0.9561	0.9426
gi|82699297	F0F1 ATP synthase subunit A	BAB1_0411	1.0581	0.9937	0.9771	1.0389
gi|82699386	ribosomal protein S7	BAB1_0505	0.8512	1.209	1.2257	0.8629
gi|82700890	ABC transporter ATPase	BAB1_2144	1.0548	1.0292	0.962	0.9859
gi|82700252	cytoplasmic peptidoglycan synthetase	BAB1_1454	0.8558	1.0133	1.1578	0.9765
gi|83269308	type I restriction-modification system, S subunit	BAB2_0396	1.0131	0.9866	1.0449	1.0723
gi|82699581	ABC transporter ATPase	BAB1_0713	0.9144	1.0975	1.1076	0.9221
gi|82699374	hypothetical protein BAB1_0488	BAB1_0488	0.9607	1.026	1.0802	1.0118
gi|82699277	cytochrome c heme-binding site:cytochrome c	BAB1_0389	0.984	0.9613	0.9655	0.9876
gi|82699062	DNA mismatch repair protein	BAB1_0146	0.8603	1.0352	1.1158	0.9266
gi|83269621	hypothetical protein BAB2_0740	BAB2_0740	1.1959	0.97	0.8678	1.0688
gi|83269026	CBS domain-containing protein:cytochrome b5	BAB2_0072	0.9714	0.9847	0.9896	0.9755
gi|82700697	diaminopimelate epimerase	BAB1_1932	0.9599	1.0122	0.9351	0.8866
gi|82700419	Short-chain dehydrogenase/reductase SDR	BAB1_1635	1.1033	1.0255	0.9554	1.0268
gi|82699819	molybdenum cofactor biosynthesis protein A	BAB1_0973	0.84	0.9894	1.222	1.0381
gi|82699687	NADH dehydrogenase subunit I	BAB1_0830	1.0238	0.9854	0.9977	1.0362
gi|83269453	glutamate-binding protein	BAB2_0558	0.8809	1.0253	1.1586	0.9965
gi|83269261	hypothetical protein BAB2_0345	BAB2_0345	1.2262	1.0645	0.9071	1.0446
gi|83268961	ribokinase:carbohydrate kinase, PfkB	BAB2_0004	1.0016	0.9339	0.9467	1.0146
gi|82700363	chaperonin clpA/B:AAA ATPase	BAB1_1573	0.9169	0.9926	1.0443	0.9638
gi|82699962	CinA, C-terminal	BAB1_1144	1.1962	0.9846	0.9167	1.113
gi|82699934	queuine tRNA-ribosyltransferase	BAB1_1115	0.9042	0.9988	1.0338	0.9335
gi|82699931	acriflavin resistance protein	BAB1_1112	0.9989	0.9583	0.9637	1.0039
gi|82699878	hypothetical protein BAB1_1048	BAB1_1048	0.873	0.8472	0.9002	0.9271
gi|82699733	HAD family hydrolase	BAB1_0880	1.0615	1.0137	0.984	1.0297
gi|82699359	colicin V production protein	BAB1_0473	0.9459	0.9914	1.0851	1.0338
gi|82699351	hypothetical protein BAB1_0465	BAB1_0465	0.9222	1.0243	1.0343	0.9298
gi|82699252	pantoate--beta-alanine ligase	BAB1_0359	1.0857	0.9531	0.9126	1.0393
gi|82699197	urease subunit alpha	BAB1_0300	1.1975	1.1626	1.0772	1.1082
gi|83269841	peptide deformylase	BAB2_0997	1.0398	1.0464	0.9768	0.9699
gi|83269745	septum formation inhibitor	BAB2_0884	0.924	0.9708	1.0483	0.9965
gi|83269608	Beta and gamma crystallin	BAB2_0727	1.0715	1.0474	1.0088	1.0314
gi|83269489	alpha/beta hydrolase	BAB2_0598	0.9845	0.9757	1.0543	1.0631
gi|83269360	tetrahydrofolate dehydrogenase/cyclohydrolase	BAB2_0457	0.8824	0.9384	1.0543	0.9906
gi|83269300	hypothetical protein BAB2_0388	BAB2_0388	0.968	1.027	1.1094	1.045
gi|83269280	fructose-1,6-bisphosphatase	BAB2_0364	0.9902	1.1251	1.1007	0.9666
gi|83269087	hypothetical protein BAB2_0142	BAB2_0142	0.8593	0.8523	1.0359	1.0437
gi|83269044	GCN5-related N-acetyltransferase	BAB2_0090	1.2608	1.4395	1.0779	0.9423
gi|83268998	inositol phosphatase/fructose-1,6-bisphosphatase	BAB2_0044	0.9888	1.097	1.0869	0.9791
gi|82700881	senescence marker protein-30 (SMP-30)	BAB1_2134	0.9838	0.9396	0.966	1.0109
gi|82700732	ExsB protein	BAB1_1973	1.1461	1.0024	0.9081	1.0392

gi|82700598	hypothetical protein BAB1_1828	BAB1_1828	0.754	0.9802	1.4425	1.109
gi|82700572	proline racemase, putative	BAB1_1800	1.3059	1.3687	1.0866	1.0378
gi|82700561	4-hydroxy-3-methylbut-2-en-1-yl diphosphate synthase	BAB1_1788	1.142	1.0573	0.9459	1.021
gi|82700531	1-(5-phosphoribosyl)-5-amino-4-imidazole-carboxyl carboxylase	BAB1_1757	1.2118	0.9596	0.9924	1.2562
gi|82700528	hypothetical protein BAB1_1754	BAB1_1754	1.1702	1.1719	1.0185	1.0164
gi|82700513	hypothetical protein BAB1_1737	BAB1_1737	0.9923	0.9508	0.9768	1.0171
gi|82700510	hypothetical protein BAB1_1734	BAB1_1734	0.9588	1.0412	1.0387	0.9559
gi|82700445	ferric-uptake regulator	BAB1_1668	1.0287	1.0033	0.9884	1.0128
gi|82700355	purine nucleoside permease	BAB1_1563	1.0883	1.2611	1.1231	0.9686
gi|82700348	adenine phosphoribosyltransferase	BAB1_1556	0.9296	0.9655	1.0192	0.9811
gi|82699980	anthranilate phosphoribosyltransferase	BAB1_1163	1.2209	0.9506	0.889	1.144
gi|82699938	phosphopantetheine adenylyltransferase	BAB1_1119	0.8847	0.9327	0.9898	0.9383
gi|82699811	protein-L-isoaspartate(D-aspartate) O-methyltransferase	BAB1_0962	1.0418	1.0197	0.9454	0.9654
gi|82699756	stationary phase survival protein SurE	BAB1_0905	1.0032	1.0391	0.9938	0.9584
gi|82699640	enoyl-CoA hydratase	BAB1_0781	0.9594	1.032	1.1042	1.0244
gi|82699339	hypothetical protein BAB1_0453	BAB1_0453	1.0293	1.0038	0.9944	1.0184
gi|82699244	polysaccharide deacetylase	BAB1_0350	0.9355	1.057	1.1116	0.9848
gi|82699198	urease accessory protein UreE	BAB1_0301	0.9572	0.9443	0.9722	0.9844
gi|82698963	prephenate dehydratase	BAB1_0034	1.036	0.9572	0.9063	0.9839
gi|83269475	glycerol-3-phosphate transporter ATP-binding subunit	BAB2_0582	1.1974	1.1661	0.9679	0.9933
gi|83269381	AsnC family regulatory protein	BAB2_0478	0.9002	0.8794	0.9482	0.97
gi|83269380	hypothetical protein BAB2_0477	BAB2_0477	0.9763	0.9817	1.0637	1.0572
gi|83269282	ribose-5-phosphate isomerase B	BAB2_0366	0.9849	0.9264	0.9789	1.0417
gi|83269267	hypothetical protein BAB2_0351	BAB2_0351	1.0092	1.066	1.0108	0.9563
gi|83269232	alanine racemase	BAB2_0312	1.1848	1.2872	1.152	1.055
gi|83269173	creatininase	BAB2_0247	0.8944	0.8774	1.0784	1.0993
gi|82700685	hypothetical protein BAB1_1919	BAB1_1919	1.0752	0.9992	0.9544	1.0262
gi|82700586	hypothetical protein BAB1_1814	BAB1_1814	0.9257	0.9421	1.0129	0.9946
gi|82700339	M24 family metallopeptidase	BAB1_1547	0.9954	0.9254	0.9725	1.0449
gi|82700316	hypothetical protein BAB1_1524	BAB1_1524	0.8561	1.0809	1.0821	0.8552
gi|82700200	K+ potassium transporter	BAB1_1402	0.7971	1.0403	1.1688	0.8947
gi|82700187	camphor resistance protein CrcB	BAB1_1389	0.8651	0.8902	1.0466	1.0163
gi|82700141	hypothetical protein BAB1_1336	BAB1_1336	1.0773	0.811	0.9204	1.2196
gi|82700094	alpha/beta fold hydrolase	BAB1_1282	1.0022	0.9277	0.9378	1.0125
gi|82700051	50S ribosomal protein L18	BAB1_1239	1.0206	1.0401	0.9759	0.9568
gi|82699903	alanyl-transfer RNA synthetase	BAB1_1074	1.245	1.1906	1.0608	1.1094
gi|82699898	molybdenum cofactor biosynthesis protein	BAB1_1069	0.9603	0.9985	1.0248	0.9844
gi|82699840	arsenate reductase:arsenate reductase and related	BAB1_1008	1.0292	1.0489	1.0175	0.9975
gi|82699828	hypothetical protein BAB1_0991	BAB1_0991	1.0072	0.9231	0.9441	1.0296
gi|82699658	integration host factor subunit alpha	BAB1_0799	1.0126	0.9941	0.9488	0.9658
gi|82699650	riboflavin synthase subunit beta	BAB1_0791	0.9806	0.9707	1.0275	1.0365
gi|82699593	hypothetical protein BAB1_0725	BAB1_0725	1.0499	1.0174	1.0099	1.0415
gi|82699573	4-hydroxythreonine-4-phosphate dehydrogenase	BAB1_0705	1.0429	1.0899	1.0101	0.9658

gi|82699288	transport protein	BAB1_0402	0.8383	0.8474	0.9976	0.9858
gi|82699236	hypothetical protein BAB1_0342	BAB1_0342	1.076	1.0181	0.9166	0.9676
gi|82699022	transcriptional regulator, putative	BAB1_0100	0.9701	0.9387	0.9814	1.0137
gi|82700806	luciferase	BAB1_2052	1.0127	0.9858	0.9517	0.9771
gi|83269551	2-octaprenyl-6-methoxyphenyl hydroxylase	BAB2_0667	0.9614	1.0663	1.051	0.947
gi|82699549	ribonuclease III	BAB1_0681	1.0342	1.0144	0.9938	1.0124
gi|82699278	cytochrome c oxidase, cbb3-type, CcoQ subunit	BAB1_0390	1.0152	1.0035	1.0612	1.0729
gi|82700565	Leu/Ile/Val-binding family protein	BAB1_1792	1.9931	1.9775	0.9925	1.0007
gi|82700241	UDP-3-O-[3-hydroxymyristoyl] N-acetylglucosamine deacetylase	BAB1_1443	0.9812	1.026	1.0057	0.9615
gi|82700092	hypothetical protein BAB1_1280	BAB1_1280	0.9733	0.932	0.9547	0.9966
gi|83269147	DNA mismatch repair protein	BAB2_0212	0.8885	0.9771	1.1025	1.0019
gi|83269763	PpiC-type peptidyl-prolyl cis-trans isomerase	BAB2_0908	0.7512	0.9239	1.3233	1.0753
gi|82700121	aminotransferase, class-I:aminotransferase, class I and II	BAB1_1315	0.9188	0.8275	0.9158	1.0161
gi|82699734	glutamate-binding protein	BAB1_0881	2.0091	1.672	0.8576	1.0303
gi|82698941	solute-binding family 5 protein	BAB1_0009	1.0177	1.0003	1.0511	1.0686
gi|82700539	hypothetical protein BAB1_1765	BAB1_1765	0.9155	0.9314	0.9577	0.9407
gi|83269286	D-erythrulose 4-phosphate dehydrogenase	BAB2_0370	0.8352	0.8215	0.9484	0.9637
gi|82700603	chorismate mutase	BAB1_1833	0.9541	0.9279	0.9629	0.9888
gi|82699150	Short-chain dehydrogenase/reductase SDR	BAB1_0246	0.9672	0.9001	1.078	1.1576
gi|82700829	calcium-binding EF-hand	BAB1_2075	0.9635	0.9512	0.9944	1.0065
gi|82700018	7-cyano-7-deazaguanine reductase	BAB1_1206	0.9915	0.9028	0.9423	1.0342
gi|82699854	Beta tubulin	BAB1_1022	0.9067	1.0614	1.0815	0.9232
gi|83269254	ornithine cyclodeaminase	BAB2_0338	1.0109	1.04	1.0103	0.9815
gi|82700783	basic helix-loop-helix dimerization domain-containing protein	BAB1_2027	1.1861	1.0538	0.8468	0.9525
gi|82699506	rhodopsin-like GPCR superfamily protein	BAB1_0638	1.1025	1.0969	1.0171	1.0216
gi|83269169	putative sulfite oxidase subunit YedY	BAB2_0243	1.1342	0.9712	0.8662	1.0108
gi|82700264	peptidoglycan binding domain-containing protein	BAB1_1466				
gi|82700793	D-alanyl-D-alanine carboxypeptidase	BAB1_2037				
gi|82700887	hypothetical protein BAB1_2141	BAB1_2141	1.0562	0.9168	0.8922	1.0271
gi|82700211	serine protease family protein	BAB1_1413	1.1111	0.9667	0.8977	1.031
gi|83269226	imidazolonepropionase	BAB2_0306	0.9759	0.896	0.9199	1.0013
gi|82699719	hypothetical protein BAB1_0865	BAB1_0865	1.1469	0.9936	0.9095	1.0491
gi|82699651	transcription antitermination protein NusB	BAB1_0792	1.0867	1.0948	0.992	0.9821
gi|82699032	phenazine biosynthesis PhzC/PhzF protein	BAB1_0110	1.0744	1.0355	0.9612	0.9967
gi|83269772	sulfonate/nitrate ABC transporter periplasmic-binding protein	BAB2_0919	1.0102	0.9484	0.8745	0.9303
gi|83269832	GTPase EngB	BAB2_0987	0.9132	1.2203	1.1724	0.8768
gi|83269424	pyruvate decarboxylase	BAB2_0525	1.1256	1.3739	1.1618	0.9512
gi|82700724	tetracycline resistance protein	BAB1_1964	1.0194	0.9578	0.981	1.0432
gi|82700156	CBS/transport-associated domain-containing protein	BAB1_1353	0.9638	0.8942	1.0113	1.0898
gi|82699262	LuxR family regulatory protein	BAB1_0370	1.0047	0.9697	0.9587	0.9925
gi|82699440	mannose-6-phosphate isomerase type II	BAB1_0561	0.903	1.0058	1.1091	0.9952
gi|82700648	glutaredoxin	BAB1_1879	1.2239	1.081	0.9066	1.0253
gi|82699801	hypothetical protein BAB1_0950	BAB1_0950	1.0363	1.1556	1.1058	0.9911

gi|82700411	AsmA	BAB1_1623	0.7785	0.989	1.1321	0.8905
gi|82700699	GTP-binding signal recognition particle	BAB1_1934	1.1563	0.9521	0.85	1.0315
gi|83269137	N-6 adenine-specific DNA methylase	BAB2_0199	0.7595	1.0019	1.0898	0.8256
gi|83269025	hypothetical protein BAB2_0071	BAB2_0071	0.6227	0.4221	0.7973	1.1754
gi|82699353	peptidoglycan-binding LysM	BAB1_0467	0.9902	0.968	1.0048	1.0267
gi|82698952	3-phosphoshikimate 1-carboxyvinyltransferase	BAB1_0023	1.0515	0.9996	0.8806	0.9257
gi|82700812	DNA polymerase III subunit delta	BAB1_2058	1.0128	0.9207	1.0627	1.1683
gi|82699621	hypothetical protein BAB1_0758	BAB1_0758	0.9926	0.8888	0.9397	1.0487
gi|83268969	isochorismatase hydrolase family protein	BAB2_0013	1.0987	1.0699	1.0138	1.0404
gi|83269515	50S ribosomal protein L33	BAB2_0631	1.1863	1.1191	0.9653	1.0225
gi|82700932	30S ribosomal protein S20	BAB1_2186	1.0079	1.0132	0.9701	0.9644
gi|82699723	ribulose-phosphate 3-epimerase	BAB1_0869	0.9502	1.1284	1.053	0.8863
gi|82700894	putative lipoprotein	BAB1_2148	0.9264	0.8617	1.0974	1.179
gi|83269291	phosphoribulokinase ABC transporter ATPase	BAB2_0375	0.602	0.8169	1.497	1.1024
gi|82699802	aminotransferase, class V	BAB1_0951	1.0242	1.02	1.0299	1.0335
gi|82700540	H+-transporting two-sector ATPase subunit A	BAB1_1766	0.8509	0.9567	1.0234	0.9096
gi|82699743	AP endonuclease	BAB1_0892	0.8855	1.0194	1.1024	0.957
gi|82700248	N-acetylglucosaminyl transferase	BAB1_1450	1.0846	0.9695	0.8866	0.9912
gi|83269554	ABC transporter ATPase	BAB2_0670	1.8861	2.2351	1.3583	1.1454
gi|82699857	hypothetical protein BAB1_1025	BAB1_1025	1.1316	0.5784	0.9812	1.9183
gi|82700830	MltA family protein	BAB1_2076	0.9627	0.9676	1.1243	1.1179
gi|82700569	ABC transporter ATPase	BAB1_1796	2.3866	2.3579	1.0746	1.087
gi|82700621	gamma-glutamyl phosphate reductase	BAB1_1851				
gi|82699805	inorganic polyphosphate/ATP-NAD kinase	BAB1_0954				
gi|82699285	related:arsenate reductase and related	BAB1_0399	1.1201	0.9919	0.8889	1.0032
gi|82700415	isocitrate lyase and phosphorylmutase:isocitrate lyase	BAB1_1631	1.2402	1.0571	0.9579	1.123
gi|82698980	TonB-dependent receptor protein	BAB1_0054	0.9581	0.9862	0.9966	0.9676
gi|83269649	cupin domain-containing protein	BAB2_0770	0.8911	1.0351	1.2456	1.0716
gi|83268983	ABC transporter:AAA ATPase	BAB2_0027	1.0821	1.1228	0.9749	0.9389
gi|82700293	DNA primase	BAB1_1499	0.9226	0.9928	1.1524	1.0703
gi|82699959	ATPase-like ATP-binding protein	BAB1_1141	0.95	0.9515	0.9903	0.988
gi|82700295	hypothetical protein BAB1_1501	BAB1_1501	1.105	1.2284	1.1139	1.0014
gi|82700322	excinuclease ABC subunit B	BAB1_1530	0.8325	0.992	1.1726	0.9834
gi|83269195	binding-protein dependent transport system inner membrane protein	BAB2_0273	0.9405	0.8315	0.9967	1.1265
gi|82699813	hypothetical protein BAB1_0964	BAB1_0964	1.0297	0.9691	1.099	1.167
gi|83269888	enoyl-CoA hydratase	BAB2_1046	2.0148	2.4192	1.1415	0.95
gi|82699885	hypothetical protein BAB1_1055	BAB1_1055	0.9455	1.1301	1.1286	0.9437
RRRRRgi|832	REVERSED quinone oxidoreductase/zeta-crystallin	BAB2_0669	0.8059	0.9806	1.2795	1.0508
gi|82699181	Maf-like protein	BAB1_0281	0.9363	0.9318	1.0168	1.0211
gi|82700639	hypothetical protein BAB1_1869	BAB1_1869	1.0229	1.0255	0.9936	0.9904
gi|83269187	NAD(P) transhydrogenase, beta subunit	BAB2_0263				
gi|82699871	ABC transporter ATPase	BAB1_1039	0.9774	0.924	0.9747	1.0304
gi|83269029	ferrochelatase	BAB2_0075	0.964	1.0027	1.0434	1.0024

gi|83269863	aldehyde dehydrogenase	BAB2_1019	0.9395	0.9872	1.0696	1.0172
gi|82700784	CBS domain-containing protein	BAB1_2028	0.9709	1.0571	1.0001	0.918
gi|82700656	O-sialoglycoprotein endopeptidase	BAB1_1888	0.9688	0.9137	0.9698	1.0276
gi|83269852	penicillin-insensitive murein endopeptidase	BAB2_1008	0.7877	0.9622	1.1457	0.9373
gi|83269525	aspartate carbamoyltransferase catalytic subunit	BAB2_0641	1.0552	1.0712	1.036	1.0199
gi|82700433	hypothetical protein BAB1_1656	BAB1_1656				
gi|82700186	ABC transporter ATPase	BAB1_1388	0.8327	0.9493	1.0767	0.9439
gi|82700163	periplasmic binding protein/LacI transcriptional regulator	BAB1_1362	0.8678	1.0277	1.1481	0.9688
gi|82700099	phosphoesterase, RecJ-like:phosphoesterase, DHHA1	BAB1_1290	0.9483	0.9536	1.0925	1.0858
gi|83269361	phosphogluconate dehydratase	BAB2_0458	0.9623	0.9526	1.0417	1.0516
gi|83269209	D-aminopeptidase	BAB2_0287	1.1786	1.0027	0.9746	1.1448
gi|82699557	hypothetical protein BAB1_0689	BAB1_0689	0.9062	1.2689	1.2203	0.8709
gi|82699843	thymidylate kinase	BAB1_1011	0.9617	0.8908	0.9339	1.0075
gi|82699648	cytidine/deoxycytidylate deaminase zinc-binding subunit	BAB1_0789	0.8825	0.9453	1.2613	1.1768
gi|82699370	acyl carrier protein	BAB1_0484	0.9143	0.891	0.9682	0.9928
gi|83269538	lipase	BAB2_0654	0.8844	0.8491	0.9473	0.9862
gi|83269028	Band 7 protein:stomatin	BAB2_0074	0.8895	0.8537	0.9954	1.0364
gi|83269240	acriflavin resistance protein	BAB2_0321	0.7805	1.2998	1.5329	0.9198
gi|83269524	dihydroorotase	BAB2_0640	0.9844	0.9743	1.0155	1.0253
gi|83269405	Iron-containing alcohol dehydrogenase	BAB2_0506	1.9457	2.3143	1.1705	0.9834
gi|82699977	preprotein translocase subunit SecG	BAB1_1160	0.7375	0.862	1.1807	1.0095
gi|82699601	ATP/GTP-binding protein	BAB1_0733	1.0648	0.9894	0.936	1.0066
gi|83269688	shikimate/quinate 5-dehydrogenase	BAB2_0825	0.8816	0.8349	1.0287	1.0855
gi|82700329	MarR family regulatory protein	BAB1_1537	0.7184	0.8378	1.0845	0.9293
gi|82699804	glycosyl transferase family protein	BAB1_0953	1.0494	0.9428	0.9615	1.0696
gi|82699499	TPR repeat-containing protein	BAB1_0631	1.1236	0.9668	0.9883	1.1479
gi|162002874	bifunctional 2-C-methyl-D-erythritol 4-phosphate cytidylyltransferase	BAB1_1143				
gi|83269536	PAS domain:PAS-associated C-terminal domain:PAC motif	BAB2_0652	0.8462	1.1014	1.3978	1.0732
gi|83269170	esterase/lipase/thioesterase, active site	BAB2_0244	0.872	0.9263	1.0465	0.9844
gi|82700256	S-adenosyl-methyltransferase MraW	BAB1_1458	0.9692	1.1217	1.1578	0.9996
gi|82699354	ABC transporter ATPase	BAB1_0468	0.8505	1.0029	1.2295	1.0419
gi|82700451	hypothetical protein BAB1_1674	BAB1_1674	1.0271	0.8478	0.9423	1.1408
gi|82699752	twin argininte translocase protein A	BAB1_0901	1.5011	0.9286	0.7825	1.264
gi|82699081	helix-hairpin-helix DNA-binding motif-containing protein	BAB1_0165	0.7819	0.8892	1.1913	1.0468
gi|82700558	50S ribosomal protein L32	BAB1_1785				
gi|82699552	DNA repair protein RecO	BAB1_0684	1.0102	0.971	1.0176	1.0579
gi|82700778	von Willebrand factor, type A:cobalt chelatase, pCobT subunit	BAB1_2022	0.9065	0.9541	1.0138	0.9626
gi|82700193	endonuclease/exonuclease/phosphatase family protein	BAB1_1395	0.9771	0.9428	1.0694	1.1077
gi|83269823	aldehyde dehydrogenase	BAB2_0976	1.6482	1.5473	0.9141	0.9731
gi|82700490	Holliday junction DNA helicase B	BAB1_1714	0.9361	1.0754	1.0894	0.9476
gi|82699551	GTP-binding protein Era	BAB1_0683	0.8368	1.1846	1.0692	0.7548
gi|83268985	Short-chain dehydrogenase	BAB2_0029	0.8262	0.7806	1.0611	1.1224
gi|82700790	Pollen allergen Poa pIX/Phl pVI, C-terminal	BAB1_2034	0.9079	0.9065	1.0819	1.0828

gi|82700560	polyprenyl synthetase	BAB1_1787	0.7908	1.1088	1.3168	0.9385
gi|82699764	tRNA (uracil-5-)-methyltransferase Gid	BAB1_0913	0.8696	0.9825	1.1189	0.9898
gi|82699569	alpha-isopropylmalate	BAB1_0701	1.0325	1.2282	1.1288	0.9484
gi|82699395	HAD family hydrolase	BAB1_0514	1.0463	0.95	0.9524	1.0483
gi|82700181	Urea transporter	BAB1_1383	1.0674	0.66	0.8921	1.4419
gi|82700149	low PH-induced protein A	BAB1_1346	1.201	1.0631	1.1212	1.2658
gi|82700093	WW/Rsp5/WWP domain-/bacterial transferase	BAB1_1281	0.9984	1.0313	1.0073	0.9745
gi|82699995	hypothetical protein BAB1_1178	BAB1_1178	0.7222	0.873	1.1692	0.9666
gi|82699713	glutathione S-transferase	BAB1_0859	1.7797	1.8539	1.0118	0.9706
gi|82699554	hypothetical protein BAB1_0686	BAB1_0686	0.7699	1.2495	1.4057	0.8656
gi|83269449	cell division protein FtsJ	BAB2_0554	1.0511	1.1787	1.2004	1.0697
gi|83269317	FMN/related compound-binding core	BAB2_0405	1.0773	0.9616	1.0297	1.1529
gi|82700924	TrkA potassium uptake protein	BAB1_2178	0.7839	0.9418	1.2105	1.0069
gi|82700902	hypothetical protein BAB1_2156	BAB1_2156	0.9136	1.018	1.1348	1.0177
gi|82700870	50S ribosomal protein L35	BAB1_2123	1.0178	0.9464	0.9259	0.9951
gi|82700727	universal stress protein	BAB1_1967	0.8972	0.9103	0.8642	0.8512
gi|82700116	uroporphyrin-III C/tetrapyrrole methyltransferase	BAB1_1307	0.9081	0.9694	1.0471	0.9802
gi|82699935	S-adenosylmethionine:tRNA ribosyltransferase-isomerase	BAB1_1116	1.0361	0.9572	1.1494	1.2434
gi|82699694	Beta-lactamase-like	BAB1_0837	0.9978	1.1252	1.0683	0.9468
gi|82699375	guanylate kinase	BAB1_0489	1.0544	0.7137	0.9715	1.4344
gi|82699304	hypothetical protein BAB1_0418	BAB1_0418	1.0424	0.8255	0.9636	1.2161
gi|82700815	glucose-inhibited division protein B	BAB1_2061	1.0078	1.02	1.0883	1.0746
gi|83269402	GntR family regulatory protein	BAB2_0503	0.7814	1.1564	1.3702	0.9252
gi|82699034	ribokinase:carbohydrate kinase, PfkB	BAB1_0112	1.0602	1.055	1.0484	1.0529
gi|82700133	cobalamin synthesis protein P47K	BAB1_1327	1.1478	1.1494	0.9841	0.982
gi|82700095	hypothetical protein BAB1_1283	BAB1_1283	1.076	0.9072	0.8807	1.0439
gi|82699779	TPR repeat-containing protein	BAB1_0928	0.8885	1.4231	1.554	0.9696
gi|82700534	TPR repeat-containing protein	BAB1_1760	0.9469	1.0728	1.2601	1.1116
gi|82699145	ABC transporter ATPase	BAB1_0241	0.9482	0.9354	0.965	0.9776
gi|82698964	3-deoxy-manno-octulosonate cytidylyltransferase	BAB1_0035	0.9372	0.9783	1.0297	0.9858
gi|82700785	3-dehydroquinate synthase	BAB1_2029	1.092	0.8872	0.8589	1.0564
gi|82700294	Na+/Pi-cotransporter	BAB1_1500	1.0406	0.9897	1.0218	1.0736
gi|83269666	methionine sulfoxide reductase B	BAB2_0792	1.0291	1.021	1.0124	1.0197
gi|82699604	Short-chain dehydrogenase/reductase SDR:glucose	BAB1_0736	1.0133	1.0223	0.9516	0.9425
gi|82700366	hypothetical protein BAB1_1576	BAB1_1576	0.9496	1.1046	1.1446	0.9833
gi|83269687	glucose-methanol-choline oxidoreductase:GMC oxidoreductase	BAB2_0824	0.7309	0.8744	1.1224	0.9376
gi|82700746	Generic methyltransferase	BAB1_1987	0.8372	0.9157	0.9627	0.8795
gi|82700618	SPOUT methyltransferase superfamily protein	BAB1_1848	0.9802	0.8571	1.0726	1.2258
gi|82699382	4-hydroxy-3-methylbut-2-enyl diphosphate reductase	BAB1_0132	0.9414	1.1519	1.2102	0.9883
gi|82699050	ATPase-like ATP-binding protein	BAB1_0132	0.8806	1.0571	1.159	0.9648
gi|83269229	beta alanine--pyruvate transaminase	BAB2_0309	0.9989	1.314	1.2612	0.958
gi|83269090	hypothetical protein BAB2_0145	BAB2_0145	0.8915	0.8359	0.996	1.0615
gi|83269088	AsnC family regulatory protein	BAB2_0143	0.76	0.8739	1.0882	0.9456

gi|83268978	GntR family regulatory protein	BAB2_0022	0.8114	0.9832	1.1161	0.9204
gi|82700893	putative lipoprotein	BAB1_2147	1.1678	0.7119	0.7488	1.2275
gi|82700236	hypothetical protein BAB1_1438	BAB1_1438	0.907	0.9688	1.0918	1.0216
gi|82700100	D-alanine--D-alanine ligase	BAB1_1291	0.88	0.9555	1.0221	0.9407
gi|82699958	response regulator receiver	BAB1_1140	0.9054	0.8622	0.8977	0.9421
gi|82699865	NAD synthetase	BAB1_1033	0.9389	1.0227	1.053	0.966
gi|82699758	peptidoglycan-binding LysM:peptidase M23/M37	BAB1_0907				
gi|82699700	general secretion pathway protein H	BAB1_0843	0.991	0.9467	0.9584	1.0026
gi|82699362	methyltransferase	BAB1_0476	1.1598	1.0398	0.9692	1.0804
gi|83269839	tRNA pseudouridine synthase A	BAB2_0995	0.9606	1.0133	1.0248	0.9708
gi|83269598	2-oxoisovalerate dehydrogenase E1 component, alpha subunit	BAB2_0715	1.1402	0.9656	0.8926	1.0533
gi|83269474	cytidine/deoxycytidylate deaminase, zinc-binding region	BAB2_0579	1.2253	1.2723	1.0763	1.0359
gi|83269429	transcriptional regulator LysR	BAB2_0530	0.9603	0.9232	0.9752	1.0137
gi|83269396	ABC transporter ATPase	BAB2_0493	1.3038	1.817	1.2475	0.8945
gi|83269193	TPR repeat-containing protein	BAB2_0271	0.9503	1.0848	1.062	0.9296
gi|83269161	TonB-dependent receptor protein	BAB2_0233	0.9462	0.9727	1.0438	1.0147
gi|83269037	keto-hydroxyglutarate-aldolase/keto-deoxy-phosphogluconate aldolase	BAB2_0083	1.023	1.1686	1.2006	1.0503
gi|82700848	PTS system fructose subfamily IIA component	BAB1_2096	0.9694	0.9677	1.0125	1.0136
gi|82700309	transcriptional regulator LysR	BAB1_1517	1.0811	1.2387	1.1045	0.9634
gi|82700289	antifreeze protein, type I	BAB1_1495	1.1002	0.9614	0.8417	0.9625
gi|82700263	glycoside hydrolase family protein	BAB1_1465	0.9657	0.9038	0.9944	1.0617
gi|82700123	uroporphyrin-III C/tetrapyrrole methyltransferase	BAB1_1317	0.8062	1.0681	1.0195	0.769
gi|82700082	preprotein translocase subunit SecE	BAB1_1270	0.962	0.9396	0.9519	0.9739
gi|82700039	transcriptional regulatory protein	BAB1_1227	0.9399	0.8751	0.9076	0.9741
gi|82699848	Beta-lactamase-like	BAB1_1016	0.9405	0.9469	1.0757	1.0678
gi|82699761	vacuolar H+-transporting two-sector ATPase subunit C	BAB1_0910	0.8234	0.9969	1.2029	0.9929
gi|82699707	inositol phosphatase/fructose-1,6-bisphosphatase	BAB1_0853	0.963	0.9734	1.0462	1.0344
gi|82699652	membrane-bound proton-translocating pyrophosphatase	BAB1_0793	0.8337	0.9546	1.1413	0.9961
gi|82699555	glycine cleavage T protein (aminomethyl transferase)	BAB1_0687	0.7512	0.9759	1.2074	0.9288
gi|82699523	antifreeze protein, type I	BAB1_0655	1.1105	1.0079	0.9986	1.0996
gi|82699505	ATPase-like ATP-binding protein	BAB1_0637	1.7178	0.8765	1.1201	2.1938
gi|82699335	ATP/GTP-binding motif-containing protein	BAB1_0449	0.6961	0.8218	1.0845	0.918
gi|82699222	ATPase-like ATP-binding protein	BAB1_0328	0.9287	0.9386	0.9735	0.9626
gi|82699078	heat shock protein Hsp20	BAB1_0162				
gi|82699063	hypothetical protein BAB1_0147	BAB1_0147	1.3143	1.0184	0.8077	1.0417
gi|82698977	hypothetical protein BAB1_0051	BAB1_0051	1.0639	0.8012	0.9545	1.2666
gi|83269922	hypothetical protein BAB2_1083	BAB2_1083	0.8507	1.0212	1.1731	0.9766
gi|83269872	methionine sulfoxide reductase A	BAB2_1029	0.9885	1.0834	1.0054	0.9167
gi|83269799	lipase	BAB2_0947	1.079	0.9991	1.0896	1.176
gi|83269785	hypothetical protein BAB2_0932	BAB2_0932	0.9253	1.0028	0.9194	0.8478
gi|83269762	nitrate reductase, gamma subunit	BAB2_0907	1.1128	1.0216	0.9128	0.9936
gi|83269717	T4 family peptidase	BAB2_0854	1.072	1.1137	1.0165	0.9778
gi|83269290	hypothetical protein BAB2_0374	BAB2_0374				

gi|83269243	N-acetylglucosamine-6-phosphate deacetylase:amidohydrolase	BAB2_0324	0.7644	1.0192	1.2118	0.9081
gi|83269224	N-formylglutamate amidohydrolase	BAB2_0304	0.924	1.0695	1.0908	0.9418
gi|83269177	TrkA potassium uptake protein	BAB2_0251	0.8784	0.9737	1.0171	0.917
gi|83269144	3-deoxy-D-manno-octulosonic-acid transferase	BAB2_0209	0.9638	1.1242	1.0951	0.9382
gi|83269049	transcriptional regulator LysR	BAB2_0096	0.9917	0.9768	1.064	1.0795
gi|83269043	ABC transporter ATPase	BAB2_0089				
gi|82700897	glycoprotease (M22) metalloprotease	BAB1_2151	0.7784	0.9605	1.1667	0.9449
gi|82700758	hypothetical protein BAB1_1999	BAB1_1999	1.0262	0.9197	0.9548	1.0647
gi|82700733	putative 6-pyruvoyl tetrahydropterin synthase	BAB1_1974	0.8138	0.9573	1.2458	1.0584
gi|82700695	lipoprotein Omp19	BAB1_1930	0.9177	0.9305	0.967	0.9531
gi|82700670	hypothetical protein BAB1_1902	BAB1_1902	0.9848	0.8606	0.9261	1.059
gi|82700641	N-6 adenine-specific DNA methylase	BAB1_1871	1.0088	0.9735	0.9629	0.9971
gi|82700546	M48 family peptidase	BAB1_1773	0.9876	1.0139	0.9939	0.9674
gi|82700543	thiamine transporter substrate binding subunit	BAB1_1770	0.9678	1.0118	1.1185	1.0691
gi|82700488	MotA/TolQ/ExbB proton channel	BAB1_1712	1.0022	0.8929	0.8811	0.9883
gi|82700457	biopolymer transport protein ExbD/TolR	BAB1_1680	0.7609	0.7823	1.0058	0.9776
gi|82700385	ABC transporter ATPase	BAB1_1595	1.0947	1.0011	0.9218	1.0074
gi|82700344	peptidyl-tRNA hydrolase	BAB1_1552				
gi|82700267	hypothetical protein BAB1_1469	BAB1_1469	1.0116	1.0008	1.0859	1.097
gi|82700266	methylenetetrahydrofolate reductase	BAB1_1468	0.7532	0.959	1.2379	0.9716
gi|82700204	ATP/GTP-binding motif-containing protein	BAB1_1406	0.856	0.9171	1.0765	1.0042
gi|82700104	hypothetical protein BAB1_1295	BAB1_1295	0.9456	0.806	1.0612	1.2442
gi|82700003	endoribonuclease L-PSP	BAB1_1187	1.0402	0.9718	0.9584	1.0253
gi|82699983	molybdenum cofactor biosynthesis protein MoeA	BAB1_1166	0.9432	1.0179	1.0343	0.9577
gi|82699955	potassium transporter peripheral membrane component	BAB1_1137	0.935	1.0253	1.0111	0.9215
gi|82699952	ATP/GTP-binding motif-containing protein	BAB1_1133	0.7356	1.0582	1.1664	0.8102
gi|82699945	single-strand binding protein	BAB1_1126	0.9084	1.0155	0.9753	0.8718
gi|82699911	nucleoside triphosphate pyrophosphohydrolase	BAB1_1089	1.1466	0.9141	0.8386	1.0512
gi|82699795	anhydro-N-acetylmuramic acid kinase	BAB1_0944				
gi|82699778	DSBA oxidoreductase	BAB1_0927	0.8948	0.9631	1.0665	0.9902
gi|82699774	leucyl/phenylalanyl-tRNA--protein transferase	BAB1_0923	0.8967	0.853	0.9278	0.9747
gi|82699759	ATP/GTP-binding motif-containing protein	BAB1_0908	0.9097	0.849	0.9557	1.0233
gi|82699671	phenylacetic acid degradation-related protein	BAB1_0812	1.138	1.1236	1.0022	1.0145
gi|82699563	hypothetical protein BAB1_0695	BAB1_0695	1.0839	1.3953	1.1602	0.9007
gi|82699541	orotate phosphoribosyltransferase	BAB1_0673	0.9377	1.064	1.0692	0.9416
gi|82699517	glutathione S-transferase	BAB1_0649	1.4728	1.0426	0.9579	1.3521
gi|82699447	xylose isomerase	BAB1_0570	1.0575	1.1356	1.0673	0.9933
gi|82699239	LuxR family regulatory protein	BAB1_0345	1.115	1.0876	0.9308	0.9536
gi|82699129	transcriptional regulator MerR	BAB1_0222	1.1124	1.044	0.9751	1.0383
gi|82699069	Clp protease:peptidase U7:Signal peptide peptidase	BAB1_0153	0.9444	0.9274	0.9581	0.9749
gi|82699015	cytochrome c assembly protein	BAB1_0093	0.8443	0.8948	0.9613	0.9064
gi|82699010	hypothetical protein BAB1_0088	BAB1_0088	0.9424	1.2532	1.1323	0.8509
gi|82699006	sugar ABC transporter ATPase	BAB1_0082				

gi|82698961	hit1 protein	BAB1_0032	0.9011	0.9554	0.9893	0.9324
gi|83269897	solute-binding family 5 protein	BAB2_1055	1.8839	2.8282	1.3922	0.9268
gi|83269840	methionyl-tRNA formyltransferase	BAB2_0996	0.9958	1.0073	1.032	1.0196
gi|83269793	Crp family regulatory protein	BAB2_0941	0.9133	0.894	1.0082	1.0293
gi|83269743	cell division topological specificity factor MinE	BAB2_0882	1.0671	1.0153	0.9987	1.049
gi|83269690	ABC transporter ATPase	BAB2_0827	0.7278	0.6934	0.8821	0.9252
gi|83269633	sodium/alanine symporter	BAB2_0754	0.9289	0.8451	0.9994	1.0977
gi|83269607	ybgT protein	BAB2_0726	1.0324	0.9971	1.0455	1.0818
gi|83269584	binding-protein-dependent transport systems inner membrane	BAB2_0701	1.3136	1.253	0.9677	1.0138
gi|83269535	lipoyltransferase	BAB2_0651	0.9908	0.9917	0.9394	0.9379
gi|83269497	saccharopine dehydrogenase	BAB2_0610	1.0706	1.2051	1.1856	1.0525
gi|83269473	xanthine/uracil/vitamin C permease family protein	BAB2_0578				
gi|83269455	hypothetical protein BAB2_0560	BAB2_0560	1.063	0.9446	1.1257	1.266
gi|83269413	glycine cleavage system protein H	BAB2_0514	1.1995	1.2238	0.9525	0.933
gi|83269364	3-ketoacyl-(acyl-carrier-protein) reductase	BAB2_0461	0.9461	1.0238	1.0324	0.9533
gi|83269272	hypothetical protein BAB2_0356	BAB2_0356				
gi|83269189	HAD family hydrolase	BAB2_0265	1.0708	1.1971	1.1483	1.0265
gi|83269159	biphenyl-2,3-diol 1,2-dioxygenase III	BAB2_0231	1.0694	1.1519	1.0942	1.0152
gi|83269134	nickel-dependent hydrogenase b-type cytochrome subunit	BAB2_0196	0.9704	0.9122	0.9152	0.973
gi|83269125	hypothetical protein BAB2_0187	BAB2_0187	0.991	0.8979	0.9923	1.0945
gi|83269048	hypothetical protein BAB2_0095	BAB2_0095	0.8578	1.2385	1.2749	0.8824
gi|83268982	ABC transporter ATPase	BAB2_0026	0.9062	1.0394	1.1305	0.985
gi|83268977	extracytoplasmic function alternative sigma factor	BAB2_0021	0.8667	0.9565	1.0521	0.9527
gi|83268976	sigma-70 region 2	BAB2_0020	0.9143	1.0842	0.962	0.8108
gi|83268962	inosine/uridine-preferring nucleoside hydrolase	BAB2_0005	1.0502	1.05	0.9902	0.9897
gi|82700865	hypothetical protein BAB1_2114	BAB1_2114	0.9648	0.964	1.0181	1.0183
gi|82700849	phosphocarrier HPr protein	BAB1_2097	0.9156	1.1923	1.0131	0.7775
gi|82700822	hypothetical protein BAB1_2068	BAB1_2068	1.143	0.7974	1.1222	1.6075
gi|82700751	hypothetical protein BAB1_1992	BAB1_1992	0.8774	0.9744	1.1041	0.9935
gi|82700742	hypothetical protein BAB1_1983	BAB1_1983	1.0936	1.0615	0.9995	1.0291
gi|82700711	hypothetical protein BAB1_1948	BAB1_1948	0.8848	0.9641	1.1116	1.0195
gi|82700701	Beta-lactamase-like	BAB1_1936	1.0583	0.9974	1.0115	1.0725
gi|82700680	tRNA (guanine-N(1)-)-methyltransferase	BAB1_1914	0.9721	0.8003	1.0091	1.2248
gi|82700671	succinate dehydrogenase, cytochrome b subunit	BAB1_1903	1.048	0.9345	1.0081	1.1298
gi|82700665	Acyl-CoA thioesterase	BAB1_1897	0.9934	1.0379	1.0084	0.9645
gi|82700654	uroporphyrinogen-III synthase	BAB1_1886	0.9831	0.9972	1.1104	1.094
gi|82700557	hypothetical protein BAB1_1784	BAB1_1784	1.0131	1.1023	1.1568	1.0624
gi|82700514	hypothetical protein BAB1_1738	BAB1_1738	0.9842	1.0179	0.9516	0.9195
gi|82700468	thromboxane receptor	BAB1_1692	0.8638	0.9257	1.047	0.9763
gi|82700444	hypothetical protein BAB1_1667	BAB1_1667	0.8811	0.9329	1.0342	0.9761
gi|82700398	hypothetical protein BAB1_1610	BAB1_1610	1.0906	1.0959	1.0243	1.0186
gi|82700377	transcriptional regulator LysR	BAB1_1587	2.0973	2.134	1.0183	1.0001
gi|82700349	cytochrome c heme-binding site	BAB1_1557	1.2005	1.0171	0.9185	1.0834

gi|82700340	putative lipoprotein	BAB1_1548	0.9963	0.9074	1.0026	1.1001
gi|82700288	immunoreactive 28 kDa outer membrane protein	BAB1_1494	0.9167	0.9769	1.0339	0.9695
gi|82700260	peptidoglycan binding domain-containing protein	BAB1_1462	0.7586	1.0729	1.138	0.8041
gi|82700234	ribosomal protein L11 methyltransferase	BAB1_1436				
gi|82700216	thymidylate synthase	BAB1_1418	0.8454	0.982	1.0904	0.9381
gi|82700182	ATP-dependent DNA ligase	BAB1_1384	0.9038	1.138	1.1918	0.9458
gi|82700026	hypothetical protein BAB1_1214	BAB1_1214	0.8815	0.9569	0.9951	0.9161
gi|82700015	MerR family regulatory protein	BAB1_1201	0.8134	0.9246	0.9465	0.832
gi|82700008	ATP-dependent Clp protease adaptor protein ClpS	BAB1_1192	1.2165	1.1394	0.9649	1.0296
gi|82699982	molybdenum cofactor biosynthesis protein C	BAB1_1165	0.6974	0.9887	1.2773	0.9003
gi|82699918	nitrogen-fixing NifU-like, N-terminal	BAB1_1096	0.9805	0.9172	0.9356	0.9996
gi|82699873	hypothetical protein BAB1_1041	BAB1_1041	1.1953	1.091	1.015	1.1113
gi|82699870	Sulfate transporter	BAB1_1038	0.8633	1.1115	1.0793	0.8377
gi|82699809	heavy metal transport/detoxification protein	BAB1_0960	0.9818	0.9767	1.1202	1.1253
gi|82699803	hypothetical protein BAB1_0952	BAB1_0952	0.9806	1.0885	1.0595	0.9539
gi|82699771	NADH dehydrogenase	BAB1_0920	1.0542	1.0182	0.974	1.0077
gi|82699757	protein-L-isoaspartate O-methyltransferase	BAB1_0906	1.1164	1.0155	0.9298	1.0215
gi|82699714	phosphoribosylformylglycinamidine synthase subunit I	BAB1_0860	1.217	1.1121	0.9424	1.0307
gi|82699674	hypothetical protein BAB1_0817	BAB1_0817	1.0115	0.9988	0.9452	0.9566
gi|82699668	agmatinase	BAB1_0809	0.7673	1.0642	1.3824	0.996
gi|82699638	hypothetical protein BAB1_0779	BAB1_0779	0.952	1.0296	1.0625	0.9818
gi|82699630	hypothetical protein BAB1_0771	BAB1_0771	1.1013	0.9384	0.8689	1.0191
gi|82699628	ABC transporter ATPase	BAB1_0769	1.0456	1.3211	1.2246	0.9686
gi|82699586	thiamineS	BAB1_0718	1.203	0.9615	0.8275	1.0345
gi|82699536	uracil-DNA glycosylase superfamily protein	BAB1_0668	0.9702	0.9412	1.0072	1.0375
gi|82699531	hypothetical protein BAB1_0663	BAB1_0663	0.8918	0.9456	0.9888	0.9319
gi|82699502	cytochrome C biogenesis protein	BAB1_0634	0.935	0.9513	1.0467	1.0281
gi|82699441	glycosyl transferase, group 1	BAB1_0563	1.185	0.8605	0.8948	1.2314
gi|82699412	transthyretin	BAB1_0532	1.1254	1.1341	0.9761	0.9679
gi|82699325	enoyl-CoA hydratase	BAB1_0439	0.9791	1.0444	1.0878	1.0191
gi|82699323	hypothetical protein BAB1_0437	BAB1_0437	1.0257	1.1288	0.935	0.849
gi|82699298	F0F1 ATP synthase subunit C	BAB1_0412	0.9666	1.0104	1.0147	0.97
gi|82699296	ATP synthase KO: K02116 ATP synthase protein I	BAB1_0410	0.8888	0.8023	1.103	1.2212
gi|82699265	hypothetical protein BAB1_0374	BAB1_0374	0.8899	1.1357	1.0221	0.8004
gi|82699242	large-conductance mechanosensitive channel	BAB1_0348	0.9462	0.9853	0.9734	0.9342
gi|82699237	hypothetical protein BAB1_0343	BAB1_0343	0.9284	1.0614	1.17	1.0228
gi|82699151	fumarylacetoacetate hydrolase	BAB1_0247	0.9141	1.0005	0.9677	0.8835
gi|82699113	DeoR family regulatory protein	BAB1_0199	0.6655	1.0354	1.2279	0.7887
gi|82699070	hypothetical protein BAB1_0154	BAB1_0154	1.0591	0.9945	0.9703	1.0325
gi|82699046	esterase/lipase/thioesterase, active site:putative esterase	BAB1_0124	0.9266	0.8659	1.0549	1.128
gi|162002875	phosphoribosyl-AMP cyclohydrolase	BAB1_1098	1.0923	1.0969	1.0334	1.0284
RRRRRgi|826	REVERSED PII uridylyl-transferase	BAB1_0143	1.0047	0.8509	0.9572	1.1295
gi|82699912	nitrilotriacetate monooxygenase component B	BAB1_1090	0.9162	0.9475	1.1281	1.0901

gi|83269035	response regulator receiver	BAB2_0081				
gi|82700755	hypothetical protein BAB1_1996	BAB1_1996	0.9648	0.9998	0.9779	0.943
gi|82700683	hypothetical protein BAB1_1917	BAB1_1917				
gi|82699039	3'-5' exonuclease	BAB1_0117	1.2426	0.9257	0.8506	1.141
RRRRRgi|827	REVERSED orotidine 5'-phosphate decarboxylase	BAB1_2132				
gi|82699031	nicotinate phosphoribosyltransferase	BAB1_0109	1.11	0.8923	0.8625	1.0722
RRRRRgi|826	REVERSED amidohydrolase 2	BAB1_0236				
gi|82699433	glycosyl transferase, group 1	BAB1_0553	0.9781	0.9562	1.0782	1.1021
gi|83269655	GntR family regulatory protein	BAB2_0777				
gi|82699919	GTP cyclohydrolase I	BAB1_1097	1.0831	1.0094	1.0242	1.0982

Table S1. Oligonucleotide primers used in this study.

Primer name	Sequence (5'→3')
AbcR-Northern	GGCAAACCTCCAGAGGGGAACACT
AbcR1-Northern	GAAGTCCGGCCAAGTTATGAAGGTGCCACT
AbcR2-Northern	CGTCCGGCTTTTGAATTTTGAAGGTGCCAT
5S rRNA-Northern	AGTTCGGAATGGGATCGGGTGCAGCC
AbcR1-5'-RACE	TGGGAAGTCCGGCCAAGTTATG
AbcR2-5'-RACE	AACGTCCGGCTTTTGAATTTTG
Δ*abcR1*-Up-For	GCGGATCCCTGATCGACTATGGTTTCCA
Δ*abcR1*-Up-Rev	GCCTGAAATCTAAAATTTCC
Δ*abcR1*-Dn-For	TGCTCTATTCTTCAACCCCAA
Δ*abcR1*-Dn-Rev	GCCTGCAGCGATCTTATTATTACCTCCTATGA
Δ*abcR2*-Up-For	GCGGATCCCGAAGTCATCATTCCCGCCC
Δ*abcR2*-Up-Rev	GGCTTTTGCCCGGTTGTCCA
Δ*abcR2*-Dn-For	GCACTGAGATGATCTTTATATGC
Δ*abcR2*-Dn-Rev	GCCTGCAGAAACGCTTTATCGTACGGC
AbcR1-express-For	ACTTACCGTTGTGCCTCCTCC
AbcR1-express-Rev	GCTCTAGACGTGATGGGGAAATTTTAGATT
AbcR2-express-For	ATCTCAGTGCTGCGTTTCCTC
AbcR2-express-Rev	GCTCTAGACATTCAGGAATGGACAACCGG
Nonsense sRNA-express-For	GGCCGCAAGGCCCCTTTTTCAT
Nonsense sRNA-express-Rev	GCTCTAGACGTTTCCTCCTCCCATTTTGCG
BAB1_0314-*gfp*-For	GCATGCATCGGAAAAACAGCAGCTTTGC
BAB1_0314-*gfp*-Rev	GCGCTAGCTGCTGATCCCGTGTGTTTCAT
BAB2_0879-*gfp*-For	GCATGCATCCGATCACGTTAGCATGTGAGTAA
BAB2_0879-*gfp*-Rev	GCGCTAGCAATTCCGCCCATAAGGGCA
BAB2_0612-*gfp*-For	GCATGCATGGGACGCGCAAAATGGGGC
BAB2_0612-*gfp*-Rev	GCGCTAGCGCCGGCGAATACTATGGCCT
BAB1_0310-North-For	GCTATAATACGACTCACTATAGGGCAACCACCAAAGGCCCTG
BAB1_0310-North-Rev	CCAATGAGGAAGGTACGCGC
BAB1_0314-North-For	GCTATAATACGACTCACTATAGGGCCTCGAAGATCGTCACCTGAT
BAB1_0314-North-Rev	ACATTCTGGGCGGCATGTGC
BAB1_0578-North-For	GCTATAATACGACTCACTATAGGGACGGATATAAAGCCCGTCGATC
BAB1_0578-North-Rev	TCTCAACGTGGCGATCAAACA
BAB1_1799-North-For	GCTATAATACGACTCACTATAGGGCCGTCAGCGAACGAAATCAC
BAB1_1799-North-Rev	GTTCCTACGAGCTGTTCGGCA
BAB2_0508-North-For	GCTATAATACGACTCACTATAGGGTAATAAACGCGATCGGCAGGC
BAB2_0508-North-Rev	GCATGGCGCGCATCGACTT
BAB2_0879-North-For	GCTATAATACGACTCACTATAGGGTGCCCGGCCAGACGACCTTGAAAT
BAB2_0879-North-Rev	CGATCGCTGCGCAAGAGTGCGAAA

*Underlined sections indicate restriction enzyme recognition sequences.

Table S2. Plasmids used in this study.

Plasmid name	Description	Reference
pNPTS138	Cloning vector; contains *sacB* gene; Kan^R	Spratt, 1986
pXG10	*gfp* fusion vector for UTR of target genes; Cm^R	Urban and Vogel, 2007
pZE12	sRNA expression vector; Amp^R	Urban and Vogel, 2007
pC^{3}022	Deletion of *abcR1* plus 1 kb of each flanking region in pNPTS138	This study
pC^{3}023	Deletion of *abcR2* plus 1 kb of each flanking region in pNPTS138	This study
pC^{3}024	*abcR1* in pZE12	This study
pC^{3}025	*abcR2* in pZE12	This study
pC^{3}026	Nonsense sRNA in pZE12	This study
pC^{3}027	5'-UTR of BAB1_0314 in pXG10	This study
pC^{3}028	5'-UTR of BAB2_0879 in pXG10	This study
pC^{3}032	wild-type *abcR1* plus 1 kb of each flanking region in pNPTS138	This study
pC^{3}033	wild-type *abcR2* plus 1 kb of each flanking region in pNPTS138	This study
pC^{3}034	5'-UTR of BAB2_0612 in pXG10	This study