Supplementary Table 3. Global data for transcriptomic assays

E. coli ATCC 25922 pBK-QnrS1 (EC14) versus *E. coli* ATCC 25922 pBK-CMV

Significant differential expression (greater than or equal to two-fold, P value <0,05)

Gene Name (ProbeID)	Fold Change	logSignal (A)	logRatio (M)	logControl	StdErr (logControl)	logExperiment	StdErr (logExperiment)	pval (limma)	FDR (limma)	Oligo	Systematic Name	Description
aaeA	-16.08	9.83	-4.01	11.83	0.1	7.82	0.1	0.00000220	0.00026540	A_07_P012680	b3241	cmr|putative membrane protein [b3241]
aaeB	-4.94	8.03	-2.31	9.18	0.1	6.88	0.0	0.00003059	0.00078194	A_07_P012673	b3240	cmr|orf, hypothetical protein [b3240]
aaeX	-4.10	8.13	-2.04	9.15	0.0	7.11	0.1	0.00004379	0.00094590	A_07_P010572	b3242	cmr|orf, hypothetical protein [b3242]
ABE-0285085	-3.42	8.51	-1.77	9.40	0.1	7.63	0.2	0.00033640	0.00367028	A_07_P010678	ABE-0285085	asap|IS1 transposase InsAB', C-ter fragment (pseudogene) [b4564]
ABH-0247453	-25.66	11.59	-4.68	13.94	0.0	9.25	0.1	0.00000074	0.00019431	A_07_P048654	ABH-0247453	asap|predicted protein []
ABR-0081747	-4.30	12.62	-2.10	13.67	0.0	11.57	0.0	0.00003172	0.00079523	A_07_P035421	ABR-0081747	asap|toxic membrane protein []
ABR-0081751	-3.96	8.80	-1.99	9.79	0.1	7.81	0.1	0.00010635	0.00164315	A_07_P041043	ABR-0081751	asap|predicted ferredoxin []
ABR-0081753	+6.78	10.99	+2.76	9.61	0.1	12.37	0.0	0.00001117	0.00048574	A_07_P041110	ABR-0081753	asap|predicted protein []
ABR-0081754	+2.65	7.54	+1.41	6.84	0.4	8.24	0.0	0.00577464	0.02947988	A_07_P041114	ABR-0081754	asap|predicted protein []
ACA-0244210	-3.16	11.50	-1.66	12.33	0.1	10.67	0.4	0.00246207	0.01543104	A_07_P059088	ACA-0244210	asap|predicted protein []
ACA-0285117	-2.79	11.88	-1.48	12.62	0.2	11.14	0.2	0.00104963	0.00821752	A_07_P062850	ACA-0285117	asap|toxic polypeptide, small []
accB	+4.40	10.79	+2.14	9.72	0.1	11.85	0.0	0.00003995	0.00090512	A_07_P012745	b3255	cmr|acetylCoA carboxylase, BCCP subunit; carrier of biotin [b3255]
accC	+2.00	10.52	+1.00	10.02	0.1	11.02	0.0	0.00190573	0.01273506	A_07_P012747	b3256	cmr|acetyl CoA carboxylase, biotin carboxylase subunit [b3256]
aceA	+6.63	9.18	+2.73	7.82	0.0	10.54	0.0	0.00000871	0.00042757	A_07_P008720	b4015	cmr|isocitrate lyase [b4015]
aceA	+6.26	8.97	+2.65	7.64	0.3	10.29	0.1	0.00008519	0.00142692	A_07_P037462	c_4972	cmr|Isocitrate lyase [c_4972]
aceB	+23.04	9.49	+4.53	7.23	0.0	11.76	0.0	0.00000071	0.00019431	A_07_P008715	b4014	cmr|malate synthase A [b4014]
aceE	+27.60	11.24	+4.79	8.85	0.0	13.64	0.1	0.00000063	0.00019431	A_07_P002535	b0114	cmr|pyruvate dehydrogenase [b0114]
aceF	+7.87	11.69	+2.98	10.20	0.1	13.18	0.0	0.00000907	0.00043556	A_07_P002536	b0115	cmr|pyruvate dehydrogenase [b0115]
ackA	+4.66	12.75	+2.22	11.64	0.1	13.87	0.0	0.00002945	0.00076000	A_07_P013766	b2296	cmr|acetate kinase [b2296]
acnA	+2.72	9.01	+1.44	8.29	0.1	9.74	0.1	0.00034781	0.00375837	A_07_P014361	b1276	cmr|aconitate hydrase 1 [b1276]
acnB	+7.16	10.24	+2.84	8.82	0.0	11.66	0.1	0.00000809	0.00041095	A_07_P002554	b0118	cmr|aconitate hydrase B [b0118]
acpD	+3.43	8.65	+1.78	7.76	0.1	9.53	0.1	0.00012727	0.00183667	A_07_P052470	Z2315	cmr|acyl carrier protein phosphodiesterase [Z2315]
acpD	+3.03	9.19	+1.60	8.39	0.2	9.99	0.0	0.00029674	0.00335322	A_07_P063175	ECs2014	cmr|acyl carrier protein phosphodiesterase [ECs2014]
acpP	+2.17	16.08	+1.12	15.52	0.0	16.64	0.1	0.00115284	0.00883229	A_07_P001671	b1094	cmr|acyl carrier protein [b1094]
acpS	+2.59	8.37	+1.37	7.68	0.1	9.06	0.0	0.00043162	0.00435473	A_07_P019720	b2563	cmr|CoA:apo- [b2563]
acpS	+2.98	8.44	+1.58	7.65	0.0	9.23	0.1	0.00015331	0.00211360	A_07_P053485	ECs3429	cmr|CoA:apo- [ECs3429]
acpS	+2.08	8.36	+1.05	7.83	0.1	8.89	0.0	0.00139171	0.01006017	A_07_P042915	Z3844	cmr|CoA:apo- [Z3844]
acs	+10.15	8.58	+3.34	6.91	0.1	10.26	0.1	0.00000660	0.00038136	A_07_P052329	Z5668	cmr|acetyl-CoA synthetase [Z5668]
acs	+6.57	8.49	+2.72	7.13	0.2	9.85	0.2	0.00009019	0.00146989	A_07_P008986	b4069	cmr|acetyl-CoA synthetase [b4069]
actP	+2.18	7.66	+1.12	7.10	0.2	8.22	0.1	0.00370526	0.02100672	A_07_P063696	ECs5049	cmr|putative transport protein [ECs5049]
actP	+2.68	7.56	+1.42	6.85	0.1	8.28	0.0	0.00042444	0.00430129	A_07_P052321	Z5666	cmr|putative transport protein [Z5666]
ade	+2.52	8.18	+1.33	7.52	0.0	8.85	0.1	0.00043204	0.00435473	A_07_P017261	b3665	cmr|probable adenine deaminase [b3665]
adhE	+2.03	8.13	+1.02	7.62	0.1	8.64	0.0	0.00130811	0.00968257	A_07_P007143	b1241	cmr|CoA-linked acetaldehyde dehydrogenase and iron-dependent alcohol dehydrogenase; pyruvate-formate-lyase deactivase [b1241]
aefA	-2.69	8.75	-1.43	9.47	0.0	8.04	0.0	0.00020331	0.00257851	A_07_P031187	c_0584	cmr|Potassium efflux system kefA [c_0584]
aes	-19.95	10.61	-4.32	12.77	0.1	8.45	0.0	0.00000141	0.00022371	A_07_P021486	b0476	cmr|putative lipase [b0476]
agaB	+2.11	7.34	+1.08	6.80	0.0	7.88	0.0	0.00083427	0.00700522	A_07_P000415	b3138	cmr|PTS system, cytoplasmic, N-acetylgalactosamine-specific IIB component 1 [b3138]
agaS	+13.70	8.73	+3.78	6.84	0.1	10.62	0.0	0.00000308	0.00028863	A_07_P034110	c_3893	cmr|Putative tagatose-6-phosphate ketose/aldose isomerase [c_3893]
agaS	+9.24	8.61	+3.21	7.01	0.1	10.22	0.0	0.00000492	0.00034758	A_07_P000404	b3136	cmr|putative tagatose-6-phosphate aldose/ketose isomerase [b3136]
agaV	+9.38	8.11	+3.23	6.50	0.1	9.73	0.1	0.00000531	0.00034950	A_07_P000390	b3133	cmr|PTS system, cytoplasmic, N-acetylgalactosamine-specific IIB component 2 [b3133]
agaW	+4.73	8.64	+2.24	7.52	0.3	9.76	0.2	0.00025275	0.00301002	A_07_P000391	b3134	cmr|PTS system N-acetylgalactosameine-specific IIC component 2 [b3134]
agp	+2.27	9.54	+1.18	8.95	0.3	10.13	0.1	0.00317787	0.01874573	A_07_P033935	c_1137	cmr|Glucose-1-phosphatase precursor [c_1137]
agp	+2.62	9.40	+1.39	8.71	0.1	10.10	0.2	0.00089902	0.00739123	A_07_P001241	b1002	cmr|periplasmic glucose-1-phosphatase [b1002]
ahpC	+2.50	15.39	+1.32	14.73	0.1	16.05	0.1	0.00039188	0.00405638	A_07_P016781	b0605	cmr|alkyl hydroperoxide reductase, C22 subunit; detoxification of hydroperoxides [b0605]
aidB	-2.92	9.26	-1.55	10.03	0.3	8.48	0.0	0.00192466	0.01280417	A_07_P011655	b4187	cmr|putative acyl coenzyme A dehydrogenase [b4187]
aldA	+3.12	8.28	+1.64	7.46	0.1	9.10	0.2	0.00033709	0.00367526	A_07_P009166	b1415	cmr|aldehyde dehydrogenase, NAD-linked [b1415]
allA	+2.76	8.86	+1.47	8.12	0.5	9.59	0.1	0.00695603	0.03382203	A_07_P016314	b0505	cmr|orf, hypothetical protein [b0505]
allB	+3.22	9.19	+1.69	8.34	0.2	10.03	0.1	0.00034946	0.00376840	A_07_P016349	b0512	cmr|putative hydrolase [b0512]
allD	+4.77	8.12	+2.25	6.99	0.0	9.24	0.2	0.00005402	0.00107118	A_07_P016372	b0517	cmr|putative malate dehydrogenase [b0517]
alr	-2.53	10.01	-1.34	10.68	0.0	9.34	0.1	0.00044888	0.00448424	A_07_P008909	b4053	cmr|alanine racemase 1 [b4053]
alsB	+9.06	9.29	+3.18	7.70	0.1	10.88	0.0	0.00000426	0.00033352	A_07_P011177	b4088	cmr|putative LACI-type transcriptional regulator [b4088]
amiA	-6.34	12.23	-2.66	13.56	0.0	10.90	0.1	0.00001089	0.00047910	A_07_P042594	c_2969	cmr|Probable N-acetylmuramoyl-L-alanine amidase amiA precursor [c_2969]
amiA	-6.35	12.20	-2.67	13.53	0.0	10.86	0.0	0.00001047	0.00047118	A_07_P052703	Z3700	cmr|N-acetylmuramoyl-l-alanine amidase I [Z3700]
amiA	-5.66	11.72	-2.50	12.97	0.0	10.47	0.0	0.00001332	0.00052521	A_07_P013234	b2435	cmr|N-acetylmuramoyl-l-alanine amidase I [b2435]
amiB	-2.54	10.66	-1.34	11.33	0.1	9.98	0.0	0.00030309	0.00339633	A_07_P011563	b4169	cmr|N-acetylmuramoyl-l-alanine amidase II; a murein hydrolase [b4169]
amn	+6.05	9.03	+2.60	7.73	0.4	10.33	0.0	0.00027270	0.00315462	A_07_P015257	b1982	cmr|AMP nucleosidase [b1982]
ampD	+2.85	12.12	+1.51	11.36	0.1	12.87	0.0	0.00019589	0.00250745	A_07_P041423	c_0129	cmr|AmpD protein [c_0129]
ampD	+3.65	10.90	+1.87	9.97	0.0	11.84	0.2	0.00016366	0.00221361	A_07_P002511	b0110	cmr|regulates ampC [b0110]
ampE	+2.06	9.14	+1.04	8.62	0.0	9.66	0.1	0.00121441	0.00913944	A_07_P002518	b0111	cmr|regulates ampC [b0111]
amyA	-2.57	8.04	-1.36	8.72	0.2	7.36	0.0	0.00106954	0.00833602	A_07_P044659	Z3017	cmr|cytoplasmic alpha-amylase [Z3017]
anmK	-2.02	9.52	-1.01	10.02	0.1	9.01	0.1	0.00200074	0.01316324	A_07_P020831	b1640	cmr|orf, hypothetical protein [b1640]
ansB	+15.30	12.19	+3.94	10.22	0.1	14.15	0.0	0.00000152	0.00022581	A_07_P011926	b2957	cmr|periplasmic L-asparaginase II [b2957]
apbA	+2.67	9.54	+1.41	8.84	0.1	10.25	0.0	0.00028897	0.00328960	A_07_P031138	c_0536	cmr|2-dehydropantoate 2-reductase [c_0536]
aphA	+2.22	8.25	+1.15	7.67	0.2	8.82	0.1	0.00259418	0.01604388	A_07_P008919	b4055	cmr|diadenosine tetraphosphatase [b4055]
apt	+7.43	12.30	+2.89	10.85	0.0	13.74	0.1	0.00000681	0.00038477	A_07_P021451	b0469	cmr|adenine phosphoribosyltransferase [b0469]
araA	+4.53	8.35	+2.18	7.26	0.1	9.44	0.0	0.00003715	0.00087028	A_07_P010999	b0062	cmr|L-arabinose isomerase [b0062]
araB	+2.83	8.05	+1.50	7.29	0.0	8.80	0.2	0.00078245	0.00665883	A_07_P011001	b0063	cmr|L-ribulokinase [b0063]
araC	+2.15	11.06	+1.10	10.50	0.0	11.61	0.0	0.00073874	0.00636601	A_07_P011010	b0064	cmr|transcriptional regulator for ara operon [b0064]
argE	+3.12	8.62	+1.64	7.80	0.2	9.44	0.1	0.00048189	0.00470068	A_07_P039521	c_4916	cmr|Acetylornithine deacetylase [c_4916]
argE	+3.25	7.85	+1.70	6.99	0.2	8.70	0.1	0.00032654	0.00359518	A_07_P008486	b3957	cmr|acetylornithine deacetylase [b3957]
argG	+2.09	7.96	+1.06	7.42	0.2	8.49	0.0	0.00254197	0.01579499	A_07_P000576	b3172	cmr|argininosuccinate synthetase [b3172]
argG	+2.06	8.57	+1.05	8.04	0.1	9.09	0.1	0.00181163	0.01228992	A_07_P041781	c_3929	cmr|Argininosuccinate synthase [c_3929]
argO	-2.03	7.90	-1.02	8.41	0.0	7.39	0.2	0.00362200	0.02069114	A_07_P011764	b2923	cmr|orf, hypothetical protein [b2923]
argR	-2.36	11.47	-1.24	12.08	0.0	10.85	0.0	0.00044476	0.00444871	A_07_P012656	b3237	cmr|repressor of arg regulon; cer-mediated site specific recombination [b3237]
arnT	+2.02	8.18	+1.01	7.67	0.2	8.69	0.1	0.00388747	0.02182751	A_07_P001072	b2257	cmr|orf, hypothetical protein [b2257]
aroD	+2.05	7.38	+1.03	6.86	0.1	7.89	0.1	0.00191791	0.01278929	A_07_P018517	b1693	cmr|3-dehydroquinate dehydratase [b1693]
aroL	-2.45	9.99	-1.29	10.63	0.1	9.34	0.0	0.00049035	0.00476059	A_07_P021052	b0388	cmr|shikimate kinase II [b0388]
aroM	-2.39	7.93	-1.26	8.56	0.0	7.30	0.1	0.00050690	0.00488112	A_07_P031086	c_0498	cmr|AroM protein [c_0498]
aroM	-2.77	7.82	-1.47	8.56	0.0	7.09	0.1	0.00021620	0.00268655	A_07_P043806	Z0486	cmr|protein of aro operon, regulated by aroR [Z0486]
arrD	+15.18	9.92	+3.92	7.96	0.1	11.88	0.1	0.00000237	0.00027039	A_07_P016536	b0555	cmr|bacteriophage lambda lysozyme homolog [b0555]
artI	+2.97	8.53	+1.57	7.75	0.1	9.32	0.1	0.00032893	0.00361129	A_07_P004766	b0863	cmr|arginine 3rd transport system periplasmic binding protein [b0863]
artP	+6.73	9.24	+2.75	7.87	0.2	10.62	0.1	0.00003721	0.00087055	A_07_P004773	b0864	cmr|ATP-binding component of 3rd arginine transport system [b0864]
asd	+3.63	9.52	+1.86	8.59	0.1	10.45	0.0	0.00006644	0.00120815	A_07_P018194	b3433	cmr|aspartate-semialdehyde dehydrogenase [b3433]
asnB	+2.66	9.43	+1.41	8.72	0.1	10.13	0.1	0.00041609	0.00423720	A_07_P046247	Z0821	cmr|asparagine synthetase B [Z0821]
asnB	+2.33	9.32	+1.22	8.71	0.2	9.93	0.1	0.00189978	0.01272086	A_07_P056567	ECs0704	cmr|asparagine synthetase B [ECs0704]
aspA	+5.99	15.44	+2.58	14.15	0.0	16.73	0.0	0.00001089	0.00047910	A_07_P011426	b4139	cmr|aspartate ammonia-lyase [b4139]
aspC	+5.75	9.54	+2.52	8.28	0.2	10.80	0.0	0.00002937	0.00076000	A_07_P052047	Z1275	cmr|aspartate aminotransferase [Z1275]
aspC	+6.18	10.90	+2.63	9.58	0.1	12.21	0.0	0.00001596	0.00056395	A_07_P005088	b0928	cmr|aspartate aminotransferase [b0928]
asr	-5.81	10.46	-2.54	11.73	0.0	9.19	0.1	0.00002243	0.00067002	A_07_P020616	b1597	cmr|acid shock protein [b1597]
astA	+3.05	8.31	+1.61	7.51	0.0	9.11	0.1	0.00016911	0.00225435	A_07_P018783	b1747	cmr|orf, hypothetical protein [b1747]
astC	+2.07	7.10	+1.05	6.58	0.1	7.62	0.1	0.00114177	0.00876450	A_07_P018786	b1748	cmr|acetylornithine delta-aminotransferase [b1748]
atpA	+3.07	14.98	+1.62	14.18	0.0	15.79	0.0	0.00012124	0.00178598	A_07_P005591	b3734	cmr|membrane-bound ATP synthase, F1 sector, alpha-subunit [b3734]
atpB	+2.15	12.51	+1.10	11.96	0.0	13.06	0.0	0.00072413	0.00627400	A_07_P005614	b3738	cmr|membrane-bound ATP synthase, F0 sector, subunit a [b3738]
atpD	+3.17	11.27	+1.67	10.44	0.0	12.10	0.0	0.00009419	0.00150861	A_07_P005582	b3732	cmr|membrane-bound ATP synthase, F1 sector, beta-subunit [b3732]
atpE	+4.40	12.62	+2.14	11.55	0.0	13.69	0.0	0.00003335	0.00081556	A_07_P005607	b3737	cmr|membrane-bound ATP synthase, F0 sector, subunit c [b3737]
atpG	+3.77	12.10	+1.92	11.14	0.0	13.06	0.0	0.00005306	0.00105884	A_07_P005587	b3733	cmr|membrane-bound ATP synthase, F1 sector, gamma-subunit [b3733]
atpH	+7.95	13.09	+2.99	11.60	0.1	14.59	0.1	0.00000792	0.00041039	A_07_P005596	b3735	cmr|membrane-bound ATP synthase, F1 sector, delta-subunit [b3735]
azoR	+2.60	8.88	+1.38	8.19	0.2	9.57	0.1	0.00122668	0.00920538	A_07_P009153	b1412	cmr|acyl carrier protein phosphodiesterase [b1412]
b0322	-5.16	9.24	-2.37	10.43	0.1	8.06	0.1	0.00004256	0.00093353	A_07_P008305	b0322	cmr|orf, hypothetical protein [b0322]
b0359	-2.25	8.60	-1.17	9.18	0.3	8.01	0.1	0.00402529	0.02229975	A_07_P020924	b0359	cmr|putative transferase [b0359]
b0359	-2.32	7.78	-1.22	8.38	0.1	7.17	0.0	0.00068608	0.00602876	A_07_P010289	b0359	cmr|putative transferase [b0359]
b0362	-2.23	7.10	-1.16	7.68	0.3	6.52	0.2	0.00463381	0.02479764	A_07_P020932	b0362	cmr|orf, hypothetical protein [b0362]
b0374	-5.61	8.35	-2.49	9.60	0.1	7.11	0.0	0.00001907	0.00061714	A_07_P020983	b0374	cmr|putative flagellin structural protein [b0374]
b0395	+2.57	7.55	+1.36	6.87	0.0	8.23	0.1	0.00054608	0.00516365	A_07_P021086	b0395	cmr|orf, hypothetical protein [b0395]
b0538	+2.25	7.97	+1.17	7.39	0.0	8.56	0.2	0.00156643	0.01104171	A_07_P016479	b0538	cmr|putative sensory transduction regulator [b0538]
b0671	-3.14	8.15	-1.65	8.98	0.0	7.33	0.2	0.00056765	0.00528823	A_07_P009885	b0671	cmr|putative RNA [b0671]
b0701	+2.17	8.91	+1.12	8.35	0.1	9.47	0.3	0.00711103	0.03444804	A_07_P010022	b0701	cmr|protein in rhs element [b0701]
b0725	+12.15	8.71	+3.60	6.91	0.0	10.51	0.1	0.00000313	0.00028944	A_07_P010142	b0725	cmr|orf, hypothetical protein [b0725]
b1170	-3.45	8.19	-1.78	9.09	0.1	7.30	0.0	0.00007884	0.00134340	A_07_P006805	b1170	cmr|putative part of putative ATP-binding component of a transport system [b1170]
b1543	-2.76	7.36	-1.46	8.09	0.0	6.63	0.2	0.00096859	0.00775143	A_07_P020361	b1543	cmr|putative transport protein [b1543]
b1995	-4.93	8.18	-2.30	9.34	0.0	7.03	0.1	0.00004494	0.00095618	A_07_P015310	b1995	cmr|orf, hypothetical protein [b1995]
b2087	+2.15	7.46	+1.11	6.91	0.1	8.02	0.0	0.00123195	0.00922733	A_07_P003208	b2087	cmr|split galactitol utilization operon repressor, interrupted [b2087]
b2680	-2.16	7.79	-1.11	8.34	0.2	7.23	0.0	0.00343917	0.01990336	A_07_P001871	b2680	cmr|orf, hypothetical protein [b2680]
b3016	-2.16	9.55	-1.11	10.11	0.0	9.00	0.1	0.00089191	0.00735583	A_07_P012215	b3016	cmr|orf, hypothetical protein [b3016]
b3111	+5.79	9.07	+2.53	7.80	0.0	10.34	0.1	0.00002355	0.00068545	A_07_P000282	b3111	cmr|putative L-serine dehydratase [b3111]
b3112	+4.39	8.38	+2.13	7.31	0.1	9.45	0.1	0.00005645	0.00109452	A_07_P000290	b3112	cmr|putative L-serine dehydratase [b3112]
b3763	+2.55	8.51	+1.35	7.83	0.0	9.19	0.1	0.00030764	0.00342294	A_07_P005708	b3763	cmr|regulator of pssA [b3763]
b3837	-3.65	11.98	-1.87	12.91	0.0	11.04	0.1	0.00007228	0.00126864	A_07_P018994	b3837	cmr|putative histone [b3837]
b3841	-3.54	10.13	-1.83	11.05	0.0	9.22	0.1	0.00007592	0.00131203	A_07_P019013	b3841	cmr|orf, hypothetical protein [b3841]
b3914	-2.01	12.33	-1.01	12.83	0.0	11.82	0.0	0.00113026	0.00870163	A_07_P019349	b3914	cmr|orf, hypothetical protein [b3914]
b4285	-2.60	15.23	-1.38	15.92	0.0	14.54	0.2	0.00092963	0.00755603	A_07_P003953	b4285	cmr|putative transposase [b4285]
bamD	-2.20	11.75	-1.14	12.32	0.1	11.19	0.0	0.00067416	0.00595430	A_07_P019860	b2595	cmr|orf, hypothetical protein [b2595]
basR	+2.37	9.78	+1.25	9.15	0.1	10.40	0.2	0.00189154	0.01267793	A_07_P037777	c_5118	cmr|Transcriptional Regulatory protein basR/pmrA [c_5118]
basS	-2.56	12.63	-1.36	13.31	0.5	11.95	0.1	0.01062794	0.04700177	A_07_P011296	b4112	cmr|sensor protein for basR [b4112]
bax	-6.61	12.16	-2.72	13.53	0.0	10.80	0.0	0.00000853	0.00042498	A_07_P007778	b3570	cmr|putative ATP-binding protein [b3570]
bcp	+11.85	10.07	+3.57	8.28	0.1	11.85	0.0	0.00000266	0.00027706	A_07_P013456	b2480	cmr|bacterioferritin comigratory protein [b2480]
bcsA	-3.05	8.67	-1.61	9.48	0.1	7.87	0.1	0.00020561	0.00259797	A_07_P007596	b3533	cmr|putative cellulose synthase [b3533]
bcsF	-3.29	7.94	-1.72	8.80	0.1	7.08	0.1	0.00011046	0.00167703	A_07_P007618	b3537	cmr|orf, hypothetical protein [b3537]
betA	+2.55	9.08	+1.35	8.41	0.0	9.76	0.1	0.00059532	0.00547004	A_07_P043676	Z0398	cmr|choline dehydrogenase, a flavoprotein [Z0398]
betA	+3.67	9.64	+1.88	8.70	0.2	10.58	0.1	0.00031830	0.00352414	A_07_P008247	b0311	cmr|choline dehydrogenase, a flavoprotein [b0311]
betA	+3.98	10.31	+1.99	9.31	0.2	11.30	0.0	0.00009776	0.00154382	A_07_P030984	c_0431	cmr|Choline dehydrogenase [c_0431]
betB	+2.90	12.14	+1.53	11.37	0.1	12.90	0.1	0.00018926	0.00244038	A_07_P008251	b0312	cmr|NAD+-dependent betaine aldehyde dehydrogenase [b0312]
bfr	-2.16	9.65	-1.11	10.21	0.1	9.10	0.2	0.00211430	0.01376089	A_07_P017709	b3336	cmr|bacterioferrin, an iron storage homoprotein [b3336]
bhsA	-9.66	11.09	-3.27	12.73	0.1	9.46	0.0	0.00000390	0.00032155	A_07_P001765	b1112	cmr|orf, hypothetical protein [b1112]
bioB	+2.00	7.43	+1.00	6.93	0.2	7.93	0.0	0.00389569	0.02185785	A_07_P004326	b0775	cmr|biotin synthesis, sulfur insertion? [b0775]
birA	-2.70	11.22	-1.44	11.94	0.0	10.51	0.0	0.00021972	0.00271742	A_07_P008550	b3973	cmr|biotin- [b3973]
bolA	+12.50	9.95	+3.64	8.13	0.0	11.78	0.0	0.00000208	0.00026053	A_07_P021288	b0435	cmr|possible regulator of murein genes [b0435]
borD	+2.16	9.18	+1.11	8.63	0.0	9.74	0.0	0.00073483	0.00634270	A_07_P016549	b0557	cmr|bacteriophage lambda Bor protein homolog [b0557]
bssS	-10.62	13.10	-3.41	14.80	0.0	11.39	0.0	0.00000287	0.00028251	A_07_P001504	b1060	cmr|orf, hypothetical protein [b1060]
btuB	-5.02	11.33	-2.33	12.49	0.0	10.17	0.1	0.00002328	0.00068274	A_07_P008533	b3966	cmr|outer membrane receptor for transport of vitamin B12, E colicins, and bacteriophage BF23 [b3966]
btuE	-2.07	10.79	-1.05	11.31	0.1	10.26	0.2	0.00428059	0.02334963	A_07_P035160	c_2106	cmr|Vitamin B12 transport periplasmic protein btuE [c_2106]
c_0036	+2.42	8.73	+1.28	8.10	0.2	9.37	0.1	0.00102614	0.00807690	A_07_P035658	c_0036	cmr|Hypothetical protein [c_0036]
c_0059	-2.43	11.77	-1.28	12.41	0.1	11.13	0.1	0.00100872	0.00798031	A_07_P035683	c_0059	cmr|Putative antitoxin of gyrase inhibiting toxin-antitoxin system [c_0059]
c_0062	-2.74	7.76	-1.45	8.48	0.1	7.03	0.2	0.00088084	0.00727980	A_07_P035698	c_0062	cmr|Hypothetical protein [c_0062]
c_0086	-2.26	10.58	-1.18	11.17	0.2	9.99	0.0	0.00133286	0.00975571	A_07_P035735	c_0086	cmr|Transposase [c_0086]
c_0088	-2.75	9.14	-1.46	9.87	0.1	8.40	0.1	0.00026470	0.00309464	A_07_P035738	c_0088	cmr|Hypothetical protein [c_0088]
c_0120	-4.85	9.83	-2.28	10.97	0.0	8.69	0.1	0.00004695	0.00098031	A_07_P035766	c_0120	cmr|Hypothetical protein [c_0120]
c_0138	-2.95	9.16	-1.56	9.94	0.0	8.38	0.3	0.00188395	0.01265396	A_07_P035783	c_0138	cmr|Unknown protein of IS629 encoded within prophage [c_0138]
c_0226	-2.11	9.43	-1.08	9.96	0.1	8.89	0.1	0.00120437	0.00909682	A_07_P035924	c_0226	cmr|Putative cell cycle protein mesJ [c_0226]
c_0256	-2.24	8.14	-1.17	8.72	0.1	7.55	0.0	0.00080857	0.00682945	A_07_P035961	c_0256	cmr|Hypothetical protein [c_0256]
c_0257	-6.24	10.70	-2.64	12.02	0.0	9.38	0.0	0.00001054	0.00047145	A_07_P035967	c_0257	cmr|Unknown in ISEc8 [c_0257]
c_0258	-3.00	11.46	-1.59	12.25	0.2	10.67	0.3	0.00132772	0.00973617	A_07_P035972	c_0258	cmr|Unknown in ISEc8 [c_0258]
c_0260	-2.43	7.83	-1.28	8.47	0.1	7.19	0.1	0.00089799	0.00739046	A_07_P035978	c_0260	cmr|Hypothetical protein [c_0260]
c_0261	-2.64	7.73	-1.40	8.43	0.0	7.03	0.1	0.00030620	0.00341417	A_07_P035987	c_0261	cmr|Hypothetical protein [c_0261]
c_0264	-3.10	8.09	-1.63	8.91	0.0	7.28	0.1	0.00013542	0.00192967	A_07_P036004	c_0264	cmr|Hypothetical protein [c_0264]
c_0274	-2.21	8.34	-1.14	8.91	0.1	7.77	0.2	0.00162382	0.01133721	A_07_P036041	c_0274	cmr|Hypothetical protein [c_0274]
c_0279	-3.27	7.80	-1.71	8.65	0.2	6.94	0.3	0.00133984	0.00979769	A_07_P036068	c_0279	cmr|Hypothetical protein ykfF [c_0279]
c_0281	-2.48	10.41	-1.31	11.07	0.0	9.75	0.1	0.00042408	0.00430129	A_07_P036079	c_0281	cmr|Hypothetical protein [c_0281]
c_0286	-4.41	9.75	-2.14	10.82	0.1	8.68	0.0	0.00003331	0.00081556	A_07_P036101	c_0286	cmr|Conserved hypothetical protein [c_0286]
c_0289	-4.66	8.37	-2.22	9.48	0.1	7.26	0.1	0.00004710	0.00098224	A_07_P036114	c_0289	cmr|Hypothetical protein [c_0289]
c_0301	-2.44	7.54	-1.29	8.18	0.0	6.90	0.1	0.00065632	0.00585114	A_07_P036159	c_0301	cmr|Hypothetical protein [c_0301]
c_0305	-2.14	10.25	-1.10	10.80	0.3	9.70	0.0	0.00729231	0.03517466	A_07_P036170	c_0305	cmr|Hypothetical protein [c_0305]
c_0309	-3.29	8.26	-1.72	9.11	0.1	7.40	0.0	0.00010537	0.00163463	A_07_P036181	c_0309	cmr|Conserved hypothetical protein [c_0309]
c_0313	-2.82	12.97	-1.49	13.72	0.3	12.22	0.3	0.00403642	0.02233720	A_07_P036201	c_0313	cmr|Hypothetical protein [c_0313]
c_0316	-2.96	8.56	-1.56	9.34	0.1	7.78	0.1	0.00017123	0.00227395	A_07_P036219	c_0316	cmr|Hypothetical protein [c_0316]
c_0328	-2.81	8.16	-1.49	8.91	0.0	7.41	0.1	0.00020740	0.00261010	A_07_P036267	c_0328	cmr|Hypothetical protein [c_0328]
c_0331	+2.62	8.29	+1.39	7.60	0.0	8.99	0.0	0.00023073	0.00281851	A_07_P036277	c_0331	cmr|Putative ribokinase [c_0331]
c_0337	-8.57	10.44	-3.10	11.99	0.0	8.89	0.2	0.00001356	0.00052725	A_07_P030738	c_0337	cmr|Putative conserved protein [c_0337]
c_0339	-2.64	9.40	-1.40	10.10	0.1	8.70	0.0	0.00030504	0.00340368	A_07_P030741	c_0339	cmr|Hypothetical protein [c_0339]
c_0340	-3.07	8.70	-1.62	9.51	0.0	7.89	0.1	0.00018156	0.00237762	A_07_P030749	c_0340	cmr|Conserved hypothetical protein [c_0340]
c_0348	-2.08	9.26	-1.06	9.79	0.0	8.73	0.1	0.00136343	0.00991481	A_07_P030761	c_0348	cmr|Hypothetical protein [c_0348]
c_0349	-3.47	7.98	-1.79	8.88	0.2	7.08	0.1	0.00028803	0.00328124	A_07_P030767	c_0349	cmr|Putative Transposase within prophage [c_0349]
c_0352	-4.68	9.79	-2.23	10.90	0.1	8.67	0.0	0.00002667	0.00073020	A_07_P030781	c_0352	cmr|Partial Transposase [c_0352]
c_0355	-3.62	9.32	-1.86	10.25	0.2	8.39	0.2	0.00037099	0.00392997	A_07_P030788	c_0355	cmr|Hypothetical protein [c_0355]
c_0357	-2.38	8.22	-1.25	8.85	0.1	7.60	0.4	0.00766725	0.03655758	A_07_P030794	c_0357	cmr|Hypothetical protein [c_0357]
c_0358	-2.44	8.57	-1.29	9.21	0.1	7.93	0.1	0.00062207	0.00563493	A_07_P030798	c_0358	cmr|Hypothetical protein [c_0358]
c_0365	-4.16	8.34	-2.06	9.37	0.1	7.32	0.1	0.00004787	0.00099032	A_07_P030828	c_0365	cmr|Hypothetical protein [c_0365]
c_0385	-3.65	8.26	-1.87	9.19	0.0	7.33	0.0	0.00006422	0.00118391	A_07_P030859	c_0385	cmr|Hypothetical protein [c_0385]
c_0386	+2.00	9.98	+1.00	9.48	0.1	10.48	0.0	0.00154186	0.01093470	A_07_P041475	c_0386	cmr|Hypothetical protein yafA [c_0386]
c_0396	-2.48	7.63	-1.31	8.29	0.0	6.98	0.1	0.00043303	0.00435910	A_07_P030886	c_0396	cmr|Insertion element IS1 1/2/3/5/6 protein insA [c_0396]
c_0397	-2.77	7.99	-1.47	8.73	0.0	7.26	0.1	0.00027043	0.00313734	A_07_P030892	c_0397	cmr|InsB protein [c_0397]
c_0410	+4.08	8.65	+2.03	7.64	0.0	9.67	0.0	0.00003972	0.00090487	A_07_P030916	c_0410	cmr|Hypothetical protein ycjY [c_0410]
c_0412	-2.09	9.79	-1.06	10.32	0.1	9.26	0.0	0.00113391	0.00872521	A_07_P030929	c_0412	cmr|Hypothetical transcriptional regulator ycjZ [c_0412]
c_0413	+3.16	7.48	+1.66	6.65	0.2	8.31	0.1	0.00061065	0.00556489	A_07_P030931	c_0413	cmr|Putative aldo/keto reductase [c_0413]
c_0414	+3.73	8.37	+1.90	7.42	0.0	9.32	0.2	0.00011679	0.00174120	A_07_P030940	c_0414	cmr|2,5-diketo-D-gluconic acid reductase A [c_0414]
c_0427	-3.54	8.06	-1.82	8.97	0.3	7.15	0.0	0.00088054	0.00727980	A_07_P030962	c_0427	cmr|Conserved hypothetical protein [c_0427]
c_0444	+2.01	7.77	+1.01	7.26	0.2	8.27	0.0	0.00430865	0.02346263	A_07_P031002	c_0444	cmr|Carbamate kinase-like protein yahI [c_0444]
c_0481	-2.65	8.82	-1.40	9.52	0.0	8.12	0.0	0.00022165	0.00273628	A_07_P031085	c_0481	cmr|Hypothetical protein [c_0481]
c_0487	-3.20	11.67	-1.68	12.51	0.0	10.83	0.1	0.00010677	0.00164437	A_07_P041502	c_0487	cmr|D-alanine--D-alanine ligase A [c_0487]
c_0503	+2.36	9.39	+1.24	8.77	0.1	10.01	0.1	0.00098623	0.00783803	A_07_P031097	c_0503	cmr|Hypothetical protein yajF [c_0503]
c_0550	+3.82	7.62	+1.93	6.65	0.1	8.58	0.1	0.00007556	0.00131017	A_07_P031150	c_0550	cmr|Hypothetical protein [c_0550]
c_0552	+2.07	7.07	+1.05	6.55	0.1	7.60	0.0	0.00116466	0.00890119	A_07_P031156	c_0552	cmr|Hypothetical protein [c_0552]
c_0583	-3.49	10.61	-1.80	11.51	0.1	9.71	0.0	0.00012441	0.00181695	A_07_P031182	c_0583	cmr|Hypothetical protein [c_0583]
c_0608	-2.32	10.24	-1.21	10.85	0.0	9.64	0.0	0.00047317	0.00465311	A_07_P031211	c_0608	cmr|Hypothetical protein [c_0608]
c_0638	-2.33	8.44	-1.22	9.05	0.1	7.83	0.1	0.00108042	0.00840005	A_07_P031250	c_0638	cmr|Hypothetical protein [c_0638]
c_0640	+2.59	7.79	+1.37	7.10	0.1	8.47	0.0	0.00037748	0.00396055	A_07_P031257	c_0640	cmr|Conserved hypothetical protein [c_0640]
c_0697	-2.79	8.78	-1.48	9.52	0.1	8.04	0.2	0.00045565	0.00453750	A_07_P031357	c_0697	cmr|Conserved hypothetical protein [c_0697]
c_0719	-2.58	8.08	-1.37	8.77	0.1	7.40	0.1	0.00049063	0.00476059	A_07_P033287	c_0719	cmr|Conserved hypothetical protein [c_0719]
c_0778	+7.10	8.15	+2.83	6.73	0.0	9.56	0.2	0.00001972	0.00062719	A_07_P033361	c_0778	cmr|Hypothetical protein [c_0778]
c_0784	-6.02	8.62	-2.59	9.92	0.0	7.33	0.2	0.00006854	0.00122908	A_07_P033375	c_0784	cmr|Hypothetical protein [c_0784]
c_0888	+2.23	8.53	+1.16	7.95	0.0	9.11	0.0	0.00063352	0.00570950	A_07_P042104	c_0888	cmr|Hypothetical protein ybiI [c_0888]
c_0897	+17.64	13.21	+4.14	11.14	0.1	15.28	0.1	0.00000209	0.00026053	A_07_P033506	c_0897	cmr|Hypothetical protein [c_0897]
c_0953	+2.00	7.09	+1.00	6.59	0.2	7.59	0.2	0.00654861	0.03227968	A_07_P033627	c_0953	cmr|Terminase, endonuclease subunit [c_0953]
c_1166	+3.03	8.79	+1.60	7.99	0.2	9.59	0.1	0.00057619	0.00534565	A_07_P033974	c_1166	cmr|Conserved hypothetical protein [c_1166]
c_1172	-4.71	8.05	-2.23	9.17	0.1	6.93	0.0	0.00003094	0.00078443	A_07_P034010	c_1172	cmr|Hypothetical protein [c_1172]
c_1173	-3.08	11.64	-1.62	12.46	0.1	10.83	0.3	0.00084253	0.00704450	A_07_P034004	c_1173	cmr|Hypothetical protein [c_1173]
c_1174	-2.80	9.75	-1.49	10.49	0.1	9.01	0.1	0.00035343	0.00379046	A_07_P040226	c_1174	cmr|Hypothetical protein [c_1174]
c_1174	-3.62	9.78	-1.86	10.70	0.2	8.85	0.3	0.00058340	0.00539033	A_07_P040226	c_1174	cmr|Hypothetical protein [c_1174]
c_1174	-3.56	9.58	-1.83	10.50	0.1	8.67	0.3	0.00062276	0.00563493	A_07_P040226	c_1174	cmr|Hypothetical protein [c_1174]
c_1174	-3.47	9.63	-1.79	10.53	0.2	8.73	0.5	0.00394459	0.02201473	A_07_P040226	c_1174	cmr|Hypothetical protein [c_1174]
c_1174	-3.39	9.66	-1.76	10.54	0.2	8.78	0.4	0.00279979	0.01698430	A_07_P040226	c_1174	cmr|Hypothetical protein [c_1174]
c_1175	+3.43	7.76	+1.78	6.87	0.1	8.65	0.2	0.00027580	0.00318111	A_07_P040232	c_1175	cmr|Putative aminotransferase [c_1175]
c_1186	-2.19	9.03	-1.13	9.60	0.1	8.47	0.1	0.00092040	0.00750815	A_07_P040258	c_1186	cmr|Putative beta-ketoacyl-ACP synthase [c_1186]
c_1197	-2.19	9.00	-1.13	9.56	0.0	8.43	0.2	0.00164534	0.01143172	A_07_P040310	c_1197	cmr|Putative enzyme [c_1197]
c_1198	-2.69	8.74	-1.43	9.45	0.0	8.02	0.2	0.00052319	0.00499828	A_07_P040314	c_1198	cmr|Conserved hypothetical protein [c_1198]
c_1199	-2.64	10.70	-1.40	11.41	0.0	10.00	0.0	0.00025102	0.00299696	A_07_P040317	c_1199	cmr|Putative acyl carrier protein [c_1199]
c_1202	-2.59	7.59	-1.37	8.28	0.0	6.91	0.0	0.00025967	0.00307016	A_07_P040334	c_1202	cmr|Conserved hypothetical protein [c_1202]
c_1203	-3.32	9.40	-1.73	10.27	0.1	8.54	0.0	0.00008761	0.00144743	A_07_P040338	c_1203	cmr|Putative O-methyltransferase [c_1203]
c_1204	-3.83	9.79	-1.94	10.76	0.1	8.82	0.0	0.00008318	0.00140064	A_07_P040344	c_1204	cmr|Conserved hypothetical protein [c_1204]
c_1204	-4.57	10.12	-2.19	11.22	0.0	9.02	0.1	0.00002756	0.00073830	A_07_P040344	c_1204	cmr|Conserved hypothetical protein [c_1204]
c_1204	-3.72	10.13	-1.89	11.07	0.1	9.18	0.0	0.00007479	0.00129967	A_07_P040344	c_1204	cmr|Conserved hypothetical protein [c_1204]
c_1204	-4.06	9.89	-2.02	10.90	0.1	8.88	0.0	0.00005793	0.00111357	A_07_P040344	c_1204	cmr|Conserved hypothetical protein [c_1204]
c_1204	-4.32	9.98	-2.11	11.04	0.1	8.93	0.1	0.00005705	0.00110340	A_07_P040344	c_1204	cmr|Conserved hypothetical protein [c_1204]
c_1209	-2.42	9.59	-1.27	10.23	0.2	8.95	0.1	0.00113682	0.00873918	A_07_P040366	c_1209	cmr|Hypothetical protein [c_1209]
c_1214	+2.83	12.42	+1.50	11.67	0.1	13.17	0.1	0.00021751	0.00269643	A_07_P040383	c_1214	cmr|Cea protein [c_1214]
c_1215	-4.45	12.59	-2.15	13.67	0.0	11.52	0.0	0.00002748	0.00073821	A_07_P040390	c_1215	cmr|Entry exclusion protein 2 [c_1215]
c_1219	-2.22	8.30	-1.15	8.88	0.0	7.73	0.2	0.00307548	0.01823741	A_07_P040407	c_1219	cmr|Putative Transposase [c_1219]
c_1225	-2.43	10.09	-1.28	10.73	0.1	9.45	0.0	0.00065722	0.00585582	A_07_P040430	c_1225	cmr|Transposase insE for insertion sequence IS3A/B/C/D/E/fA/fB [c_1225]
c_1235	-10.31	8.83	-3.37	10.51	0.0	7.14	0.1	0.00000412	0.00032560	A_07_P040469	c_1235	cmr|Conserved hypothetical protein [c_1235]
c_1236	-4.88	9.14	-2.29	10.29	0.0	8.00	0.5	0.00146771	0.01050345	A_07_P040474	c_1236	cmr|Conserved hypothetical protein [c_1236]
c_1253	-5.00	9.55	-2.32	10.72	0.1	8.39	0.1	0.00002892	0.00075516	A_07_P040560	c_1253	cmr|ATP binding cassette [c_1253]
c_1257	-23.41	11.02	-4.55	13.29	0.1	8.74	0.0	0.00000088	0.00019431	A_07_P040573	c_1257	cmr|Putative conserved protein [c_1257]
c_1258	-2.24	7.77	-1.17	8.35	0.4	7.18	0.0	0.00758089	0.03625561	A_07_P040577	c_1258	cmr|Hypothetical protein [c_1258]
c_1261	-2.11	9.49	-1.08	10.03	0.0	8.96	0.0	0.00081180	0.00684205	A_07_P040595	c_1261	cmr|Hypothetical protein [c_1261]
c_1267	-3.53	8.48	-1.82	9.39	0.5	7.57	0.1	0.00397885	0.02211190	A_07_P040614	c_1267	cmr|Hypothetical protein [c_1267]
c_1268	-2.08	8.45	-1.06	8.98	0.0	7.92	0.1	0.00126934	0.00944895	A_07_P040616	c_1268	cmr|Hypothetical protein [c_1268]
c_1271	-2.35	8.50	-1.23	9.12	0.1	7.89	0.0	0.00049393	0.00478257	A_07_P040631	c_1271	cmr|Hypothetical protein [c_1271]
c_1272	-4.34	8.07	-2.12	9.13	0.1	7.01	0.0	0.00003790	0.00087581	A_07_P040636	c_1272	cmr|Hypothetical protein yeeP [c_1272]
c_1273	+4.01	11.44	+2.00	10.43	0.1	12.44	0.1	0.00006645	0.00120815	A_07_P040643	c_1273	cmr|Antigen 43 precursor [c_1273]
c_1284	-2.84	11.51	-1.50	12.26	0.2	10.75	0.5	0.01033846	0.04588910	A_07_P040687	c_1284	cmr|Hypothetical protein yeeT [c_1284]
c_1286	-5.42	10.23	-2.44	11.45	0.0	9.01	0.6	0.00131315	0.00970625	A_07_P040696	c_1286	cmr|Hypothetical protein [c_1286]
c_1294	-3.68	7.70	-1.88	8.64	0.0	6.76	0.0	0.00005423	0.00107304	A_07_P040732	c_1294	cmr|Hypothetical protein [c_1294]
c_1363	+2.29	8.02	+1.20	7.42	0.1	8.62	0.1	0.00064173	0.00576675	A_07_P040789	c_1363	cmr|Hypothetical protein [c_1363]
c_1406	-3.46	8.26	-1.79	9.16	0.1	7.37	0.2	0.00018722	0.00242003	A_07_P040862	c_1406	cmr|Hypothetical protein [c_1406]
c_1421	-9.27	9.73	-3.21	11.34	0.1	8.12	0.0	0.00000594	0.00036511	A_07_P040925	c_1421	cmr|Hypothetical protein [c_1421]
c_1436	-2.08	8.97	-1.06	9.50	0.2	8.44	0.0	0.00385479	0.02169043	A_07_P042220	c_1436	cmr|Probable lysozyme from lambdoid prophage Qin [c_1436]
c_1445	+2.61	10.68	+1.39	9.98	0.2	11.37	0.1	0.00093603	0.00758059	A_07_P041010	c_1445	cmr|Putative DNA packaging protein of prophage terminase [c_1445]
c_1446	+3.01	10.88	+1.59	10.09	0.3	11.68	0.1	0.00184013	0.01242327	A_07_P041015	c_1446	cmr|Putative DNA packaging protein of prophage [c_1446]
c_1448	+23.01	11.32	+4.52	9.05	0.1	13.58	0.0	0.00000082	0.00019431	A_07_P041021	c_1448	cmr|Putative capsid assembly protein of prophage [c_1448]
c_1453	+12.23	11.45	+3.61	9.64	0.1	13.25	0.2	0.00000783	0.00041039	A_07_P038108	c_1453	cmr|Putative head-tail joining protein of prophage [c_1453]
c_1456	-2.07	11.26	-1.05	11.78	0.2	10.73	0.2	0.00725882	0.03504535	A_07_P038121	c_1456	cmr|Putative tail fiber component V of prophage [c_1456]
c_1478	+3.08	8.67	+1.62	7.86	0.1	9.48	0.0	0.00013550	0.00192967	A_07_P038214	c_1478	cmr|Hypothetical protein [c_1478]
c_1484	-2.25	9.11	-1.17	9.70	0.4	8.53	0.1	0.00790421	0.03747183	A_07_P038229	c_1484	cmr|Unknown protein encoded by prophage [c_1484]
c_1487	-2.18	10.41	-1.12	10.98	0.1	9.85	0.1	0.00117338	0.00894178	A_07_P038235	c_1487	cmr|Hypothetical protein [c_1487]
c_1499	+2.37	8.59	+1.25	7.97	0.0	9.21	0.1	0.00061432	0.00558100	A_07_P038295	c_1499	cmr|Putative capsid protein of prophage [c_1499]
c_1501	+3.04	8.97	+1.60	8.17	0.0	9.78	0.1	0.00018346	0.00238910	A_07_P038305	c_1501	cmr|Hypothetical protein [c_1501]
c_1516	+2.50	7.34	+1.32	6.68	0.2	8.00	0.1	0.00151988	0.01081784	A_07_P038337	c_1516	cmr|Hypothetical protein [c_1516]
c_1519	+14.69	8.96	+3.88	7.02	0.3	10.89	0.2	0.00004663	0.00097506	A_07_P038347	c_1519	cmr|Prophage lambda integrase [c_1519]
c_1522	+112.15	11.07	+6.81	7.66	0.4	14.47	0.1	0.00000258	0.00027706	A_07_P038354	c_1522	cmr|Hypothetical protein [c_1522]
c_1523	+68.86	12.31	+6.11	9.26	0.1	15.36	0.1	0.00000025	0.00019431	A_07_P035459	c_1523	cmr|Unknown protein encoded by bacteriophage [c_1523]
c_1524	+84.18	11.31	+6.40	8.12	0.0	14.51	0.0	0.00000011	0.00019431	A_07_P038365	c_1524	cmr|Hypothetical protein [c_1524]
c_1525	+85.60	12.65	+6.42	9.44	0.0	15.86	0.0	0.00000013	0.00019431	A_07_P038369	c_1525	cmr|Hypothetical protein [c_1525]
c_1526	+83.64	10.95	+6.39	7.76	0.1	14.15	0.1	0.00000024	0.00019431	A_07_P038374	c_1526	cmr|Hypothetical protein [c_1526]
c_1527	+65.16	10.66	+6.03	7.65	0.3	13.67	0.0	0.00000246	0.00027471	A_07_P038377	c_1527	cmr|Hypothetical protein [c_1527]
c_1528	+117.66	11.09	+6.88	7.65	0.3	14.53	0.1	0.00000081	0.00019431	A_07_P038381	c_1528	cmr|Hypothetical protein [c_1528]
c_1531	+134.56	11.60	+7.07	8.06	0.0	15.13	0.0	0.00000007	0.00019431	A_07_P038395	c_1531	cmr|Hypothetical protein [c_1531]
c_1532	+41.70	11.68	+5.38	8.99	0.3	14.37	0.2	0.00000618	0.00036832	A_07_P038400	c_1532	cmr|Unknown protein encoded within prophage [c_1532]
c_1533	+5.71	13.07	+2.51	11.81	0.3	14.33	0.1	0.00010487	0.00162985	A_07_P038402	c_1533	cmr|Hypothetical protein [c_1533]
c_1536	+5.71	14.23	+2.51	12.98	0.1	15.49	0.1	0.00002464	0.00070547	A_07_P038406	c_1536	cmr|Putative recombination protein Bet of prophage [c_1536]
c_1538	+31.45	13.16	+4.98	10.67	0.0	15.65	0.0	0.00000044	0.00019431	A_07_P038419	c_1538	cmr|Hypothetical protein [c_1538]
c_1540	+8.29	14.93	+3.05	13.40	0.1	16.45	0.0	0.00000542	0.00034972	A_07_P038423	c_1540	cmr|Lambda Regulatory protein CIII [c_1540]
c_1541	+20.00	14.41	+4.32	12.24	0.0	16.57	0.0	0.00000089	0.00019431	A_07_P038427	c_1541	cmr|Putative single-stranded DNA binding protein of prophage [c_1541]
c_1544	-2.07	8.48	-1.05	9.01	0.0	7.96	0.0	0.00095699	0.00769111	A_07_P038443	c_1544	cmr|Hypothetical protein [c_1544]
c_1546	-5.53	12.18	-2.47	13.42	0.0	10.95	0.1	0.00002038	0.00063193	A_07_P038451	c_1546	cmr|Repressor protein [c_1546]
c_1547	+5.28	13.02	+2.40	11.82	0.1	14.22	0.1	0.00003088	0.00078408	A_07_P038456	c_1547	cmr|Hypothetical protein [c_1547]
c_1548	+5.05	12.47	+2.34	11.30	0.2	13.64	0.0	0.00005610	0.00109168	A_07_P038465	c_1548	cmr|Putative Regulatory protein CII of bacteriophage [c_1548]

c_1549	+10.42	13.56	+3.38	11.87	0.0	15.25	0.0	0.00000282	0.00028143	A_07_P038470	c_1549	cmr|Putative replication protein O of bacteriophage [c_1549]
c_1550	+7.03	15.04	+2.81	13.63	0.1	16.45	0.0	0.00001063	0.00047201	A_07_P038471	c_1550	cmr|Putative replication protein P of bacteriophage [c_1550]
c_1554	+61.33	10.90	+5.94	7.93	0.2	13.87	0.2	0.00000092	0.00019431	A_07_P038485	c_1554	cmr|Unknown protein encoded within prophage [c_1554]
c_1555	+47.13	10.13	+5.56	7.35	0.1	12.91	0.0	0.00000035	0.00019431	A_07_P038490	c_1555	cmr|Putative DNA N-6-adenine-methyltransferase of bacteriophage [c_1555]
c_1556	+152.03	10.91	+7.25	7.28	0.2	14.53	0.0	0.00000015	0.00019431	A_07_P038492	c_1556	cmr|Hypothetical protein [c_1556]
c_1565	+4.38	12.58	+2.13	11.51	0.2	13.65	0.0	0.00016624	0.00223475	A_07_P038514	c_1565	cmr|Partial tonB-like membrane protein encoded within prophage [c_1565]
c_1567	+6.07	10.16	+2.60	8.86	0.1	11.46	0.0	0.00001316	0.00052315	A_07_P038518	c_1567	cmr|Hypothetical protein [c_1567]
c_1569	+2.29	10.50	+1.20	9.90	0.0	11.09	0.1	0.00064805	0.00580043	A_07_P038528	c_1569	cmr|Putative DNA packaging protein of prophage terminase [c_1569]
c_1570	+3.99	11.21	+2.00	10.21	0.4	12.21	0.1	0.00118025	0.00897241	A_07_P038532	c_1570	cmr|Putative DNA packaging protein of prophage [c_1570]
c_1571	+9.96	9.76	+3.32	8.10	0.0	11.42	0.1	0.00000509	0.00034758	A_07_P038538	c_1571	cmr|Putative capsid protein of prophage [c_1571]
c_1572	+60.26	10.81	+5.91	7.86	0.1	13.77	0.0	0.00000022	0.00019431	A_07_P038541	c_1572	cmr|Putative capsid assembly protein of prophage [c_1572]
c_1574	+25.07	10.65	+4.65	8.32	0.1	12.97	0.0	0.00000090	0.00019431	A_07_P038551	c_1574	cmr|Putative capsid protein of prophage [c_1574]
c_1575	+23.31	9.61	+4.54	7.34	0.2	11.88	0.1	0.00000321	0.00029243	A_07_P038556	c_1575	cmr|Putative capsid protein of prophage [c_1575]
c_1576	+15.42	9.62	+3.95	7.65	0.2	11.59	0.0	0.00000786	0.00041039	A_07_P038564	c_1576	cmr|Hypothetical protein [c_1576]
c_1577	+20.87	9.22	+4.38	7.03	0.1	11.41	0.1	0.00000189	0.00025064	A_07_P038569	c_1577	cmr|Putative head-tail joining protein of prophage [c_1577]
c_1579	+9.79	11.19	+3.29	9.55	0.1	12.84	0.0	0.00000627	0.00036832	A_07_P038580	c_1579	cmr|Putative tail component of prophage [c_1579]
c_1580	+47.82	9.82	+5.58	7.03	0.0	12.61	0.2	0.00000070	0.00019431	A_07_P038581	c_1580	cmr|Tail protein [c_1580]
c_1583	+13.48	9.77	+3.75	7.89	0.0	11.65	0.1	0.00000238	0.00027039	A_07_P038594	c_1583	cmr|Putative tail component of prophage [c_1583]
c_1585	+5.71	10.15	+2.51	8.89	0.2	11.41	0.0	0.00005566	0.00108730	A_07_P038605	c_1585	cmr|Putative tail component of prophage [c_1585]
c_1587	+2.97	9.75	+1.57	8.96	0.1	10.53	0.3	0.00146740	0.01050345	A_07_P038615	c_1587	cmr|Putative tail component of prophage [c_1587]
c_1588	+2.39	11.31	+1.26	10.68	0.3	11.93	0.1	0.00470663	0.02512617	A_07_P038617	c_1588	cmr|Putative tail component of prophage [c_1588]
c_1590	+2.68	9.68	+1.42	8.97	0.1	10.40	0.2	0.00068310	0.00601156	A_07_P038626	c_1590	cmr|Putative tail component of prophage [c_1590]
c_1591	+3.27	9.57	+1.71	8.72	0.3	10.43	0.2	0.00171954	0.01183830	A_07_P038637	c_1591	cmr|Hypothetical protein [c_1591]
c_1593	+4.57	8.27	+2.19	7.17	0.2	9.36	0.0	0.00006914	0.00123557	A_07_P038645	c_1593	cmr|Hypothetical protein [c_1593]
c_1596	-3.15	8.87	-1.66	9.70	0.0	8.05	0.1	0.00016016	0.00218551	A_07_P038656	c_1596	cmr|Hypothetical protein [c_1596]
c_1605	-2.56	11.85	-1.36	12.52	0.1	11.17	0.1	0.00065167	0.00582613	A_07_P038687	c_1605	cmr|Hypothetical protein [c_1605]
c_1640	-3.43	11.96	-1.78	12.85	0.1	11.07	0.1	0.00018399	0.00239209	A_07_P038726	c_1640	cmr|Putative Na [c_1640]
c_1657	+2.61	7.88	+1.38	7.19	0.1	8.57	0.1	0.00040724	0.00416878	A_07_P038777	c_1657	cmr|Protein ycgS [c_1657]
c_1660	-2.64	9.68	-1.40	10.38	0.0	8.98	0.0	0.00026068	0.00307888	A_07_P038788	c_1660	cmr|Hypothetical protein [c_1660]
c_1714	-5.80	10.99	-2.54	12.25	0.1	9.72	0.0	0.00001601	0.00056395	A_07_P038863	c_1714	cmr|Hypothetical protein [c_1714]
c_1755	+2.05	8.93	+1.04	8.41	0.0	9.44	0.1	0.00132361	0.00972818	A_07_P038912	c_1755	cmr|Conserved hypothetical protein [c_1755]
c_1819	+2.53	8.92	+1.34	8.25	0.2	9.59	0.1	0.00087705	0.00726750	A_07_P034790	c_1819	cmr|Putative conserved protein [c_1819]
c_1825	+3.91	10.23	+1.97	9.25	0.3	11.22	0.2	0.00044208	0.00442752	A_07_P034801	c_1825	cmr|Hypothetical protein [c_1825]
c_1884	+2.37	7.16	+1.24	6.54	0.3	7.78	0.0	0.00342932	0.01985699	A_07_P034884	c_1884	cmr|Hypothetical protein [c_1884]
c_1887	-2.08	8.33	-1.06	8.86	0.1	7.80	0.1	0.00126651	0.00943235	A_07_P034897	c_1887	cmr|Hypothetical protein [c_1887]
c_1935	-2.86	8.89	-1.52	9.65	0.2	8.13	0.0	0.00036974	0.00392997	A_07_P034987	c_1935	cmr|Chaperone protein fimC precursor [c_1935]
c_1955	-2.07	6.97	-1.05	7.49	0.1	6.44	0.2	0.00313742	0.01855583	A_07_P035036	c_1955	cmr|6-phospho-beta-glucosidase bglA [c_1955]
c_1956	-2.46	11.29	-1.30	11.94	0.2	10.64	0.1	0.00181709	0.01230990	A_07_P035043	c_1956	cmr|Putative outer membrane protein yieC precursor [c_1956]
c_1989	-10.96	10.50	-3.45	12.23	0.1	8.77	0.1	0.00000368	0.00030737	A_07_P035078	c_1989	cmr|Putative acid shock protein [c_1989]
c_2059	+2.21	9.33	+1.14	8.76	0.1	9.90	0.1	0.00137422	0.00997041	A_07_P035140	c_2059	cmr|Protein ydhR precursor [c_2059]
c_2148	+2.78	7.97	+1.47	7.24	0.4	8.71	0.1	0.00470243	0.02512617	A_07_P035198	c_2148	cmr|Succinylornithine transaminase [c_2148]
c_2155	+3.23	9.12	+1.69	8.28	0.2	9.97	0.1	0.00055263	0.00520656	A_07_P042371	c_2155	cmr|Protein ynjB [c_2155]
c_2158	+7.24	9.77	+2.86	8.34	0.0	11.20	0.0	0.00000662	0.00038136	A_07_P041171	c_2158	cmr|Putative thiosulfate sulfurtransferase ynjE precursor [c_2158]
c_2255	-16.55	10.32	-4.05	12.35	0.0	8.30	0.1	0.00000177	0.00024644	A_07_P035318	c_2255	cmr|Hypothetical protein [c_2255]
c_2273	-2.42	9.90	-1.27	10.54	0.0	9.27	0.1	0.00043298	0.00435910	A_07_P035336	c_2273	cmr|High-affinity zinc uptake system membrane protein znuB [c_2273]
c_2348	+22.28	9.69	+4.48	7.45	0.4	11.93	0.1	0.00001880	0.00061398	A_07_P035389	c_2348	cmr|Outer membrane porin protein nmpC precursor [c_2348]
c_2392	-2.88	9.46	-1.53	10.23	0.2	8.70	0.4	0.00565433	0.02897843	A_07_P031413	c_2392	cmr|Putative P4-family integrase [c_2392]
c_2409	+2.37	7.71	+1.25	7.09	0.1	8.33	0.0	0.00044014	0.00441938	A_07_P031493	c_2409	cmr|Hypothetical protein [c_2409]
c_2418	-2.89	9.05	-1.53	9.82	0.3	8.29	0.1	0.00123068	0.00922659	A_07_P031531	c_2418	cmr|Prophage P4 integrase [c_2418]
c_2423	-2.06	8.02	-1.04	8.54	0.1	7.50	0.1	0.00243279	0.01529017	A_07_P031557	c_2423	cmr|Putataive AraC type regulator [c_2423]
c_2455	-2.90	13.20	-1.53	13.96	0.1	12.43	0.1	0.00034552	0.00373874	A_07_P031671	c_2455	cmr|Putative peptide synthetase [c_2455]
c_2458	-3.06	9.56	-1.61	10.37	0.1	8.75	0.2	0.00028353	0.00325162	A_07_P031686	c_2458	cmr|Putative peptide synthetase [c_2458]
c_2460	+3.64	7.47	+1.86	6.54	0.2	8.41	0.1	0.00022080	0.00272866	A_07_P031697	c_2460	cmr|Putative polyketide synthase [c_2460]
c_2461	+2.26	8.26	+1.18	7.67	0.1	8.85	0.2	0.00156620	0.01104171	A_07_P031704	c_2461	cmr|Hypothetical protein [c_2461]
c_2481	-4.02	8.38	-2.01	9.39	0.0	7.38	0.0	0.00003799	0.00087581	A_07_P031773	c_2481	cmr|Hypothetical protein [c_2481]
c_2482	-6.86	8.34	-2.78	9.73	0.1	6.95	0.1	0.00001274	0.00051704	A_07_P031779	c_2482	cmr|Putative outer membrane receptor for iron compound [c_2482]
c_2484	-5.76	11.54	-2.53	12.80	0.0	10.28	0.1	0.00001445	0.00054604	A_07_P031782	c_2484	cmr|Hypothetical protein ybdM [c_2484]
c_2489	-2.44	7.83	-1.29	8.47	0.1	7.18	0.0	0.00065846	0.00586029	A_07_P031799	c_2489	cmr|Putative transferase [c_2489]
c_2495	-2.69	9.58	-1.43	10.30	0.2	8.87	0.1	0.00092727	0.00755215	A_07_P031824	c_2495	cmr|Putative phosphotriesterase-related protein [c_2495]
c_2500	-3.96	8.73	-1.98	9.72	0.1	7.74	0.0	0.00006010	0.00114415	A_07_P031846	c_2500	cmr|Hypothetical protein [c_2500]
c_2501	-2.03	9.02	-1.02	9.53	0.0	8.51	0.1	0.00159129	0.01116952	A_07_P031851	c_2501	cmr|Hypothetical protein [c_2501]
c_2512	+2.87	8.46	+1.52	7.70	0.2	9.22	0.0	0.00040910	0.00418234	A_07_P031888	c_2512	cmr|Transposase [c_2512]
c_2514	+4.10	8.76	+2.04	7.74	0.1	9.78	0.1	0.00004642	0.00097317	A_07_P031900	c_2514	cmr|Hypothetical protein [c_2514]
c_2520	+8.81	10.91	+3.14	9.34	0.1	12.48	0.0	0.00000536	0.00034972	A_07_P031907	c_2520	cmr|Conserved hypothetical protein [c_2520]
c_2523	+2.79	9.92	+1.48	9.18	0.0	10.66	0.1	0.00037336	0.00394177	A_07_P031921	c_2523	cmr|Conserved hypothetical protein [c_2523]
c_2524	+4.85	9.40	+2.28	8.26	0.2	10.53	0.1	0.00011255	0.00169568	A_07_P031927	c_2524	cmr|Hypothetical protein [c_2524]
c_2525	+5.90	9.37	+2.56	8.08	0.3	10.65	0.1	0.00010178	0.00159601	A_07_P031934	c_2525	cmr|Hypothetical protein [c_2525]
c_2528	-2.77	9.06	-1.47	9.80	0.1	8.33	0.1	0.00025108	0.00299696	A_07_P031949	c_2528	cmr|Hypothetical protein [c_2528]
c_2558	+4.71	10.67	+2.24	9.56	0.2	11.79	0.0	0.00008006	0.00135829	A_07_P031994	c_2558	cmr|Mannose-1-phosphate guanylyltransferase [c_2558]
c_2559	+2.24	11.51	+1.16	10.93	0.2	12.09	0.0	0.00242223	0.01522987	A_07_P031999	c_2559	cmr|Hypothetical protein [c_2559]
c_2562	-2.59	12.90	-1.37	13.58	0.0	12.21	0.1	0.00027825	0.00319999	A_07_P032014	c_2562	cmr|Glycosyl transferase [c_2562]
c_2566	-2.35	11.64	-1.24	12.25	0.0	11.02	0.1	0.00046950	0.00463439	A_07_P032030	c_2566	cmr|Hypothetical protein [c_2566]
c_2662	-2.09	8.40	-1.06	8.93	0.1	7.87	0.0	0.00162942	0.01136119	A_07_P032204	c_2662	cmr|Hypothetical protein [c_2662]
c_2670	-2.76	9.38	-1.46	10.11	0.2	8.65	0.1	0.00064418	0.00577889	A_07_P032229	c_2670	cmr|Putative conserved protein [c_2670]
c_2729	-3.42	8.74	-1.77	9.63	0.1	7.86	0.0	0.00009950	0.00156646	A_07_P032291	c_2729	cmr|Hypothetical protein [c_2729]
c_2897	+2.23	7.46	+1.16	6.88	0.2	8.04	0.1	0.00291415	0.01745165	A_07_P032543	c_2897	cmr|Type 1 fimbriae Regulatory protein fimB [c_2897]
c_3030	-2.36	8.21	-1.24	8.83	0.1	7.59	0.0	0.00076650	0.00656218	A_07_P030168	c_3030	cmr|SinI homolog [c_3030]
c_3031	-5.16	8.81	-2.37	9.99	0.0	7.63	0.0	0.00001813	0.00060098	A_07_P030171	c_3031	cmr|SinH homolog [c_3031]
c_3053	-4.60	12.08	-2.20	13.19	0.2	10.98	0.0	0.00006430	0.00118410	A_07_P041244	c_3053	cmr|Protein yfhF [c_3053]
c_3116	-2.49	11.38	-1.32	12.03	0.0	10.72	0.0	0.00032938	0.00361129	A_07_P030232	c_3116	cmr|Ribosomal large subunit pseudouridine synthase D [c_3116]
c_3156	+3.42	8.56	+1.77	7.67	0.1	9.44	0.1	0.00016472	0.00222409	A_07_P030311	c_3156	cmr|Putative tail fiber component K of prophage [c_3156]
c_3158	+8.14	8.55	+3.02	7.04	0.1	10.06	0.3	0.00004053	0.00091288	A_07_P030320	c_3158	cmr|Putative tail component of prophage [c_3158]
c_3159	+4.19	10.42	+2.07	9.39	0.5	11.46	0.1	0.00170948	0.01178890	A_07_P030328	c_3159	cmr|Putative tail component of prophage [c_3159]
c_3160	+3.19	9.99	+1.67	9.15	0.4	10.83	0.2	0.00395909	0.02205659	A_07_P030331	c_3160	cmr|Putative tail component of prophage [c_3160]
c_3161	+8.64	8.45	+3.11	6.90	0.2	10.01	0.1	0.00001470	0.00054604	A_07_P030336	c_3161	cmr|Putative tail component of prophage [c_3161]
c_3162	+2.44	10.91	+1.28	10.27	0.1	11.56	0.1	0.00077832	0.00663808	A_07_P030343	c_3162	cmr|Putative tail component of prophage [c_3162]
c_3163	+14.52	8.87	+3.86	6.94	0.2	10.80	0.0	0.00000496	0.00034758	A_07_P030350	c_3163	cmr|Putative tail component of prophage [c_3163]
c_3164	+38.04	9.60	+5.25	6.98	0.1	12.23	0.0	0.00000052	0.00019431	A_07_P030353	c_3164	cmr|Putative tail component of prophage [c_3164]
c_3165	+10.51	9.68	+3.39	7.98	0.6	11.37	0.1	0.00053588	0.00507637	A_07_P030358	c_3165	cmr|Putative tail fiber component Z of prophage [c_3165]
c_3176	+16.58	11.69	+4.05	9.67	0.1	13.72	0.1	0.00000240	0.00027039	A_07_P030411	c_3176	cmr|GnsB protein [c_3176]
c_3214	-2.30	8.42	-1.20	9.02	0.0	7.82	0.3	0.00336946	0.01960412	A_07_P030524	c_3214	cmr|Hypothetical protein [c_3214]
c_3224	-2.00	8.93	-1.00	9.43	0.2	8.43	0.1	0.00396671	0.02208340	A_07_P030537	c_3224	cmr|Conserved hypothetical protein [c_3224]
c_3225	+2.50	8.44	+1.32	7.78	0.0	9.11	0.1	0.00040186	0.00414060	A_07_P030542	c_3225	cmr|Conserved hypothetical protein [c_3225]
c_3252	-5.69	12.08	-2.51	13.33	0.0	10.82	0.2	0.00005271	0.00105307	A_07_P041659	c_3252	cmr|Regulatory protein recX [c_3252]
c_3270	-2.72	8.54	-1.44	9.26	0.0	7.82	0.2	0.00044198	0.00442752	A_07_P030625	c_3270	cmr|Hypothetical protein [c_3270]
c_3273	-3.28	13.19	-1.71	14.05	0.1	12.33	0.1	0.00011158	0.00169030	A_07_P030635	c_3273	cmr|Hypothetical protein ygjM [c_3273]
c_3276	-2.13	8.37	-1.09	8.92	0.0	7.83	0.1	0.00088138	0.00728041	A_07_P030650	c_3276	cmr|Hypothetical protein [c_3276]
c_3305	-2.49	7.85	-1.32	8.51	0.1	7.19	0.2	0.00135308	0.00986703	A_07_P030690	c_3305	cmr|Hypothetical protein [c_3305]
c_3343	-2.29	7.54	-1.20	8.14	0.1	6.94	0.1	0.00112483	0.00867256	A_07_P032631	c_3343	cmr|Hypothetical protein [c_3343]
c_3389	-2.27	8.72	-1.18	9.31	0.2	8.13	0.0	0.00137316	0.00996727	A_07_P032681	c_3389	cmr|Hypothetical protein [c_3389]
c_3394	-4.96	8.22	-2.31	9.37	0.1	7.06	0.2	0.00008874	0.00145375	A_07_P032706	c_3394	cmr|Hypothetical protein [c_3394]
c_3395	-2.55	7.45	-1.35	8.12	0.1	6.77	0.1	0.00037059	0.00392997	A_07_P032713	c_3395	cmr|Hypothetical protein [c_3395]
c_3396	-5.02	8.66	-2.33	9.82	0.0	7.50	0.1	0.00002213	0.00066628	A_07_P032716	c_3396	cmr|Hypothetical protein [c_3396]
c_3397	-2.81	7.75	-1.49	8.49	0.0	7.00	0.0	0.00017137	0.00227395	A_07_P032722	c_3397	cmr|Hypothetical protein [c_3397]
c_3432	-2.37	11.51	-1.25	12.13	0.1	10.88	0.0	0.00072202	0.00626395	A_07_P032816	c_3432	cmr|Transposase [c_3432]
c_3506	+6.42	10.63	+2.68	9.29	0.1	11.97	0.0	0.00001477	0.00054604	A_07_P032900	c_3506	cmr|Hypothetical protein [c_3506]
c_3507	+12.04	9.27	+3.59	7.48	0.3	11.07	0.0	0.00001614	0.00056732	A_07_P032905	c_3507	cmr|Hypothetical protein [c_3507]
c_3508	+4.47	8.86	+2.16	7.78	0.0	9.94	0.3	0.00023586	0.00285424	A_07_P032907	c_3508	cmr|Hypothetical protein [c_3508]
c_3513	-2.56	12.61	-1.36	13.29	0.1	11.93	0.4	0.00629175	0.03135720	A_07_P032930	c_3513	cmr|Putative conserved protein [c_3513]
c_3518	-4.29	8.37	-2.10	9.42	0.1	7.32	0.0	0.00003868	0.00088510	A_07_P032938	c_3518	cmr|Hypothetical protein [c_3518]
c_3523	-2.13	7.12	-1.09	7.67	0.2	6.58	0.0	0.00251977	0.01569898	A_07_P032958	c_3523	cmr|Conserved hypothetical protein [c_3523]
c_3557	-5.29	9.26	-2.40	10.46	0.1	8.06	0.1	0.00002256	0.00067139	A_07_P032997	c_3557	cmr|ShiA homolog [c_3557]
c_3560	-3.91	8.18	-1.97	9.17	0.1	7.20	0.0	0.00008652	0.00143544	A_07_P033008	c_3560	cmr|Unknown protein encoded by ISEc8 within prophage [c_3560]
c_3561	-2.31	10.14	-1.21	10.74	0.0	9.54	0.2	0.00138485	0.01002730	A_07_P033015	c_3561	cmr|Unknown protein encoded by ISEc8 [c_3561]
c_3564	-3.37	9.74	-1.75	10.62	0.4	8.87	0.3	0.00452332	0.02435539	A_07_P033028	c_3564	cmr|Hypothetical protein [c_3564]
c_3565	-5.81	10.16	-2.54	11.43	0.2	8.89	0.0	0.00005330	0.00106045	A_07_P033031	c_3565	cmr|Putative response regulator [c_3565]
c_3575	-2.54	8.45	-1.35	9.13	0.2	7.78	0.2	0.00200891	0.01320585	A_07_P033084	c_3575	cmr|Transposase insF for insertion sequence IS3A/B/C/D/E/fA [c_3575]
c_3576	-3.13	8.77	-1.65	9.59	0.0	7.95	0.1	0.00012782	0.00183942	A_07_P033087	c_3576	cmr|Unknown in IS [c_3576]
c_3579	-5.08	10.15	-2.34	11.32	0.0	8.98	0.1	0.00002584	0.00072358	A_07_P033108	c_3579	cmr|Hypothetical protein [c_3579]
c_3580	-8.44	11.74	-3.08	13.28	0.0	10.20	0.0	0.00000483	0.00034614	A_07_P033102	c_3580	cmr|Hypothetical protein [c_3580]
c_3581	-5.93	11.50	-2.57	12.78	0.0	10.21	0.1	0.00001482	0.00054604	A_07_P033112	c_3581	cmr|Hypothetical protein [c_3581]
c_3594	-10.62	10.94	-3.41	12.64	0.1	9.24	0.1	0.00000494	0.00034758	A_07_P033172	c_3594	cmr|Putative Transposase [c_3594]
c_3595	-6.28	10.87	-2.65	12.19	0.0	9.54	0.2	0.00003731	0.00087155	A_07_P033176	c_3595	cmr|Transposase [c_3595]
c_3596	-7.01	11.56	-2.81	12.96	0.1	10.15	0.0	0.00000789	0.00041039	A_07_P033185	c_3596	cmr|Hypothetical protein in IS [c_3596]
c_3597	-3.53	10.24	-1.82	11.15	0.0	9.33	0.0	0.00006310	0.00116867	A_07_P033190	c_3597	cmr|Transposase [c_3597]
c_3598	-4.29	9.53	-2.10	10.58	0.0	8.48	0.1	0.00004043	0.00091288	A_07_P033191	c_3598	cmr|Hypothetical protein [c_3598]
c_3598	-5.13	9.74	-2.36	10.92	0.1	8.55	0.0	0.00002199	0.00066568	A_07_P033191	c_3598	cmr|Hypothetical protein [c_3598]
c_3598	-4.50	9.73	-2.17	10.82	0.1	8.65	0.1	0.00004518	0.00095882	A_07_P033191	c_3598	cmr|Hypothetical protein [c_3598]
c_3598	-5.48	9.71	-2.45	10.94	0.0	8.49	0.0	0.00001516	0.00055633	A_07_P033191	c_3598	cmr|Hypothetical protein [c_3598]
c_3598	-5.10	9.64	-2.35	10.81	0.1	8.46	0.1	0.00003235	0.00079881	A_07_P033191	c_3598	cmr|Hypothetical protein [c_3598]
c_3600	-2.14	10.09	-1.09	10.64	0.0	9.54	0.2	0.00289411	0.01739116	A_07_P033203	c_3600	cmr|Hypothetical protein [c_3600]
c_3601	-11.66	9.48	-3.54	11.25	0.1	7.71	0.2	0.00001349	0.00052666	A_07_P033207	c_3601	cmr|Hypothetical protein [c_3601]
c_3602	-3.87	11.97	-1.95	12.94	0.2	10.99	0.1	0.00019646	0.00250894	A_07_P033212	c_3602	cmr|Hypothetical protein [c_3602]
c_3603	-2.07	10.41	-1.05	10.93	0.1	9.88	0.1	0.00153880	0.01091792	A_07_P033216	c_3603	cmr|Hypothetical protein [c_3603]
c_3604	-2.24	8.37	-1.16	8.95	0.0	7.78	0.1	0.00063614	0.00571983	A_07_P033222	c_3604	cmr|Hypothetical protein [c_3604]
c_3605	+2.26	10.61	+1.18	10.02	0.1	11.20	0.1	0.00101482	0.00801272	A_07_P033227	c_3605	cmr|Hypothetical protein [c_3605]
c_3606	+3.89	9.71	+1.96	8.73	0.1	10.69	0.1	0.00005903	0.00112656	A_07_P033231	c_3606	cmr|Hypothetical protein [c_3606]
c_3609	-2.28	8.94	-1.19	9.53	0.1	8.35	0.4	0.00942330	0.04268139	A_07_P033238	c_3609	cmr|Hypothetical protein [c_3609]
c_3612	-2.47	10.91	-1.30	11.56	0.2	10.26	0.1	0.00087203	0.00723355	A_07_P033247	c_3612	cmr|Transposase insC for insertion element IS2A/D/F/H/I/K [c_3612]
c_3614	-2.96	9.50	-1.56	10.28	0.1	8.71	0.1	0.00035151	0.00378015	A_07_P033257	c_3614	cmr|Hypothetical protein [c_3614]
c_3615	-2.14	8.86	-1.10	9.41	0.0	8.32	0.0	0.00075730	0.00650463	A_07_P033261	c_3615	cmr|Unknown in ISEc8 [c_3615]
c_3616	-3.93	10.71	-1.97	11.70	0.1	9.72	0.0	0.00008572	0.00143229	A_07_P033266	c_3616	cmr|Unknown in ISEc8 [c_3616]
c_3617	-2.68	8.28	-1.42	8.99	0.1	7.57	0.0	0.00029748	0.00335322	A_07_P036281	c_3617	cmr|Unknown in putative ISEc8 [c_3617]
c_3618	-10.11	9.52	-3.34	11.19	0.1	7.85	0.0	0.00000380	0.00031465	A_07_P036289	c_3618	cmr|Hypothetical protein [c_3618]
c_3618	-10.73	9.57	-3.42	11.29	0.1	7.86	0.0	0.00000443	0.00033535	A_07_P036289	c_3618	cmr|Hypothetical protein [c_3618]
c_3618	-9.75	9.21	-3.29	10.86	0.1	7.57	0.1	0.00000518	0.00034758	A_07_P036289	c_3618	cmr|Hypothetical protein [c_3618]
c_3618	-11.17	9.63	-3.48	11.37	0.1	7.89	0.1	0.00000339	0.00029832	A_07_P036289	c_3618	cmr|Hypothetical protein [c_3618]
c_3618	-9.02	9.27	-3.17	10.86	0.0	7.68	0.1	0.00000730	0.00040349	A_07_P036289	c_3618	cmr|Hypothetical protein [c_3618]
c_3620	-5.09	10.78	-2.35	11.95	0.1	9.60	0.0	0.00001976	0.00062719	A_07_P036293	c_3620	cmr|Hypothetical protein [c_3620]
c_3630	-3.84	9.38	-1.94	10.35	0.1	8.41	0.1	0.00006362	0.00117563	A_07_P036335	c_3630	cmr|Hypothetical protein yjhS precursor [c_3630]
c_3631	-3.84	9.28	-1.94	10.25	0.1	8.31	0.2	0.00018493	0.00240029	A_07_P036340	c_3631	cmr|Hypothetical protein [c_3631]
c_3639	+3.48	9.02	+1.80	8.12	0.0	9.92	0.1	0.00008579	0.00143229	A_07_P036375	c_3639	cmr|N-acetylneuraminate lyase subunit [c_3639]
c_3641	-3.06	9.58	-1.61	10.39	0.2	8.78	0.2	0.00086129	0.00716707	A_07_P036385	c_3641	cmr|Unknown in ISEc8 [c_3641]
c_3643	-2.08	10.95	-1.05	11.48	0.0	10.42	0.1	0.00105307	0.00824036	A_07_P036391	c_3643	cmr|Unknown in ISEc8 [c_3643]
c_3646	-3.43	12.32	-1.78	13.21	0.3	11.44	0.3	0.00269198	0.01651697	A_07_P036409	c_3646	cmr|Hypothetical protein [c_3646]
c_3652	-3.36	9.17	-1.75	10.04	0.1	8.29	0.1	0.00013841	0.00196138	A_07_P036440	c_3652	cmr|Hypothetical protein yfjI [c_3652]
c_3654	-4.04	8.12	-2.01	9.13	0.0	7.11	0.2	0.00009699	0.00154244	A_07_P036449	c_3654	cmr|Hypothetical protein yeeP [c_3654]
c_3655	+3.74	11.21	+1.90	10.26	0.1	12.17	0.1	0.00012776	0.00183942	A_07_P036451	c_3655	cmr|Antigen 43 precursor [c_3655]
c_3658	-34.46	14.06	-5.11	16.62	0.0	11.51	0.0	0.00000041	0.00019431	A_07_P036466	c_3658	cmr|Hypothetical protein [c_3658]
c_3659	-35.89	9.92	-5.17	12.50	0.0	7.34	0.0	0.00000036	0.00019431	A_07_P036474	c_3659	cmr|Unknown protein encoded by ISEc8 [c_3659]
c_3660	-28.57	10.11	-4.84	12.53	0.0	7.70	0.0	0.00000048	0.00019431	A_07_P036480	c_3660	cmr|Unknown protein encoded by ISEc8 [c_3660]
c_3662	-4.74	11.21	-2.25	12.33	0.1	10.09	0.2	0.00006188	0.00115851	A_07_P036488	c_3662	cmr|Unknown protein encoded by ISEc8 [c_3662]
c_3663	-5.94	8.53	-2.57	9.82	0.1	7.24	0.1	0.00001796	0.00059912	A_07_P036493	c_3663	cmr|Hypothetical protein [c_3663]
c_3666	-2.65	7.97	-1.41	8.68	0.0	7.27	0.1	0.00029775	0.00335322	A_07_P036509	c_3666	cmr|Hypothetical protein ykfF [c_3666]
c_3670	-3.07	9.16	-1.62	9.97	0.0	8.35	0.2	0.00048546	0.00472965	A_07_P036530	c_3670	cmr|Hypothetical protein [c_3670]
c_3681	-13.24	11.82	-3.73	13.68	0.0	9.96	0.0	0.00000185	0.00025064	A_07_P036583	c_3681	cmr|Hypothetical protein [c_3681]
c_3682	-18.88	10.66	-4.24	12.78	0.0	8.55	0.0	0.00000094	0.00019431	A_07_P036586	c_3682	cmr|Hypothetical protein [c_3682]
c_3683	-61.63	11.89	-5.95	14.86	0.0	8.92	0.1	0.00000021	0.00019431	A_07_P036593	c_3683	cmr|Hypothetical protein [c_3683]
c_3686	+8.10	10.19	+3.02	8.68	0.1	11.70	0.0	0.00001013	0.00046432	A_07_P036604	c_3686	cmr|Hypothetical protein yrbH [c_3686]
c_3689	+3.73	8.98	+1.90	8.04	0.1	9.93	0.1	0.00011009	0.00167356	A_07_P036619	c_3689	cmr|3-deoxy-manno-octulosonate cytidylyltransferase [c_3689]
c_3693	+4.90	9.28	+2.29	8.14	0.2	10.43	0.1	0.00011787	0.00175230	A_07_P036636	c_3693	cmr|Hypothetical protein [c_3693]
c_3693	+4.32	9.71	+2.11	8.66	0.3	10.77	0.1	0.00030719	0.00342042	A_07_P036636	c_3693	cmr|Hypothetical protein [c_3693]
c_3693	+4.88	9.56	+2.29	8.42	0.0	10.71	0.0	0.00002021	0.00063193	A_07_P036636	c_3693	cmr|Hypothetical protein [c_3693]
c_3693	+4.65	9.52	+2.22	8.41	0.1	10.62	0.0	0.00002868	0.00075016	A_07_P036636	c_3693	cmr|Hypothetical protein [c_3693]
c_3693	+5.01	9.60	+2.32	8.44	0.1	10.76	0.0	0.00003479	0.00083884	A_07_P036636	c_3693	cmr|Hypothetical protein [c_3693]
c_3694	+3.30	11.51	+1.72	10.64	0.0	12.37	0.0	0.00008598	0.00143251	A_07_P036641	c_3694	cmr|Hypothetical protein [c_3694]
c_3695	+5.36	10.16	+2.42	8.95	0.2	11.37	0.2	0.00020928	0.00262336	A_07_P036649	c_3695	cmr|Hypothetical protein [c_3695]
c_3774	-2.31	7.90	-1.21	8.51	0.0	7.30	0.0	0.00050885	0.00488792	A_07_P036820	c_3774	cmr|Ferric enterobactin transport ATP-binding protein fepC [c_3774]
c_3819	-5.87	15.03	-2.55	16.30	0.0	13.75	0.1	0.00001309	0.00052207	A_07_P036906	c_3819	cmr|Putative conserved protein [c_3819]
c_3873	+17.65	9.40	+4.14	7.33	0.1	11.47	0.0	0.00000124	0.00021441	A_07_P034083	c_3873	cmr|Putative conserved protein [c_3873]
c_3891	+2.89	8.19	+1.53	7.43	0.3	8.96	0.3	0.00358837	0.02058117	A_07_P034105	c_3891	cmr|Putative phosphotransferase system enzyme subunit [c_3891]
c_3928	+2.00	7.40	+1.00	6.90	0.0	7.90	0.1	0.00124156	0.00928541	A_07_P034139	c_3928	cmr|Hypothetical protein [c_3928]
c_3976	+5.37	8.19	+2.42	6.97	0.1	9.40	0.1	0.00002164	0.00065900	A_07_P041300	c_3976	cmr|Hypothetical protein yhcI [c_3976]
c_4013	-2.73	11.16	-1.45	11.88	0.0	10.43	0.1	0.00023555	0.00285318	A_07_P034204	c_4013	cmr|Hypothetical protein [c_4013]
c_4014	-7.61	8.76	-2.93	10.22	0.1	7.29	0.1	0.00001144	0.00049545	A_07_P034207	c_4014	cmr|Hypothetical protein [c_4014]
c_4016	-6.26	8.56	-2.65	9.88	0.0	7.23	0.2	0.00003128	0.00078813	A_07_P034216	c_4016	cmr|Ribose transport ATP-binding protein rbsA [c_4016]
c_4053	-2.29	11.28	-1.19	11.88	0.0	10.68	0.1	0.00067564	0.00595930	A_07_P041813	c_4053	cmr|Zn [c_4053]
c_4059	+3.33	7.70	+1.74	6.83	0.3	8.56	0.0	0.00061757	0.00560084	A_07_P034273	c_4059	cmr|Hypothetical protein [c_4059]
c_4067	+2.16	7.32	+1.11	6.76	0.2	7.87	0.1	0.00288845	0.01737417	A_07_P034282	c_4067	cmr|Hypothetical protein [c_4067]
c_4084	+2.95	7.76	+1.56	6.98	0.0	8.54	0.1	0.00019787	0.00252367	A_07_P034310	c_4084	cmr|Hypothetical protein [c_4084]
c_4086	+2.06	7.52	+1.04	7.00	0.0	8.04	0.0	0.00094782	0.00763687	A_07_P034312	c_4086	cmr|Hypothetical protein [c_4086]
c_4209	-2.19	10.23	-1.13	10.80	0.0	9.67	0.1	0.00122602	0.00920482	A_07_P034472	c_4209	cmr|Putative minor fimbrial subunit precursor [c_4209]
c_4277	+2.03	7.78	+1.02	7.27	0.3	8.30	0.0	0.00873074	0.04038097	A_07_P034581	c_4277	cmr|Putative phosphotransferase system enzyme subunit [c_4277]
c_4278	+3.07	8.69	+1.62	7.88	0.3	9.50	0.0	0.00101889	0.00803271	A_07_P034587	c_4278	cmr|Putative phosphotransferase system enzyme subunit [c_4278]
c_4360	-2.60	9.48	-1.38	10.16	0.1	8.79	0.0	0.00029643	0.00335277	A_07_P039592	c_4360	cmr|Hypothetical protein [c_4360]
c_4422	-2.48	12.32	-1.31	12.98	0.2	11.67	0.0	0.00068642	0.00602876	A_07_P039723	c_4422	cmr|Hypothetical protein [c_4422]
c_4437	+2.74	7.49	+1.45	6.76	0.0	8.22	0.2	0.00056391	0.00527744	A_07_P039756	c_4437	cmr|Hypothetical protein [c_4437]
c_4437	+2.59	7.67	+1.38	6.98	0.1	8.36	0.1	0.00041837	0.00425500	A_07_P039756	c_4437	cmr|Hypothetical protein [c_4437]
c_4437	+3.24	7.83	+1.70	6.98	0.1	8.68	0.0	0.00010729	0.00164539	A_07_P039756	c_4437	cmr|Hypothetical protein [c_4437]
c_4437	+2.74	7.68	+1.45	6.95	0.1	8.41	0.2	0.00071650	0.00622895	A_07_P039756	c_4437	cmr|Hypothetical protein [c_4437]
c_4437	+2.56	7.81	+1.36	7.13	0.2	8.49	0.2	0.00158342	0.01112418	A_07_P039756	c_4437	cmr|Hypothetical protein [c_4437]
c_4481	-2.11	10.36	-1.08	10.89	0.1	9.82	0.1	0.00130882	0.00968327	A_07_P039839	c_4481	cmr|Conserved hypothetical protein [c_4481]
c_4487	+2.05	7.67	+1.04	7.16	0.1	8.19	0.0	0.00132913	0.00973744	A_07_P039870	c_4487	cmr|Putative phosphotransferase system [c_4487]
c_4493	-2.38	8.41	-1.25	9.03	0.0	7.78	0.1	0.00050563	0.00487485	A_07_P039886	c_4493	cmr|Hypothetical protein [c_4493]
c_4523	-3.81	8.40	-1.93	9.36	0.2	7.43	0.0	0.00017581	0.00231945	A_07_P040008	c_4523	cmr|Conserved hypothetical protein [c_4523]
c_4528	-2.09	7.70	-1.06	8.24	0.1	7.17	0.0	0.00096407	0.00772037	A_07_P040032	c_4528	cmr|Ethanolamine utilization protein eutN [c_4528]
c_4548	-2.62	9.33	-1.39	10.02	0.2	8.63	0.0	0.00110096	0.00853027	A_07_P040129	c_4548	cmr|Hypothetical protein [c_4548]
c_4576	+2.35	8.02	+1.23	7.40	0.0	8.64	0.1	0.00073327	0.00633274	A_07_P038942	c_4576	cmr|Hypothetical protein yeeV [c_4576]
c_4580	-3.52	9.00	-1.81	9.91	0.2	8.10	0.1	0.00032200	0.00355257	A_07_P038963	c_4580	cmr|Hypothetical protein [c_4580]
c_4762	-2.62	7.97	-1.39	8.67	0.2	7.28	0.0	0.00055343	0.00520817	A_07_P039201	c_4762	cmr|Putative permease [c_4762]
c_4776	+2.53	8.41	+1.34	7.74	0.3	9.08	0.0	0.00189005	0.01267793	A_07_P039258	c_4776	cmr|Hypothetical protein [c_4776]
c_4777	+3.53	7.85	+1.82	6.94	0.0	8.76	0.2	0.00017666	0.00232751	A_07_P039263	c_4777	cmr|Putative conserved protein [c_4777]
c_4778	+2.45	8.07	+1.29	7.43	0.1	8.72	0.1	0.00068658	0.00602876	A_07_P039269	c_4778	cmr|Putative conserved protein [c_4778]
c_4779	+3.19	8.35	+1.67	7.51	0.1	9.18	0.2	0.00029411	0.00333849	A_07_P039274	c_4779	cmr|Putative transcriptional regulator [c_4779]
c_4780	+2.42	12.64	+1.27	12.00	0.0	13.27	0.0	0.00037301	0.00394177	A_07_P039276	c_4780	cmr|Hypothetical protein [c_4780]
c_4836	+5.75	11.34	+2.52	10.08	0.0	12.60	0.1	0.00001834	0.00060558	A_07_P039365	c_4836	cmr|Putative lipase [c_4836]
c_4837	-21.77	12.52	-4.44	14.74	0.0	10.29	0.0	0.00000072	0.00019431	A_07_P039369	c_4837	cmr|Hypothetical protein [c_4837]
c_4838	-4.67	12.24	-2.22	13.35	0.1	11.13	0.2	0.00006854	0.00122908	A_07_P039373	c_4838	cmr|Hypothetical protein [c_4838]
c_4839	-19.72	11.40	-4.30	13.55	0.1	9.25	0.0	0.00000122	0.00021323	A_07_P039376	c_4839	cmr|Hypothetical protein [c_4839]
c_4858	+2.42	7.30	+1.28	6.66	0.0	7.94	0.0	0.00036284	0.00387759	A_07_P039424	c_4858	cmr|Hypothetical protein [c_4858]
c_4924	-3.37	7.82	-1.75	8.70	0.0	6.95	0.0	0.00007425	0.00129689	A_07_P039536	c_4924	cmr|Putative hippuricase [c_4924]
c_4925	-2.92	8.28	-1.54	9.05	0.1	7.50	0.1	0.00027246	0.00315418	A_07_P039541	c_4925	cmr|Putative citrate permease [c_4925]
c_4928	-2.84	8.92	-1.51	9.67	0.1	8.17	0.0	0.00020983	0.00262814	A_07_P037396	c_4928	cmr|tRNA [c_4928]
c_4938	+3.12	7.30	+1.64	6.48	0.0	8.12	0.0	0.00011823	0.00175446	A_07_P037425	c_4938	cmr|Hypothetical protein [c_4938]
c_4942	+3.63	7.79	+1.86	6.86	0.2	8.72	0.5	0.00411103	0.02272614	A_07_P037427	c_4942	cmr|Hypothetical protein [c_4942]
c_4953	+2.30	9.54	+1.20	8.94	0.2	10.14	0.0	0.00117774	0.00896134	A_07_P037440	c_4953	cmr|NADH pyrophosphatase [c_4953]
c_4986	-2.04	7.64	-1.03	8.16	0.1	7.13	0.2	0.00348791	0.02010465	A_07_P037506	c_4986	cmr|D-glucitol-6-phosphate dehydrogenase [c_4986]
c_5012	+2.24	11.21	+1.16	10.63	0.1	11.79	0.0	0.00066812	0.00592275	A_07_P037546	c_5012	cmr|Hypothetical protein [c_5012]
c_5019	-4.70	8.85	-2.23	9.96	0.0	7.73	0.3	0.00027234	0.00315418	A_07_P035565	c_5019	cmr|Hypothetical protein yjbO [c_5019]
c_5033	-2.03	8.33	-1.02	8.84	0.1	7.82	0.0	0.00198592	0.01309861	A_07_P037610	c_5033	cmr|Hypothetical protein [c_5033]
c_5035	+2.43	8.11	+1.28	7.47	0.1	8.75	0.0	0.00075786	0.00650583	A_07_P037619	c_5035	cmr|Putative 2-oxoglutarate dehydrogenase [c_5035]
c_5055	+3.61	8.58	+1.85	7.65	0.0	9.50	0.1	0.00008885	0.00145399	A_07_P037658	c_5055	cmr|Hypothetical protein [c_5055]
c_5058	-2.44	8.98	-1.28	9.62	0.2	8.34	0.1	0.00171514	0.01182274	A_07_P037663	c_5058	cmr|Putative transcriptional regulator [c_5058]
c_5061	-2.12	8.37	-1.08	8.92	0.2	7.83	0.1	0.00461841	0.02473656	A_07_P037671	c_5061	cmr|Hypothetical protein [c_5061]
c_5061	-2.71	8.60	-1.44	9.32	0.1	7.88	0.1	0.00055942	0.00525198	A_07_P037671	c_5061	cmr|Hypothetical protein [c_5061]
c_5062	+4.00	8.52	+2.00	7.52	0.1	9.52	0.1	0.00013732	0.00194847	A_07_P037679	c_5062	cmr|Putative symporter yjcG [c_5062]
c_5088	-2.41	7.61	-1.27	8.24	0.0	6.98	0.2	0.00080939	0.00683275	A_07_P037733	c_5088	cmr|Hypothetical protein [c_5088]
c_5153	-3.78	9.81	-1.92	10.77	0.0	8.85	0.0	0.00004899	0.00100424	A_07_P037845	c_5153	cmr|Hypothetical protein [c_5153]
c_5154	-3.11	9.07	-1.64	9.89	0.1	8.25	0.1	0.00022337	0.00274527	A_07_P037850	c_5154	cmr|Hypothetical protein [c_5154]
c_5166	-4.02	9.52	-2.01	10.52	0.0	8.51	0.4	0.00079857	0.00677409	A_07_P037902	c_5166	cmr|Partial Transposase [c_5166]
c_5207	-2.39	11.48	-1.26	12.11	0.2	10.86	0.1	0.00202867	0.01329867	A_07_P038058	c_5207	cmr|Hypothetical protein [c_5207]
c_5233	-2.33	8.49	-1.22	9.10	0.1	7.88	0.1	0.00062327	0.00563628	A_07_P036933	c_5233	cmr|Hypothetical protein [c_5233]
c_5269	-2.07	7.96	-1.05	8.49	0.0	7.44	0.1	0.00140249	0.01012879	A_07_P036952	c_5269	cmr|Hypothetical protein [c_5269]
c_5293	+3.85	8.38	+1.94	7.41	0.0	9.35	0.2	0.00025929	0.00307016	A_07_P036987	c_5293	cmr|Hypothetical protein [c_5293]
c_5295	-7.09	10.41	-2.83	11.82	0.0	8.99	0.1	0.00001025	0.00046640	A_07_P036994	c_5295	cmr|Hypothetical protein [c_5295]
c_5296	-15.18	12.16	-3.92	14.12	0.0	10.20	0.2	0.00000653	0.00038079	A_07_P037000	c_5296	cmr|Hypothetical protein [c_5296]
c_5297	-3.54	8.96	-1.82	9.87	0.2	8.05	0.2	0.00043753	0.00439592	A_07_P037001	c_5297	cmr|Hypothetical protein [c_5297]
c_5334	+3.86	8.73	+1.95	7.76	0.6	9.71	0.1	0.00364540	0.02076451	A_07_P037056	c_5334	cmr|Hypothetical protein [c_5334]
c_5341	-39.25	12.29	-5.29	14.93	0.1	9.64	0.1	0.00000078	0.00019431	A_07_P042071	c_5341	cmr|Mg [c_5341]
c_5343	-40.65	9.65	-5.35	12.33	0.1	6.98	0.1	0.00000056	0.00019431	A_07_P037072	c_5343	cmr|Hypothetical protein [c_5343]
c_5356	-2.83	7.68	-1.50	8.43	0.1	6.93	0.1	0.00026161	0.00308181	A_07_P037109	c_5356	cmr|Hypothetical protein [c_5356]
c_5375	-2.29	9.81	-1.20	10.41	0.4	9.21	0.1	0.00730859	0.03522085	A_07_P037145	c_5375	cmr|Hypothetical protein [c_5375]
c_5448	-2.37	7.87	-1.24	8.49	0.0	7.25	0.2	0.00134247	0.00981235	A_07_P037329	c_5448	cmr|Hypothetical protein [c_5448]
c_5455	+6.33	9.10	+2.66	7.77	0.1	10.43	0.1	0.00002028	0.00063193	A_07_P037341	c_5455	cmr|Hypothetical protein [c_5455]
caiA	-6.26	12.08	-2.65	13.41	0.0	10.76	0.0	0.00000976	0.00045680	A_07_P010884	b0039	cmr|probable carnitine operon oxidoreductase [b0039]
caiT	+2.00	6.79	+1.00	6.29	0.0	7.28	0.0	0.00110998	0.00858747	A_07_P010887	b0040	cmr|probable carnitine transporter [b0040]
carA	+4.81	8.83	+2.27	7.70	0.2	9.97	0.1	0.00006544	0.00119937	A_07_P010846	b0032	cmr|carbamoyl-phosphate synthetase, glutamine [b0032]
carB	+8.71	10.16	+3.12	8.60	0.2	11.72	0.1	0.00001921	0.00061714	A_07_P010855	b0033	cmr|carbamoyl-phosphate synthase large subunit [b0033]
cbl	-5.16	13.04	-2.37	14.23	0.0	11.86	0.0	0.00001835	0.00060558	A_07_P015271	b1987	cmr|transcriptional regulator cys regulon; accessory regulatory circuit affecting cysM [b1987]
cbpA	+6.40	8.67	+2.68	7.33	0.2	10.01	0.0	0.00003939	0.00090005	A_07_P001235	b1000	cmr|curved DNA-binding protein; functions closely related to DnaJ [b1000]
cbpM	+4.90	8.38	+2.29	7.23	0.0	9.53	0.0	0.00002002	0.00063193	A_07_P001226	b0999	cmr|orf, hypothetical protein [b0999]
cbrA	-3.65	7.76	-1.87	8.70	0.4	6.83	0.1	0.00131909	0.00971976	A_07_P017384	b3690	cmr|orf, hypothetical protein [b3690]
ccmG	-2.28	9.64	-1.19	10.23	0.1	9.04	0.2	0.00145687	0.01044487	A_07_P000765	b2195	cmr|disulfide oxidoreductase [b2195]
cdh	-2.41	8.13	-1.27	8.76	0.1	7.49	0.0	0.00059663	0.00547399	A_07_P019370	b3918	cmr|CDP-diacylglycerol phosphotidylhydrolase [b3918]
cdsA	-2.19	11.26	-1.13	11.83	0.2	10.69	0.0	0.00203345	0.01331170	A_07_P002831	b0175	cmr|CDP-diglyceride synthetase [b0175]
cedA	-4.71	11.18	-2.24	12.30	0.1	10.07	0.0	0.00002592	0.00072358	A_07_P018702	b1731	cmr|orf, hypothetical protein [b1731]
chaC	-2.13	8.03	-1.09	8.58	0.2	7.49	0.1	0.00244928	0.01537539	A_07_P007044	b1218	cmr|cation transport regulator [b1218]
cheZ	-3.02	11.76	-1.60	12.56	0.1	10.96	0.1	0.00026422	0.00309464	A_07_P016084	b1881	cmr|chemotactic response; CheY protein phophatase; antagonist of CheY as switch regulator [b1881]
chpB	-2.08	10.85	-1.05	11.37	0.0	10.32	0.1	0.00159278	0.01117504	A_07_P003680	b4225	cmr|probable growth inhibitor, PemK-like, autoregulated [b4225]
clpA	+3.99	9.95	+1.99	8.95	0.0	10.95	0.1	0.00008816	0.00145271	A_07_P004862	b0882	cmr|ATP-binding component of serine protease [b0882]
clpP	+4.74	12.22	+2.24	11.09	0.1	13.34	0.0	0.00002762	0.00073830	A_07_P021300	b0437	cmr|ATP-dependent proteolytic subunit of clpA-clpP serine protease, heat shock protein F21.5 [b0437]
clpS	+3.66	10.47	+1.87	9.53	0.1	11.40	0.0	0.00009328	0.00149973	A_07_P004856	b0881	cmr|orf, hypothetical protein [b0881]
cmr	-2.31	8.13	-1.21	8.73	0.1	7.53	0.0	0.00056846	0.00529264	A_07_P004661	b0842	cmr|proton motive force efflux pump [b0842]
cmtA	-2.94	11.34	-1.55	12.11	0.4	10.56	0.1	0.00272924	0.01664824	A_07_P011811	b2933	cmr|PTS system, mannitol-specific enzyme II component, cryptic [b2933]
cobS	-3.30	8.77	-1.72	9.63	0.1	7.91	0.2	0.00055408	0.00521111	A_07_P015292	b1992	cmr|cobalamin 5-phosphate synthase [b1992]
cobU	-2.87	9.32	-1.52	10.08	0.0	8.56	0.0	0.00015453	0.00212664	A_07_P015296	b1993	cmr|cobinamide kinase/cobinamide phosphate guanylyltransferase [b1993]
codA	+4.72	8.89	+2.24	7.77	0.0	10.01	0.2	0.00008894	0.00145399	A_07_P008378	b0337	cmr|cytosine deaminase [b0337]
codB	+3.89	7.83	+1.96	6.85	0.0	8.81	0.2	0.00014676	0.00204652	A_07_P031022	c_0455	cmr|Cytosine permease [c_0455]

codB	+2.09	7.73	+1.06	7.19	0.1	8.26	0.1	0.00282372	0.01707992	A_07_P008371	b0336	cmr|cytosine permease/transport [b0336]
cpdA	-2.04	12.73	-1.03	13.24	0.1	12.21	0.1	0.00116605	0.00890744	A_07_P012295	b3032	cmr|regulator of lacZ [b3032]
cpxR	+3.83	10.88	+1.94	9.91	0.0	11.85	0.0	0.00004520	0.00095882	A_07_P019340	b3912	cmr|transcriptional regulator in 2-component system [b3912]
cpxR	+3.48	11.24	+1.80	10.34	0.0	12.14	0.0	0.00006620	0.00120763	A_07_P041979	c_4864	cmr|Transcriptional Regulatory protein cpxR [c_4864]
creD	-3.82	9.12	-1.93	10.09	0.1	8.15	0.0	0.00005717	0.00110431	A_07_P017684	b4400	cmr|tolerance to colicin E2 [b4400]
crp	-2.44	12.94	-1.28	13.59	0.0	12.30	0.0	0.00034200	0.00370834	A_07_P017815	b3357	cmr|cyclic AMP receptor protein [b3357]
crr	+2.65	10.24	+1.41	9.54	0.0	10.94	0.1	0.00031070	0.00345228	A_07_P013145	b2417	cmr|PTS system, glucose-specific IIA component [b2417]
csdA	-3.20	11.28	-1.68	12.11	0.0	10.44	0.1	0.00012054	0.00178030	A_07_P006050	b2810	cmr|orf, hypothetical protein [b2810]
csiD	-3.97	9.02	-1.99	10.02	0.1	8.03	0.0	0.00006667	0.00120840	A_07_P020146	b2659	cmr|orf, hypothetical protein [b2659]
csiE	+3.57	7.93	+1.84	7.01	0.1	8.85	0.0	0.00008296	0.00139835	A_07_P019579	b2535	cmr|orf, hypothetical protein [b2535]
cspB	+2.15	11.49	+1.10	10.94	0.1	12.04	0.0	0.00088915	0.00733692	A_07_P020429	b1557	cmr|cold shock protein; may affect transcription [b1557]
cspC	+3.44	14.09	+1.78	13.20	0.1	14.98	0.0	0.00014268	0.00200567	A_07_P015809	b1823	cmr|cold shock protein [b1823]
cspD	+22.92	10.20	+4.52	7.94	0.1	12.45	0.0	0.00000110	0.00020547	A_07_P004854	b0880	cmr|cold shock protein [b0880]
cspE	+6.54	12.96	+2.71	11.61	0.1	14.32	0.1	0.00001278	0.00051714	A_07_P035444	c_0714	cmr|Cold shock-like protein cspE [c_0714]
cspE	+5.88	12.71	+2.55	11.43	0.1	13.98	0.2	0.00004632	0.00097245	A_07_P009684	b0623	cmr|cold shock protein [b0623]
cstA	+6.30	10.15	+2.66	8.82	0.4	11.48	0.1	0.00026794	0.00311300	A_07_P016748	b0598	cmr|carbon starvation protein [b0598]
cvpA	+6.06	12.90	+2.60	11.60	0.1	14.20	0.0	0.00001564	0.00056283	A_07_P013855	b2313	cmr|membrane protein required for colicin V production [b2313]
cvpA	+5.31	11.02	+2.41	9.82	0.1	12.23	0.0	0.00001947	0.00062241	A_07_P042620	Z3575	cmr|membrane protein required for colicin V production [Z3575]
cvrA	-2.94	12.72	-1.55	13.49	0.2	11.94	0.3	0.00251109	0.01565726	A_07_P006906	b1191	cmr|orf, hypothetical protein [b1191]
cyaY	+2.85	10.47	+1.51	9.72	0.1	11.23	0.0	0.00017144	0.00227395	A_07_P005904	b3807	cmr|orf, hypothetical protein [b3807]
cyaY	+2.38	11.50	+1.25	10.87	0.1	12.12	0.1	0.00069705	0.00609686	A_07_P041940	c_4726	cmr|CyaY protein [c_4726]
cybC	+2.56	11.65	+1.36	10.97	0.2	12.33	0.0	0.00075604	0.00649734	A_07_P037063	c_5335	cmr|Soluble cytochrome b562 precursor [c_5335]
cybC	+3.04	10.51	+1.60	9.71	0.0	11.31	0.1	0.00013737	0.00194847	A_07_P003731	b4236	cmr|cytochrome b [b4236]
cydA	+11.22	11.99	+3.49	10.24	0.0	13.73	0.1	0.00000440	0.00033535	A_07_P010185	b0733	cmr|cytochrome d terminal oxidase, polypeptide subunit I [b0733]
cydB	+8.49	11.65	+3.09	10.11	0.1	13.20	0.0	0.00000519	0.00034758	A_07_P010187	b0734	cmr|cytochrome d terminal oxidase polypeptide subunit II [b0734]
cyoB	+2.95	13.90	+1.56	13.12	0.0	14.68	0.1	0.00015079	0.00208799	A_07_P021268	b0431	cmr|cytochrome o ubiquinol oxidase subunit I [b0431]
cyoC	+2.76	12.71	+1.46	11.98	0.0	13.44	0.1	0.00021587	0.00268458	A_07_P021261	b0430	cmr|cytochrome o ubiquinol oxidase subunit III [b0430]
cyoD	+3.89	8.69	+1.96	7.71	0.2	9.67	0.0	0.00010062	0.00157948	A_07_P051941	Z0532	cmr|cytochrome o ubiquinol oxidase subunit IV [Z0532]
cyoD	+3.19	11.29	+1.68	10.45	0.1	12.13	0.0	0.00011753	0.00174890	A_07_P021258	b0429	cmr|cytochrome o ubiquinol oxidase subunit IV [b0429]
cyoE	+2.88	10.53	+1.52	9.77	0.0	11.29	0.0	0.00015989	0.00218551	A_07_P021254	b0428	cmr|protoheme IX farnesyltransferase [b0428]
cysA	-3.43	9.29	-1.78	10.18	0.2	8.40	0.1	0.00019199	0.00246351	A_07_P013166	b2422	cmr|ATP-binding component of sulfate permease A protein; chromate resistance [b2422]
cysB	-2.41	9.30	-1.27	9.94	0.0	8.67	0.1	0.00046899	0.00463227	A_07_P014359	b1275	cmr|positive transcriptional regulator for cysteine regulon [b1275]
cysC	-4.19	9.41	-2.07	10.44	0.0	8.37	0.1	0.00004371	0.00094590	A_07_P002196	b2750	cmr|adenosine 5-phosphosulfate kinase [b2750]
cysD	-2.11	9.97	-1.08	10.51	0.1	9.43	0.1	0.00135926	0.00990294	A_07_P002209	b2752	cmr|ATP:sulfurylase [b2752]
cysH	-3.65	10.82	-1.87	11.76	0.0	9.89	0.1	0.00009217	0.00148959	A_07_P002256	b2762	cmr|3-phosphoadenosine 5-phosphosulfate reductase [b2762]
cysI	-5.44	11.51	-2.44	12.74	0.0	10.29	0.1	0.00002647	0.00072866	A_07_P002265	b2763	cmr|sulfite reductase, alpha subunit [b2763]
cysJ	-4.25	11.19	-2.09	12.23	0.0	10.14	0.1	0.00003522	0.00084015	A_07_P032576	c_3323	cmr|Sulfite reductase [c_3323]
cysJ	-2.07	10.05	-1.05	10.58	0.0	9.53	0.1	0.00103769	0.00814024	A_07_P002266	b2764	cmr|sulfite reductase [b2764]
cysM	-2.13	10.19	-1.09	10.74	0.1	9.65	0.1	0.00097747	0.00779599	A_07_P030051	c_2955	cmr|Cysteine synthase B [c_2955]
cysN	-2.88	7.80	-1.53	8.56	0.2	7.04	0.1	0.00039934	0.00412279	A_07_P002205	b2751	cmr|ATP-sulfurylase [b2751]
cysN	-4.75	9.11	-2.25	10.24	0.1	7.99	0.1	0.00003576	0.00084433	A_07_P043152	Z4059	cmr|ATP-sulfurylase [Z4059]
cysN	-5.14	9.64	-2.36	10.83	0.1	8.46	0.1	0.00003792	0.00087581	A_07_P030710	c_3318	cmr|Sulfate adenylyltransferase subunit 1 [c_3318]
cysN	-4.38	9.27	-2.13	10.33	0.0	8.20	0.2	0.00006985	0.00124629	A_07_P056037	ECs3605	cmr|ATP-sulfurylase [ECs3605]
cysP	-4.48	11.61	-2.16	12.70	0.0	10.53	0.2	0.00008108	0.00137285	A_07_P013181	b2425	cmr|thiosulfate binding protein [b2425]
cysP	-5.90	12.48	-2.56	13.77	0.0	11.20	0.1	0.00001351	0.00052666	A_07_P030063	c_2959	cmr|Thiosulfate-binding protein precursor [c_2959]
cysP	-4.54	11.14	-2.18	12.23	0.0	10.04	0.1	0.00004067	0.00091477	A_07_P042814	Z3690	cmr|thiosulfate binding protein [Z3690]
cysU	-3.81	12.00	-1.93	12.96	0.1	11.03	0.0	0.00005893	0.00112656	A_07_P013177	b2424	cmr|sulfate, thiosulfate transport system permease T protein [b2424]
cysU	-4.62	11.09	-2.21	12.19	0.0	9.98	0.2	0.00006160	0.00115828	A_07_P042582	c_2958	cmr|Sulfate transport system permease protein cysT [c_2958]
cysW	-12.38	10.92	-3.63	12.73	0.0	9.10	0.1	0.00000230	0.00026836	A_07_P013174	b2423	cmr|sulfate transport system permease W protein [b2423]
dadA	+10.10	9.98	+3.34	8.31	0.0	11.65	0.0	0.00000300	0.00028496	A_07_P006899	b1189	cmr|D-amino acid dehydrogenase subunit [b1189]
dadA	+8.46	10.12	+3.08	8.58	0.1	11.66	0.1	0.00001174	0.00050228	A_07_P038722	c_1638	cmr|D-amino acid dehydrogenase small subunit [c_1638]
dadX	+5.04	9.37	+2.33	8.21	0.0	10.54	0.0	0.00001857	0.00061157	A_07_P006905	b1190	cmr|alanine racemase 2, catabolic [b1190]
damX	-2.31	10.91	-1.21	11.52	0.0	10.31	0.1	0.00056994	0.00530327	A_07_P017966	b3388	cmr|putative membrane protein; interferes with cell division [b3388]
dapA	+2.74	11.49	+1.45	10.76	0.0	12.21	0.1	0.00023797	0.00287537	A_07_P013447	b2478	cmr|dihydrodipicolinate synthase [b2478]
dapB	+3.64	9.33	+1.86	8.39	0.0	10.26	0.1	0.00006743	0.00121740	A_07_P010842	b0031	cmr|dihydrodipicolinate reductase [b0031]
dapD	+2.78	8.62	+1.48	7.89	0.0	9.36	0.1	0.00024466	0.00293818	A_07_P041442	c_0201	cmr|2,3,4,5-tetrahydropyridine-2,6-dicarboxylate N-succinyltransferase [c_0201]
dapE	-4.24	10.91	-2.09	11.95	0.1	9.87	0.0	0.00003602	0.00084763	A_07_P013420	b2472	cmr|N-succinyl-diaminopimelate deacylase [b2472]
dcd	-3.54	12.31	-1.82	13.22	0.0	11.39	0.0	0.00006817	0.00122531	A_07_P003102	b2065	cmr|2-deoxycytidine 5-triphosphate deaminase [b2065]
dctA	+17.35	10.51	+4.12	8.46	0.1	12.57	0.0	0.00000152	0.00022581	A_07_P007574	b3528	cmr|uptake of C4-dicarboxylic acids [b3528]
dcuA	+3.24	10.23	+1.69	9.38	0.1	11.08	0.1	0.00014143	0.00199367	A_07_P011423	b4138	cmr|anaerobic dicarboxylate transport [b4138]
dcuB	-2.56	8.28	-1.36	8.96	0.0	7.61	0.2	0.00102756	0.00808088	A_07_P011354	b4123	cmr|anaerobic dicarboxylate transport [b4123]
dcuC	+2.11	8.05	+1.08	7.52	0.0	8.59	0.1	0.00087549	0.00725841	A_07_P009671	b0621	cmr|transport of dicarboxylates [b0621]
dcyD	-6.15	11.41	-2.62	12.72	0.0	10.10	0.0	0.00001054	0.00047145	A_07_P014958	b1919	cmr|putative 1-aminocyclopropane-1-carboxylate deaminase [b1919]
ddl	-2.94	11.59	-1.56	12.37	0.0	10.81	0.0	0.00014337	0.00201178	A_07_P062950	ECs0431	cmr|D-alanine-D-alanine ligase A [ECs0431]
ddl	-2.66	11.53	-1.41	12.24	0.0	10.83	0.1	0.00040431	0.00415498	A_07_P051920	Z0477	cmr|putative enzyme Cell envelop: Murein sacculus, peptidoglycan [Z0477]
ddlA	-4.06	9.81	-2.02	10.82	0.1	8.80	0.0	0.00005623	0.00109182	A_07_P021019	b0381	cmr|D-alanine-D-alanine ligase A [b0381]
deaD	-14.08	11.48	-3.82	13.39	0.0	9.57	0.1	0.00000182	0.00025064	A_07_P000534	b3162	cmr|inducible ATP-independent RNA helicase [b3162]
degP	-2.10	11.14	-1.07	11.68	0.0	10.61	0.0	0.00078568	0.00668277	A_07_P002766	b0161	cmr|periplasmic serine protease Do; heat shock protein HtrA [b0161]
degQ	+3.81	8.77	+1.93	7.80	0.0	9.73	0.1	0.00006245	0.00116220	A_07_P041306	c_3989	cmr|Protease degQ precursor [c_3989]
degS	-3.60	9.39	-1.85	10.31	0.1	8.47	0.0	0.00006994	0.00124629	A_07_P034177	c_3990	cmr|Protease degS precursor [c_3990]
deoB	+4.53	11.00	+2.18	9.91	0.1	12.09	0.0	0.00003022	0.00077353	A_07_P017598	b4383	cmr|phosphopentomutase [b4383]
deoC	-6.14	14.49	-2.62	15.80	0.0	13.18	0.0	0.00001067	0.00047201	A_07_P017589	b4381	cmr|2-deoxyribose-5-phosphate aldolase [b4381]
deoD	+2.15	11.15	+1.10	10.60	0.1	11.71	0.1	0.00080621	0.00682418	A_07_P017603	b4384	cmr|purine-nucleoside phosphorylase [b4384]
deoR	-8.03	10.23	-3.01	11.74	0.1	8.73	0.3	0.00006115	0.00115710	A_07_P042124	c_0925	cmr|Deoxyribose operon repressor [c_0925]
deoR	-11.73	10.57	-3.55	12.34	0.1	8.79	0.1	0.00000311	0.00028944	A_07_P004651	b0840	cmr|transcriptional repressor for deo operon, tsx, nupG [b0840]
dhaK	+3.89	8.89	+1.96	7.91	0.1	9.87	0.0	0.00007676	0.00132177	A_07_P006953	b1200	cmr|putative dihydroxyacetone kinase [b1200]
dhaL	+2.72	7.70	+1.45	6.98	0.1	8.43	0.1	0.00047985	0.00468366	A_07_P006948	b1199	cmr|putative dihydroxyacetone kinase [b1199]
diaA	+2.61	9.41	+1.38	8.72	0.1	10.10	0.1	0.00042591	0.00430780	A_07_P000466	b3149	cmr|orf, hypothetical protein [b3149]
dinB	-3.37	12.07	-1.75	12.95	0.1	11.19	0.0	0.00012234	0.00179502	A_07_P007867	b0231	cmr|damage-inducible protein P; putative tRNA synthetase [b0231]
dinF	-3.12	10.11	-1.64	10.93	0.0	9.29	0.0	0.00010654	0.00164437	A_07_P008863	b4044	cmr|DNA-damage-inducible protein F [b4044]
dinG	+4.36	11.26	+2.12	10.20	0.1	12.33	0.1	0.00006253	0.00116220	A_07_P004448	b0799	cmr|probably ATP-dependent helicase [b0799]
dinI	-2.31	14.34	-1.21	14.94	0.0	13.73	0.1	0.00049084	0.00476059	A_07_P001507	b1061	cmr|damage-inducible protein I [b1061]
djlB	-3.83	11.81	-1.94	12.78	0.1	10.84	0.0	0.00006046	0.00114826	A_07_P009800	b0646	cmr|putative enzyme of polynucleotide modification [b0646]
dkgA	+2.85	8.75	+1.51	7.99	0.0	9.50	0.0	0.00015105	0.00208974	A_07_P012193	b3012	cmr|orf, hypothetical protein [b3012]
dkgB	-3.84	8.94	-1.94	9.91	0.1	7.97	0.1	0.00008853	0.00145271	A_07_P002965	b0207	cmr|putative aldose reductase [b0207]
dmsA	+5.26	10.01	+2.39	8.81	0.2	11.21	0.0	0.00004400	0.00094686	A_07_P033816	c_1031	cmr|Anaerobic dimethyl sulfoxide reductase chain A precursor [c_1031]
dmsA	+4.75	8.27	+2.25	7.15	0.1	9.39	0.1	0.00004053	0.00091288	A_07_P004916	b0894	cmr|anaerobic dimethyl sulfoxide reductase subunit A [b0894]
dmsB	+3.71	8.43	+1.89	7.49	0.1	9.38	0.1	0.00009178	0.00148821	A_07_P004924	b0895	cmr|anaerobic dimethyl sulfoxide reductase subunit B [b0895]
dmsC	+2.38	7.78	+1.25	7.15	0.1	8.40	0.1	0.00059996	0.00549480	A_07_P052033	Z1242	cmr|anaerobic dimethyl sulfoxide reductase subunit C [Z1242]
dmsC	+2.88	8.13	+1.52	7.37	0.0	8.90	0.0	0.00016021	0.00218551	A_07_P004926	b0896	cmr|anaerobic dimethyl sulfoxide reductase subunit C [b0896]
dnaA	-2.07	14.01	-1.05	14.54	0.0	13.49	0.1	0.00109608	0.00849666	A_07_P005441	b3702	cmr|DNA biosynthesis; initiation of chromosome replication; can be transcription regulator [b3702]
dnaB	-2.22	9.30	-1.15	9.88	0.0	8.73	0.0	0.00054978	0.00518615	A_07_P008903	b4052	cmr|replicative DNA helicase; part of primosome [b4052]
dnaC	+2.00	11.91	+1.00	11.41	0.1	12.41	0.1	0.00210341	0.01370701	A_07_P017504	b4361	cmr|chromosome replication; initiation and chain elongation [b4361]
dnaG	-5.32	11.70	-2.41	12.91	0.0	10.49	0.0	0.00001587	0.00056388	A_07_P000065	b3066	cmr|DNA biosynthesis; DNA primase [b3066]
dnaN	-3.06	13.24	-1.61	14.05	0.0	12.44	0.1	0.00012751	0.00183834	A_07_P005436	b3701	cmr|DNA polymerase III, beta-subunit [b3701]
dnaQ	+3.07	9.18	+1.62	8.37	0.0	9.99	0.0	0.00011279	0.00169761	A_07_P051886	Z0241	cmr|DNA polymerase III, epsilon subunit [Z0241]
dnaQ	+3.08	9.80	+1.62	8.99	0.1	10.61	0.0	0.00023399	0.00284423	A_07_P003004	b0215	cmr|DNA polymerase III, epsilon subunit [b0215]
dnaX	+6.83	11.14	+2.77	9.76	0.1	12.53	0.0	0.00000887	0.00042982	A_07_P021457	b0470	cmr|DNA polymerase III, tau and gamma subunits; DNA elongation factor III [b0470]
dps	+4.24	11.69	+2.08	10.64	0.1	12.73	0.1	0.00008620	0.00143428	A_07_P004515	b0812	cmr|global regulator, starvation conditions [b0812]
dsbA	+4.11	9.47	+2.04	8.45	0.1	10.49	0.0	0.00004476	0.00095355	A_07_P019081	b3860	cmr|protein disulfide isomerase I, essential for cytochrome c synthesis and formate-dependent reduction [b3860]
dsdX	+2.38	7.57	+1.25	6.95	0.3	8.20	0.1	0.00335565	0.01955992	A_07_P014107	b2365	cmr|transport system permease [b2365]
dtd	+3.00	9.81	+1.58	9.02	0.3	10.60	0.1	0.00136593	0.00992393	A_07_P019212	b3887	cmr|orf, hypothetical protein [b3887]
dusB	+3.72	11.89	+1.89	10.94	0.1	12.83	0.1	0.00008195	0.00138289	A_07_P012768	b3260	cmr|putative dehydrogenase [b3260]
E1A_r60_a104	-2.21	9.95	-1.14	10.52	0.1	9.37	0.3	0.00581046	0.02964352	(+)E1A_r60_a104	E1A_r60_a104	
E1A_r60_a104	-2.26	10.00	-1.18	10.59	0.0	9.41	0.1	0.00064411	0.00577889	(+)E1A_r60_a104	E1A_r60_a104	
E1A_r60_a104	-3.20	10.17	-1.68	11.01	0.3	9.33	0.0	0.00057391	0.00533670	(+)E1A_r60_a104	E1A_r60_a104	
E1A_r60_a104	-2.23	9.74	-1.15	10.32	0.1	9.16	0.1	0.00116791	0.00891302	(+)E1A_r60_a104	E1A_r60_a104	
E1A_r60_a104	-2.13	10.03	-1.09	10.57	0.1	9.48	0.2	0.00278233	0.01690661	(+)E1A_r60_a104	E1A_r60_a104	
E1A_r60_a104	-2.16	10.14	-1.11	10.70	0.3	9.59	0.1	0.00582787	0.02964589	(+)E1A_r60_a104	E1A_r60_a104	
E1A_r60_a107	-2.94	9.73	-1.56	10.51	0.3	8.96	0.3	0.00402784	0.02229975	(+)E1A_r60_a107	E1A_r60_a107	
E1A_r60_a107	-2.15	9.12	-1.10	9.68	0.1	8.57	0.0	0.00104769	0.00821045	(+)E1A_r60_a107	E1A_r60_a107	
E1A_r60_a135	-2.47	9.56	-1.30	10.21	0.3	8.91	0.2	0.00365353	0.02080082	(+)E1A_r60_a135	E1A_r60_a135	
E1A_r60_a20	-2.43	10.25	-1.28	10.89	0.1	9.61	0.0	0.00041082	0.00419719	(+)E1A_r60_a20	E1A_r60_a20	
E1A_r60_a20	-2.09	10.11	-1.06	10.64	0.3	9.58	0.2	0.00685332	0.03344661	(+)E1A_r60_a20	E1A_r60_a20	
E1A_r60_a20	-2.03	10.31	-1.02	10.82	0.3	9.80	0.1	0.00768295	0.03662136	(+)E1A_r60_a20	E1A_r60_a20	
E1A_r60_a20	-2.16	10.32	-1.11	10.88	0.0	9.77	0.1	0.00136401	0.00991481	(+)E1A_r60_a20	E1A_r60_a20	
E1A_r60_a22	-2.02	10.98	-1.02	11.49	0.1	10.47	0.2	0.00458755	0.02460027	(+)E1A_r60_a22	E1A_r60_a22	
E1A_r60_a97	-2.26	8.22	-1.18	8.81	0.2	7.63	0.0	0.00218404	0.01409245	(+)E1A_r60_a97	E1A_r60_a97	
E1A_r60_n11	-3.11	8.19	-1.64	9.01	0.2	7.37	0.1	0.00077007	0.00658197	(+)E1A_r60_n11	E1A_r60_n11	
eaeH	-2.16	12.33	-1.11	12.89	0.1	11.78	0.2	0.00281771	0.01706630	A_07_P008177	b0297	cmr|attaching and effacing protein, pathogenesis factor [b0297]
ebgR	+2.20	9.19	+1.13	8.62	0.3	9.76	0.0	0.00519127	0.02711724	A_07_P041749	c_3832	cmr|Ebg operon repressor [c_3832]
ECs0016	-3.96	12.44	-1.98	13.44	0.0	11.45	0.0	0.00004206	0.00093353	A_07_P058872	ECs0016	cmr|Gef protein [ECs0016]
ECs0031	+2.34	9.98	+1.23	9.37	0.2	10.60	0.2	0.00223052	0.01433372	A_07_P062890	ECs0031	cmr|putative FKBX-type 16KD peptidyl-prolyl cis-trans isomerase [ECs0031]
ECs0052	-2.21	11.93	-1.14	12.50	0.0	11.36	0.0	0.00059481	0.00547004	A_07_P059413	ECs0052	cmr|CcdA-like protein [ECs0052]
ECs0127	-2.06	9.91	-1.04	10.44	0.2	9.39	0.0	0.00230787	0.01468676	A_07_P062900	ECs0127	cmr|hypothetical protein [ECs0127]
ECs0132	-2.41	8.58	-1.27	9.21	0.1	7.94	0.1	0.00092771	0.00755215	A_07_P059452	ECs0132	cmr|hypothetical protein [ECs0132]
ECs0211	+3.12	9.38	+1.64	8.56	0.0	10.20	0.1	0.00012866	0.00184826	A_07_P062916	ECs0211	cmr|DNA polymerase III epsilon subunit [ECs0211]
ECs0278	+3.09	13.44	+1.63	12.63	0.0	14.25	0.0	0.00011209	0.00169030	A_07_P053587	ECs0278	cmr|replication protein [ECs0278]
ECs0309	+2.18	7.73	+1.12	7.17	0.2	8.29	0.1	0.00401692	0.02227627	A_07_P053736	ECs0309	cmr|putative transcriptional regulator [ECs0309]
ECs0325	-2.43	8.29	-1.28	8.93	0.2	7.65	0.3	0.00327560	0.01919557	A_07_P053765	ECs0325	cmr|hypothetical protein [ECs0325]
ECs0330	-3.21	8.74	-1.68	9.58	0.1	7.90	0.1	0.00017284	0.00229052	A_07_P053789	ECs0330	cmr|hypothetical protein [ECs0330]
ECs0332	+3.45	8.46	+1.79	7.57	0.3	9.36	0.1	0.00064963	0.00581122	A_07_P053796	ECs0332	cmr|hypothetical protein [ECs0332]
ECs0357	+2.66	9.14	+1.41	8.43	0.0	9.84	0.0	0.00021437	0.00267014	A_07_P053871	ECs0357	cmr|choline dehydrogenase [ECs0357]
ECs0440	-2.74	7.96	-1.45	8.68	0.2	7.23	0.2	0.00171965	0.01183830	A_07_P054001	ECs0440	cmr|aroM protein [ECs0440]
ECs0449	-5.27	11.65	-2.40	12.85	0.0	10.45	0.1	0.00002686	0.00073391	A_07_P054018	ECs0449	cmr|positive response regulator for pho regulon PhoB [ECs0449]
ECs0483	+3.67	8.77	+1.87	7.83	0.2	9.71	0.0	0.00026118	0.00308044	A_07_P062971	ECs0483	cmr|cytochrome o ubiquinol oxidase subunit IV [ECs0483]
ECs0551	-3.17	10.64	-1.67	11.48	0.1	9.81	0.1	0.00015056	0.00208675	A_07_P054138	ECs0551	cmr|hypothetical protein [ECs0551]
ECs0573	+2.25	7.50	+1.17	6.92	0.0	8.08	0.0	0.00053244	0.00505894	A_07_P054146	ECs0573	cmr|allantoinase [ECs0573]
ECs0679	-2.69	10.30	-1.43	11.01	0.0	9.59	0.2	0.00061403	0.00558100	A_07_P054223	ECs0679	cmr|minor lipoprotein [ECs0679]
ECs0711	-2.16	10.26	-1.11	10.81	0.1	9.70	0.0	0.00140827	0.01016201	A_07_P056574	ECs0711	cmr|hypothetical protein [ECs0711]
ECs0778	-2.10	8.97	-1.07	9.50	0.1	8.43	0.0	0.00090116	0.00739560	A_07_P056671	ECs0778	cmr|quinolinate synthetase A protein [ECs0778]
ECs0794	+2.50	10.08	+1.32	9.42	0.1	10.75	0.0	0.00051120	0.00490750	A_07_P056677	ECs0794	cmr|putative phosphatase [ECs0794]
ECs0805	+164.56	11.31	+7.36	7.63	0.0	14.99	0.1	0.00000013	0.00019431	A_07_P056700	ECs0805	cmr|hypothetical C4-type zinc finger protein TraR-family [ECs0805]
ECs0806	+12.84	11.77	+3.68	9.93	0.3	13.61	0.2	0.00003555	0.00084290	A_07_P056701	ECs0806	cmr|hypothetical protein [ECs0806]
ECs0807	+42.89	10.56	+5.42	7.85	0.0	13.27	0.2	0.00000127	0.00021491	A_07_P056708	ECs0807	cmr|hypothetical protein [ECs0807]
ECs0808	+9.96	12.17	+3.32	10.52	0.2	13.83	0.2	0.00004304	0.00093596	A_07_P056712	ECs0808	cmr|hypothetical protein [ECs0808]
ECs0809	+6.25	13.12	+2.64	11.80	0.1	14.44	0.1	0.00001732	0.00058395	A_07_P056720	ECs0809	cmr|exonuclease [ECs0809]
ECs0810	+27.97	10.56	+4.81	8.15	0.1	12.96	0.1	0.00000062	0.00019431	A_07_P056725	ECs0810	cmr|NinE protein [ECs0810]
ECs0819	+24.51	10.29	+4.62	7.99	0.1	12.60	0.1	0.00000148	0.00022429	A_07_P056765	ECs0819	cmr|endolysin [ECs0819]
ECs0820	+14.27	8.77	+3.83	6.85	0.1	10.69	0.0	0.00000240	0.00027039	A_07_P056766	ECs0820	cmr|putative endopeptidase [ECs0820]
ECs0825	-3.19	8.57	-1.68	9.41	0.2	7.73	0.1	0.00025975	0.00307016	A_07_P056791	ECs0825	cmr|putative terminase large subunit [ECs0825]
ECs0827	-2.05	9.90	-1.04	10.42	0.1	9.38	0.1	0.00286931	0.01731483	A_07_P056801	ECs0827	cmr|putative portal protein [ECs0827]
ECs0828	-2.70	8.18	-1.43	8.90	0.1	7.47	0.2	0.00064463	0.00577966	A_07_P056809	ECs0828	cmr|hypothetical protein [ECs0828]
ECs0839	+2.52	9.64	+1.33	8.97	0.2	10.31	0.1	0.00120470	0.00909682	A_07_P056861	ECs0839	cmr|putative minor tail protein [ECs0839]
ECs0840	+7.62	9.58	+2.93	8.11	0.2	11.04	0.0	0.00001938	0.00062155	A_07_P056866	ECs0840	cmr|putative tail assembly protein [ECs0840]
ECs0841	+3.08	8.69	+1.62	7.88	0.2	9.50	0.2	0.00096893	0.00775143	A_07_P056872	ECs0841	cmr|putative tail assembly protein [ECs0841]
ECs0878	+2.85	10.13	+1.51	9.38	0.0	10.89	0.1	0.00020856	0.00262051	A_07_P056933	ECs0878	cmr|putative enzyme [ECs0878]
ECs0901	+2.40	7.26	+1.27	6.62	0.1	7.89	0.2	0.00178083	0.01216899	A_07_P056937	ECs0901	cmr|hypothetical protein [ECs0901]
ECs0906	+2.43	10.63	+1.28	9.99	0.2	11.27	0.0	0.00124787	0.00931993	A_07_P056943	ECs0906	cmr|hypothetical protein [ECs0906]
ECs0950	-2.02	11.51	-1.01	12.02	0.1	11.00	0.2	0.00245419	0.01539194	A_07_P056991	ECs0950	cmr|hypothetical protein [ECs0950]
ECs0981	+2.81	7.98	+1.49	7.23	0.2	8.72	0.1	0.00053277	0.00505906	A_07_P063053	ECs0981	cmr|anaerobic dimethyl sulfoxide reductase subunit C [ECs0981]
ECs1011	+4.91	9.74	+2.30	8.59	0.1	10.89	0.0	0.00002655	0.00072942	A_07_P063067	ECs1011	cmr|aspartate aminotransferase [ECs1011]
ECs1015	+5.36	9.25	+2.42	8.04	0.0	10.46	0.1	0.00001876	0.00061398	A_07_P063074	ECs1015	cmr|aminopeptidase N [ECs1015]
ECs1081	-3.82	9.15	-1.93	10.11	0.1	8.18	0.0	0.00005492	0.00107955	A_07_P057173	ECs1081	cmr|hypothetical protein [ECs1081]
ECs1092	+6.84	11.43	+2.77	10.05	0.3	12.82	0.0	0.00007088	0.00125539	A_07_P057221	ECs1092	cmr|putative lipoprotein Rz1 protein precursor [ECs1092]
ECs1093	+2.67	7.32	+1.41	6.61	0.0	8.03	0.1	0.00028768	0.00327971	A_07_P057227	ECs1093	cmr|putative endopeptidase [ECs1093]
ECs1105	-2.88	12.22	-1.53	12.98	0.1	11.46	0.3	0.00217496	0.01405686	A_07_P057269	ECs1105	cmr|putative terminase small subunit [ECs1105]
ECs1106	+4.06	9.16	+2.02	8.15	0.0	10.17	0.0	0.00003737	0.00087155	A_07_P057274	ECs1106	cmr|putative terminase large subunit [ECs1106]
ECs1107	+7.66	8.71	+2.94	7.24	0.0	10.17	0.1	0.00000724	0.00040140	A_07_P057276	ECs1107	cmr|putative portal protein [ECs1107]
ECs1108	+45.22	10.81	+5.50	8.06	0.2	13.56	0.1	0.00000094	0.00019431	A_07_P057281	ECs1108	cmr|putative head-tail preconnector protein [ECs1108]
ECs1109	+39.03	10.31	+5.29	7.67	0.3	12.95	0.1	0.00000220	0.00026540	A_07_P057290	ECs1109	cmr|putative head decoration protein [ECs1109]
ECs1110	+27.81	9.24	+4.80	6.84	0.0	11.64	0.2	0.00000197	0.00025681	A_07_P057293	ECs1110	cmr|putative major head protein [ECs1110]
ECs1115	+3.01	8.36	+1.59	7.57	0.1	9.16	0.1	0.00038712	0.00402821	A_07_P057316	ECs1115	cmr|putative minor tail protein [ECs1115]
ECs1119	-2.11	10.77	-1.08	11.31	0.2	10.24	0.1	0.00336452	0.01958264	A_07_P057336	ECs1119	cmr|hypothetical protein [ECs1119]
ECs1160	-2.02	10.48	-1.01	10.99	0.0	9.97	0.3	0.00858206	0.03982196	A_07_P061927	ECs1160	cmr|putative integrase [ECs1160]
ECs1163	+42.62	9.84	+5.41	7.13	0.0	12.54	0.1	0.00000031	0.00019431	A_07_P061944	ECs1163	cmr|hypothetical protein [ECs1163]
ECs1170	+59.08	10.61	+5.88	7.66	0.2	13.55	0.1	0.00000104	0.00020391	A_07_P061980	ECs1170	cmr|C4-type zinc finger protein [ECs1170]
ECs1173	+7.59	10.37	+2.92	8.91	0.6	11.83	0.1	0.00065453	0.00584189	A_07_P061991	ECs1173	cmr|hypothetical protein [ECs1173]
ECs1174	+19.62	12.65	+4.29	10.50	0.3	14.80	0.2	0.00001473	0.00054604	A_07_P061996	ECs1174	cmr|exonuclease [ECs1174]
ECs1175	+8.74	15.25	+3.13	13.69	0.0	16.82	0.0	0.00000442	0.00033535	A_07_P062005	ECs1175	cmr|recombination protein Bet [ECs1175]
ECs1176	+35.96	13.05	+5.17	10.47	0.1	15.64	0.1	0.00000057	0.00019431	A_07_P062008	ECs1176	cmr|host-nuclease inhibitor protein Gam [ECs1176]
ECs1177	+2.83	14.38	+1.50	13.63	0.0	15.13	0.0	0.00017068	0.00227100	A_07_P062011	ECs1177	cmr|Kil protein [ECs1177]
ECs1179	+21.08	13.97	+4.40	11.77	0.2	16.17	0.0	0.00000204	0.00025889	A_07_P062021	ECs1179	cmr|single strand binding protein Ea10 [ECs1179]
ECs1185	-4.10	13.22	-2.04	14.24	0.0	12.20	0.0	0.00003527	0.00084015	A_07_P062053	ECs1185	cmr|putative cI repressor protein [ECs1185]
ECs1186	+11.56	11.53	+3.53	9.77	0.2	13.30	0.0	0.00000679	0.00038477	A_07_P062059	ECs1186	cmr|putative regulatory protein [ECs1186]
ECs1187	+7.41	12.07	+2.89	10.63	0.1	13.52	0.1	0.00000818	0.00041270	A_07_P062064	ECs1187	cmr|regulatory protein CII [ECs1187]
ECs1197	+57.27	9.94	+5.84	7.02	0.0	12.86	0.1	0.00000025	0.00019431	A_07_P062106	ECs1197	cmr|NinE protein [ECs1197]
ECs1207	-2.00	8.25	-1.00	8.75	0.1	7.75	0.1	0.00177437	0.01213541	A_07_P062157	ECs1207	cmr|hypothetical protein [ECs1207]
ECs1234	+2.32	7.53	+1.21	6.92	0.1	8.13	0.3	0.00272304	0.01663479	A_07_P062282	ECs1234	cmr|putative outer membrane protein [ECs1234]
ECs1249	-2.34	12.04	-1.23	12.66	0.2	11.43	0.1	0.00192438	0.01280417	A_07_P062357	ECs1249	cmr|hypothetical protein [ECs1249]
ECs1273	-3.38	7.85	-1.76	8.72	0.6	6.97	0.0	0.00816684	0.03837586	A_07_P062382	ECs1273	cmr|FidL-like protein [ECs1273]
ECs1276	-2.59	8.95	-1.37	9.64	0.4	8.27	0.0	0.00643008	0.03186500	A_07_P062400	ECs1276	cmr|putative chaperone protein [ECs1276]
ECs1283	-2.38	8.29	-1.25	8.92	0.2	7.67	0.0	0.00193226	0.01282529	A_07_P062434	ECs1283	cmr|hemolysin activator-related protein [ECs1283]
ECs1299	-2.25	11.11	-1.17	11.69	0.4	10.53	0.1	0.01117072	0.04896207	A_07_P062501	ECs1299	cmr|putative integrase [ECs1299]
ECs1300	+3.57	8.66	+1.84	7.75	0.2	9.58	0.2	0.00046683	0.00461378	A_07_P062509	ECs1300	cmr|putative membrane protein [ECs1300]
ECs1328	-2.59	8.18	-1.38	8.87	0.1	7.49	0.0	0.00038603	0.00402231	A_07_P062631	ECs1328	cmr|hypothetical protein [ECs1328]
ECs1338	-3.05	9.78	-1.61	10.59	0.1	8.98	0.1	0.00028359	0.00325162	A_07_P062685	ECs1338	cmr|hypothetical protein [ECs1338]
ECs1339	-2.94	8.79	-1.56	9.57	0.3	8.01	0.1	0.00090378	0.00739560	A_07_P062686	ECs1339	cmr|hypothetical protein [ECs1339]
ECs1359	-2.30	8.30	-1.20	8.90	0.1	7.70	0.1	0.00065424	0.00584189	A_07_P060342	ECs1359	cmr|hypothetical protein [ECs1359]
ECs1363	-12.59	9.92	-3.65	11.75	0.1	8.09	0.3	0.00001719	0.00058318	A_07_P060356	ECs1363	cmr|hypothetical protein [ECs1363]
ECs1369	-2.53	7.70	-1.34	8.37	0.1	7.03	0.1	0.00059619	0.00547315	A_07_P060383	ECs1369	cmr|hypothetical protein [ECs1369]
ECs1380	-8.39	9.97	-3.07	11.50	0.1	8.43	0.1	0.00000624	0.00036832	A_07_P060427	ECs1380	cmr|putative transposase OrfB protein of insertion sequence IS629 [ECs1380]
ECs1381	-2.94	9.87	-1.56	10.65	0.1	9.09	0.1	0.00041201	0.00420666	A_07_P060432	ECs1381	cmr|putative transposase OrfA protein of insertion sequence IS629 [ECs1381]
ECs1387	-2.45	8.52	-1.29	9.17	0.0	7.88	0.1	0.00039574	0.00409097	A_07_P060457	ECs1387	cmr|hypothetical protein [ECs1387]
ECs1392	-4.71	8.93	-2.24	10.05	0.0	7.81	0.3	0.00017996	0.00236303	A_07_P060482	ECs1392	cmr|hypothetical protein [ECs1392]
ECs1395	-2.55	7.65	-1.35	8.32	0.1	6.97	0.1	0.00072447	0.00627400	A_07_P060497	ECs1395	cmr|hypothetical protein [ECs1395]
ECs1494	-2.09	9.67	-1.06	10.20	0.2	9.13	0.0	0.00288192	0.01736433	A_07_P063103	ECs1494	cmr|hypothetical protein [ECs1494]
ECs1511	-2.48	12.33	-1.31	12.98	0.1	11.67	0.4	0.00762094	0.03637851	A_07_P060633	ECs1511	cmr|hypothetical protein [ECs1511]
ECs1518	+17.31	10.17	+4.11	8.12	0.3	12.23	0.0	0.00001004	0.00046359	A_07_P060667	ECs1518	cmr|hypothetical protein [ECs1518]
ECs1526	-5.92	8.67	-2.57	9.95	0.0	7.39	0.1	0.00001250	0.00051423	A_07_P060699	ECs1526	cmr|hypothetical protein [ECs1526]
ECs1537	-3.10	11.82	-1.63	12.64	0.1	11.00	0.4	0.00231620	0.01472790	A_07_P060748	ECs1537	cmr|hypothetical protein [ECs1537]
ECs1558	+4.01	8.97	+2.00	7.97	0.3	9.97	0.1	0.00052965	0.00503852	A_07_P060837	ECs1558	cmr|putative tail assembly protein [ECs1558]
ECs1595	-3.83	11.29	-1.94	12.25	0.3	10.32	0.4	0.00304539	0.01807261	A_07_P061000	ECs1595	cmr|hypothetical protein [ECs1595]
ECs1607	-3.43	13.82	-1.78	14.71	0.0	12.93	0.2	0.00036405	0.00388583	A_07_P061030	ECs1607	cmr|hypothetical protein [ECs1607]
ECs1608	+3.27	8.51	+1.71	7.65	0.1	9.36	0.1	0.00023140	0.00282329	A_07_P061034	ECs1608	cmr|isocitrate dehydrogenase [ECs1608]
ECs1609	+17.16	8.86	+4.10	6.81	0.1	10.91	0.2	0.00000457	0.00033765	A_07_P061036	ECs1609	cmr|intergrase [ECs1609]
ECs1610	+95.49	10.66	+6.58	7.37	0.3	13.94	0.0	0.00000093	0.00019431	A_07_P061042	ECs1610	cmr|excisionase [ECs1610]
ECs1612	+5.64	12.66	+2.50	11.41	0.0	13.90	0.0	0.00001412	0.00053964	A_07_P061055	ECs1612	cmr|replication protein P [ECs1612]
ECs1623	+20.88	9.65	+4.38	7.45	0.4	11.84	0.0	0.00003064	0.00078195	A_07_P061089	ECs1623	cmr|putative endopeptidase [ECs1623]
ECs1625	+2.36	7.56	+1.24	6.94	0.0	8.17	0.2	0.00143959	0.01035874	A_07_P061095	ECs1625	cmr|Bor protein precursor [ECs1625]
ECs1638	+35.31	10.61	+5.14	8.04	0.1	13.18	0.0	0.00000052	0.00019431	A_07_P061143	ECs1638	cmr|minor tail protein [ECs1638]
ECs1639	+5.90	11.21	+2.56	9.93	0.0	12.49	0.1	0.00001524	0.00055785	A_07_P061148	ECs1639	cmr|minor tail protein [ECs1639]
ECs1640	+28.79	9.67	+4.85	7.24	0.1	12.09	0.1	0.00000064	0.00019431	A_07_P061154	ECs1640	cmr|major tail protein [ECs1640]
ECs1641	+26.59	9.54	+4.73	7.17	0.1	11.91	0.2	0.00000286	0.00028251	A_07_P061159	ECs1641	cmr|minor tail protein [ECs1641]
ECs1642	+7.62	8.32	+2.93	6.85	0.0	9.78	0.2	0.00001809	0.00060095	A_07_P061162	ECs1642	cmr|minor tail protein [ECs1642]
ECs1643	+6.36	10.19	+2.67	8.86	0.0	11.53	0.0	0.00001017	0.00046432	A_07_P061170	ECs1643	cmr|tail length tape measure protein precursor [ECs1643]
ECs1644	+6.43	10.05	+2.68	8.71	0.2	11.40	0.2	0.00012273	0.00179744	A_07_P061173	ECs1644	cmr|minor tail protein [ECs1644]
ECs1645	+4.27	9.75	+2.10	8.70	0.2	10.79	0.1	0.00018629	0.00241201	A_07_P061180	ECs1645	cmr|minor tail protein [ECs1645]
ECs1666	-4.62	9.71	-2.21	10.82	0.2	8.61	0.1	0.00006738	0.00121740	A_07_P058060	ECs1666	cmr|putative transposase OrfB protein of insertion sequence IS629 [ECs1666]
ECs1702	-2.23	8.11	-1.15	8.69	0.1	7.53	0.2	0.00219478	0.01415011	A_07_P058124	ECs1702	cmr|trehalase [ECs1702]
ECs1724	+3.38	9.35	+1.76	8.47	0.0	10.23	0.0	0.00007581	0.00131154	A_07_P058147	ECs1724	cmr|hypothetical protein [ECs1724]
ECs1726	+3.37	11.12	+1.75	10.24	0.1	12.00	0.0	0.00016061	0.00218551	A_07_P063128	ECs1726	cmr|nitrate/nitrite response regulator protein NarL [ECs1726]
ECs1743	+21.39	11.02	+4.42	8.81	0.3	13.23	0.0	0.00000616	0.00036832	A_07_P063132	ECs1743	cmr|oligopeptide transport periplasmic binding protein [ECs1743]
ECs1751	+10.22	10.24	+3.35	8.56	0.0	11.91	0.0	0.00000299	0.00028496	A_07_P058156	ECs1751	cmr|hypothetical protein [ECs1751]
ECs1773	-2.43	15.57	-1.28	16.21	0.0	14.93	0.0	0.00036682	0.00391011	A_07_P058245	ECs1773	cmr|putative prophage maintenance protein [ECs1773]
ECs1827	-4.05	9.31	-2.02	10.32	0.0	8.30	0.2	0.00022439	0.00275355	A_07_P058453	ECs1827	cmr|IS630 hypothetical protein [ECs1827]
ECs1833	+3.69	8.61	+1.88	7.67	0.1	9.55	0.1	0.00006503	0.00119336	A_07_P058463	ECs1833	cmr|tryptophan synthase beta protein [ECs1833]
ECs1839	-2.31	8.96	-1.21	9.57	0.1	8.36	0.0	0.00089888	0.00739123	A_07_P058472	ECs1839	cmr|hypothetical protein [ECs1839]
ECs1839	-2.36	8.76	-1.24	9.38	0.0	8.14	0.1	0.00052261	0.00499575	A_07_P058472	ECs1839	cmr|hypothetical protein [ECs1839]
ECs1839	-2.39	9.06	-1.26	9.69	0.0	8.43	0.0	0.00037277	0.00394177	A_07_P058472	ECs1839	cmr|hypothetical protein [ECs1839]
ECs1839	-2.38	9.07	-1.25	9.70	0.0	8.45	0.0	0.00037871	0.00396960	A_07_P058472	ECs1839	cmr|hypothetical protein [ECs1839]
ECs1900	-2.76	12.10	-1.47	12.83	0.0	11.36	0.2	0.00059551	0.00547004	A_07_P058536	ECs1900	cmr|putative enzyme [ECs1900]
ECs1906	+2.17	8.45	+1.12	7.90	0.2	9.01	0.1	0.00234582	0.01486822	A_07_P058547	ECs1906	cmr|hypothetical protein [ECs1906]
ECs1930	-2.21	10.16	-1.14	10.73	0.0	9.59	0.2	0.00184752	0.01244116	A_07_P058575	ECs1930	cmr|hypothetical protein [ECs1930]
ECs1951	+56.52	10.09	+5.82	7.18	0.2	13.00	0.1	0.00000099	0.00020340	A_07_P058631	ECs1951	cmr|hypothetical protein [ECs1951]
ECs2049	-2.32	7.66	-1.21	8.27	0.1	7.05	0.0	0.00095827	0.00769355	A_07_P058915	ECs2049	cmr|hypothetical protein [ECs2049]
ECs2081	-2.18	10.06	-1.12	10.62	0.1	9.50	0.1	0.00133959	0.00979769	A_07_P058916	ECs2081	cmr|hypothetical protein [ECs2081]
ECs2113	+2.11	8.29	+1.08	7.75	0.1	8.83	0.1	0.00114409	0.00877803	A_07_P054316	ECs2113	cmr|putative type 1 fimbrial protein precursor [ECs2113]
ECs2139	+2.37	7.87	+1.25	7.24	0.3	8.49	0.2	0.00467360	0.02498512	A_07_P054346	ECs2139	cmr|multiple antibiotic resistance protein [ECs2139]
ECs2177	+3.21	8.34	+1.68	7.50	0.0	9.18	0.1	0.00060345	0.00551728	A_07_P054468	ECs2177	cmr|putative portal protein [ECs2177]
ECs2183	+9.60	9.65	+3.26	8.01	0.1	11.28	0.0	0.00000490	0.00034758	A_07_P054491	ECs2183	cmr|putative lipoprotein Rz1 precursor [ECs2183]
ECs2184	+12.93	8.89	+3.69	7.05	0.0	10.74	0.0	0.00000188	0.00025264	A_07_P054498	ECs2184	cmr|putative endopeptidase [ECs2184]
ECs2234	+4.76	8.35	+2.25	7.22	0.0	9.48	0.0	0.00002391	0.00066473	A_07_P054691	ECs2234	cmr|putative host specificity protein [ECs2234]
ECs2241	-2.64	11.84	-1.40	12.54	0.2	11.14	0.2	0.00156265	0.01102754	A_07_P054726	ECs2241	cmr|putative tail protein [ECs2241]
ECs2319	+2.52	8.51	+1.33	7.84	0.3	9.17	0.1	0.00328762	0.01925605	A_07_P054872	ECs2319	cmr|mannose-6-phosphate isomerase [ECs2319]
ECs2356	+2.23	9.57	+1.15	9.00	0.1	10.15	0.1	0.00056480	0.00527744	A_07_P054895	ECs2356	cmr|hypothetical protein [ECs2356]
ECs2431	+4.04	8.70	+2.01	7.69	0.0	9.70	0.1	0.00026646	0.00310509	A_07_P054909	ECs2431	cmr|hypothetical protein [ECs2431]
ECs2471	+8.13	11.20	+3.02	9.69	0.2	12.71	0.1	0.00001780	0.00059515	A_07_P054922	ECs2471	cmr|hypothetical protein [ECs2471]
ECs2477	-3.10	9.39	-1.63	10.00	0.1	8.37	0.3	0.00009521	0.00788955	A_07_P054931	ECs2477	cmr|putative transposase OrfA protein of insertion sequence IS629 [ECs2477]
ECs2478	-2.72	8.43	-1.44	9.15	0.1	7.71	0.4	0.00093111	0.00376342	A_07_P054936	ECs2478	cmr|putative transposase OrfB protein of insertion sequence IS629 [ECs2478]
ECs2526	+3.65	8.26	+1.87	7.32	0.1	9.19	0.1	0.00038260	0.00399182	A_07_P054984	ECs2526	cmr|hypothetical protein [ECs2526]
ECs2547	-2.35	9.24	-1.23	9.85	0.1	8.62	0.1	0.00041874	0.00425603	A_07_P054991	ECs2547	cmr|hypothetical protein [ECs2547]
ECs2555	-5.65	10.34	-2.50	11.59	0.2	9.09	0.1	0.00004535	0.00095882	A_07_P063252	ECs2555	cmr|protease II [ECs2555]
ECs2619	-2.29	10.88	-1.20	11.48	0.2	10.28	0.1	0.00235605	0.01490900	A_07_P055016	ECs2619	cmr|putative membrane protein [ECs2619]
ECs2658	-3.77	9.92	-1.91	10.87	0.1	8.96	0.1	0.00007092	0.00125539	A_07_P055157	ECs2658	cmr|hypothetical protein [ECs2658]
ECs2668	+4.51	9.99	+2.17	8.90	0.1	11.08	0.1	0.00002816	0.00074298	A_07_P063276	ECs2668	cmr|putative transport system permease protein [ECs2668]
ECs2700	-2.05	8.23	-1.17	8.81	0.0	7.64	0.1	0.00096215	0.00770892	A_07_P063287	ECs2700	cmr|hypothetical protein [ECs2700]
ECs2720	+4.55	8.94	+2.19	7.85	0.0	10.04	0.1	0.00003855	0.00088510	A_07_P055245	ECs2720	cmr|putative host specificity protein [ECs2720]
ECs2720	+4.35	8.94	+2.12	7.88	0.1	10.00	0.1	0.00008627	0.00143428	A_07_P055249	ECs2720	cmr|putative host specificity protein [ECs2720]
ECs2734	+5.37	10.85	+2.42	9.64	0.1	12.06	0.0	0.00001695	0.00058050	A_07_P055282	ECs2734	cmr|putative head completion protein [ECs2734]
ECs2748	+2.58	8.28	+1.37	7.60	0.0	8.96	0.3	0.00351794	0.02022393	A_07_P055335	ECs2748	cmr|hypothetical protein [ECs2748]
ECs2754	-2.76	15.46	-1.19	16.06	0.1	14.87	0.1	0.00054731	0.00516907	A_07_P055361	ECs2754	cmr|prophage maintenance protein [ECs2754]
ECs2773	-2.34	11.19	-1.23	11.81	0.0	10.58	0.0	0.00044512	0.00449498	A_07_P055453	ECs2773	cmr|putative integrase [ECs2773]
ECs2782	-8.54	8.61	-3.09	10.16	0.1	7.07	0.1	0.00000712	0.00039666	A_07_P055462	ECs2782	cmr|hypothetical protein [ECs2782]
ECs2792	-8.02	8.55	-3.00	10.06	0.0	7.05	0.1	0.00000524	0.00034950	A_07_P055475	ECs2792	cmr|hypothetical protein [ECs2792]
ECs2793	-3.61	8.68	-1.85	9.60	0.1	7.75	0.4	0.00121028	0.00912855	A_07_P055479	ECs2793	cmr|hypothetical protein [ECs2793]
ECs2795	-7.45	10.66	-2.90	12.10	0.1	9.21	0.1	0.00001200	0.00050646	A_07_P055487	ECs2795	cmr|putative transposase OrfB protein of insertion sequence IS629 [ECs2795]
ECs2800	+2.25	9.46	+1.17	8.88	0.2	10.05	0.1	0.00220375	0.01419051	A_07_P055513	ECs2800	cmr|hypothetical protein [ECs2800]

ECs2825	+6.84	8.67	+2.77	7.28	0.2	10.05	0.0	0.00005026	0.00101969	A_07_P062811	ECs2825	cmr|N- [ECs2825]
ECs2828	-2.26	8.93	-1.18	9.52	0.1	8.34	0.0	0.00056586	0.00528183	A_07_P055560	ECs2828	cmr|regulator of length of O-antigen component of lipopolysaccharide chains [ECs2828]
ECs2829	-4.03	8.73	-2.01	9.73	0.0	7.72	0.0	0.00004252	0.00093353	A_07_P055562	ECs2829	cmr|UDP-glucose 6-dehydrogenase [ECs2829]
ECs2835	+2.10	10.27	+1.07	9.74	0.1	10.81	0.1	0.00114753	0.00879585	A_07_P055581	ECs2835	cmr|phosphomannomutase [ECs2835]
ECs2845	-2.80	10.47	-1.49	11.22	0.0	9.73	0.3	0.00198508	0.01309851	A_07_P055631	ECs2845	cmr|putative glycosyl transferase [ECs2845]
ECs2905	-3.03	8.58	-1.60	9.38	0.1	7.78	0.2	0.00057798	0.00535596	A_07_P062818	ECs2905	cmr|hypothetical protein [ECs2905]
ECs2933	-3.84	9.14	-1.94	10.11	0.1	8.17	0.1	0.00006569	0.00120118	A_07_P055796	ECs2933	cmr|putative transposase OrfA protein of insertion sequence IS629 [ECs2933]
ECs2978	-2.02	8.63	-1.02	9.14	0.1	8.12	0.1	0.00162210	0.01133021	A_07_P052883	ECs2978	cmr|hypothetical protein [ECs2978]
ECs2981	+34.60	9.06	+5.11	6.50	0.2	11.62	0.0	0.00000093	0.00019431	A_07_P052891	ECs2981	cmr|putative DNA methylase [ECs2981]
ECs2985	+9.24	13.08	+3.21	11.47	0.0	14.68	0.0	0.00000397	0.00032449	A_07_P052912	ECs2985	cmr|Ren protein [ECs2985]
ECs2986	+7.23	14.54	+2.85	13.11	0.1	15.96	0.1	0.00001029	0.00046680	A_07_P052916	ECs2986	cmr|phage replication protein P [ECs2986]
ECs2987	+13.89	11.35	+3.80	9.45	0.2	13.25	0.0	0.00000453	0.00033765	A_07_P052921	ECs2987	cmr|phage replication protein O [ECs2987]
ECs2988	+4.86	9.54	+2.28	8.39	0.2	10.68	0.0	0.00008858	0.00145271	A_07_P052928	ECs2988	cmr|regulatory protein CII [ECs2988]
ECs2996	+16.55	13.74	+4.05	11.71	0.1	15.76	0.0	0.00000131	0.00021824	A_07_P052967	ECs2996	cmr|putative single-stranded DNA binding protein [ECs2996]
ECs2997	+11.70	13.60	+3.55	11.82	0.1	15.37	0.0	0.00000354	0.00030339	A_07_P052972	ECs2997	cmr|regulatory protein cIII [ECs2997]
ECs2998	+3.08	13.78	+1.62	12.97	0.0	14.59	0.0	0.00011299	0.00169761	A_07_P052976	ECs2998	cmr|Kil protein [ECs2998]
ECs2999	+30.13	12.73	+4.91	10.27	0.2	15.19	0.0	0.00000119	0.00021323	A_07_P052981	ECs2999	cmr|host-nuclease inhibitor protein gam [ECs2999]
ECs3000	+23.29	11.41	+4.54	9.14	0.0	13.68	0.1	0.00000136	0.00022125	A_07_P052986	ECs3000	cmr|putative host-nuclease inhibitor protein Gam [ECs3000]
ECs3001	+7.56	13.54	+2.92	12.08	0.1	15.00	0.1	0.00001238	0.00051423	A_07_P052993	ECs3001	cmr|recombination protein Bet [ECs3001]
ECs3002	+5.88	12.34	+2.56	11.06	0.0	13.62	0.1	0.00001547	0.00056253	A_07_P053000	ECs3002	cmr|exonuclease [ECs3002]
ECs3003	+40.59	11.98	+5.34	9.31	0.1	14.65	0.3	0.00000501	0.00034758	A_07_P053004	ECs3003	cmr|hypothetical protein [ECs3003]
ECs3004	+53.38	10.60	+5.74	7.73	0.2	13.47	0.2	0.00000147	0.00022429	A_07_P053006	ECs3004	cmr|hypothetical protein [ECs3004]
ECs3005	+37.52	11.64	+5.23	9.03	0.3	14.26	0.2	0.00000606	0.00036814	A_07_P053011	ECs3005	cmr|hypothetical protein [ECs3005]
ECs3006	+64.74	9.77	+6.02	6.77	0.1	12.78	0.1	0.00000031	0.00019431	A_07_P053018	ECs3006	cmr|putative C4-type zinc finger protein [ECs3006]
ECs3042	+14.47	10.08	+3.86	8.15	0.1	12.00	0.1	0.00000185	0.00025064	A_07_P053100	ECs3042	cmr|galactose-binding transport protein [ECs3042]
ECs3104	+2.42	10.42	+1.28	9.78	0.0	11.06	0.0	0.00035054	0.00377532	A_07_P053132	ECs3104	cmr|outer membrane protein C OmpC [ECs3104]
ECs3152	+2.02	8.91	+1.01	8.41	0.3	9.42	0.1	0.00798753	0.03777581	A_07_P053169	ECs3152	cmr|2-oxoglutarate decarboxylase [ECs3152]
ECs3160	+3.66	7.70	+1.87	6.77	0.1	8.64	0.1	0.00010823	0.00165600	A_07_P062826	ECs3160	cmr|NADH dehydrogenase I chain N [ECs3160]
ECs3163	+10.44	8.79	+3.38	7.10	0.1	10.48	0.3	0.00003442	0.00083231	A_07_P053173	ECs3163	cmr|NADH dehydrogenase I chain K [ECs3163]
ECs3167	+8.06	9.77	+3.01	8.26	0.1	11.27	0.1	0.00001206	0.00050646	A_07_P053176	ECs3167	cmr|NADH dehydrogenase I chain G [ECs3167]
ECs3169	+5.45	11.63	+2.45	10.41	0.2	12.86	0.1	0.00007987	0.00135656	A_07_P063350	ECs3169	cmr|NADH dehydrogenase I chain E [ECs3169]
ECs3179	+3.34	10.23	+1.74	9.37	0.0	11.10	0.0	0.00007634	0.00131755	A_07_P053181	ECs3179	cmr|hypothetical protein [ECs3179]
ECs3196	+5.83	9.18	+2.54	7.90	0.0	10.45	0.1	0.00002699	0.00073391	A_07_P053197	ECs3196	cmr|amidophosphoribosyltransferase [ECs3196]
ECs3197	+5.55	10.93	+2.47	9.69	0.0	12.17	0.0	0.00001362	0.00052801	A_07_P053205	ECs3197	cmr|membrane protein required for colicin V production [ECs3197]
ECs3243	-2.70	8.14	-1.43	8.86	0.1	7.43	0.2	0.00092896	0.00755454	A_07_P053337	ECs3243	cmr|sucrose-6 phosphate hydrolase [ECs3243]
ECs3296	-4.87	11.15	-2.28	12.30	0.1	10.01	0.1	0.00003186	0.00079613	A_07_P053399	ECs3296	cmr|thiosulfate binding protein [ECs3296]
ECs3306	-5.23	11.79	-2.39	12.99	0.0	10.60	0.1	0.00002209	0.00066624	A_07_P063373	ECs3306	cmr|N-acetylmuramoyl-l-alanine amidase I [ECs3306]
ECs3370	+4.74	11.25	+2.25	10.12	0.1	12.37	0.0	0.00004444	0.00094837	A_07_P053430	ECs3370	cmr|IMP dehydrogenase [ECs3370]
ECs3382	-2.32	11.49	-1.22	12.10	0.1	10.88	0.2	0.00155263	0.01097764	A_07_P053440	ECs3382	cmr|putative anaerobic dimethyl sulfoxide reductase chain C [ECs3382]
ECs3398	-5.31	13.60	-2.41	14.81	0.0	12.40	0.0	0.00001676	0.00058010	A_07_P053458	ECs3398	cmr|putative ATP synthase beta subunit [ECs3398]
ECs3442	+4.18	8.71	+2.06	7.68	0.3	9.74	0.0	0.00053507	0.00507319	A_07_P053491	ECs3442	cmr|ATP-dependent RNA helicase [ECs3442]
ECs3450	+2.73	9.45	+1.45	8.73	0.0	10.18	0.1	0.00038797	0.00402870	A_07_P053496	ECs3450	cmr|hypothetical protein [ECs3450]
ECs3492	-3.48	8.70	-1.80	9.60	0.0	7.80	0.1	0.00014289	0.00200686	A_07_P055876	ECs3492	cmr|hypothetical protein [ECs3492]
ECs3521	-2.21	9.17	-1.14	9.74	0.1	8.60	0.2	0.00363596	0.02074077	A_07_P055974	ECs3521	cmr|hypothetical protein [ECs3521]
ECs3535	+2.79	8.33	+1.48	7.59	0.0	9.07	0.2	0.00046241	0.00457870	A_07_P055985	ECs3535	cmr|hypothetical protein [ECs3535]
ECs3569	-3.19	8.06	-1.68	8.90	0.1	7.22	0.2	0.00061077	0.00556489	A_07_P055993	ECs3569	cmr|electron transport protein HydN [ECs3569]
ECs3585	+2.15	9.31	+1.10	8.75	0.1	9.86	0.1	0.00121244	0.00913448	A_07_P056003	ECs3585	cmr|hydrogenase isoenzyme HypD [ECs3585]
ECs3607	-2.11	7.48	-1.08	8.02	0.1	6.94	0.0	0.00113979	0.00875357	A_07_P063410	ECs3607	cmr|alkaline phosphatase isozyme conversion [ECs3607]
ECs3649	+3.15	8.06	+1.65	7.23	0.1	8.88	0.0	0.00012560	0.00182757	A_07_P063411	ECs3649	cmr|putative transport protein [ECs3649]
ECs3663	+3.87	11.51	+1.95	10.53	0.0	12.48	0.0	0.00004347	0.00094275	A_07_P056139	ECs3663	cmr|L-fuculokinase [ECs3663]
ECs3670	-2.17	9.35	-1.12	9.91	0.1	8.79	0.1	0.00155412	0.01097764	A_07_P056142	ECs3670	cmr|hypothetical protein [ECs3670]
ECs3683	+2.40	7.85	+1.26	7.22	0.2	8.49	0.1	0.00135229	0.00986580	A_07_P056146	ECs3683	cmr|prepilin peptidase dependent protein A [ECs3683]
ECs3758	-2.96	8.80	-1.56	9.58	0.2	8.02	0.1	0.00045989	0.00456818	A_07_P056278	ECs3758	cmr|putative oxidoreductase Fe-S subunit [ECs3758]
ECs3764	-3.52	9.27	-1.82	10.17	0.2	8.36	0.0	0.00014428	0.00202100	A_07_P056285	ECs3764	cmr|ssDNA exonuclease RecJ [ECs3764]
ECs3772	+2.27	7.84	+1.18	7.25	0.1	8.43	0.0	0.00067970	0.00598833	A_07_P056288	ECs3772	cmr|hypothetical protein [ECs3772]
ECs3774	+3.18	8.55	+1.67	7.71	0.1	9.38	0.1	0.00025353	0.00301482	A_07_P063454	ECs3774	cmr|glycine decarboxylase [ECs3774]
ECs3778	+2.49	11.95	+1.31	11.29	0.0	12.61	0.0	0.00029545	0.00334773	A_07_P056295	ECs3778	cmr|2-octaprenyl-6-methoxyphenol 4-monoxygenase [ECs3778]
ECs3792	-2.33	7.19	-1.22	7.80	0.2	6.58	0.4	0.00798410	0.03777094	A_07_P056301	ECs3792	cmr|putative transcriptional regulator LYSR-type [ECs3792]
ECs3799	+2.11	7.27	+1.08	6.74	0.1	7.81	0.2	0.00395595	0.02205159	A_07_P056312	ECs3799	cmr|hypothetical protein [ECs3799]
ECs3800	+7.47	8.28	+2.90	6.83	0.1	9.73	0.0	0.00000878	0.00042939	A_07_P056318	ECs3800	cmr|putative transporter [ECs3800]
ECs3801	+2.89	8.30	+1.53	7.53	0.1	9.06	0.0	0.00021258	0.00265188	A_07_P056323	ECs3801	cmr|hypothetical lipoprotein [ECs3801]
ECs3802	+2.14	7.29	+1.10	6.74	0.0	7.84	0.0	0.00068820	0.00603958	A_07_P056330	ECs3802	cmr|putative ABC transporter ATP-binding subunit [ECs3802]
ECs3837	-2.01	12.11	-1.00	12.61	0.1	11.61	0.0	0.00172526	0.01186652	A_07_P063461	ECs3837	cmr|adenine glycosylase [ECs3837]
ECs3844	-4.92	9.67	-2.30	10.82	0.0	8.52	0.1	0.00002943	0.00076000	A_07_P056361	ECs3844	cmr|hypothetical protein [ECs3844]
ECs3853	-2.00	8.43	-1.00	8.93	0.0	7.93	0.0	0.00106076	0.00827993	A_07_P056407	ECs3853	cmr|putative transposase [ECs3853]
ECs3858	-2.65	7.56	-1.41	8.26	0.5	6.85	0.2	0.01018590	0.04533978	A_07_P056433	ECs3858	cmr|hypothetical protein [ECs3858]
ECs3869	-2.56	11.82	-1.36	12.50	0.1	11.15	0.1	0.00032927	0.00361129	A_07_P056468	ECs3869	cmr|hypothetical protein [ECs3869]
ECs3870	-3.23	9.05	-1.69	9.89	0.3	8.20	0.1	0.00131797	0.00971976	A_07_P056475	ECs3870	cmr|hypothetical protein [ECs3870]
ECs3874	+2.14	9.62	+1.10	9.07	0.2	10.17	0.0	0.00226472	0.01450600	A_07_P056483	ECs3874	cmr|hypothetical protein [ECs3874]
ECs3916	-2.65	8.15	-1.40	8.85	0.1	7.44	0.1	0.00035114	0.00377879	A_07_P056524	ECs3916	cmr|putative ABC-type iron-siderophore transport system ATP-binding protein [ECs3916]
ECs3930	-2.40	13.15	-1.26	13.78	0.1	12.52	0.2	0.00111264	0.00860386	A_07_P056534	ECs3930	cmr|hypothetical protein [ECs3930]
ECs3966	+2.17	8.96	+1.11	8.40	0.0	9.52	0.0	0.00071400	0.00621064	A_07_P059647	ECs3966	cmr|putative enzyme [ECs3966]
ECs3995	+14.38	9.18	+3.85	7.25	0.2	11.10	0.0	0.00000613	0.00036832	A_07_P059659	ECs3995	cmr|putative kinase [ECs3995]
ECs4006	+4.64	9.22	+2.21	8.11	0.1	10.32	0.1	0.00003798	0.00087581	A_07_P059666	ECs4006	cmr|putative hydrolase [ECs4006]
ECs4014	+2.58	7.79	+1.37	7.10	0.1	8.47	0.2	0.00110162	0.00853121	A_07_P059680	ECs4014	cmr|N-acetyl-galactosamine / galactosamine PTS system enzyme IIA component [ECs4014]
ECs4014	+2.64	7.85	+1.40	7.15	0.3	8.55	0.1	0.00220217	0.01418618	A_07_P059680	ECs4014	cmr|N-acetyl-galactosamine / galactosamine PTS system enzyme IIA component [ECs4014]
ECs4014	+2.52	8.23	+1.33	7.56	0.1	8.89	0.1	0.00062968	0.00568443	A_07_P059680	ECs4014	cmr|N-acetyl-galactosamine / galactosamine PTS system enzyme IIA component [ECs4014]
ECs4023	-30.04	11.84	-4.91	14.29	0.1	9.39	0.1	0.00000060	0.00019431	A_07_P059688	ECs4023	cmr|truncated putative fimbrial protein [ECs4023]
ECs4052	+2.09	8.27	+1.07	7.74	0.1	8.80	0.2	0.00290426	0.01741803	A_07_P059701	ECs4052	cmr|argininosuccinate synthetase [ECs4052]
ECs4086	+4.49	9.83	+2.17	8.74	0.0	10.91	0.0	0.00002693	0.00073391	A_07_P063500	ECs4086	cmr|hypothetical protein [ECs4086]
ECs4094	+3.11	7.89	+1.64	7.07	0.0	8.71	0.1	0.00012156	0.00178700	A_07_P059712	ECs4094	cmr|hypothetical protein [ECs4094]
ECs4098	+2.04	7.67	+1.03	7.15	0.0	8.19	0.0	0.00103267	0.00811298	A_07_P059716	ECs4098	cmr|N-acetylneuraminate lyase [ECs4098]
ECs4115	-3.37	8.32	-1.75	9.20	0.1	7.45	0.2	0.00034044	0.00369388	A_07_P058957	ECs4115	cmr|hypothetical protein [ECs4115]
ECs4150	+2.96	10.91	+1.57	10.13	0.0	11.70	0.1	0.00015917	0.00217908	A_07_P059737	ECs4150	cmr|hypothetical protein [ECs4150]
ECs4237	+2.04	7.18	+1.03	6.67	0.1	7.69	0.1	0.00199118	0.01312227	A_07_P059765	ECs4237	cmr|hypothetical protein [ECs4237]
ECs4253	-2.36	9.32	-1.24	9.94	0.1	8.70	0.3	0.00349972	0.02014611	A_07_P063536	ECs4253	cmr|hypothetical protein [ECs4253]
ECs4260	+3.57	8.14	+1.83	7.23	0.2	9.06	0.1	0.00018400	0.00239209	A_07_P063542	ECs4260	cmr|positive regulator of mal regulon [ECs4260]
ECs4325	-2.92	8.32	-1.55	9.09	0.0	7.54	0.0	0.00014797	0.00205794	A_07_P059892	ECs4325	cmr|putative O-methyltransferase [ECs4325]
ECs4329	-3.10	10.49	-1.63	11.30	0.0	9.67	0.0	0.00010809	0.00165548	A_07_P059912	ECs4329	cmr|putative acyl carrier protein [ECs4329]
ECs4331	-2.33	7.85	-1.22	8.46	0.2	7.24	0.2	0.00261667	0.01616670	A_07_P059921	ECs4331	cmr|putative surfactin synthetase [ECs4331]
ECs4332	-2.27	7.53	-1.18	8.12	0.0	6.94	0.0	0.00052102	0.00498353	A_07_P059928	ECs4332	cmr|putative [ECs4332]
ECs4337	+2.05	7.48	+1.03	6.96	0.0	7.99	0.0	0.00094090	0.00760835	A_07_P059955	ECs4337	cmr|hypothetical lipoprotein [ECs4337]
ECs4339	+2.29	7.10	+1.19	6.51	0.2	7.70	0.1	0.00144895	0.01040556	A_07_P059965	ECs4339	cmr|putative beta-hydroxydecanoyl-ACP dehydrase [ECs4339]
ECs4353	-2.58	8.61	-1.37	9.30	0.1	7.93	0.2	0.00102922	0.00808988	A_07_P060001	ECs4353	cmr|putative sugar kinase [ECs4353]
ECs4367	+6.22	11.85	+2.64	10.53	0.1	13.17	0.0	0.00001898	0.00061693	A_07_P060029	ECs4367	cmr|universal stress protein UspA [ECs4367]
ECs4407	-2.42	9.40	-1.27	10.03	0.1	8.76	0.1	0.00065903	0.00586205	A_07_P060081	ECs4407	cmr|hypothetical protein [ECs4407]
ECs4457	-2.86	9.21	-1.52	9.97	0.3	8.46	0.3	0.00649773	0.03207913	A_07_P060122	ECs4457	cmr|putative transcriptional regulator [ECs4457]
ECs4475	+3.19	8.05	+1.67	7.21	0.1	8.88	0.1	0.00011744	0.00174890	A_07_P060156	ECs4475	cmr|mannitol-specific PTS system enzyme IIABC components [ECs4475]
ECs4505	-3.96	10.11	-1.99	11.10	0.2	9.12	0.3	0.00049106	0.00476059	A_07_P060214	ECs4505	cmr|lipopolysaccharide core biosynthesis protein RfaP [ECs4505]
ECs4587	-2.13	7.76	-1.09	8.31	0.0	7.22	0.1	0.00093066	0.00756053	A_07_P057552	ECs4587	cmr|hypothetical protein [ECs4587]
ECs4630	-2.52	7.41	-1.34	8.08	0.0	6.74	0.2	0.00121540	0.00914253	A_07_P062852	ECs4630	cmr|hypothetical protein [ECs4630]
ECs4643	+2.37	8.40	+1.24	7.77	0.2	9.02	0.0	0.00212384	0.01380587	A_07_P057644	ECs4643	cmr|hypothetical protein [ECs4643]
ECs4786	+2.93	8.43	+1.55	7.66	0.2	9.21	0.0	0.00047865	0.00468356	A_07_P063635	ECs4786	cmr|DNA polymerase I [ECs4786]
ECs4787	+4.11	9.46	+2.04	8.44	0.0	10.48	0.1	0.00004281	0.00093353	A_07_P057780	ECs4787	cmr|essential GTPase for cell cycle [ECs4787]
ECs4819	+2.68	11.01	+1.42	10.30	0.0	11.72	0.0	0.00021523	0.00267878	A_07_P057834	ECs4819	cmr|formate dehydrogenase-O iron-sulfur subunit [ECs4819]
ECs4832	+2.13	7.69	+1.09	7.14	0.0	8.23	0.0	0.00073110	0.00632113	A_07_P057869	ECs4832	cmr|positive regulator for rhaBAD operon [ECs4832]
ECs4847	+2.94	8.34	+1.55	7.57	0.2	9.12	0.1	0.00070347	0.00614276	A_07_P057876	ECs4847	cmr|hypothetical protein [ECs4847]
ECs4848	+2.38	9.60	+1.25	8.97	0.1	10.22	0.0	0.00043716	0.00439510	A_07_P057881	ECs4848	cmr|putative regulator [ECs4848]
ECs4866	-2.59	9.57	-1.37	10.26	0.1	8.89	0.1	0.00040676	0.00416878	A_07_P063657	ECs4866	cmr|hypothetical protein [ECs4866]
ECs4892	-3.10	12.44	-1.63	13.26	0.5	11.62	0.2	0.00856238	0.03977756	A_07_P057920	ECs4892	cmr|putative amino acid amidohydrolase [ECs4892]
ECs4893	-3.31	12.02	-1.73	12.88	0.3	11.15	0.1	0.00117798	0.00896134	A_07_P057923	ECs4893	cmr|putative membrane transport / symporter protein [ECs4893]
ECs4893	-2.15	11.93	-1.10	12.48	0.1	11.38	0.1	0.00132564	0.00973002	A_07_P057923	ECs4893	cmr|putative membrane transport / symporter protein [ECs4893]
ECs4896	-2.85	9.11	-1.51	9.86	0.1	8.35	0.1	0.00041964	0.00426244	A_07_P057927	ECs4896	cmr|tRNA [ECs4896]
ECs4921	+6.25	9.52	+2.64	8.20	0.0	10.84	0.0	0.00001032	0.00046700	A_07_P057952	ECs4921	cmr|endonuclease V [ECs4921]
ECs4956	-2.07	9.20	-1.05	9.72	0.0	8.67	0.1	0.00180110	0.01225015	A_07_P061239	ECs4956	cmr|hypothetical protein [ECs4956]
ECs4963	+2.64	8.15	+1.40	7.45	0.1	8.85	0.1	0.00056693	0.00528775	A_07_P061274	ECs4963	cmr|hypothetical protein [ECs4963]
ECs4978	-2.09	8.70	-1.06	9.23	0.2	8.17	0.1	0.00310066	0.01836601	A_07_P061350	ECs4978	cmr|hypothetical protein [ECs4978]
ECs5003	-2.11	7.62	-1.08	8.16	0.1	7.08	0.3	0.00524741	0.02732890	A_07_P061472	ECs5003	cmr|putative sorbitol-6-phosphate 2-dehydrogenase [ECs5003]
ECs5043	-2.64	8.32	-1.40	9.02	0.1	7.62	0.1	0.00045061	0.00449586	A_07_P063693	ECs5043	cmr|hypothetical protein [ECs5043]
ECs5051	+10.86	8.62	+3.44	6.90	0.2	10.35	0.1	0.00001535	0.00055949	A_07_P063704	ECs5051	cmr|acetyl-CoA synthetase [ECs5051]
ECs5065	-2.50	7.86	-1.32	8.52	0.0	7.20	0.0	0.00029832	0.00335727	A_07_P061508	ECs5065	cmr|hypothetical protein [ECs5065]
ECs5129	-3.22	9.54	-1.69	10.39	0.0	8.70	0.1	0.00010981	0.00167356	A_07_P058973	ECs5129	cmr|suppressor of groEL [ECs5129]
ECs5165	+11.02	11.05	+3.46	9.32	0.0	12.78	0.0	0.00000282	0.00028143	A_07_P058980	ECs5165	cmr|hypothetical protein [ECs5165]
ECs5273	-2.14	7.36	-1.09	7.91	0.0	6.82	0.1	0.00080478	0.00681577	A_07_P061747	ECs5273	cmr|major type 1 subunit fimbrin [ECs5273]
ECs5282	+4.60	8.31	+2.20	7.21	0.1	9.41	0.0	0.00003278	0.00080633	A_07_P061751	ECs5282	cmr|D-mannonate oxidoreductase [ECs5282]
ECs5296	+2.74	7.76	+1.45	7.03	0.1	8.49	0.0	0.00028603	0.00327271	A_07_P061800	ECs5296	cmr|hypothetical protein [ECs5296]
ECs5338	+4.80	10.35	+2.26	9.22	0.1	11.48	0.0	0.00002536	0.00071770	A_07_P061864	ECs5338	cmr|hypothetical protein [ECs5338]
ECs5344	+2.09	8.70	+1.06	8.17	0.2	9.23	0.1	0.00290293	0.01741803	A_07_P061868	ECs5344	cmr|hypothetical protein [ECs5344]
ECs5345	+5.21	8.88	+2.38	7.69	0.1	10.07	0.1	0.00002925	0.00076000	A_07_P061871	ECs5345	cmr|putative lipoate-protein ligase A [ECs5345]
ECs5350	+2.11	7.67	+1.08	7.13	0.0	8.21	0.0	0.00081088	0.00684165	A_07_P062875	ECs5350	cmr|soluble lytic murein transglycosylase [ECs5350]
edd	+2.56	8.40	+1.36	7.72	0.1	9.07	0.2	0.00084412	0.00705035	A_07_P015931	b1851	cmr|6-phosphogluconate dehydratase [b1851]
elaA	+2.42	8.02	+1.28	7.39	0.0	8.66	0.1	0.00064304	0.00577530	A_07_P032393	c_2811	cmr|Protein elaA [c_2811]
elbB	+4.80	10.08	+2.26	8.95	0.1	11.22	0.0	0.00002625	0.00072778	A_07_P012521	b3209	cmr|sigma cross-reacting protein 27A [b3209]
emrA	-2.00	11.03	-1.00	11.53	0.0	10.53	0.1	0.00132054	0.00971976	A_07_P001896	b2685	cmr|multidrug resistance secretion protein [b2685]
emrD	-5.87	9.97	-2.55	11.24	0.0	8.69	0.3	0.00012603	0.00183113	A_07_P017297	b3673	cmr|2-module integral membrane pump; multidrug resistance [b3673]
emtA	-2.32	10.53	-1.21	11.14	0.2	9.93	0.0	0.00160614	0.01123368	A_07_P006916	b1193	cmr|murein transglycosylase E [b1193]
eno	+3.90	10.35	+1.96	9.37	0.1	11.33	0.0	0.00005551	0.00108557	A_07_P002342	b2779	cmr|enolase [b2779]
epd	+3.18	10.63	+1.67	9.80	0.2	11.47	0.0	0.00035616	0.00381456	A_07_P011783	b2927	cmr|D-erythrose 4-phosphate dehydrogenase [b2927]
eptA	+2.34	8.46	+1.23	7.85	0.0	9.08	0.1	0.00049506	0.00478762	A_07_P011307	b4114	cmr|orf, hypothetical protein [b4114]
eptB	+2.32	7.99	+1.22	7.38	0.0	8.59	0.1	0.00083915	0.00702801	A_07_P007657	b3546	cmr|orf, hypothetical protein [b3546]
EQC	-2.09	9.05	-1.06	9.59	0.2	8.52	0.2	0.00582192	0.02964589	(+)eQC-42	EQC	
erpA	-12.08	11.18	-3.59	12.98	0.1	9.38	0.1	0.00000297	0.00028496	A_07_P002744	b0156	cmr|orf, hypothetical protein [b0156]
essD	+22.15	9.78	+4.47	7.55	0.2	12.01	0.0	0.00000428	0.00033352	A_07_P016531	b0554	cmr|orf, hypothetical protein [b0554]
essQ	+2.53	7.70	+1.34	7.03	0.2	8.37	0.1	0.00162713	0.01135023	A_07_P010455	b1556	cmr|orf, hypothetical protein [b1556]
ETG10_234183	-2.63	12.08	-1.39	12.77	0.2	11.38	0.2	0.00211567	0.01376413	ETG10_234183	ETG10_234183	
ETG10_234183	-2.91	12.53	-1.54	13.31	0.2	11.76	0.5	0.00622418	0.03105973	ETG10_234183	ETG10_234183	
ETG10_236652	+2.61	7.47	+1.39	6.78	0.1	8.17	0.0	0.00042201	0.00428377	ETG10_236652	ETG10_236652	
etpO	-2.07	9.18	-1.05	9.70	0.1	8.65	0.2	0.00336110	0.01957722	A_07_P048849	ABH-0244075	asap|type II secretion protein [L7044]
eutA	+2.27	7.33	+1.19	6.74	0.1	7.92	0.2	0.00294589	0.01761493	A_07_P013311	b2451	cmr|orf, hypothetical protein [b2451]
eutC	+2.14	7.29	+1.10	6.74	0.1	7.84	0.1	0.00124206	0.00928541	A_07_P042830	Z3705	cmr|ethanolamine ammonia-lyase, light chain [Z3705]
exoD	+6.21	13.03	+2.63	11.71	0.0	14.34	0.2	0.00005105	0.00103301	A_07_P016473	b0539	cmr|putative exonuclease [b0539]
exuR	-2.41	12.59	-1.27	13.22	0.1	11.95	0.2	0.00109157	0.00847006	A_07_P000199	b3094	cmr|negative regulator of exu regulon, exuT, uxaAC, and uxuB [b3094]
exuT	+6.58	8.61	+2.72	7.25	0.1	9.97	0.1	0.00001473	0.00054604	A_07_P000192	b3093	cmr|transport of hexuronates [b3093]
fabB	+7.57	12.20	+2.92	10.74	0.0	13.66	0.0	0.00000589	0.00036511	A_07_P013901	b2323	cmr|3-oxoacyl- [b2323]
fabD	+5.00	12.81	+2.32	11.65	0.1	13.97	0.1	0.00002697	0.00073391	A_07_P001661	b1092	cmr|malonyl-CoA- [b1092]
fabG	+5.97	12.37	+2.58	11.08	0.1	13.66	0.1	0.00002062	0.00063650	A_07_P001668	b1093	cmr|3-oxoacyl- [b1093]
fabH	+3.80	12.63	+1.93	11.66	0.1	13.59	0.3	0.00039229	0.00405794	A_07_P001656	b1091	cmr|3-oxoacyl- [b1091]
fabZ	-2.09	14.37	-1.06	14.90	0.0	13.84	0.0	0.00087923	0.00727980	A_07_P002859	b0180	cmr|(3R)-hydroxymyristol acyl carrier protein dehydratase [b0180]
fadI	-3.34	11.34	-1.74	12.21	0.2	10.47	0.0	0.00034038	0.00369388	A_07_P053270	ECs3225	cmr|putative acyltransferase [ECs3225]
fadI	-3.40	10.78	-1.77	11.67	0.1	9.90	0.1	0.00009887	0.00155813	A_07_P014000	b2342	cmr|putative acyltransferase [b2342]
fadI	-2.93	11.08	-1.55	11.86	0.4	10.31	0.1	0.00254529	0.01580792	A_07_P042685	Z3605	cmr|putative acyltransferase [Z3605]
fadJ	+2.07	11.06	+1.05	10.53	0.0	11.59	0.0	0.00090348	0.00739560	A_07_P013995	b2341	cmr|putative enzyme [b2341]
fadL	+5.84	8.20	+2.55	6.93	0.1	9.48	0.1	0.00002052	0.00063471	A_07_P032506	c_2889	cmr|Long-chain fatty acid transport protein precursor [c_2889]
fbaA	+9.27	11.27	+3.21	9.67	0.1	12.88	0.1	0.00000597	0.00036562	A_07_P011772	b2925	cmr|fructose-bisphosphate aldolase, class II [b2925]
fbaB	+2.23	10.10	+1.16	9.52	0.0	10.68	0.0	0.00061149	0.00556489	A_07_P003250	b2097	cmr|orf, hypothetical protein [b2097]
fbp	-2.53	14.13	-1.34	14.80	0.0	13.46	0.0	0.00027061	0.00313734	A_07_P003714	b4232	cmr|fructose-bisphosphatase [b4232]
fdhE	+2.22	9.89	+1.15	9.32	0.2	10.47	0.1	0.00144569	0.01039310	A_07_P039385	c_4841	cmr|Protein fdhE [c_4841]
fdhE	+2.02	10.02	+1.01	9.52	0.1	10.53	0.1	0.00209039	0.01364472	A_07_P039385	c_4841	cmr|Protein fdhE [c_4841]
fdhE	+2.10	10.30	+1.07	9.77	0.0	10.84	0.0	0.00082053	0.00690825	A_07_P039385	c_4841	cmr|Protein fdhE [c_4841]
fdnG	+3.44	9.71	+1.78	8.82	0.2	10.60	0.2	0.00040855	0.00417949	A_07_P009461	b1474	cmr|formate dehydrogenase-N, nitrate-inducible, alpha subunit [b1474]
fdnH	+3.10	8.51	+1.63	7.69	0.1	9.32	0.1	0.00020594	0.00260014	A_07_P009468	b1475	cmr|formate dehydrogenase-N, nitrate-inducible, iron-sulfur beta subunit [b1475]
fdoG	+2.86	8.55	+1.52	7.79	0.0	9.31	0.1	0.00024255	0.00291707	A_07_P019246	b3894	cmr|formate dehydrogenase-O, major subunit [b3894]
fdoH	+3.36	9.53	+1.75	8.66	0.2	10.41	0.2	0.00058420	0.00539455	A_07_P019241	b3893	cmr|formate dehydrogenase-O, iron-sulfur subunit [b3893]
fdoH	+3.34	10.14	+1.74	9.26	0.0	11.01	0.0	0.00007682	0.00132177	A_07_P039386	c_4843	cmr|Formate dehydrogenase-O beta subunit [c_4843]
fdoH	+2.65	11.07	+1.41	10.36	0.0	11.77	0.0	0.00021702	0.00269339	A_07_P047064	Z5435	cmr|formate dehydrogenase-O, iron-sulfur subunit [Z5435]
fdoI	+4.80	9.81	+2.26	8.67	0.1	10.94	0.1	0.00002635	0.00072866	A_07_P019239	b3892	cmr|formate dehydrogenase, cytochrome B556 [b3892]
fecB	-2.32	9.95	-1.22	10.56	0.1	9.34	0.1	0.00083922	0.00702801	A_07_P003977	b4290	cmr|citrate-dependent iron transport, periplasmic protein [b4290]
fecI	-2.39	8.64	-1.26	9.26	0.1	8.01	0.2	0.00109393	0.00848418	A_07_P003994	b4293	cmr|probable RNA polymerase sigma factor [b4293]
fepE	-19.90	11.28	-4.31	13.43	0.0	9.12	0.2	0.00000237	0.00027039	A_07_P031316	c_0674	cmr|Ferric enterobactin transport protein fepE [c_0674]
ffh	-2.68	13.72	-1.42	14.43	0.0	13.00	0.0	0.00022177	0.00273628	A_07_P019926	b2610	cmr|GTP-binding export factor binds to signal sequence, GTP and RNA [b2610]
fhuD	-2.25	7.90	-1.17	8.48	0.0	7.31	0.0	0.00054860	0.00517818	A_07_P002724	b0152	cmr|hydroxamate-dependent iron uptake, cytoplasmic membrane component [b0152]
fimA	-3.78	9.03	-1.92	9.99	0.0	8.07	0.1	0.00005837	0.00111936	A_07_P004096	b4314	cmr|major type 1 subunit fimbrin [b4314]
fimC	-2.53	8.36	-1.34	9.03	0.1	7.69	0.1	0.00050673	0.00488112	A_07_P004109	b4316	cmr|periplasmic chaperone, required for type 1 fimbriae [b4316]
fimD	-12.14	9.45	-3.60	11.25	0.0	7.65	0.2	0.00000749	0.00040630	A_07_P004111	b4317	cmr|outer membrane protein; export and assembly of type 1 fimbriae, interrupted [b4317]
fimF	-16.44	9.29	-4.04	11.31	0.2	7.27	0.1	0.00000406	0.00032474	A_07_P004120	b4318	cmr|fimbrial morphology [b4318]
fimF	-8.58	8.26	-3.10	9.82	0.1	6.71	0.1	0.00000758	0.00040630	A_07_P041401	c_5397	cmr|FimF protein precursor [c_5397]
fimG	-8.60	10.88	-3.10	12.43	0.1	9.32	0.1	0.00001105	0.00048316	A_07_P004124	b4319	cmr|fimbrial morphology [b4319]
fimH	-3.66	7.83	-1.87	8.77	0.1	6.90	0.0	0.00007113	0.00125539	A_07_P004128	b4320	cmr|minor fimbrial subunit, D-mannose specific adhesin [b4320]
fimI	-2.02	9.13	-1.01	9.64	0.1	8.63	0.1	0.00262177	0.01618712	A_07_P004101	b4315	cmr|fimbrial protein [b4315]
fis	+4.74	10.54	+2.24	9.41	0.1	11.66	0.0	0.00002913	0.00075920	A_07_P012772	b3261	cmr|site-specific DNA inversion stimulation factor; DNA-binding protein; a trans activator for transcription [b3261]
fklB	+2.42	11.68	+1.28	11.04	0.1	12.32	0.1	0.00077145	0.00659019	A_07_P011753	b4207	cmr|FKBP-type 22KD peptidyl-prolyl cis-trans isomerase [b4207]
fkpB	+4.25	10.50	+2.09	9.46	0.0	11.55	0.0	0.00003384	0.00082101	A_07_P010829	b0028	cmr|probable FKBX-type 16KD peptidyl-prolyl cis-trans isomerase [b0028]
flgK	-2.05	9.47	-1.04	9.99	0.1	8.96	0.2	0.00229730	0.01464911	A_07_P001612	b1082	cmr|flagellar biosynthesis, hook-filament junction protein 1 [b1082]
flgL	-2.31	8.59	-1.21	9.19	0.2	7.98	0.1	0.00157810	0.01109673	A_07_P001620	b1083	cmr|flagellar biosynthesis; hook-filament junction protein [b1083]
flhD	+2.72	8.55	+1.44	7.83	0.0	9.27	0.1	0.00025783	0.00305666	A_07_P016140	b1892	cmr|regulator of flagellar biosynthesis, acting on class 2 operons; transcriptional initiation factor [b1892]
fliA	-3.91	7.96	-1.97	8.94	0.1	6.97	0.1	0.00008935	0.00145767	A_07_P014973	b1922	cmr|flagellar biosynthesis; alternative sigma factor 28; regulation of flagellar operons [b1922]
fliI	-2.95	12.39	-1.56	13.16	0.3	11.61	0.1	0.00122183	0.00918208	A_07_P044691	Z3031	cmr|flagellum-specific ATP synthase [Z3031]
fliI	-2.80	12.49	-1.49	13.23	0.4	11.75	0.1	0.00371157	0.02103173	A_07_P055201	ECs2680	cmr|flagellum-specific ATP synthase [ECs2680]
fliI	-2.32	12.02	-1.22	12.63	0.4	11.41	0.1	0.01000488	0.04476184	A_07_P015066	b1941	cmr|flagellum-specific ATP synthase [b1941]
fliI	-2.81	11.78	-1.49	12.53	0.2	11.03	0.0	0.00042456	0.00430129	A_07_P035407	c_2358	cmr|Flagellum-specific ATP synthase [c_2358]
fliY	-6.88	12.76	-2.78	14.15	0.0	11.36	0.0	0.00000760	0.00040630	A_07_P041209	c_2335	cmr|Cystine-binding periplasmic protein precursor [c_2335]
fliY	-6.03	11.64	-2.59	12.93	0.1	10.34	0.0	0.00001250	0.00051423	A_07_P014964	b1920	cmr|putative periplasmic binding transport protein [b1920]
flu	+3.06	10.51	+1.62	9.70	0.5	11.31	0.0	0.00723627	0.03496863	A_07_P015330	b2000	cmr|outer membrane fluffing protein, similar to adhesin [b2000]
fmt	-2.71	11.97	-1.44	12.69	0.0	11.25	0.2	0.00044950	0.00448761	A_07_P012874	b3288	cmr|10-formyltetrahydrofolate:L-methionyl-tRNA [b3288]
fnr	-10.73	13.62	-3.42	15.33	0.0	11.91	0.2	0.00001341	0.00052642	A_07_P014647	b1334	cmr|transcriptional regulation of aerobic, anaerobic respiration, osmotic balance [b1334]
focA	+3.50	10.70	+1.81	9.80	0.1	11.60	0.1	0.00011177	0.00169030	A_07_P004969	b0904	cmr|probable formate transporter [b0904]
focA	+40.43	12.66	+5.34	9.99	0.0	15.33	0.1	0.00000065	0.00019431	A_07_P040486	c_1239	cmr|F1C major fimbrial subunit precursor [c_1239]
focC	+6.88	9.56	+2.78	8.16	0.1	10.95	0.0	0.00001310	0.00052207	A_07_P040500	c_1241	cmr|F1C periplasmic chaperone [c_1241]
focD	+3.56	10.43	+1.83	9.52	0.3	11.35	0.1	0.00052728	0.00502204	A_07_P040505	c_1242	cmr|F1C fimbrial usher [c_1242]
focF	+3.53	9.81	+1.82	8.90	0.2	10.72	0.1	0.00018230	0.00238186	A_07_P040507	c_1243	cmr|F1C minor fimbrial subunit F precursor [c_1243]
focX	-2.87	10.63	-1.52	11.39	0.2	9.87	0.1	0.00055293	0.00520656	A_07_P040530	c_1247	cmr|Putative Regulatory protein [c_1247]
folA	+2.54	9.24	+1.35	8.56	0.1	9.91	0.1	0.00043446	0.00437074	A_07_P010929	b0048	cmr|dihydrofolate reductase type I; trimethoprim resistance [b0048]
folA	+2.36	10.35	+1.24	9.73	0.1	10.97	0.0	0.00067081	0.00593666	A_07_P035679	c_0058	cmr|Dihydrofolate reductase [c_0058]
folA	+2.49	9.20	+1.32	8.54	0.0	9.86	0.1	0.00035211	0.00378335	A_07_P049144	Z0055	cmr|dihydrofolate reductase type I trimethoprim resistance [Z0055]
folA	+2.62	9.29	+1.39	8.60	0.0	9.98	0.0	0.00023169	0.00282329	A_07_P059409	ECs0051	cmr|dihydrofolate reductase type I; trimethoprim resistance [ECs0051]
fpr	+3.18	9.38	+1.67	8.54	0.1	10.21	0.1	0.00033822	0.00367995	A_07_P039438	c_4876	cmr|Ferredoxin--NADP reductase [c_4876]
fpr	+3.89	8.89	+1.96	7.91	0.1	9.87	0.1	0.00010565	0.00163561	A_07_P019396	b3924	cmr|ferredoxin-NADP reductase [b3924]
frdB	+2.66	12.30	+1.41	11.59	0.1	13.01	0.0	0.00030073	0.00337715	A_07_P011497	b4153	cmr|fumarate reductase, anaerobic, iron-sulfur protein subunit [b4153]
frdC	+2.61	11.48	+1.38	10.79	0.2	12.17	0.0	0.00084519	0.00705338	A_07_P011491	b4152	cmr|fumarate reductase, anaerobic, membrane anchor polypeptide [b4152]
frdD	+2.39	9.69	+1.26	9.06	0.2	10.32	0.0	0.00085517	0.00712456	A_07_P011487	b4151	cmr|fumarate reductase, anaerobic, membrane anchor polypeptide [b4151]
frmR	+6.50	10.64	+2.70	9.29	0.1	11.99	0.1	0.00001700	0.00058050	A_07_P020911	b0357	cmr|putative alpha helix chain [b0357]
frr	-2.15	13.50	-1.10	14.05	0.0	12.95	0.0	0.00070711	0.00617112	A_07_P002818	b0172	cmr|ribosome releasing factor [b0172]
fruR	+2.89	10.03	+1.53	9.26	0.1	10.79	0.1	0.00021876	0.00270977	A_07_P011076	b0080	cmr|transcriptional repressor of fru operon and others [b0080]
fryB	-2.13	7.38	-1.09	7.92	0.0	6.83	0.0	0.00081774	0.00688848	A_07_P014219	b2387	cmr|putative PTS system enzyme IIB component [b2387]
ftnA	+17.48	10.12	+4.13	8.05	0.0	12.18	0.0	0.00000107	0.00020503	A_07_P016193	b1905	cmr|cytoplasmic ferritin [b1905]
ftnB	+4.17	10.14	+2.06	9.11	0.1	11.17	0.1	0.00004097	0.00091779	A_07_P016180	b1902	cmr|ferritin-like protein [b1902]
ftsE	-8.42	11.03	-3.07	12.57	0.0	9.50	0.0	0.00000524	0.00034781	A_07_P007255	b3463	cmr|ATP-binding component of a membrane-associated complex involved in cell division [b3463]
ftsY	-4.40	13.17	-2.14	14.24	0.1	12.10	0.1	0.00005157	0.00103969	A_07_P007256	b3464	cmr|cell division membrane protein [b3464]
fucA	+2.64	10.69	+1.40	9.99	0.0	11.39	0.0	0.00023000	0.00281576	A_07_P005999	b2800	cmr|L-fuculose-1-phosphate aldolase [b2800]
fucK	+3.29	9.36	+1.72	8.50	0.1	10.22	0.0	0.00018109	0.00237584	A_07_P006014	b2803	cmr|L-fuculokinase [b2803]
fucK	+3.39	11.60	+1.76	10.72	0.3	12.49	0.0	0.00076736	0.00656593	A_07_P043254	Z4120	cmr|L-fuculokinase [Z4120]
fucO	+4.09	9.78	+2.03	8.77	0.0	10.80	0.1	0.00004092	0.00091779	A_07_P005991	b2799	cmr|L-1,2-propanediol oxidoreductase [b2799]
fucP	-2.14	10.38	-1.10	10.93	0.3	9.84	0.0	0.00393053	0.02197522	A_07_P006001	b2801	cmr|fucose permease [b2801]
fucR	+4.13	8.28	+2.05	7.26	0.1	9.31	0.0	0.00004770	0.00098950	A_07_P006024	b2805	cmr|positive regulator of the fuc operon [b2805]
fucU	+3.26	11.16	+1.71	10.30	0.1	12.01	0.0	0.00009335	0.00149973	A_07_P006018	b2804	cmr|protein of fucose operon [b2804]
fumA	+14.13	10.51	+3.82	8.60	0.0	12.42	0.0	0.00000166	0.00023773	A_07_P020691	b1612	cmr|fumarase A = fumarate hydratase Class I; aerobic isozyme [b1612]
fumB	+3.06	10.37	+1.61	9.56	0.4	11.17	0.0	0.00215863	0.01397427	A_07_P011347	b4122	cmr|fumarase B= fumarate hydratase Class I; anaerobic isozyme [b4122]
fumC	+5.11	8.64	+2.35	7.46	0.0	9.81	0.1	0.00002107	0.00064399	A_07_P042312	c_2003	cmr|Fumarate hydratase class II [c_2003]
fumC	+8.08	8.82	+3.02	7.32	0.1	10.33	0.0	0.00000566	0.00035797	A_07_P020689	b1611	cmr|fumarase C= fumarate hydratase Class II; isozyme [b1611]
galF	+3.14	10.29	+1.65	9.46	0.1	11.11	0.0	0.00019018	0.00245020	A_07_P015526	b2042	cmr|homolog of Salmonella UTP--glucose-1-P uridylyltransferase, probably a UDP-gal transferase [b2042]
galK	+7.17	11.57	+2.84	10.15	0.1	13.00	0.1	0.00000898	0.00043361	A_07_P004240	b0757	cmr|galactokinase [b0757]
galM	+6.86	10.77	+2.78	9.38	0.1	12.16	0.1	0.00001329	0.00052521	A_07_P004231	b0756	cmr|galactose-1-epimerase [b0756]
galS	+2.87	9.57	+1.52	8.80	0.2	10.33	0.0	0.00064761	0.00579974	A_07_P032245	c_2685	cmr|Mgl repressor and galactose ultrainduction factor [c_2685]
galT	+2.25	10.30	+1.17	9.72	0.0	10.89	0.0	0.00055909	0.00525198	A_07_P004241	b0758	cmr|galactose-1-phosphate uridylyltransferase [b0758]
gamW	+20.43	13.28	+4.35	11.10	0.2	15.45	0.0	0.00000404	0.00032474	A_07_P038414	c_1537	cmr|Putative host-nuclease inhibitor protein Gam of bacteriphage [c_1537]
gapA	+14.88	10.66	+3.90	8.71	0.1	12.61	0.1	0.00000354	0.00030339	A_07_P015590	b1779	cmr|glyceraldehyde-3-phosphate dehydrogenase A [b1779]
gcd	-2.59	8.73	-1.37	9.42	0.2	8.05	0.1	0.00093147	0.00756060	A_07_P002585	b0124	cmr|glucose dehydrogenase [b0124]
gcvH	+76.66	11.01	+6.26	7.88	0.0	14.14	0.0	0.00000015	0.00019431	A_07_P041711	c_3484	cmr|Glycine cleavage system H protein [c_3484]
gcvH	+48.16	10.28	+5.59	7.49	0.2	13.08	0.0	0.00000075	0.00019431	A_07_P006489	b2904	cmr|in glycine cleavage complex, carrier of aminomethyl moiety via covalently bound lipoyl cofactor [b2904]
gcvH	+44.64	11.31	+5.48	8.57	0.3	14.05	0.0	0.00000188	0.00025064	A_07_P041275	c_3484	cmr|Glycine cleavage system H protein [c_3484]
gcvP	+3.23	8.70	+1.69	7.86	0.1	9.55	0.1	0.00023559	0.00285318	A_07_P032879	c_3483	cmr|Glycine dehydrogenase [c_3483]
gcvP	+3.73	8.60	+1.90	7.65	0.2	9.55	0.1	0.00016661	0.00223623	A_07_P052779	Z4240	cmr|glycine decarboxylase, P protein of glycine cleavage [Z4240]
gcvP	+5.62	8.29	+2.49	7.04	0.0	9.53	0.1	0.00002015	0.00063193	A_07_P006481	b2903	cmr|glycine decarboxylase, P protein of glycine cleavage system [b2903]
gcvR	+6.92	9.17	+2.79	7.78	0.1	10.57	0.0	0.00000882	0.00042982	A_07_P013453	b2479	cmr|transcriptional regulation of gcv operon [b2479]
gcvT	+46.68	10.72	+5.54	7.95	0.0	13.49	0.1	0.00000028	0.00019431	A_07_P006491	b2905	cmr|aminomethyltransferase [b2905]
gef	-4.59	12.55	-2.20	13.65	0.0	11.45	0.0	0.00002726	0.00073404	A_07_P048482	Z0016	cmr|Gef protein interferes with membrane function when [Z0016]
gef	-2.42	10.72	-1.28	11.36	0.1	10.08	0.0	0.00044094	0.00442459	A_07_P048478	Z0016	cmr|Gef protein interferes with membrane function when [Z0016]
gfcA	-3.40	11.94	-1.77	12.83	0.0	11.06	0.2	0.00031542	0.00349707	A_07_P005379	b0987	cmr|orf, hypothetical protein [b0987]
gfcD	-2.06	15.14	-1.04	15.66	0.0	14.62	0.2	0.00323447	0.01901548	A_07_P005364	b0984	cmr|orf, hypothetical protein [b0984]
ggt	-2.25	7.58	-1.17	8.16	0.0	6.99	0.1	0.00087198	0.00723355	A_07_P034524	c_4236	cmr|Gamma-glutamyltranspeptidase precursor [c_4236]
glcB	+3.34	9.20	+1.74	8.33	0.1	10.08	0.0	0.00009231	0.00148959	A_07_P012016	b2976	cmr|malate synthase G [b2976]
glcB	+4.78	11.22	+2.26	10.09	0.1	12.34	0.1	0.00004896	0.00100424	A_07_P041726	c_3705	cmr|Malate synthase G [c_3705]
glcD	+4.07	8.64	+2.02	7.62	0.0	9.65	0.0	0.00004252	0.00093353	A_07_P012031	b2979	cmr|glycolate oxidase subunit D [b2979]
glcF	+11.09	9.31	+3.47	7.58	0.1	11.05	0.1	0.00000593	0.00036511	A_07_P012026	b2978	cmr|glycolate oxidase iron-sulfur subunit [b2978]
glcG	+39.37	9.66	+5.30	7.01	0.0	12.31	0.0	0.00000030	0.00019431	A_07_P012024	b2977	cmr|orf, hypothetical protein [b2977]
gldA	+6.23	12.06	+2.64	10.74	0.2	13.38	0.1	0.00003134	0.00078813	A_07_P019501	b3945	cmr|glycerol dehydrogenase, [b3945]
glgA	+4.45	10.50	+2.15	9.42	0.1	11.58	0.1	0.00004587	0.00096667	A_07_P018171	b3429	cmr|glycogen synthase [b3429]
glgB	+2.58	9.19	+1.37	8.50	0.1	9.87	0.1	0.00044167	0.00442752	A_07_P018189	b3432	cmr|1,4-alpha-glucan branching enzyme [b3432]
glgC	+6.25	9.90	+2.64	8.57	0.1	11.22	0.0	0.00001456	0.00054604	A_07_P018179	b3430	cmr|glucose-1-phosphate adenylyltransferase [b3430]
glgP	+2.70	8.17	+1.43	7.46	0.3	8.89	0.1	0.00185063	0.01245671	A_07_P018166	b3428	cmr|glycogen phosphorylase [b3428]
glgS	+5.19	9.98	+2.38	8.79	0.0	11.17	0.0	0.00001740	0.00058395	A_07_P012366	b3049	cmr|glycogen biosynthesis, rpoS dependent [b3049]
glgX	+4.10	10.89	+2.04	9.87	0.1	11.91	0.1	0.00006778	0.00122099	A_07_P018182	b3431	cmr|part of glycogen operon, a glycosyl hydrolase, debranching enzyme [b3431]
glmM	+3.27	11.18	+1.71	10.32	0.1	12.03	0.0	0.00010259	0.00160236	A_07_P000591	b3176	cmr|similar to phosphoglucomutases and phosphomannomutases [b3176]
glnA	-4.89	13.16	-2.29	14.30	0.0	12.01	0.2	0.00005624	0.00109182	A_07_P019129	b3870	cmr|glutamine synthetase [b3870]
glnB	+3.68	11.06	+1.88	10.12	0.1	12.00	0.0	0.00006001	0.00114386	A_07_P019668	b2553	cmr|regulatory protein P-II for glutamine synthetase [b2553]
glnH	-3.21	14.65	-1.68	15.49	0.0	13.81	0.2	0.00030440	0.00340122	A_07_P004510	b0811	cmr|periplasmic glutamine-binding protein; permease [b0811]
gloA	+4.38	9.53	+2.13	8.47	0.2	10.60	0.1	0.00011152	0.00169030	A_07_P020890	b1651	cmr|lactoylglutathione lyase [b1651]
glpB	-2.16	10.46	-1.11	11.02	0.1	9.91	0.2	0.00197928	0.01307121	A_07_P000998	b2242	cmr|sn-glycerol-3-phosphate dehydrogenase [b2242]

glpE	-2.13	9.81	-1.09	10.36	0.0	9.26	0.1	0.00100097	0.00793120	A_07_P018153	b3425	cmr|protein of glp regulon [b3425]
glpF	+10.50	9.75	+3.39	8.05	0.1	11.44	0.0	0.00000328	0.00029330	A_07_P019412	b3927	cmr|facilitated diffusion of glycerol [b3927]
glpK	+2.01	9.90	+1.01	9.40	0.1	10.41	0.1	0.00143802	0.01035215	A_07_P019409	b3926	cmr|glycerol kinase [b3926]
glpT	+6.19	8.95	+2.63	7.63	0.1	10.26	0.2	0.00004123	0.00092082	A_07_P063326	ECs3125	cmr|sn-glycerol-3-phosphate permease [ECs3125]
glpT	+5.08	9.04	+2.35	7.87	0.1	10.21	0.0	0.00002284	0.00067725	A_07_P052656	Z3498	cmr|sn-glycerol-3-phosphate permease [Z3498]
glpT	+4.24	9.44	+2.08	8.39	0.2	10.48	0.0	0.00007958	0.00135303	A_07_P000990	b2240	cmr|sn-glycerol-3-phosphate permease [b2240]
gltA	+19.85	13.20	+4.31	11.04	0.1	15.35	0.1	0.00000273	0.00028012	A_07_P056596	ECs0745	cmr|citrate synthase [ECs0745]
gltA	+9.71	10.83	+3.28	9.19	0.2	12.47	0.1	0.00001454	0.00054604	A_07_P010118	b0720	cmr|citrate synthase [b0720]
gltA	+18.48	13.83	+4.21	11.72	0.1	15.93	0.0	0.00000132	0.00021824	A_07_P046286	Z0873	cmr|citrate synthase [Z0873]
gltD	+2.30	8.71	+1.20	8.11	0.1	9.31	0.1	0.00097072	0.00775788	A_07_P012545	b3213	cmr|glutamate synthase, small subunit [b3213]
gltK	+2.83	8.31	+1.50	7.56	0.1	9.06	0.0	0.00020281	0.00257504	A_07_P009831	b0653	cmr|glutamate/aspartate transport system permease [b0653]
gltL	+3.05	8.77	+1.61	7.97	0.1	9.57	0.1	0.00015262	0.00210589	A_07_P009830	b0652	cmr|ATP-binding protein of glutamate/aspartate transport system [b0652]
gltP	+3.20	8.66	+1.68	7.82	0.2	9.50	0.0	0.00047020	0.00463832	A_07_P009026	b4077	cmr|glutamate-aspartate symport protein [b4077]
glvG	-3.24	9.45	-1.70	10.30	0.4	8.61	0.0	0.00226923	0.01451717	A_07_P010606	ABE-0285077	asap|C-terminal fragment of predicted 6-phospho-beta-glucosidase (pseudogene) [b4556]
glyA	+9.22	11.83	+3.20	10.23	0.1	13.43	0.1	0.00000747	0.00040630	A_07_P019657	b2551	cmr|serine hydroxymethyltransferase [b2551]
gmhA	+3.69	9.34	+1.89	8.40	0.0	10.28	0.0	0.00005502	0.00108015	A_07_P053536	ECs0249	cmr|phosphoheptose isomerase [ECs0249]
gmhA	+3.25	9.24	+1.70	8.39	0.2	10.10	0.1	0.00041460	0.00423040	A_07_P043366	Z0280	cmr|phosphoheptose isomerase [Z0280]
gmhA	+5.41	11.54	+2.44	10.32	0.0	12.76	0.0	0.00001573	0.00056283	A_07_P030845	c_0372	cmr|Phosphoheptose isomerase [c_0372]
gmk	-13.48	12.61	-3.75	14.48	0.0	10.73	0.0	0.00000176	0.00024644	A_07_P017181	b3648	cmr|guanylate kinase [b3648]
gnd	+2.82	8.54	+1.50	7.79	0.4	9.29	0.0	0.00248644	0.01554664	A_07_P015470	b2029	cmr|gluconate-6-phosphate dehydrogenase, decarboxylating [b2029]
gnd	+2.80	10.09	+1.48	9.35	0.1	10.83	0.1	0.00035858	0.00383789	A_07_P042488	c_2556	cmr|6-phosphogluconate dehydrogenase, decarboxylating [c_2556]
gnsA	+2.72	11.11	+1.45	10.39	0.1	11.83	0.0	0.00031563	0.00349707	A_07_P010343	ABE-0285038	asap|predicted regulator of phosphatidylethanolamine synthesis [b4517]
gnsB	+14.71	10.00	+3.88	8.07	0.5	11.94	0.0	0.00009282	0.00149582	A_07_P020394	b1550	cmr|orf, hypothetical protein [b1550]
gntX	+3.10	11.79	+1.63	10.98	0.1	12.61	0.0	0.00019812	0.00252367	A_07_P018091	b3413	cmr|orf, hypothetical protein [b3413]
gntY	-3.65	10.94	-1.87	11.87	0.1	10.00	0.2	0.00024665	0.00295753	A_07_P018096	b3414	cmr|orf, hypothetical protein [b3414]
gntY	-3.26	11.27	-1.70	12.12	0.1	10.42	0.0	0.00016924	0.00225435	A_07_P018096	b3414	cmr|orf, hypothetical protein [b3414]
gntY	-2.90	11.21	-1.54	11.97	0.1	10.44	0.0	0.00017691	0.00232877	A_07_P018096	b3414	cmr|orf, hypothetical protein [b3414]
gntY	-3.49	11.11	-1.80	12.02	0.1	10.21	0.1	0.00010703	0.00164539	A_07_P018096	b3414	cmr|orf, hypothetical protein [b3414]
gntY	-3.16	11.10	-1.66	11.93	0.1	10.27	0.0	0.00018167	0.00237762	A_07_P018096	b3414	cmr|orf, hypothetical protein [b3414]
gph	+4.97	9.87	+2.31	8.72	0.1	11.03	0.0	0.00002588	0.00072358	A_07_P017954	b3385	cmr|phosphoglycolate phosphatase [b3385]
gpmA	+3.20	7.85	+1.68	7.01	0.2	8.69	0.2	0.00076106	0.00652976	A_07_P004227	b0755	cmr|phosphoglyceromutase 1 [b0755]
greB	-2.75	10.86	-1.46	11.59	0.1	10.13	0.1	0.00040567	0.00416132	A_07_P018057	b3406	cmr|transcription elongation factor and transcript cleavage [b3406]
groL	+4.22	12.63	+2.08	11.59	0.0	13.67	0.1	0.00004000	0.00090512	A_07_P011446	b4143	cmr|GroEL, chaperone Hsp60, peptide-dependent ATPase, heat shock protein [b4143]
groS	+5.01	13.34	+2.32	12.17	0.1	14.50	0.0	0.00002517	0.00071646	A_07_P011443	b4142	cmr|GroES, 10 Kd chaperone binds to Hsp60 in pres. Mg-ATP, suppressing its ATPase activity [b4142]
grxB	+9.27	9.69	+3.21	8.08	0.2	11.29	0.0	0.00001273	0.00051704	A_07_P001521	b1064	cmr|glutaredoxin 2 [b1064]
gshA	-3.47	10.31	-1.79	11.21	0.0	9.41	0.1	0.00010631	0.00164315	A_07_P001912	b2688	cmr|gamma-glutamate-cysteine ligase [b2688]
gshB	+2.46	11.33	+1.30	10.68	0.1	11.98	0.0	0.00040572	0.00416132	A_07_P011876	b2947	cmr|glutathione synthetase [b2947]
gspD	-2.87	7.81	-1.52	8.57	0.0	7.05	0.2	0.00040273	0.00414691	A_07_P013055	b3325	cmr|putative general protein secretion protein [b3325]
gspL	-2.94	9.82	-1.56	10.60	0.1	9.04	0.1	0.00030397	0.00340122	A_07_P013091	b3333	cmr|putative general protein secretion protein [b3333]
gspM	-3.59	7.80	-1.84	8.72	0.1	6.88	0.2	0.00025942	0.00307016	A_07_P017699	b3334	cmr|putative general secretion [b3334]
gst	+9.67	10.30	+3.27	8.66	0.1	11.94	0.0	0.00000602	0.00036752	A_07_P020808	b1635	cmr|glutathionine S-transferase [b1635]
guaA	+2.38	10.68	+1.25	10.05	0.1	11.30	0.1	0.00071081	0.00619446	A_07_P013594	b2507	cmr|GMP synthetase [b2507]
guaB	+3.92	11.28	+1.97	10.29	0.0	12.27	0.0	0.00004122	0.00092082	A_07_P030153	c_3027	cmr|Inosine-5-monophosphate dehydrogenase [c_3027]
guaB	+4.40	11.30	+2.14	10.23	0.1	12.37	0.0	0.00006555	0.00120005	A_07_P042850	Z3772	cmr|IMP dehydrogenase [Z3772]
gudP	+3.50	7.54	+1.81	6.64	0.1	8.44	0.1	0.00017079	0.00227100	A_07_P002391	b2789	cmr|putative transport protein [b2789]
gyrA	-4.50	12.96	-2.17	14.04	0.0	11.88	0.1	0.00003358	0.00081707	A_07_P000942	b2231	cmr|DNA gyrase, subunit A, type II topoisomerase [b2231]
gyrB	-5.65	12.53	-2.50	13.78	0.0	11.28	0.0	0.00001281	0.00051714	A_07_P005429	b3699	cmr|DNA gyrase subunit B, type II topoisomerase, ATPase activity [b3699]
hchA	+2.15	10.24	+1.11	9.69	0.3	10.79	0.0	0.00432030	0.02350338	A_07_P015194	b1967	cmr|orf, hypothetical protein [b1967]
hda	-3.77	10.72	-1.92	11.68	0.0	9.76	0.0	0.00004956	0.00100951	A_07_P013536	b2496	cmr|putative DNA replication factor [b2496]
hdeA	+3.10	8.23	+1.63	7.41	0.1	9.05	0.0	0.00019561	0.00250584	A_07_P007483	b3510	cmr|orf, hypothetical protein [b3510]
hdhA	+2.24	9.69	+1.16	9.11	0.1	10.27	0.1	0.00122866	0.00921583	A_07_P035106	c_2011	cmr|7-alpha-hydroxysteroid dehydrogenase [c_2011]
hemC	+4.70	11.59	+2.23	10.47	0.1	12.70	0.1	0.00002969	0.00076491	A_07_P039097	c_4724	cmr|Porphobilinogen deaminase [c_4724]
hemC	+3.42	9.77	+1.77	8.88	0.1	10.66	0.3	0.00067735	0.00597099	A_07_P005892	b3805	cmr|porphobilinogen deaminase = hydroxymethylbilane synthase [b3805]
hemE	+4.29	9.24	+2.10	8.19	0.1	10.29	0.0	0.00004879	0.00100402	A_07_P008648	b3997	cmr|uroporphyrinogen decarboxylase [b3997]
hemF	-2.22	11.37	-1.15	11.95	0.0	10.80	0.4	0.00864329	0.04005886	A_07_P013240	b2436	cmr|coproporphyrinogen III oxidase [b2436]
hemN	+2.32	8.20	+1.21	7.59	0.0	8.80	0.1	0.00087017	0.00722955	A_07_P041357	c_4816	cmr|Oxygen-independent coproporphyrinogen III oxidase [c_4816]
hepA	-4.18	10.67	-2.06	11.70	0.1	9.64	0.0	0.00003864	0.00088510	A_07_P010981	b0059	cmr|probable ATP-dependent RNA helicase [b0059]
hflB	-3.13	13.17	-1.65	13.99	0.0	12.35	0.0	0.00011208	0.00169030	A_07_P000601	b3178	cmr|degrades sigma32, integral membrane peptidase, cell division protein [b3178]
hflK	-2.26	12.12	-1.18	12.71	0.1	11.54	0.1	0.00072212	0.00626395	A_07_P011588	b4174	cmr|protease specific for phage lambda cII repressor [b4174]
hha	-4.61	10.04	-2.21	11.15	0.1	8.94	0.1	0.00004098	0.00091779	A_07_P021406	b0460	cmr|haemolysin expression modulating protein [b0460]
hisA	+4.57	8.92	+2.19	7.82	0.1	10.01	0.1	0.00005447	0.00107551	A_07_P015442	b2024	cmr|N- [b2024]
hisA	+4.77	8.80	+2.25	7.67	0.2	9.92	0.1	0.00006998	0.00124629	A_07_P051776	Z3186	cmr|N- [Z3186]
hisB	+8.20	9.00	+3.04	7.48	0.2	10.52	0.0	0.00001228	0.00051423	A_07_P015435	b2022	cmr|imidazoleglycerolphosphate dehydratase and histidinol-phosphate phosphatase [b2022]
hisC	+7.24	8.86	+2.86	7.43	0.1	10.28	0.1	0.00001723	0.00058333	A_07_P015429	b2021	cmr|histidinol-phosphate aminotransferase [b2021]
hisD	+8.49	9.38	+3.09	7.83	0.1	10.92	0.1	0.00000886	0.00042982	A_07_P015421	b2020	cmr|L-histidinal:NAD+ oxidoreductase; L-histidinol:NAD+ oxidoreductase [b2020]
hisF	+9.23	9.76	+3.21	8.16	0.6	11.36	0.1	0.00048796	0.00474808	A_07_P015446	b2025	cmr|imidazole glycerol phosphate synthase subunit in heterodimer with HisH = imidazole glycerol phsphate synthase holoenzyme [b2025]
hisG	+3.82	8.19	+1.93	7.22	0.0	9.16	0.1	0.00005751	0.00110693	A_07_P031978	c_2546	cmr|ATP phosphoribosyltransferase [c_2546]
hisG	+2.42	7.68	+1.28	7.04	0.2	8.32	0.0	0.00089680	0.00738456	A_07_P015420	b2019	cmr|ATP phosphoribosyltransferase [b2019]
hisH	+13.76	9.38	+3.78	7.49	0.1	11.27	0.1	0.00000327	0.00029330	A_07_P015440	b2023	cmr|glutamine amidotransferase subunit of heterodimer with HisF = imidazole glycerol phosphate synthase holoenzyme [b2023]
hisI	+3.83	8.10	+1.94	7.13	0.2	9.07	0.0	0.00013556	0.00192967	A_07_P042478	c_2553	cmr|Histidine biosynthesis bifunctional protein hisIE [c_2553]
hisJ	+4.46	10.86	+2.16	9.78	0.0	11.94	0.1	0.00003254	0.00080182	A_07_P013834	b2309	cmr|histidine-binding periplasmic protein of high-affinity histidine transport system [b2309]
hisM	+2.46	8.98	+1.30	8.33	0.1	9.63	0.1	0.00082745	0.00695536	A_07_P013822	b2307	cmr|histidine transport, membrane protein M [b2307]
hlyB	-2.32	8.38	-1.22	8.99	0.0	7.77	0.1	0.00067385	0.00595430	A_07_P033071	c_3573	cmr|Hemolysin B [c_3573]
hlyC	+3.58	9.16	+1.84	8.24	0.1	10.08	0.1	0.00012544	0.00182701	A_07_P033053	c_3569	cmr|Hemolysin C [c_3569]
hmp	+7.83	9.04	+2.97	7.56	0.2	10.52	0.0	0.00001250	0.00051423	A_07_P019661	b2552	cmr|dihydropteridine reductase, ferrisiderophore reductase activity [b2552]
hmpA	+10.00	9.38	+3.32	7.72	0.4	11.04	0.1	0.00008336	0.00140212	A_07_P041601	c_3075	cmr|Flavohemoprotein [c_3075]
hofH	-2.10	8.06	-1.07	8.60	0.2	7.53	0.2	0.00721878	0.03491522	A_07_P034333	c_4100	cmr|Putative general secretion pathway protein H precursor [c_4100]
hokD	-2.47	15.61	-1.31	16.26	0.0	14.95	0.0	0.00030452	0.00340122	A_07_P020454	b1562	cmr|polypeptide destructive to membrane potential [b1562]
holC	+5.90	10.12	+2.56	8.84	0.2	11.40	0.1	0.00004243	0.00093353	A_07_P003845	b4259	cmr|DNA polymerase III, chi subunit [b4259]
holE	+5.56	9.06	+2.48	7.82	0.1	10.29	0.0	0.00002209	0.00066624	A_07_P015890	b1842	cmr|DNA polymerase III, theta subunit [b1842]
holE	+4.20	9.32	+2.07	8.28	0.3	10.35	0.0	0.00042602	0.00430780	A_07_P035500	c_2252	cmr|DNA polymerase III, theta subunit [c_2252]
hpf	+13.82	11.98	+3.79	10.09	0.0	13.88	0.1	0.00000177	0.00024644	A_07_P012495	b3203	cmr|probable sigma-54 modulation protein [b3203]
hpt	-2.87	12.71	-1.52	13.47	0.0	11.95	0.0	0.00014795	0.00205794	A_07_P002588	b0125	cmr|hypoxanthine phosphoribosyltransferase [b0125]
hrpB	-2.68	10.21	-1.42	10.92	0.0	9.49	0.2	0.00051186	0.00491089	A_07_P035880	c_0181	cmr|ATP-dependent helicase hrpB [c_0181]
hscA	+2.03	11.00	+1.02	10.49	0.1	11.51	0.0	0.00124767	0.00931993	A_07_P019531	b2526	cmr|heat shock protein, chaperone, member of Hsp70 protein family [b2526]
hslU	+2.28	8.27	+1.19	7.67	0.2	8.86	0.0	0.00115471	0.00884231	A_07_P019432	b3931	cmr|heat shock protein hslVU, ATPase subunit, homologous to chaperones [b3931]
hslV	+3.91	11.76	+1.97	10.78	0.1	12.75	0.1	0.00008173	0.00138058	A_07_P019439	b3932	cmr|heat shock protein hslVU, proteasome-related peptidase subunit [b3932]
hspQ	-4.54	13.85	-2.18	14.94	0.1	12.76	0.1	0.00003110	0.00078710	A_07_P005278	b0966	cmr|orf, hypothetical protein [b0966]
htpG	+3.46	8.87	+1.79	7.97	0.2	9.77	0.0	0.00021039	0.00263076	A_07_P021471	b0473	cmr|chaperone Hsp90, heat shock protein C 62.5 [b0473]
htrG	-4.61	10.10	-2.20	11.20	0.1	8.99	0.1	0.00004726	0.00098397	A_07_P000008	b3055	cmr|orf, hypothetical protein [b3055]
hupA	+16.81	12.69	+4.07	10.65	0.0	14.72	0.0	0.00000121	0.00021323	A_07_P008662	b4000	cmr|DNA-binding protein HU-alpha [b4000]
hupB	+3.09	12.16	+1.63	11.35	0.1	12.98	0.1	0.00016794	0.00224832	A_07_P021314	b0440	cmr|DNA-binding protein HU-beta, NS1 [b0440]
hybA	+2.61	10.50	+1.38	9.81	0.1	11.19	0.1	0.00030391	0.00340122	A_07_P012111	b2996	cmr|hydrogenase-2 small subunit [b2996]
hybB	+5.95	11.25	+2.57	9.96	0.0	12.53	0.0	0.00001169	0.00050224	A_07_P012108	b2995	cmr|probable cytochrome Ni/Fe component of hydrogenase-2 [b2995]
hybC	+3.28	10.08	+1.71	9.22	0.0	10.94	0.1	0.00011187	0.00169030	A_07_P012105	b2994	cmr|probable large subunit, hydrogenase-2 [b2994]
hybD	+2.38	10.81	+1.25	10.18	0.2	11.44	0.0	0.00093339	0.00756708	A_07_P012100	b2993	cmr|probable processing element for hydrogenase-2 [b2993]
hydN	-3.65	8.14	-1.87	9.07	0.0	7.20	0.2	0.00026442	0.00309464	A_07_P043108	Z4021	cmr|involved in electron transport from formate to [Z4021]
hydN	-4.78	8.46	-2.26	9.58	0.0	7.33	0.1	0.00002665	0.00073020	A_07_P002014	b2713	cmr|involved in electron transport from formate to hydrogen, Fe-S centers [b2713]
hydN	-4.35	8.32	-2.12	9.38	0.1	7.26	0.1	0.00005211	0.00104646	A_07_P030619	c_3269	cmr|Electron transport protein hydN [c_3269]
hypB	+2.64	9.94	+1.40	9.24	0.1	10.64	0.1	0.00031931	0.00353038	A_07_P002083	b2727	cmr|guanine-nucleotide binding protein, functions as nickel donor for large subunit of hydrogenase 3 [b2727]
hypC	+2.13	12.30	+1.09	11.76	0.2	12.85	0.0	0.00177969	0.01216649	A_07_P002090	b2728	cmr|pleiotrophic effects on 3 hydrogenase isozymes [b2728]
hypD	+2.56	9.17	+1.36	8.49	0.1	9.85	0.1	0.00057455	0.00533670	A_07_P002091	b2729	cmr|pleiotrophic effects on 3 hydrogenase isozymes [b2729]
iap	-2.75	7.81	-1.46	8.54	0.1	7.08	0.4	0.00452729	0.02436236	A_07_P041682	c_3320	cmr|Alkaline phosphatase isozyme conversion protein precursor [c_3320]
ibpB	-3.78	10.61	-1.92	11.57	0.1	9.65	0.1	0.00008574	0.00143229	A_07_P017361	b3686	cmr|heat shock protein [b3686]
icd	+2.68	9.93	+1.42	9.22	0.1	10.64	0.2	0.00084538	0.00705338	A_07_P006631	b1136	cmr|isocitrate dehydrogenase, specific for NADP+ [b1136]
icdA	+5.30	8.44	+2.41	7.24	0.0	9.64	0.1	0.00002248	0.00067042	A_07_P050489	Z1865	cmr|isocitrate dehydrogenase, specific for NADP+ [Z1865]
icdA	+15.00	13.47	+3.91	11.51	0.0	15.42	0.1	0.00000289	0.00028300	A_07_P038343	c_1517	cmr|Isocitrate dehydrogenase [c_1517]
iclR	+7.49	8.47	+2.90	7.01	0.1	9.92	0.0	0.00000742	0.00040580	A_07_P008735	b4018	cmr|repressor of aceBA operon [b4018]
iclR	+12.70	8.95	+3.67	7.12	0.1	10.79	0.0	0.00000219	0.00026540	A_07_P041378	c_4975	cmr|Acetate operon repressor [c_4975]
idnO	-3.03	11.67	-1.60	12.47	0.3	10.87	0.2	0.00173536	0.01192035	A_07_P003879	b4266	cmr|5-keto-D-gluconate 5-reductase [b4266]
ihfA	+3.34	12.33	+1.74	11.46	0.0	13.20	0.1	0.00009415	0.00150861	A_07_P018614	b1712	cmr|integration host factor [b1712]
ihfB	+4.55	9.87	+2.18	8.78	0.0	10.96	0.1	0.00002860	0.00074930	A_07_P005009	b0912	cmr|integration host factor [b0912]
ilvB	+2.58	10.70	+1.37	10.01	0.2	11.38	0.0	0.00066917	0.00592567	A_07_P017291	b3671	cmr|acetolactate synthase I,valine-sensitive, large subunit [b3671]
ilvD	+3.95	9.04	+1.98	8.04	0.0	10.03	0.0	0.00003977	0.00090487	A_07_P039071	c_4693	cmr|Dihydroxy-acid dehydratase [c_4693]
ilvM	+3.89	8.35	+1.96	7.37	0.0	9.33	0.1	0.00004761	0.00098891	A_07_P005727	b3769	cmr|acetolactate synthase II, valine insensitive, small subunit [b3769]
ilvN	+2.22	8.68	+1.15	8.11	0.0	9.26	0.1	0.00070140	0.00613147	A_07_P038986	c_4595	cmr|Acetolactate synthase isozyme I small subunit [c_4595]
inaA	-2.76	7.82	-1.46	8.55	0.0	7.09	0.1	0.00021274	0.00265188	A_07_P000971	b2237	cmr|pH-inducible protein involved in stress response [b2237]
infB	-2.33	13.05	-1.22	13.66	0.0	12.44	0.1	0.00049932	0.00481991	A_07_P000561	b3168	cmr|protein chain initiation factor IF-2 [b3168]
infC	-3.27	14.77	-1.71	15.63	0.0	13.91	0.0	0.00008682	0.00143726	A_07_P018636	b1718	cmr|protein chain initiation factor IF-3 [b1718]
insA	-3.41	9.09	-1.77	9.97	0.1	8.20	0.1	0.00009048	0.00147268	A_07_P008028	b0265	cmr|IS1 protein InsA [b0265]
insA	-4.05	10.16	-2.02	11.17	0.0	9.15	0.1	0.00007937	0.00135096	A_07_P003998	b4294	cmr|IS1 protein InsA [b4294]
insB	-2.80	9.45	-1.48	10.19	0.3	8.71	0.2	0.00322447	0.01897086	A_07_P005381	b0988	cmr|IS1 protein InsB [b0988]
insB	-3.66	9.51	-1.87	10.45	0.0	8.57	0.3	0.00038104	0.00398343	A_07_P010675	b0021	cmr|IS1 protein InsB [b0021]
insD	-2.87	12.25	-1.52	13.01	0.2	11.49	0.3	0.00179736	0.01225015	A_07_P020927	b0361	cmr|IS2 hypothetical protein [b0361]
insG	-20.13	10.77	-4.33	12.94	0.0	8.61	0.1	0.00000103	0.00020391	A_07_P003924	b4278	cmr|IS4 hypothetical protein [b4278]
iroN	-5.50	8.86	-2.46	10.09	0.1	7.63	0.3	0.00011805	0.00175334	A_07_P040541	c_1250	cmr|Siderophore receptor IroN [c_1250]
iscA	-4.70	11.42	-2.23	12.53	0.1	10.30	0.1	0.00006458	0.00118644	A_07_P019544	b2528	cmr|putative regulator [b2528]
iscR	-3.31	10.69	-1.73	11.55	0.1	9.82	0.1	0.00012327	0.00180375	A_07_P019560	b2531	cmr|orf, hypothetical protein [b2531]
iscS	-2.12	12.19	-1.08	12.74	0.1	11.65	0.1	0.00096057	0.00770017	A_07_P019553	b2530	cmr|putative aminotransferase [b2530]
iscX	-2.28	12.45	-1.19	13.04	0.1	11.85	0.0	0.00055147	0.00519904	A_07_P013676	b2524	cmr|orf, hypothetical protein [b2524]
ispG	+2.09	10.08	+1.07	9.54	0.2	10.61	0.1	0.00201586	0.01322404	A_07_P013631	b2515	cmr|orf, hypothetical protein [b2515]
iucC	-2.09	8.38	-1.06	8.91	0.1	7.84	0.1	0.00116126	0.00888380	A_07_P036313	c_3625	cmr|IucC protein [c_3625]
iutA	-2.44	8.29	-1.29	8.93	0.0	7.64	0.2	0.00086890	0.00722279	A_07_P036302	c_3623	cmr|IutA protein [c_3623]
katG	+3.42	10.20	+1.77	9.31	0.1	11.08	0.0	0.00008109	0.00137285	A_07_P019488	b3942	cmr|catalase; hydroperoxidase HPI [b3942]
kbaZ	+4.97	8.17	+2.31	7.01	0.1	9.32	0.0	0.00002838	0.00074722	A_07_P000381	b3132	cmr|putative tagatose 6-phosphate kinase 2 [b3132]
kbl	+16.32	11.09	+4.03	9.07	0.1	13.10	0.1	0.00000363	0.00030703	A_07_P017030	b3617	cmr|2-amino-3-ketobutyrate CoA ligase [b3617]
kdpA	-2.70	8.68	-1.43	9.40	0.1	7.96	0.0	0.00025130	0.00299733	A_07_P010006	b0698	cmr|ATPase of high-affinity potassium transport system, A chain [b0698]
kdsA	-2.32	11.91	-1.21	12.51	0.0	11.30	0.1	0.00049464	0.00478647	A_07_P007028	b1215	cmr|2-dehydro-3-deoxyphosphooctulonate aldolase [b1215]
kdsC	-2.09	13.04	-1.07	13.57	0.0	12.51	0.2	0.00181527	0.01230406	A_07_P012468	b3198	cmr|orf, hypothetical protein [b3198]
kefA	-2.56	8.72	-1.36	9.40	0.0	8.04	0.1	0.00041635	0.00423720	A_07_P021433	b0465	cmr|putative alpha helix protein [b0465]
kpsC	+2.00	7.42	+1.00	6.92	0.0	7.92	0.1	0.00195408	0.01294824	A_07_P036625	c_3690	cmr|KpsC protein [c_3690]
kpsE	+2.96	9.24	+1.56	8.46	0.1	10.02	0.1	0.00028602	0.00327271	A_07_P036606	c_3687	cmr|KpsE protein [c_3687]
kpsS	-2.06	8.57	-1.04	9.09	0.2	8.05	0.1	0.00266590	0.01640169	A_07_P036626	c_3691	cmr|KpsS protein [c_3691]
kpsT	+2.87	9.99	+1.52	9.23	0.1	10.75	0.3	0.00117822	0.00896134	A_07_P036658	c_3697	cmr|KpsT protein [c_3697]
ksgA	-2.53	11.81	-1.34	12.48	0.0	11.14	0.1	0.00032451	0.00357524	A_07_P010944	b0051	cmr|S-adenosylmethionine-6-N,N-adenosyl [b0051]
L7002	-4.30	12.40	-2.10	13.45	0.4	11.35	0.2	0.00121065	0.00912855	A_07_P048661	ABH-0243999	asap|unknown [L7002]
L7055	-2.85	10.97	-1.51	11.73	0.1	10.22	0.2	0.00050036	0.00482696	A_07_P048893	ABH-0244096	asap|replication protein [L7055]
L7079	-2.00	11.65	-1.00	12.15	0.0	11.15	0.1	0.00233153	0.01478359	A_07_P048996	ABH-0244148	asap|unknown [L7079]
lacI	+2.81	8.40	+1.49	7.65	0.1	9.14	0.1	0.00039006	0.00404551	A_07_P008419	b0345	cmr|transcriptional repressor of the lac operon [b0345]
lacZ	+2.39	7.68	+1.26	7.05	0.2	8.31	0.1	0.00118095	0.00897338	A_07_P031027	c_0459	cmr|Beta-galactosidase [c_0459]
lamB	+14.52	9.75	+3.86	7.82	0.1	11.68	0.1	0.00000210	0.00026053	A_07_P008822	b4036	cmr|phage lambda receptor protein; maltose high-affinity receptor [b4036]
lamB	+14.30	9.25	+3.84	7.33	0.0	11.17	0.1	0.00000274	0.00028012	A_07_P037538	c_5006	cmr|Maltoporin precursor [c_5006]
leuB	+2.14	9.36	+1.10	8.81	0.0	9.91	0.2	0.00275200	0.01675359	A_07_P035745	c_0090	cmr|3-isopropylmalate dehydrogenase [c_0090]
leuE	-9.69	8.94	-3.28	10.57	0.1	7.30	0.2	0.00001564	0.00056283	A_07_P015685	b1798	cmr|orf, hypothetical protein [b1798]
ligB	-2.88	8.07	-1.53	8.83	0.0	7.30	0.1	0.00030196	0.00338846	A_07_P017180	b3647	cmr|putative enzyme [b3647]
ligT	-2.81	10.45	-1.49	11.20	0.1	9.71	0.1	0.00040385	0.00415342	A_07_P002698	b0147	cmr|orf, hypothetical protein [b0147]
lipA	+2.30	12.86	+1.20	12.26	0.0	13.46	0.1	0.00060601	0.00553423	A_07_P009709	b0628	cmr|lipoate synthesis, sulfur insertion? [b0628]
lipB	-7.99	12.43	-3.00	13.93	0.0	10.93	0.0	0.00000513	0.00034758	A_07_P009718	b0630	cmr|protein of lipoate biosynthesis [b0630]
livK	-4.49	8.09	-2.17	9.17	0.1	7.00	0.2	0.00007699	0.00132177	A_07_P034548	c_4248	cmr|Leucine-specific binding protein precursor [c_4248]
lldD	+4.56	8.65	+2.19	7.56	0.5	9.75	0.1	0.00107515	0.00836324	A_07_P016968	b3605	cmr|L-lactate dehydrogenase [b3605]
lldP	+2.29	7.12	+1.20	6.52	0.1	7.72	0.1	0.00094727	0.00763638	A_07_P016959	b3603	cmr|L-lactate permease [b3603]
lldR	+3.30	8.21	+1.72	7.35	0.1	9.07	0.1	0.00016858	0.00225120	A_07_P016965	b3604	cmr|transcriptional regulator [b3604]
lolA	+2.32	9.41	+1.21	8.80	0.0	10.01	0.0	0.00051250	0.00491401	A_07_P004904	b0891	cmr|periplasmic protein effects translocation of lipoproteins from inner membrane to outer [b0891]
lolC	-2.26	9.95	-1.18	10.54	0.2	9.36	0.0	0.00119454	0.00904608	A_07_P040818	c_1391	cmr|Lipoprotein releasing system transmembrane protein lolC [c_1391]
lpcA	+5.18	10.73	+2.37	9.54	0.0	11.91	0.0	0.00001716	0.00058318	A_07_P007824	b0222	cmr|phosphoheptose isomerase [b0222]
lpxA	-2.59	11.68	-1.37	12.36	0.0	10.99	0.0	0.00025108	0.00299696	A_07_P002865	b0181	cmr|UDP-N-acetylglucosamine acetyltransferase; lipid A biosynthesis [b0181]
lpxB	-2.42	10.59	-1.27	11.22	0.1	9.95	0.1	0.00080810	0.00682912	A_07_P002870	b0182	cmr|tetraacyldisaccharide-1-P; lipid A biosynthesis, penultimate step [b0182]
lpxC	-6.01	14.46	-2.59	15.76	0.0	13.17	0.0	0.00001094	0.00047993	A_07_P002451	b0096	cmr|UDP-3-O-acyl N-acetylglucosamine deacetylase; lipid A biosynthesis [b0096]
lpxK	-4.40	10.09	-2.14	11.16	0.0	9.02	0.1	0.00004195	0.00093286	A_07_P005022	b0915	cmr|putative EC 1.2 enzyme [b0915]
lpxL	-3.90	11.64	-1.96	12.62	0.0	10.65	0.0	0.00004405	0.00094686	A_07_P001480	b1054	cmr|heat shock protein [b1054]
lpxP	-2.33	11.53	-1.22	12.14	0.0	10.92	0.1	0.00048620	0.00473388	A_07_P014174	b2378	cmr|putative heat shock protein [b2378]
lrhA	-4.38	11.83	-2.13	12.90	0.0	10.77	0.0	0.00002789	0.00073912	A_07_P013734	b2289	cmr|NADH dehydrogenase transcriptional regulator, LysR family [b2289]
lrp	+3.59	9.83	+1.84	8.90	0.1	10.75	0.1	0.00016627	0.00223475	A_07_P004893	b0889	cmr|regulator for leucine [b0889]
lsrK	-2.15	9.23	-1.11	9.79	0.3	8.68	0.1	0.00664756	0.03266514	A_07_P020203	b1511	cmr|putative kinase [b1511]
ltaE	+3.19	9.10	+1.67	8.26	0.0	9.94	0.0	0.00010256	0.00160236	A_07_P004805	b0870	cmr|putative arylsulfatase [b0870]
lysS	-2.78	11.64	-1.47	12.38	0.1	10.90	0.0	0.00020470	0.00259073	A_07_P006416	b2890	cmr|lysine tRNA synthetase, constitutive; suppressor of ColE1 mutation in primer RNA [b2890]
lyxK	+2.37	7.50	+1.25	6.87	0.1	8.12	0.1	0.00067415	0.00595430	A_07_P039671	c_4403	cmr|Cryptic L-xylulose kinase [c_4403]
maa	-7.32	9.57	-2.87	11.01	0.1	8.14	0.0	0.00000978	0.00045680	A_07_P021405	b0459	cmr|putative transferase [b0459]
macB	-2.50	8.55	-1.32	9.21	0.0	7.88	0.1	0.00037915	0.00397162	A_07_P004848	b0879	cmr|putative ATP-binding component of a transport system [b0879]
maeA	+2.52	8.54	+1.33	7.87	0.1	9.20	0.1	0.00057557	0.00534303	A_07_P009486	b1479	cmr|NAD-linked malate dehydrogenase [b1479]
maeB	+2.10	10.55	+1.07	10.02	0.2	11.09	0.0	0.00229563	0.01464440	A_07_P013371	b2463	cmr|putative multimodular enzyme [b2463]
malE	+6.32	10.18	+2.66	8.85	0.1	11.51	0.0	0.00001716	0.00058318	A_07_P008811	b4034	cmr|periplasmic maltose-binding protein; substrate recognition for transport and chemotaxis [b4034]
malI	-2.28	10.11	-1.19	10.70	0.1	9.51	0.0	0.00098079	0.00781063	A_07_P020735	b1620	cmr|repressor of malX and Y genes [b1620]
malI	-2.56	10.23	-1.36	10.91	0.1	9.55	0.2	0.00108460	0.00842841	A_07_P042320	c_2012	cmr|Maltose regulon Regulatory protein malI [c_2012]
malK	+2.67	7.30	+1.41	6.59	0.0	8.01	0.0	0.00023413	0.00284423	A_07_P008816	b4035	cmr|ATP-binding component of transport system for maltose [b4035]
malP	+6.10	9.15	+2.61	7.85	0.1	10.46	0.1	0.00003540	0.00084182	A_07_P018111	b3417	cmr|maltodextrin phosphorylase [b3417]
malT	+3.71	8.20	+1.89	7.25	0.0	9.14	0.0	0.00005391	0.00107039	A_07_P034438	c_4196	cmr|MalT Regulatory protein [c_4196]
malT	+2.39	7.80	+1.26	7.17	0.0	8.43	0.2	0.00081156	0.00684205	A_07_P018118	b3418	cmr|positive regulator of mal regulon [b3418]
malT	+2.77	8.18	+1.47	7.44	0.1	8.91	0.0	0.00033321	0.00364059	A_07_P052157	Z4774	cmr|positive regulator of mal regulon [Z4774]
malX	+3.80	9.78	+1.93	8.81	0.0	10.74	0.0	0.00004926	0.00100666	A_07_P020740	b1621	cmr|PTS system, maltose and glucose-specific II ABC [b1621]
malY	+2.35	9.10	+1.23	8.48	0.1	9.71	0.1	0.00117144	0.00893567	A_07_P042322	c_2014	cmr|MalY protein [c_2014]
manA	+2.37	8.82	+1.25	8.20	0.1	9.45	0.1	0.00093165	0.00756060	A_07_P020700	b1613	cmr|mannose-6-phosphate isomerase [b1613]
manA	+2.66	8.73	+1.41	8.02	0.1	9.44	0.0	0.00033738	0.00367597	A_07_P044397	Z2616	cmr|mannose-6-phosphate isomerase [Z2616]
manA	+2.32	8.73	+1.22	8.12	0.0	9.34	0.1	0.00051652	0.00494954	A_07_P035096	c_2005	cmr|Mannose-6-phosphate isomerase [c_2005]
manB	+2.03	10.47	+1.02	9.96	0.1	10.98	0.1	0.00223846	0.01436435	A_07_P045001	Z3194	cmr|phosphomannomutase [Z3194]
manB	+2.50	12.60	+1.32	11.94	0.1	13.26	0.0	0.00053522	0.00507319	A_07_P031986	c_2557	cmr|Phosphomannomutase [c_2557]
manX	+7.29	9.72	+2.87	8.29	0.0	11.16	0.2	0.00001659	0.00057541	A_07_P015778	b1817	cmr|PTS enzyme IIAB, mannose-specific [b1817]
manY	+3.06	9.29	+1.62	8.48	0.1	10.10	0.1	0.00019173	0.00246301	A_07_P015784	b1818	cmr|PTS enzyme IIC, mannose-specific [b1818]
manZ	+3.25	9.41	+1.70	8.56	0.2	10.25	0.1	0.00037537	0.00395400	A_07_P015786	b1819	cmr|PTS enzyme IID, mannose-specific [b1819]
marA	+6.16	10.41	+2.62	9.10	0.1	11.73	0.0	0.00001913	0.00061714	A_07_P020303	b1531	cmr|multiple antibiotic resistance; transcriptional activator of defense systems [b1531]
marB	+2.16	8.72	+1.11	8.16	0.1	9.27	0.1	0.00126315	0.00941621	A_07_P020307	b1532	cmr|multiple antibiotic resistance protein [b1532]
marR	+2.71	11.63	+1.44	10.91	0.2	12.35	0.1	0.00143201	0.01031835	A_07_P020299	b1530	cmr|multiple antibiotic resistance protein; repressor of mar operon [b1530]
matA	-2.13	9.36	-1.09	9.91	0.3	8.82	0.1	0.00895348	0.04122947	A_07_P041479	c_0405	cmr|Hypothetical protein ykgK [c_0405]
mchD	-2.50	11.64	-1.32	12.30	0.4	10.98	0.0	0.00451509	0.02431941	A_07_P040445	c_1230	cmr|MchD protein [c_1230]
mdaB	+5.71	9.81	+2.51	8.55	0.2	11.06	0.2	0.00009718	0.00154382	A_07_P012273	b3028	cmr|modulator of drug activity B [b3028]
mdh	+6.74	11.61	+2.75	10.24	0.0	12.99	0.0	0.00000798	0.00041039	A_07_P012651	b3236	cmr|malate dehydrogenase [b3236]
mdoC	-2.69	8.02	-1.43	8.73	0.0	7.31	0.1	0.00023076	0.00281851	A_07_P001448	b1047	cmr|orf, hypothetical protein [b1047]
mdoG	-2.52	10.95	-1.33	11.62	0.0	10.29	0.1	0.00040389	0.00415342	A_07_P001451	b1048	cmr|periplasmic glucans biosynthesis protein [b1048]
mdtH	-2.77	9.53	-1.47	10.26	0.3	8.79	0.2	0.00227272	0.01453359	A_07_P001526	b1065	cmr|orf, hypothetical protein [b1065]
mdtK	-3.18	11.17	-1.67	12.01	0.0	10.34	0.0	0.00009294	0.00149610	A_07_P018376	b1663	cmr|putative transport protein [b1663]
mdtL	-2.24	7.98	-1.16	8.56	0.3	7.40	0.1	0.00644569	0.03192183	A_07_P005475	b3710	cmr|putative transport protein [b3710]
mdtQ	-2.16	7.07	-1.11	7.62	0.0	6.51	0.0	0.00066069	0.00587078	A_07_P003459	b2139	cmr|orf, hypothetical protein [b2139]
mdtQ	-2.23	8.52	-1.16	9.10	0.1	7.94	0.1	0.00107124	0.00834272	A_07_P010504	b2139	cmr|orf, hypothetical protein [b2139]
melA	+2.85	8.83	+1.51	8.08	0.1	9.59	0.2	0.00069434	0.00608327	A_07_P011333	b4119	cmr|alpha-galactosidase [b4119]
menB	+5.33	9.64	+2.41	8.43	0.1	10.85	0.1	0.00001893	0.00061693	A_07_P001100	b2262	cmr|dihydroxynaphtoic acid synthetase [b2262]
menC	-2.39	12.52	-1.26	13.15	0.1	11.89	0.1	0.00108530	0.00842964	A_07_P001094	b2261	cmr|o-succinylbenzoyl-CoA synthase; conversion of chorismate to 2-o-succinylbenzoyl-CoA [b2261]
menD	+2.25	8.95	+1.17	8.37	0.2	9.54	0.1	0.00163683	0.01139267	A_07_P032389	c_2808	cmr|Menaquinone biosynthesis protein menD [c_2808]
metB	+2.53	8.89	+1.34	8.22	0.2	9.56	0.1	0.00091526	0.00747785	A_07_P019474	b3939	cmr|cystathionine gamma-synthase [b3939]
metH	+2.49	8.12	+1.32	7.46	0.3	8.78	0.1	0.00253811	0.01578201	A_07_P057969	ECs4937	cmr|B12-dependent homocysteine-N5-methyltetrahydrofolate transmethylase [ECs4937]
metH	+2.99	8.48	+1.58	7.69	0.0	9.27	0.0	0.00013299	0.00190006	A_07_P047219	Z5610	cmr|B12-dependent homocysteine-N5-methyltetrahydrofolate transmethylase, repressor of metE and [Z5610]
metH	+2.52	9.11	+1.33	8.44	0.1	9.77	0.1	0.00069653	0.00609566	A_07_P037467	c_4976	cmr|5-methyltetrahydrofolate--homocysteine methyltransferase [c_4976]
metN	-3.64	10.73	-1.87	11.66	0.1	9.80	0.1	0.00009758	0.00154382	A_07_P002955	b0199	cmr|ATP-binding component of a transporter [b0199]
mfd	+2.16	7.72	+1.11	7.16	0.1	8.27	0.0	0.00119228	0.00903331	A_07_P040806	c_1389	cmr|Transcription-repair coupling factor [c_1389]
mglA	+5.38	8.39	+2.43	7.17	0.1	9.60	0.1	0.00002243	0.00067002	A_07_P003507	b2149	cmr|ATP-binding component of methyl-galactoside transport and galactose taxis [b2149]
mglB	+13.26	9.19	+3.73	7.32	0.3	11.05	0.0	0.00001472	0.00054604	A_07_P003515	b2150	cmr|galactose-binding transport protein; receptor for galactose taxis [b2150]
mglB	+15.81	10.19	+3.98	8.19	0.0	12.18	0.0	0.00000138	0.00022125	A_07_P032239	c_2684	cmr|D-galactose-binding periplasmic protein precursor [c_2684]
mglB	+17.45	10.29	+4.12	8.22	0.1	12.35	0.0	0.00000117	0.00021114	A_07_P045485	Z3405	cmr|galactose-binding transport protein receptor for galactose taxis [Z3405]
mglC	+2.87	8.62	+1.52	7.86	0.0	9.38	0.1	0.00021945	0.00271616	A_07_P003504	b2148	cmr|methyl-galactoside transport and galactose taxis [b2148]
mgsA	+5.31	10.33	+2.41	9.12	0.2	11.53	0.1	0.00006353	0.00117531	A_07_P005264	b0963	cmr|methylglyoxal synthase [b0963]
mgtA	-37.54	11.77	-5.23	14.38	0.0	9.15	0.1	0.00000059	0.00019431	A_07_P003761	b4242	cmr|Mg2+ transport ATPase, P-type 1 [b4242]
miaA	+3.11	13.07	+1.64	12.26	0.0	13.89	0.0	0.00010557	0.00163561	A_07_P011571	b4171	cmr|delta [b4171]
minD	+2.18	10.21	+1.13	9.65	0.2	10.78	0.2	0.00337708	0.01962668	A_07_P006827	b1175	cmr|cell division inhibitor, a membrane ATPase, activates minC [b1175]
minE	+3.31	11.96	+1.73	11.09	0.1	12.82	0.0	0.00011655	0.00173927	A_07_P006821	b1174	cmr|cell division topological specificity factor, reverses MinC inhibition of ftsZ ring formation [b1174]
mioC	-4.91	13.92	-2.30	15.07	0.0	12.77	0.0	0.00002079	0.00063916	A_07_P005634	b3742	cmr|initiation of chromosome replication [b3742]
mipA	+4.48	11.81	+2.16	10.73	0.1	12.90	0.0	0.00003767	0.00087581	A_07_P015602	b1782	cmr|orf, hypothetical protein [b1782]
mltD	+3.16	10.65	+1.66	9.82	0.2	11.48	0.0	0.00023069	0.00281851	A_07_P002982	b0211	cmr|transcriptional regulator for nitrite reductase [b0211]
mntH	-7.86	9.79	-2.97	11.28	0.2	8.31	0.1	0.00003191	0.00079613	A_07_P014241	b2392	cmr|putative transport system permease [b2392]
moaB	+2.58	10.27	+1.37	9.59	0.1	10.96	0.1	0.00044460	0.00444871	A_07_P004361	b0782	cmr|molybdopterin biosynthesis, protein B [b0782]
mobA	+3.44	8.19	+1.78	7.30	0.4	9.08	0.1	0.00182312	0.01232958	A_07_P039291	c_4801	cmr|Molybdopterin-guanine dinucleotide biosynthesis protein A [c_4801]
moeA	-2.11	11.36	-1.08	11.90	0.0	10.82	0.1	0.00097952	0.00780447	A_07_P004586	b0827	cmr|molybdopterin biosynthesis [b0827]
moeB	-2.39	9.06	-1.26	9.69	0.1	8.43	0.1	0.00077461	0.00661362	A_07_P004583	b0826	cmr|molybdopterin biosynthesis [b0826]
mokC	-3.55	12.36	-1.83	13.27	0.1	11.44	0.0	0.00012129	0.00178598	A_07_P010256	b0018	cmr|Gef protein interferes with membrane function when in excess [b0018]
mokC	-2.41	10.92	-1.27	11.55	0.1	10.28	0.0	0.00040051	0.00412947	A_07_P010779	b0018	cmr|Gef protein interferes with membrane function when in excess [b0018]
mokP	-2.60	15.08	-1.38	15.77	0.0	14.39	0.4	0.00414157	0.02281485	A_07_P044279	Z6063	cmr|putative cell killing protein encoded within cryptic [Z6063]
motB	-2.96	8.42	-1.57	9.20	0.0	7.63	0.2	0.00033299	0.00364059	A_07_P016121	b1889	cmr|enables flagellar motor rotation, linking torque machinery to cell wall [b1889]
mpl	-2.24	12.34	-1.16	12.92	0.0	11.75	0.0	0.00059428	0.00547004	A_07_P003716	b4233	cmr|putative ligase [b4233]
mraZ	-3.20	12.31	-1.68	13.15	0.0	11.47	0.1	0.00012419	0.00181541	A_07_P011082	b0081	cmr|orf, hypothetical protein [b0081]
mrdA	-2.10	8.81	-1.07	9.35	0.1	8.28	0.1	0.00145651	0.01044487	A_07_P009743	b0635	cmr|cell elongation, e phase; peptidoglycan synthetase; penicillin-binding protein 2 [b0635]
msbA	-4.43	10.26	-2.15	11.33	0.0	9.18	0.0	0.00002776	0.00073912	A_07_P005017	b0914	cmr|ATP-binding transport protein; multicopy suppressor of htrB [b0914]
mscL	-2.02	12.30	-1.02	12.81	0.0	11.79	0.1	0.00123814	0.00926487	A_07_P034268	c_4051	cmr|Large-conductance mechanosensitive channel [c_4051]
msrA	+3.49	8.69	+1.80	7.78	0.1	9.59	0.0	0.00012626	0.00183207	A_07_P003647	b4219	cmr|peptide methionine sulfoxide reductase [b4219]
msrB	+6.54	13.44	+2.71	12.09	0.1	14.80	0.1	0.00001334	0.00052521	A_07_P015584	b1778	cmr|orf, hypothetical protein [b1778]
msyB	+2.68	10.26	+1.42	9.55	0.1	10.97	0.0	0.00042529	0.00430593	A_07_P040763	c_1318	cmr|Acidic protein msyB [c_1318]
mtfA	+2.64	7.68	+1.40	6.98	0.1	8.38	0.0	0.00033204	0.00363536	A_07_P015234	b1976	cmr|orf, hypothetical protein [b1976]
mtlA	+2.79	7.99	+1.48	7.25	0.0	8.73	0.1	0.00033997	0.00369388	A_07_P049516	Z5023	cmr|PTS system, mannitol-specific enzyme IIABC components [Z5023]
mtlA	+3.51	8.27	+1.81	7.37	0.1	9.18	0.2	0.00018306	0.00238590	A_07_P039704	c_4416	cmr|PTS system, mannitol-specific IIABC component [c_4416]
mtlD	+2.58	8.79	+1.37	8.11	0.0	9.47	0.2	0.00056596	0.00528183	A_07_P039708	c_4417	cmr|Mannitol-1-phosphate 5-dehydrogenase [c_4417]
murI	-3.44	10.51	-1.78	11.40	0.1	9.62	0.1	0.00014487	0.00202744	A_07_P008540	b3967	cmr|glutamate racemase, required for biosynthesis of D-glutamate and peptidoglycan [b3967]
mutH	-2.00	8.47	-1.00	8.97	0.0	7.97	0.1	0.00169517	0.01170047	A_07_P041691	c_3426	cmr|DNA mismatch repair protein mutH [c_3426]
mutM	-4.02	9.79	-2.01	10.80	0.0	8.79	0.1	0.00006458	0.00118644	A_07_P017118	b3635	cmr|formamidopyrimidine DNA glycosylase [b3635]
mutY	-2.91	12.02	-1.54	12.79	0.5	11.24	0.0	0.00636244	0.03164936	A_07_P011946	b2961	cmr|adenine glycosylase; G.C --> T.A transversions [b2961]
nac	-10.12	9.31	-3.34	10.98	0.1	7.64	0.0	0.00000593	0.00036511	A_07_P015279	b1988	cmr|nitrogen assimilation control protein [b1988]
nadA	-2.27	8.47	-1.18	9.06	0.2	7.88	0.1	0.00214651	0.01390728	A_07_P033430	c_0825	cmr|Quinolinate synthetase A [c_0825]
nadA	-2.04	8.70	-1.03	9.22	0.0	8.19	0.1	0.00163609	0.01139259	A_07_P046361	Z0919	cmr|quinolinate synthetase, A protein [Z0919]
nadA	-2.09	7.90	-1.06	8.43	0.1	7.37	0.1	0.00158224	0.01112091	A_07_P010232	b0750	cmr|quinolinate synthetase, A protein [b0750]
nadE	+5.78	9.53	+2.53	8.26	0.0	10.79	0.1	0.00001397	0.00053770	A_07_P018749	b1740	cmr|NAD synthetase, prefers NH3 over glutamine [b1740]
nadR	+2.03	9.17	+1.02	8.66	0.3	9.68	0.1	0.00998600	0.04470339	A_07_P017631	b4390	cmr|probable nadAB transcriptional regulator [b4390]
nagA	+2.43	9.44	+1.28	8.80	0.2	10.08	0.3	0.00365441	0.02080082	A_07_P009903	b0677	cmr|N-acetylglucosamine-6-phosphate deacetylase [b0677]
nagB	+2.20	8.40	+1.14	7.84	0.1	8.97	0.1	0.00112795	0.00868811	A_07_P009910	b0678	cmr|glucosamine-6-phosphate deaminase [b0678]
nagE	-2.05	11.96	-1.04	12.48	0.0	11.44	0.0	0.00093463	0.00757320	A_07_P009911	b0679	cmr|PTS system, N-acetylglucosamine-specific enzyme IIABC [b0679]
nagZ	+4.52	9.08	+2.18	8.00	0.0	10.17	0.0	0.00002780	0.00073912	A_07_P001737	b1107	cmr|orf, hypothetical protein [b1107]
nanA	+3.00	8.58	+1.58	7.78	0.4	9.37	0.2	0.00401424	0.02226925	A_07_P041797	c_3979	cmr|N-acetylneuraminate lyase subunit [c_3979]
nanA	+2.02	7.70	+1.01	7.20	0.1	8.21	0.1	0.00241642	0.01521155	A_07_P012599	b3225	cmr|N-acetylneuraminate lyase [b3225]
nanE	+2.91	8.15	+1.54	7.38	0.0	8.92	0.0	0.00015057	0.00208675	A_07_P012586	b3223	cmr|putative enzyme [b3223]
nanK	+2.85	7.43	+1.51	6.67	0.0	8.18	0.1	0.00021006	0.00262893	A_07_P012584	b3222	cmr|putative NAGC-like transcriptional regulator [b3222]
napB	+2.63	8.90	+1.40	8.20	0.1	9.60	0.1	0.00038737	0.00402821	A_07_P000804	b2203	cmr|cytochrome c-type protein [b2203]
napF	-4.02	11.13	-2.01	12.13	0.1	10.13	0.0	0.00004892	0.00100424	A_07_P000827	b2208	cmr|ferredoxin-type protein: electron transfer [b2208]
narL	+2.89	10.98	+1.53	10.22	0.2	11.75	0.0	0.00032707	0.00359843	A_07_P052433	Z1996	cmr|pleiotrophic regulation of anaerobic respiration: response regulator [Z1996]

narP	+2.81	8.13	+1.49	7.38	0.3	8.88	0.2	0.00179841	0.01225015	A_07_P000752	b2193	cmr|nitrate/nitrite response regulator [b2193]
ndk	+9.19	11.48	+3.20	9.88	0.1	13.08	0.0	0.00000529	0.00034950	A_07_P013646	b2518	cmr|nucleoside diphosphate kinase [b2518]
nemA	+4.44	10.47	+2.15	9.39	0.0	11.54	0.0	0.00003007	0.00077228	A_07_P020882	b1650	cmr|N-ethylmaleimide reductase [b1650]
nfi	+7.47	9.81	+2.90	8.36	0.1	11.26	0.1	0.00000805	0.00041039	A_07_P037441	c_4955	cmr|Endonuclease V [c_4955]
nfi	+6.35	9.39	+2.67	8.05	0.0	10.72	0.1	0.00001145	0.00049545	A_07_P008655	b3998	cmr|endonuclease V [b3998]
nfi	+3.56	9.41	+1.83	8.50	0.3	10.33	0.2	0.00132405	0.00972818	A_07_P047202	Z5574	cmr|endonuclease V [Z5574]
nfo	+3.03	8.50	+1.60	7.70	0.1	9.30	0.1	0.00040715	0.00416878	A_07_P003556	b2159	cmr|endonuclease IV [b2159]
nhaA	-7.26	11.57	-2.86	13.00	0.0	10.14	0.0	0.00000666	0.00038136	A_07_P010784	b0019	cmr|Na+/H antiporter, pH dependent [b0019]
nhaR	-3.26	9.55	-1.71	10.41	0.1	8.70	0.1	0.00015405	0.00212192	A_07_P035651	c_0025	cmr|Transcriptional activator protein nhaR [c_0025]
nikA	+2.62	7.70	+1.39	7.01	0.2	8.40	0.0	0.00099420	0.00788955	A_07_P007316	b3476	cmr|periplasmic binding protein for nickel [b3476]
nlpA	-4.40	8.58	-2.14	9.65	0.1	7.51	0.1	0.00005542	0.00108517	A_07_P017245	b3661	cmr|lipoprotein-28 [b3661]
nlpI	-5.78	14.84	-2.53	16.11	0.0	13.57	0.0	0.00001303	0.00052185	A_07_P000538	b3163	cmr|putative control proteins [b3163]
nmpC	+17.13	10.40	+4.10	8.36	0.5	12.45	0.0	0.00009575	0.00152759	A_07_P038497	c_1560	cmr|Outer membrane porin protein nmpC precursor [c_1560]
nohA	+7.14	10.37	+2.84	8.95	0.0	11.79	0.0	0.00000700	0.00039376	A_07_P038523	c_1568	cmr|Prophage Qin DNA packaging protein NU1 homolog [c_1568]
nrdA	+50.08	10.76	+5.65	7.93	0.1	13.58	0.1	0.00000034	0.00019431	A_07_P000956	b2234	cmr|ribonucleoside diphosphate reductase 1, alpha subunit, B1 [b2234]
nrdB	+12.18	10.65	+3.61	8.85	0.1	12.45	0.1	0.00000264	0.00027706	A_07_P000962	b2235	cmr|ribonucleoside-diphosphate reductase 1, beta subunit, B2 [b2235]
nrdD	+26.15	12.76	+4.71	10.41	0.1	15.12	0.1	0.00000105	0.00020472	A_07_P003742	b4238	cmr|anaerobic ribonucleoside-triphosphate reductase [b4238]
nrdD	+24.22	13.21	+4.60	10.91	0.0	15.51	0.1	0.00000127	0.00021491	A_07_P042066	c_5337	cmr|Anaerobic ribonucleoside-triphosphate reductase [c_5337]
nrdG	+11.44	10.17	+3.52	8.41	0.1	11.93	0.0	0.00000361	0.00030683	A_07_P003737	b4237	cmr|anaerobic ribonucleotide reductase activating protein [b4237]
nrdR	-3.38	13.39	-1.76	14.27	0.1	12.52	0.0	0.00008374	0.00140699	A_07_P021179	b0413	cmr|orf, hypothetical protein [b0413]
nudB	+2.87	10.81	+1.52	10.05	0.1	11.57	0.1	0.00025418	0.00302024	A_07_P016003	b1865	cmr|dATP pyrophosphohydrolase [b1865]
nudB	+2.92	11.13	+1.54	10.36	0.1	11.90	0.0	0.00026659	0.00310509	A_07_P016003	b1865	cmr|dATP pyrophosphohydrolase [b1865]
nudB	+2.79	11.06	+1.48	10.32	0.0	11.80	0.0	0.00018260	0.00238373	A_07_P016003	b1865	cmr|dATP pyrophosphohydrolase [b1865]
nudB	+3.25	11.03	+1.70	10.18	0.0	11.88	0.1	0.00012189	0.00179019	A_07_P016003	b1865	cmr|dATP pyrophosphohydrolase [b1865]
nudB	+2.87	10.86	+1.52	10.10	0.0	11.62	0.1	0.00017515	0.00231344	A_07_P016003	b1865	cmr|dATP pyrophosphohydrolase [b1865]
nudC	+2.14	9.65	+1.10	9.11	0.1	10.20	0.0	0.00118980	0.00902756	A_07_P008643	b3996	cmr|orf, hypothetical protein [b3996]
nudC	+2.18	9.59	+1.13	9.02	0.1	10.15	0.1	0.00090540	0.00740498	A_07_P063685	ECs4919	cmr|hypothetical protein [ECs4919]
nudE	-2.29	10.61	-1.20	11.21	0.1	10.01	0.1	0.00073152	0.00632113	A_07_P018014	b3397	cmr|orf, hypothetical protein [b3397]
nudE	-2.19	11.01	-1.13	11.57	0.1	10.44	0.1	0.00078930	0.00670628	A_07_P059766	ECs4239	cmr|hypothetical protein [ECs4239]
nudE	-2.15	11.55	-1.10	12.10	0.0	11.00	0.1	0.00099489	0.00788955	A_07_P046016	Z4751	cmr|orf, hypothetical protein [Z4751]
nudI	+2.78	8.21	+1.48	7.47	0.1	8.95	0.0	0.00022409	0.00275206	A_07_P001045	b2251	cmr|orf, hypothetical protein [b2251]
nudK	+2.41	9.14	+1.27	8.51	0.1	9.78	0.4	0.00782807	0.03723420	A_07_P013393	b2467	cmr|orf, hypothetical protein [b2467]
nuoC	+6.15	10.89	+2.62	9.58	0.0	12.20	0.0	0.00001043	0.00047057	A_07_P013718	b2286	cmr|NADH dehydrogenase I chain C, D [b2286]
nuoE	+5.24	12.78	+2.39	11.59	0.0	13.98	0.0	0.00001624	0.00056947	A_07_P042543	c_2826	cmr|NADH dehydrogenase I chain E [c_2826]
nuoE	+6.88	11.13	+2.78	9.74	0.0	12.53	0.0	0.00000741	0.00040580	A_07_P013712	b2285	cmr|NADH dehydrogenase I chain E [b2285]
nuoE	+4.42	11.16	+2.14	10.09	0.1	12.23	0.0	0.00005581	0.00108886	A_07_P052679	Z3544	cmr|NADH dehydrogenase I chain E [Z3544]
nuoF	+16.05	10.48	+4.00	8.48	0.1	12.48	0.0	0.00000281	0.00028143	A_07_P013708	b2284	cmr|NADH dehydrogenase I chain F [b2284]
nuoG	+6.15	8.62	+2.62	7.31	0.1	9.93	0.3	0.00013043	0.00186858	A_07_P013701	b2283	cmr|NADH dehydrogenase I chain G [b2283]
nuoG	+8.84	9.75	+3.14	8.18	0.0	11.32	0.2	0.00001201	0.00050646	A_07_P045556	Z3542	cmr|NADH dehydrogenase I chain G [Z3542]
nuoH	+18.80	9.64	+4.23	7.52	0.0	11.75	0.1	0.00000164	0.00023759	A_07_P013700	b2282	cmr|NADH dehydrogenase I chain H [b2282]
nuoI	+7.16	9.41	+2.84	7.99	0.7	10.83	0.0	0.00192746	0.01280417	A_07_P013694	b2281	cmr|NADH dehydrogenase I chain I [b2281]
nuoJ	+7.91	9.55	+2.98	8.06	0.3	11.04	0.1	0.00007038	0.00124928	A_07_P013686	b2280	cmr|NADH dehydrogenase I chain J [b2280]
nuoK	+9.89	8.68	+3.31	7.03	0.0	10.34	0.2	0.00001452	0.00054604	A_07_P001181	b2279	cmr|NADH dehydrogenase I chain K [b2279]
nuoK	+9.72	8.84	+3.28	7.20	0.0	10.48	0.2	0.00001564	0.00056283	A_07_P045553	Z3538	cmr|NADH dehydrogenase I chain K [Z3538]
nuoL	+6.25	8.79	+2.64	7.47	0.4	10.11	0.0	0.00018912	0.00244038	A_07_P001178	b2278	cmr|NADH dehydrogenase I chain L [b2278]
nuoM	+6.62	8.54	+2.73	7.18	0.2	9.90	0.0	0.00003127	0.00078813	A_07_P001174	b2277	cmr|NADH dehydrogenase I chain M [b2277]
nuoN	+3.33	7.59	+1.73	6.72	0.1	8.46	0.1	0.00014739	0.00205361	A_07_P051791	Z3534	cmr|NADH dehydrogenase I chain N [Z3534]
nuoN	+2.70	7.74	+1.43	7.03	0.2	8.46	0.1	0.00088384	0.00729692	A_07_P042539	c_2817	cmr|NADH dehydrogenase I chain N [c_2817]
nuoN	+2.41	7.81	+1.27	7.17	0.2	8.45	0.2	0.00228626	0.01459056	A_07_P001166	b2276	cmr|NADH dehydrogenase I chain N [b2276]
nupC	+2.58	8.30	+1.37	7.62	0.4	8.99	0.2	0.00567604	0.02908023	A_07_P014250	b2393	cmr|permease of transport system for 3 nucleosides [b2393]
nupG	+4.40	10.07	+2.14	9.00	0.1	11.14	0.0	0.00003507	0.00083975	A_07_P011964	b2964	cmr|transport of nucleosides, permease protein [b2964]
nusA	-2.85	14.77	-1.51	15.52	0.1	14.01	0.1	0.00023169	0.00282329	A_07_P000566	b3169	cmr|transcription pausing; L factor [b3169]
nusB	-6.99	12.53	-2.81	13.93	0.0	11.12	0.1	0.00000948	0.00044666	A_07_P021194	b0416	cmr|transcription termination; L factor [b0416]
nusG	+2.36	10.21	+1.24	9.58	0.2	10.83	0.0	0.00145006	0.01040556	A_07_P008575	b3982	cmr|component in transcription antitermination [b3982]
obgE	-2.11	10.18	-1.08	10.72	0.1	9.64	0.0	0.00084412	0.00705035	A_07_P012391	b3183	cmr|putative GTP-binding factor [b3183]
ompC	+5.17	9.97	+2.37	8.79	0.1	11.16	0.0	0.00002033	0.00063193	A_07_P032359	c_2758	cmr|Outer membrane protein C precursor [c_2758]
ompC	+4.54	9.14	+2.18	8.05	0.1	10.23	0.1	0.00004795	0.00099062	A_07_P000863	b2215	cmr|outer membrane protein 1b [b2215]
ompC	+2.32	10.38	+1.21	9.77	0.1	10.98	0.0	0.00084123	0.00703741	A_07_P045517	Z3473	cmr|outer membrane protein 1b [Z3473]
ompF	+6.72	10.16	+2.75	8.79	0.1	11.54	0.0	0.00001234	0.00051423	A_07_P005092	b0929	cmr|outer membrane protein 1a [b0929]
ompT	+2.12	8.18	+1.08	7.64	0.3	8.72	0.1	0.00836015	0.03904543	A_07_P031283	c_0652	cmr|Protease VII precursor [c_0652]
ompW	+35.91	9.54	+5.17	6.96	0.0	12.13	0.0	0.00000034	0.00019431	A_07_P007216	b1256	cmr|putative outer membrane protein [b1256]
ompW	+81.78	11.83	+6.35	8.65	0.0	15.00	0.1	0.00000015	0.00019431	A_07_P038872	c_1722	cmr|Outer membrane protein W precursor [c_1722]
ompX	-8.05	13.81	-3.01	15.32	0.0	12.31	0.0	0.00000518	0.00034758	A_07_P004524	b0814	cmr|outer membrane protein X [b0814]
oppA	+16.39	10.14	+4.03	8.12	0.2	12.15	0.0	0.00000556	0.00035456	A_07_P007151	b1243	cmr|oligopeptide transport; periplasmic binding protein [b1243]
oppA	+20.77	11.14	+4.38	8.95	0.0	13.33	0.0	0.00000085	0.00019431	A_07_P052437	Z2019	cmr|oligopeptide transport periplasmic binding protein [Z2019]
oppC	+2.55	7.89	+1.35	7.21	0.0	8.57	0.1	0.00035526	0.00380746	A_07_P007165	b1245	cmr|homolog of Salmonella oligopeptide transport permease protein [b1245]
oppD	+4.85	9.65	+2.28	8.51	0.2	10.79	0.1	0.00013905	0.00196871	A_07_P007166	b1246	cmr|homolog of Salmonella ATP-binding protein of oligopeptide ABC transport system [b1246]
oppF	+5.31	8.71	+2.41	7.50	0.3	9.91	0.0	0.00011319	0.00169854	A_07_P007171	b1247	cmr|homolog of Salmonella ATP-binding protein of oligopeptide ABC transport system [b1247]
osmB	-5.84	8.95	-2.55	10.22	0.1	7.67	0.0	0.00001527	0.00055785	A_07_P014396	b1283	cmr|osmotically inducible lipoprotein [b1283]
osmC	-2.34	10.91	-1.22	11.52	0.0	10.29	0.0	0.00047810	0.00468112	A_07_P009499	b1482	cmr|osmotically inducible protein [b1482]
osmE	+2.32	8.12	+1.22	7.52	0.1	8.73	0.1	0.00065802	0.00585967	A_07_P018744	b1739	cmr|activator of ntrL gene [b1739]
osmY	+2.08	8.62	+1.06	8.10	0.1	9.15	0.2	0.00304110	0.01806079	A_07_P017561	b4376	cmr|hyperosmotically inducible periplasmic protein [b4376]
oxyR	-2.24	13.78	-1.16	14.36	0.0	13.20	0.0	0.00056380	0.00527744	A_07_P008508	b3961	cmr|activator, hydrogen peroxide-inducible genes [b3961]
pal	+2.55	11.45	+1.35	10.78	0.1	12.13	0.0	0.00036801	0.00391653	A_07_P010223	b0741	cmr|peptidoglycan-associated lipoprotein [b0741]
panB	-2.58	10.60	-1.37	11.28	0.0	9.91	0.1	0.00029118	0.00331235	A_07_P002634	b0134	cmr|3-methyl-2-oxobutanoate hydroxymethyltransferase [b0134]
panB	-3.38	12.53	-1.76	13.41	0.0	11.65	0.1	0.00008665	0.00143594	A_07_P035825	c_0165	cmr|3-methyl-2-oxobutanoate hydroxymethyltransferase [c_0165]
panC	-2.08	9.58	-1.05	10.11	0.1	9.05	0.0	0.00144973	0.01040556	A_07_P049200	Z0144	cmr|pantothenate synthetase [Z0144]
panD	+3.69	11.56	+1.88	10.62	0.0	12.50	0.0	0.00005258	0.00105181	A_07_P002617	b0131	cmr|aspartate 1-decarboxylase [b0131]
panE	+2.18	8.95	+1.13	8.39	0.1	9.51	0.0	0.00134374	0.00981706	A_07_P021236	b0425	cmr|involved in thiamin biosynthesis, alternative pyrimidine biosynthesis [b0425]
panF	+2.11	8.39	+1.08	7.85	0.0	8.93	0.1	0.00105817	0.00826384	A_07_P012756	b3258	cmr|sodium/pantothenate symporter [b3258]
papA	+11.49	9.00	+3.52	7.24	0.2	10.76	0.2	0.00002704	0.00073404	A_07_P033164	c_3592	cmr|PapA protein [c_3592]
papC	+4.03	8.97	+2.01	7.97	0.1	9.98	0.1	0.00006678	0.00120840	A_07_P033151	c_3590	cmr|PapC protein [c_3590]
papD_2	+2.71	9.37	+1.44	8.65	0.1	10.09	0.1	0.00049009	0.00476059	A_07_P037957	c_5185	cmr|PapD protein [c_5185]
papE	+2.21	9.28	+1.14	8.71	0.1	9.85	0.1	0.00144027	0.01035891	A_07_P033134	c_3585	cmr|PapE protein [c_3585]
papH	+3.03	10.43	+1.60	9.62	0.3	11.23	0.0	0.00128454	0.00953955	A_07_P033156	c_3591	cmr|PapH protein [c_3591]
papH_2	+6.26	8.94	+2.65	7.62	0.2	10.27	0.1	0.00004446	0.00094837	A_07_P037969	c_5187	cmr|PapH protein [c_5187]
papI_2	+3.11	7.89	+1.63	7.07	0.2	8.71	0.1	0.00060411	0.00552011	A_07_P037980	c_5189	cmr|PapI protein [c_5189]
papK	+2.30	9.56	+1.20	8.96	0.2	10.16	0.0	0.00222564	0.01431980	A_07_P033137	c_3586	cmr|PapK protein [c_3586]
parE	-2.02	11.44	-1.02	11.94	0.3	10.93	0.0	0.00637151	0.03168450	A_07_P012284	b3030	cmr|DNA topoisomerase IV subunit B [b3030]
pbpG	+2.17	7.61	+1.12	7.05	0.3	8.17	0.0	0.00430773	0.02346263	A_07_P003433	b2134	cmr|penicillin-binding protein 7 [b2134]
pck	+4.61	14.13	+2.21	13.03	0.1	15.24	0.1	0.00004630	0.00097245	A_07_P018041	b3403	cmr|phosphoenolpyruvate carboxykinase [b3403]
pcm	-2.39	11.08	-1.25	11.71	0.2	10.46	0.1	0.00094291	0.00761295	A_07_P002163	b2743	cmr|L-isoaspartate protein carboxylmethyltransferase type II [b2743]
pdhR	+2.09	11.82	+1.06	11.28	0.1	12.35	0.1	0.00102525	0.00807477	A_07_P002527	b0113	cmr|transcriptional regulator for pyruvate dehydrogenase complex [b0113]
pdxB	+2.86	10.64	+1.52	9.89	0.0	11.40	0.2	0.00038633	0.00402277	A_07_P013888	b2320	cmr|erythronate-4-phosphate dehyrogenase [b2320]
pdxJ	+3.53	8.99	+1.82	8.08	0.0	9.90	0.0	0.00007021	0.00124769	A_07_P019721	b2564	cmr|pyridoxine biosynthesis [b2564]
pepA	+2.14	12.33	+1.10	11.78	0.0	12.87	0.0	0.00074428	0.00640677	A_07_P003848	b4260	cmr|aminopeptidase A/I [b4260]
pepB	+3.02	9.36	+1.60	8.56	0.0	10.15	0.1	0.00016925	0.00225435	A_07_P013674	b2523	cmr|putative peptidase [b2523]
pepD	+10.85	10.48	+3.44	8.76	0.1	12.20	0.0	0.00000435	0.00033435	A_07_P007896	b0237	cmr|aminoacyl-histidine dipeptidase [b0237]
pepE	+4.95	8.12	+2.31	6.96	0.1	9.27	0.1	0.00003219	0.00079793	A_07_P008748	b4021	cmr|peptidase E, a dipeptidase where amino-terminal residue is aspartate [b4021]
pepN	+5.98	9.11	+2.58	7.82	0.1	10.40	0.0	0.00001598	0.00056395	A_07_P051734	Z1280	cmr|aminopeptidase N [Z1280]
pepT	+4.66	9.20	+2.22	8.09	0.1	10.31	0.2	0.00009097	0.00147798	A_07_P006587	b1127	cmr|putative peptidase T [b1127]
perM	-2.69	9.36	-1.43	10.07	0.1	8.64	0.1	0.00056482	0.00527744	A_07_P030120	c_3009	cmr|Putative permease perM [c_3009]
pfkB	+3.22	9.11	+1.69	8.26	0.1	9.95	0.1	0.00026477	0.00309464	A_07_P041160	c_2121	cmr|6-phosphofructokinase isozyme 2 [c_2121]
pfkB	+3.73	9.26	+1.90	8.31	0.1	10.21	0.0	0.00007728	0.00132533	A_07_P018663	b1723	cmr|6-phosphofructokinase II; suppressor of pfkA [b1723]
pflA	-2.87	12.93	-1.52	13.69	0.0	12.17	0.1	0.00016825	0.00224864	A_07_P004958	b0902	cmr|pyruvate formate lyase activating enzyme 1 [b0902]
pflB	+8.96	10.90	+3.16	9.32	0.1	12.48	0.1	0.00000610	0.00036832	A_07_P004961	b0903	cmr|formate acetyltransferase 1 [b0903]
pgaD	-4.96	9.06	-2.31	10.22	0.0	7.91	0.3	0.00016697	0.00223914	A_07_P001332	b1021	cmr|orf, hypothetical protein [b1021]
pgi	+2.81	8.97	+1.49	8.22	0.3	9.71	0.0	0.00245102	0.01538016	A_07_P008767	b4025	cmr|glucosephosphate isomerase [b4025]
pgk	+4.09	12.73	+2.03	11.71	0.1	13.74	0.0	0.00004322	0.00093866	A_07_P011776	b2926	cmr|phosphoglycerate kinase [b2926]
pgl	+5.67	9.19	+2.50	7.94	0.0	10.44	0.0	0.00001264	0.00051704	A_07_P004288	b0767	cmr|putative isomerase [b0767]
pheS	+3.75	11.21	+1.91	10.26	0.0	12.17	0.2	0.00014064	0.00198761	A_07_P018621	b1714	cmr|phenylalanine tRNA synthetase, alpha-subunit [b1714]
pheT	+2.72	10.23	+1.44	9.51	0.1	10.95	0.1	0.00035229	0.00378335	A_07_P018619	b1713	cmr|phenylalanine tRNA synthetase, beta-subunit [b1713]
phnI	-2.26	11.29	-1.17	11.88	0.1	10.71	0.1	0.00078215	0.00665883	A_07_P011231	b4099	cmr|phosphonate metabolism [b4099]
phoA	-2.59	8.59	-1.37	9.28	0.2	7.91	0.1	0.00076368	0.00654155	A_07_P021029	b0383	cmr|alkaline phosphatase [b0383]
phoB	-5.63	11.81	-2.49	13.06	0.1	10.56	0.1	0.00002330	0.00068274	A_07_P031103	c_0508	cmr|Phosphate regulon transcriptional Regulatory protein phoB [c_0508]
phoB	-5.64	11.51	-2.50	12.76	0.0	10.26	0.0	0.00001293	0.00051944	A_07_P021109	b0399	cmr|positive response regulator for pho regulon, sensor is PhoR [b0399]
phoB	-5.21	11.73	-2.38	12.92	0.0	10.54	0.1	0.00002026	0.00063193	A_07_P043823	Z0497	cmr|positive response regulator for pho regulon, sensor [Z0497]
phoR	-3.16	8.25	-1.66	9.08	0.1	7.42	0.1	0.00020272	0.00257504	A_07_P021115	b0400	cmr|positive and negative sensor protein for pho regulon [b0400]
phoU	+2.14	8.70	+1.10	8.16	0.2	9.25	0.2	0.00386221	0.02172443	A_07_P005542	b3724	cmr|negative regulator for pho regulon and putative enzyme in phosphate metabolism [b3724]
pinR	-2.71	8.49	-1.44	9.20	0.1	7.77	0.0	0.00035336	0.00379046	A_07_P014850	b1374	cmr|putative transposon resolvase [b1374]
pmbA	+2.49	8.70	+1.32	8.04	0.2	9.36	0.4	0.00710987	0.03444804	A_07_P003729	b4235	cmr|maturation of antibiotic MccB17, see tld genes [b4235]
pntA	+4.90	8.57	+2.29	7.42	0.2	9.72	0.0	0.00008477	0.00142126	A_07_P020648	b1603	cmr|pyridine nucleotide transhydrogenase, alpha subunit [b1603]
polA	+3.66	8.60	+1.87	7.66	0.2	9.53	0.1	0.00022615	0.00277298	A_07_P019099	b3863	cmr|DNA polymerase I, 3 --> 5 polymerase, 5 --> 3 and 3 --> 5 exonuclease [b3863]
polA	+2.90	8.68	+1.54	7.91	0.4	9.45	0.1	0.00302621	0.01798592	A_07_P052260	Z5398	cmr|DNA polymerase I, 3 --> 5 polymerase [Z5398]
polB	-5.18	10.47	-2.37	11.66	0.0	9.29	0.1	0.00002414	0.00069739	A_07_P010989	b0060	cmr|DNA polymerase II [b0060]
potA	-2.36	10.73	-1.24	11.35	0.0	10.11	0.1	0.00047964	0.00468366	A_07_P006583	b1126	cmr|ATP-binding component of spermidine/putrescine transport [b1126]
potC	-3.46	11.88	-1.79	12.77	0.0	10.98	0.0	0.00006863	0.00122932	A_07_P006571	b1124	cmr|spermidine/putrescine transport system permease [b1124]
ppdA	+2.88	8.05	+1.53	7.28	0.2	8.81	0.0	0.00058019	0.00537009	A_07_P043261	Z4143	cmr|prepilin peptidase dependent protein A [Z4143]
ppdA	+2.74	8.23	+1.46	7.50	0.1	8.96	0.2	0.00053438	0.00507128	A_07_P032800	c_3420	cmr|Prepilin peptidase dependent protein A precursor [c_3420]
pphB	-3.41	8.00	-1.77	8.88	0.3	7.12	0.1	0.00066113	0.00587078	A_07_P002119	b2734	cmr|protein phosphatase 2 [b2734]
ppiB	+2.69	12.90	+1.43	12.18	0.1	13.61	0.0	0.00037011	0.00392997	A_07_P016413	b0525	cmr|peptidyl-prolyl cis-trans isomerase B [b0525]
ppiC	+2.18	9.35	+1.12	8.79	0.0	9.91	0.1	0.00078205	0.00665883	A_07_P041923	c_4697	cmr|Peptidyl-prolyl cis-trans isomerase C [c_4697]
ppiC	+2.15	8.25	+1.11	7.70	0.1	8.81	0.0	0.00090232	0.00739560	A_07_P005759	b3775	cmr|peptidyl-prolyl cis-trans isomerase C [b3775]
pps	+3.21	13.28	+1.68	12.44	0.0	14.12	0.1	0.00011949	0.00176668	A_07_P018562	b1702	cmr|phosphoenolpyruvate synthase [b1702]
ppx	-2.04	8.75	-1.03	9.27	0.0	8.24	0.1	0.00132907	0.00973744	A_07_P013570	b2502	cmr|exopolyphosphatase [b2502]
prfA	-2.41	10.05	-1.27	10.69	0.1	9.42	0.1	0.00082288	0.00692435	A_07_P007006	b1211	cmr|peptide chain release factor RF-1 [b1211]
prfB	-2.81	13.88	-1.49	14.62	0.0	13.13	0.2	0.00065522	0.00584467	A_07_P006421	b2891	cmr|peptide chain release factor RF-2 [b2891]
prfB	-2.64	14.38	-1.40	15.07	0.0	13.68	0.1	0.00029452	0.00334071	A_07_P032852	c_5622	cmr|Peptide chain release factor 2 [c_5622]
prfH	-8.22	10.49	-3.04	12.01	0.0	8.97	0.0	0.00000514	0.00034758	A_07_P030853	c_0382	cmr|Peptide chain release factor homolog [c_0382]
prfH	-6.36	10.94	-2.67	12.28	0.2	9.61	0.0	0.00002717	0.00073404	A_07_P007894	b0236	cmr|probable peptide chain release factor [b0236]
prfH	-6.82	9.29	-2.77	10.67	0.1	7.90	0.0	0.00000982	0.00045743	A_07_P062922	ECs0263	cmr|probable peptide chain release factor [ECs0263]
prfH	-6.43	9.33	-2.69	10.67	0.0	7.99	0.1	0.00001686	0.00058050	A_07_P051892	Z0297	cmr|probable peptide chain release factor [Z0297]
priA	-2.23	8.55	-1.15	9.12	0.1	7.97	0.0	0.00119666	0.00905341	A_07_P019451	b3935	cmr|primosomal protein N [b3935]
priA	-2.94	9.99	-1.56	10.76	0.2	9.21	0.3	0.00297784	0.01777220	A_07_P039449	c_4888	cmr|Primosomal protein N [c_4888]
prmC	-2.03	9.94	-1.02	10.45	0.1	9.43	0.1	0.00176962	0.01211343	A_07_P007012	b1212	cmr|possible protoporphyrinogen oxidase [b1212]
proP	-5.86	10.17	-2.55	11.45	0.1	8.90	0.1	0.00001484	0.00054604	A_07_P011292	b4111	cmr|low-affinity transport system; proline permease II [b4111]
proV	-3.07	8.69	-1.62	9.50	0.0	7.88	0.1	0.00015594	0.00214424	A_07_P030555	c_3230	cmr|Glycine betaine/L-proline transport ATP-binding protein proV [c_3230]
proW	-2.78	8.52	-1.47	9.26	0.0	7.78	0.1	0.00022252	0.00274273	A_07_P001861	b2678	cmr|high-affinity transport system for glycine betaine and proline [b2678]
proX	+2.62	8.19	+1.39	7.49	0.5	8.88	0.0	0.00977943	0.04395301	A_07_P001866	b2679	cmr|high-affinity transport system for glycine betaine and proline [b2679]
proX	+4.13	8.83	+2.04	7.81	0.2	9.86	0.0	0.00016096	0.00218777	A_07_P030557	c_3232	cmr|Glycine betaine-binding periplasmic protein precursor [c_3232]
prpR	-2.86	11.11	-1.52	11.87	0.3	10.35	0.0	0.00131514	0.00971180	A_07_P031011	c_0450	cmr|Propionate catabolism operon Regulatory protein [c_0450]
psiF	-2.30	8.77	-1.20	9.37	0.2	8.17	0.1	0.00213757	0.01386644	A_07_P062746	ECs0434	cmr|phosphate starvation-induced protein psiF [ECs0434]
psiF	-2.25	8.86	-1.17	9.45	0.1	8.27	0.0	0.00069415	0.00608327	A_07_P051681	Z0480	cmr|induced by phosphate starvation [Z0480]
pspB	-8.04	10.20	-3.01	11.71	0.1	8.70	0.0	0.00000775	0.00041039	A_07_P014506	b1305	cmr|phage shock protein [b1305]
pspC	-18.09	10.48	-4.18	12.57	0.0	8.40	0.1	0.00000201	0.00025681	A_07_P014514	b1306	cmr|phage shock protein: activates phage shock-protein expression [b1306]
pspE	+2.85	11.00	+1.51	10.25	0.1	11.76	0.1	0.00038818	0.00402870	A_07_P014522	b1308	cmr|phage shock protein [b1308]
pspE	+2.47	11.14	+1.31	10.49	0.1	11.80	0.0	0.00036817	0.00391653	A_07_P014522	b1308	cmr|phage shock protein [b1308]
pstC	-3.82	10.31	-1.93	11.27	0.1	9.34	0.1	0.00008397	0.00140944	A_07_P005556	b3727	cmr|high-affinity phosphate-specific transport system, cytoplasmic membrane component [b3727]
pta	+8.56	10.50	+3.10	8.96	0.1	12.05	0.1	0.00000797	0.00041039	A_07_P042552	c_2840	cmr|Phosphate acetyltransferase [c_2840]
pta	+8.49	9.55	+3.09	8.01	0.3	11.09	0.1	0.00004414	0.00094686	A_07_P013771	b2297	cmr|phosphotransacetylase [b2297]
pth	+4.73	11.11	+2.24	9.99	0.1	12.23	0.1	0.00002979	0.00076634	A_07_P006971	b1204	cmr|peptidyl-tRNA hydrolase [b1204]
ptrB	-4.36	8.33	-2.12	9.39	0.1	7.27	0.2	0.00011606	0.00173362	A_07_P015904	b1845	cmr|protease II [b1845]
ptrB	-10.69	9.81	-3.42	11.52	0.0	8.10	0.2	0.00000800	0.00041039	A_07_P035322	c_2256	cmr|Protease II [c_2256]
ptrB	-14.04	10.24	-3.81	12.14	0.2	8.33	0.2	0.00002170	0.00065941	A_07_P052572	Z2896	cmr|protease II [Z2896]
ptsH	+2.11	11.50	+1.08	10.96	0.0	12.04	0.1	0.00102195	0.00805287	A_07_P013132	b2415	cmr|PTS system protein HPr [b2415]
ptsI	+6.54	12.92	+2.71	11.57	0.1	14.28	0.2	0.00003653	0.00085835	A_07_P013136	b2416	cmr|PEP-protein phosphotransferase system enzyme I [b2416]
ptsI	+6.71	13.47	+2.75	12.10	0.1	14.84	0.1	0.00001595	0.00056395	A_07_P013136	b2416	cmr|PEP-protein phosphotransferase system enzyme I [b2416]
ptsI	+8.53	12.74	+3.09	11.19	0.1	14.28	0.0	0.00000635	0.00037147	A_07_P013136	b2416	cmr|PEP-protein phosphotransferase system enzyme I [b2416]
ptsI	+6.53	13.52	+2.71	12.17	0.1	14.87	0.0	0.00000985	0.00045743	A_07_P013136	b2416	cmr|PEP-protein phosphotransferase system enzyme I [b2416]
ptsI	+6.38	13.49	+2.67	12.16	0.1	14.83	0.1	0.00001769	0.00059256	A_07_P013136	b2416	cmr|PEP-protein phosphotransferase system enzyme I [b2416]
purB	+3.18	11.41	+1.67	10.57	0.0	12.24	0.0	0.00010311	0.00160656	A_07_P006606	b1131	cmr|adenylosuccinate lyase [b1131]
purC	+15.02	10.12	+3.91	8.16	0.1	12.07	0.0	0.00000200	0.00025681	A_07_P013440	b2476	cmr|phosphoribosylaminoimidazole-succinocarboxamide synthetase = SAICAR synthetase [b2476]
purD	+19.08	10.09	+4.25	7.96	0.5	12.21	0.0	0.00004214	0.00093353	A_07_P008690	b4005	cmr|phosphoribosylglycinamide synthetase = GAR synthetase [b4005]
purE	+5.92	9.77	+2.57	8.49	0.3	11.05	0.1	0.00010303	0.00160656	A_07_P016404	b0523	cmr|phosphoribosylaminoimidazole carboxylase = AIR carboxylase, catalytic subunit [b0523]
purF	+4.66	8.94	+2.22	7.82	0.1	10.05	0.2	0.00008705	0.00143969	A_07_P013849	b2312	cmr|amidophosphoribosyltransferase = PRPP amidotransferase [b2312]
purF	+7.33	10.16	+2.87	8.72	0.1	11.60	0.0	0.00000737	0.00040556	A_07_P032426	c_2856	cmr|Amidophosphoribosyltransferase [c_2856]
purF	+4.88	9.11	+2.29	7.97	0.2	10.26	0.1	0.00010668	0.00164437	A_07_P042612	Z3574	cmr|amidophosphoribosyltransferase = PRPP amidotransferase [Z3574]
purH	+11.78	8.71	+3.56	6.93	0.1	10.49	0.1	0.00000543	0.00034972	A_07_P057962	ECs4929	cmr|phosphoribosylaminoimidazolecarboxamideformyltra nsferase [ECs4929]
purH	+34.26	10.24	+5.10	7.69	0.0	12.79	0.1	0.00000045	0.00019431	A_07_P037451	c_4964	cmr|Purine biosynthesis protein PurH [c_4964]
purH	+12.19	8.82	+3.61	7.02	0.1	10.62	0.0	0.00000260	0.00027706	A_07_P047211	Z5583	cmr|phosphoribosylaminoimidazolecarboxamide formyltransferase = AICAR formyltransferase IMP cyclohydrolase [Z5583]
purH	+11.96	8.90	+3.58	7.11	0.1	10.69	0.0	0.00000264	0.00027706	A_07_P008693	b4006	cmr|phosphoribosylaminoimidazolecarboxamideformyltransferase = AICAR formyltransferase; IMP cyclohydrolase [b4006]
purK	+4.37	9.38	+2.13	8.32	0.1	10.44	0.1	0.00009825	0.00154998	A_07_P016397	b0522	cmr|phosphoribosylaminoimidazole carboxylase = AIR carboxylase, CO [b0522]
purL	+9.40	9.23	+3.23	7.61	0.3	10.84	0.0	0.00003554	0.00084290	A_07_P019686	b2557	cmr|phosphoribosylformyl-glycineamide synthetase = FGAM synthetase [b2557]
purM	+23.48	11.34	+4.55	9.06	0.0	13.62	0.1	0.00000075	0.00019431	A_07_P013551	b2499	cmr|phosphoribosylaminoimidazole synthetase = AIR synthetase [b2499]
purN	+13.35	10.60	+3.74	8.73	0.1	12.47	0.0	0.00000336	0.00029719	A_07_P013559	b2500	cmr|phosphoribosylglycinamide formyltransferase 1 [b2500]
purN	+11.56	11.45	+3.53	9.68	0.1	13.21	0.1	0.00000348	0.00030339	A_07_P030133	c_3018	cmr|Phosphoribosylglycinamide formyltransferase [c_3018]
purT	+15.70	9.48	+3.97	7.49	0.0	11.47	0.0	0.00000142	0.00022424	A_07_P015921	b1849	cmr|phosphoribosylglycinamide formyltransferase 2 [b1849]
putA	+5.17	10.36	+2.37	9.17	0.2	11.54	0.0	0.00005250	0.00105155	A_07_P041092	c_1151	cmr|PutA protein [c_1151]
putA	+21.48	9.78	+4.42	7.57	0.2	11.99	0.1	0.00000263	0.00027706	A_07_P001304	b1014	cmr|proline dehydrogenase, P5C dehydrogenase [b1014]
putP	+3.99	9.58	+2.00	8.58	0.5	10.58	0.0	0.00200164	0.01316364	A_07_P001306	b1015	cmr|major sodium/proline symporter [b1015]
pykA	+6.60	10.50	+2.72	9.14	0.0	11.86	0.0	0.00000872	0.00042757	A_07_P015946	b1854	cmr|pyruvate kinase II, glucose stimulated [b1854]
pyrB	+9.92	9.71	+3.31	8.06	0.3	11.37	0.0	0.00002852	0.00074846	A_07_P003778	b4245	cmr|aspartate carbamoyltransferase, catalytic subunit [b4245]
pyrC	+4.23	8.69	+2.08	7.65	0.0	9.73	0.0	0.00003346	0.00081556	A_07_P001513	b1062	cmr|dihydro-orotase [b1062]
pyrD	+2.96	9.22	+1.57	8.43	0.1	10.00	0.1	0.00019812	0.00252367	A_07_P005175	b0945	cmr|dihydro-orotate dehydrogenase [b0945]
pyrF	+3.24	9.99	+1.70	9.14	0.1	10.84	0.0	0.00013968	0.00197581	A_07_P014388	b1281	cmr|orotidine-5-phosphate decarboxylase [b1281]
pyrG	+4.05	11.37	+2.02	10.36	0.1	12.37	0.0	0.00004229	0.00093353	A_07_P002348	b2780	cmr|CTP synthetase [b2780]
pyrH	-2.45	12.49	-1.29	13.13	0.0	11.84	0.0	0.00033810	0.00367995	A_07_P002814	b0171	cmr|uridylate kinase [b0171]
pyrI	+6.06	8.98	+2.60	7.68	0.1	10.28	0.0	0.00001448	0.00054604	A_07_P003774	b4244	cmr|aspartate carbamoyltransferase, regulatory subunit [b4244]
qor	+4.75	8.91	+2.25	7.79	0.1	10.04	0.1	0.00003988	0.00090512	A_07_P008897	b4051	cmr|quinone oxidoreductase [b4051]
quuQ	-2.00	8.94	-1.00	9.43	0.2	8.44	0.0	0.00569906	0.02918868	A_07_P020436	b1559	cmr|orf, hypothetical protein [b1559]
raiA	+29.10	13.85	+4.86	11.42	0.1	16.28	0.0	0.00000090	0.00019431	A_07_P019869	b2597	cmr|putative yhbH sigma 54 modulator [b2597]
rarD	-2.14	9.22	-1.10	9.77	0.1	8.67	0.0	0.00104128	0.00816430	A_07_P005965	b3819	cmr|orf, hypothetical protein [b3819]
rbfA	-2.83	12.99	-1.50	13.74	0.0	12.24	0.0	0.00016249	0.00220162	A_07_P000559	b3167	cmr|ribosome-binding factor A [b3167]
rbn	+3.55	9.22	+1.83	8.31	0.1	10.14	0.1	0.00017474	0.00230993	A_07_P039358	c_4833	cmr|Ribonuclease BN [c_4833]
rbsB	+3.97	14.29	+1.99	13.29	0.0	15.28	0.0	0.00004380	0.00094590	A_07_P005677	b3751	cmr|D-ribose periplasmic binding protein [b3751]
rbsC	+7.95	10.25	+2.99	8.75	0.0	11.74	0.0	0.00000544	0.00034972	A_07_P005671	b3750	cmr|D-ribose high-affinity transport system [b3750]
rcsB	+2.12	10.24	+1.08	9.70	0.0	10.78	0.1	0.00127825	0.00950623	A_07_P032365	c_2760	cmr|Capsular synthesis regulator component B [c_2760]
rcsD	+6.84	9.95	+2.77	8.57	0.2	11.34	0.0	0.00002130	0.00064982	A_07_P000870	b2216	cmr|putative 2-component sensor protein [b2216]
rcsF	+2.34	11.22	+1.23	10.61	0.1	11.84	0.0	0.00053891	0.00509893	A_07_P041460	c_0237	cmr|Protein rcsF [c_0237]
rdgC	+4.14	10.32	+2.05	9.29	0.3	11.34	0.0	0.00024952	0.00298515	A_07_P021080	b0393	cmr|orf, hypothetical protein [b0393]
rdoA	+3.26	10.58	+1.71	9.73	0.1	11.43	0.0	0.00009766	0.00154382	A_07_P019079	b3859	cmr|orf, hypothetical protein [b3859]
recA	-3.27	14.69	-1.71	15.55	0.0	13.84	0.1	0.00010685	0.00164437	A_07_P001941	b2699	cmr|DNA strand exchange and renaturation, DNA-dependent ATPase, DNA- and ATP-dependent coprotease [b2699]
recF	-3.86	11.12	-1.95	12.10	0.0	10.15	0.2	0.00012265	0.00179744	A_07_P005432	b3700	cmr|ssDNA and dsDNA binding, ATP binding [b3700]
recJ	-2.54	9.23	-1.35	9.90	0.1	8.55	0.2	0.00135159	0.00986532	A_07_P045645	Z4230	cmr|ssDNA exonuclease, 5 --> 3 specific [Z4230]
recJ	-2.84	8.29	-1.51	9.04	0.1	7.54	0.1	0.00033880	0.00368379	A_07_P006426	b2892	cmr|ssDNA exonuclease, 5 --> 3 specific [b2892]
recJ	-4.31	11.10	-2.11	12.16	0.0	10.05	0.0	0.00003237	0.00079881	A_07_P032859	c_3472	cmr|Single-stranded-DNA-specific exonuclease recJ [c_3472]
recN	-3.03	13.88	-1.60	14.68	0.0	13.08	0.0	0.00011524	0.00172297	A_07_P019956	b2616	cmr|protein used in recombination and DNA repair [b2616]
recR	+8.63	11.87	+3.11	10.32	0.1	13.43	0.0	0.00000682	0.00038477	A_07_P021466	b0472	cmr|recombination and repair [b0472]
recX	-4.32	11.38	-2.11	12.44	0.0	10.33	0.1	0.00003863	0.00088510	A_07_P063405	ECs3555	cmr|regulatory protein OraA [ECs3555]
recX	-4.57	11.60	-2.19	12.69	0.0	10.50	0.2	0.00007017	0.00124769	A_07_P001938	b2698	cmr|regulator, OraA protein [b2698]
recX	-3.00	10.77	-1.58	11.56	0.1	9.98	0.2	0.00058126	0.00537678	A_07_P052735	Z4001	cmr|regulator, OraA protein [Z4001]
rep	+3.09	8.96	+1.63	8.15	0.1	9.78	0.1	0.00023461	0.00284787	A_07_P005771	b3778	cmr|rep helicase, a single-stranded DNA dependent ATPase [b3778]
rfaH	-2.63	9.52	-1.40	10.22	0.0	8.82	0.1	0.00027793	0.00319869	A_07_P019019	b3842	cmr|transcriptional activator affecting biosynthesis of lipopolysaccharide core, F pilin, and haemolysin [b3842]
rfaI	-9.02	12.44	-3.17	14.03	0.0	10.85	0.1	0.00000451	0.00033765	A_07_P039805	c_4453	cmr|Lipopolysaccharide 1,3-galactosyltransferase [c_4453]
rfaP	-3.08	12.01	-1.62	12.83	0.0	11.20	0.1	0.00017590	0.00231945	A_07_P039808	c_4454	cmr|Lipopolysaccharide core biosynthesis protein rfaP [c_4454]
rfaP	-3.20	12.36	-1.68	13.20	0.2	11.52	0.0	0.00030711	0.00342042	A_07_P039808	c_4454	cmr|Lipopolysaccharide core biosynthesis protein rfaP [c_4454]
rfaP	-2.70	12.08	-1.43	12.80	0.0	11.36	0.0	0.00021054	0.00263076	A_07_P039808	c_4454	cmr|Lipopolysaccharide core biosynthesis protein rfaP [c_4454]
rfaP	-3.09	12.41	-1.63	13.22	0.0	11.59	0.1	0.00011951	0.00176668	A_07_P039808	c_4454	cmr|Lipopolysaccharide core biosynthesis protein rfaP [c_4454]
rfaP	-2.92	12.25	-1.55	13.02	0.0	11.47	0.1	0.00015771	0.00216480	A_07_P039808	c_4454	cmr|Lipopolysaccharide core biosynthesis protein rfaP [c_4454]
rffA	+2.36	8.31	+1.24	7.69	0.1	8.93	0.0	0.00046235	0.00457870	A_07_P005832	b3791	cmr|putative regulator [b3791]
rffC	+2.68	8.03	+1.42	7.32	0.4	8.74	0.1	0.00522529	0.02723171	A_07_P005826	b3790	cmr|orf, hypothetical protein [b3790]
rffM	+2.14	7.64	+1.10	7.09	0.1	8.19	0.1	0.00099510	0.00788955	A_07_P005860	b3794	cmr|probable UDP-N-acetyl-D-mannosaminuronic acid transferase; synthesis of enterobacterial common antigen [b3794]
rhaS	+2.79	7.55	+1.48	6.81	0.3	8.29	0.0	0.00174778	0.01199888	A_07_P019305	b3905	cmr|positive regulator for rhaBAD operon [b3905]
rhaS	+2.16	7.51	+1.11	6.96	0.2	8.07	0.0	0.00332798	0.01943461	A_07_P047099	Z5449	cmr|positive regulator for rhaBAD operon [Z5449]
rhlB	+2.76	9.04	+1.47	8.31	0.0	9.78	0.1	0.00032396	0.00357174	A_07_P005782	b3780	cmr|putative ATP-dependent RNA helicase [b3780]
rhlE	+2.05	10.08	+1.04	9.56	0.1	10.60	0.0	0.00149320	0.01066650	A_07_P004438	b0797	cmr|putative ATP-dependent RNA helicase [b0797]
rho	-3.24	10.24	-1.69	11.09	0.1	9.39	0.0	0.00014363	0.00201369	A_07_P005791	b3783	cmr|transcription termination factor Rho; polarity suppressor [b3783]
ribD	-2.58	10.98	-1.37	11.67	0.0	10.30	0.0	0.00024886	0.00297954	A_07_P021185	b0414	cmr|bifunctional pyrimidine deaminase/reductase in pathway of riboflavin synthesis [b0414]
ribE	-4.51	12.81	-2.17	13.90	0.0	11.72	0.1	0.00002926	0.00076000	A_07_P021187	b0415	cmr|riboflavin synthase, beta chain [b0415]
ribE	-4.31	12.99	-2.11	14.04	0.0	11.93	0.0	0.00003384	0.00082101	A_07_P021187	b0415	cmr|riboflavin synthase, beta chain [b0415]
ribE	-4.67	12.74	-2.22	13.85	0.0	11.63	0.1	0.00002566	0.00072274	A_07_P021187	b0415	cmr|riboflavin synthase, beta chain [b0415]
ribE	-4.58	12.67	-2.20	13.77	0.0	11.58	0.0	0.00002459	0.00070547	A_07_P021187	b0415	cmr|riboflavin synthase, beta chain [b0415]
ribE	-4.73	12.73	-2.24	13.85	0.0	11.61	0.0	0.00002300	0.00067944	A_07_P021187	b0415	cmr|riboflavin synthase, beta chain [b0415]
rimI	-2.10	11.72	-1.07	12.26	0.0	11.19	0.0	0.00080706	0.00682752	A_07_P017550	b4373	cmr|acyltransferase for 30S ribosomal subunit protein S18; acetylation of N-terminal alanine [b4373]
rimJ	+3.62	10.49	+1.86	9.56	0.1	11.42	0.1	0.00014603	0.00203963	A_07_P001534	b1066	cmr|acetylation of N-terminal alanine of 30S ribosomal subunit protein S5 [b1066]
rimN	+2.46	8.67	+1.30	8.02	0.3	9.33	0.0	0.00315062	0.01862685	A_07_P012843	b3282	cmr|orf, hypothetical protein [b3282]
rlmL	+2.75	8.51	+1.46	7.78	0.2	9.24	0.1	0.00047186	0.00464602	A_07_P005186	b0948	cmr|putative oxidoreductase [b0948]
rlpA	+2.65	9.84	+1.41	9.14	0.1	10.55	0.0	0.00026191	0.00308181	A_07_P009735	b0633	cmr|a minor lipoprotein [b0633]
rlpB	-2.53	10.36	-1.34	11.03	0.1	9.69	0.0	0.00035058	0.00377532	A_07_P044023	Z0788	cmr|a minor lipoprotein [Z0788]
rlpB	-3.33	12.43	-1.73	13.30	0.1	11.56	0.0	0.00009199	0.00148849	A_07_P009773	b0641	cmr|a minor lipoprotein [b0641]
rluA	-2.51	9.73	-1.33	10.39	0.2	9.07	0.0	0.00119591	0.00905214	A_07_P010976	b0058	cmr|orf, hypothetical protein [b0058]
rluD	-2.65	10.47	-1.41	11.18	0.3	9.77	0.0	0.00127534	0.00948910	A_07_P042940	Z3888	cmr|suppressor of ftsH mutation [Z3888]
rluE	-2.37	11.26	-1.24	11.88	0.0	10.63	0.1	0.00051765	0.00495438	A_07_P006629	b1135	cmr|orf, hypothetical protein [b1135]
rmf	+25.77	11.15	+4.69	8.80	0.1	13.49	0.0	0.00000068	0.00019431	A_07_P005212	b0953	cmr|ribosome modulation factor [b0953]
rnc	-3.24	12.06	-1.69	12.91	0.0	11.21	0.1	0.00011518	0.00172297	A_07_P019740	b2567	cmr|RNase III, ds RNA [b2567]
rne	+2.77	8.18	+1.47	7.45	0.1	8.92	0.0	0.00027536	0.00317893	A_07_P001621	b1084	cmr|RNase E, membrane attachment, mRNA turnover, maturation 5S RNA [b1084]
rnhB	-4.01	11.18	-2.01	12.18	0.1	10.18	0.0	0.00005329	0.00106045	A_07_P002875	b0183	cmr|RNAse HII, degrades RNA of DNA-RNA hybrids [b0183]
rnk	+5.61	10.20	+2.49	8.95	0.2	11.44	0.1	0.00007826	0.00133632	A_07_P016807	b0610	cmr|regulator of nucleoside diphosphate kinase [b0610]
rnpA	-2.15	14.35	-1.10	14.90	0.0	13.80	0.0	0.00073125	0.00632113	A_07_P005448	b3704	cmr|RNase P, protein component; protein C5; processes tRNA, 4.5S RNA [b3704]
rob	+2.94	11.90	+1.56	11.12	0.1	12.68	0.1	0.00026432	0.00309464	A_07_P017663	b4396	cmr|right origin-binding protein [b4396]
rpe	+4.50	10.25	+2.17	9.16	0.1	11.33	0.0	0.00005485	0.00107946	A_07_P017959	b3386	cmr|D-ribulose-5-phosphate 3-epimerase [b3386]
rpiR	+10.15	9.35	+3.34	7.68	0.1	11.03	0.0	0.00000400	0.00032449	A_07_P037745	c_5095	cmr|Protein rpiR [c_5095]
rplB	+2.26	16.85	+1.18	16.26	0.0	17.44	0.1	0.00061415	0.00558100	A_07_P013013	b3317	cmr|50S ribosomal subunit protein L2 [b3317]
rplI	-2.48	15.05	-1.31	15.71	0.0	14.40	0.0	0.00031229	0.00346495	A_07_P011735	b4203	cmr|50S ribosomal subunit protein L9 [b4203]
rplN	+2.65	16.37	+1.41	15.66	0.0	17.07	0.0	0.00022312	0.00274437	A_07_P012976	b3310	cmr|50S ribosomal subunit protein L14 [b3310]
rplR	-2.40	16.43	-1.27	17.06	0.1	15.80	0.1	0.00046399	0.00459145	A_07_P012950	b3304	cmr|50S ribosomal subunit protein L18 [b3304]
rplS	-5.70	12.95	-2.51	14.21	0.0	11.69	0.0	0.00001265	0.00051704	A_07_P019906	b2606	cmr|50S ribosomal subunit protein L19 [b2606]
rplT	-5.48	13.66	-2.46	14.89	0.1	12.43	0.0	0.00001642	0.00057181	A_07_P018627	b1716	cmr|50S ribosomal subunit protein L20, and regulator [b1716]
rplY	+2.55	14.11	+1.35	13.44	0.1	14.79	0.0	0.00034820	0.00376000	A_07_P000722	b2185	cmr|50S ribosomal subunit protein L25 [b2185]
rplY	+2.90	13.99	+1.54	13.22	0.1	14.76	0.1	0.00022750	0.00278734	A_07_P035511	c_2722	cmr|50S ribosomal protein L25 [c_2722]
rpmE	-5.28	15.20	-2.40	16.40	0.0	13.99	0.0	0.00001573	0.00056283	A_07_P019460	b3936	cmr|50S ribosomal subunit protein L31 [b3936]
rpmG	-3.07	14.17	-1.62	14.98	0.0	13.36	0.1	0.00016493	0.00222503	A_07_P017122	b3636	cmr|50S ribosomal subunit protein L33 [b3636]
rpoB	+4.06	10.81	+2.02	9.80	0.0	11.82	0.1	0.00004411	0.00094686	A_07_P008600	b3987	cmr|RNA polymerase, beta subunit [b3987]
rpoC	+2.25	10.57	+1.17	9.99	0.1	11.16	0.1	0.00072018	0.00625405	A_07_P008605	b3988	cmr|RNA polymerase, beta prime subunit [b3988]
rpoD	-4.46	14.52	-2.16	15.60	0.0	13.44	0.1	0.00003133	0.00078813	A_07_P000070	b3067	cmr|RNA polymerase, sigma [b3067]
rpoE	-5.35	12.07	-2.42	13.28	0.0	10.86	0.0	0.00001583	0.00056378	A_07_P019770	b2573	cmr|RNA polymerase, sigma-E factor; heat shock and oxidative stress [b2573]
rpoH	-2.59	11.96	-1.37	12.64	0.0	11.27	0.0	0.00024105	0.00291040	A_07_P007245	b3461	cmr|RNA polymerase, sigma [b3461]
rpoN	+2.06	9.76	+1.04	9.24	0.0	10.28	0.3	0.00991105	0.04444308	A_07_P012490	b3202	cmr|RNA polymerase, sigma [b3202]

rpoZ	-4.23	13.64	-2.08	14.68	0.0	12.60	0.0	0.00003409	0.00082567	A_07_P017187	b3649	cmr|RNA polymerase, omega subunit [b3649]
rppH	-3.93	12.37	-1.97	13.35	0.1	11.38	0.0	0.00004657	0.00097501	A_07_P006135	b2830	cmr|putative invasion protein [b2830]
rpsA	-2.18	14.67	-1.12	15.23	0.0	14.11	0.0	0.00062260	0.00563493	A_07_P005002	b0911	cmr|30S ribosomal subunit protein S1 [b0911]
rpsB	-2.82	14.58	-1.49	15.33	0.0	13.83	0.0	0.00017339	0.00229590	A_07_P002803	b0169	cmr|30S ribosomal subunit protein S2 [b0169]
rpsC	-2.32	16.72	-1.21	17.32	0.0	16.11	0.1	0.00052507	0.00501311	A_07_P012998	b3314	cmr|30S ribosomal subunit protein S3 [b3314]
rpsG	-2.08	16.35	-1.06	16.88	0.0	15.82	0.0	0.00085214	0.00710601	A_07_P017731	b3341	cmr|30S ribosomal subunit protein S7, initiates assembly [b3341]
rpsI	-3.32	13.60	-1.73	14.47	0.1	12.74	0.4	0.00163480	0.01138865	A_07_P012625	b3230	cmr|30S ribosomal subunit protein S9 [b3230]
rpsO	+3.06	13.35	+1.61	12.55	0.1	14.16	0.0	0.00012937	0.00185677	A_07_P000550	b3165	cmr|30S ribosomal subunit protein S15 [b3165]
rpsQ	-4.89	15.70	-2.29	16.84	0.0	14.55	0.1	0.00002237	0.00067002	A_07_P012981	b3311	cmr|30S ribosomal subunit protein S17 [b3311]
rpsS	+2.27	15.72	+1.19	15.13	0.0	16.31	0.1	0.00061818	0.00560315	A_07_P013010	b3316	cmr|30S ribosomal subunit protein S19 [b3316]
rpsT	-3.85	13.66	-1.95	14.64	0.0	12.69	0.1	0.00004930	0.00100666	A_07_P010803	b0023	cmr|30S ribosomal subunit protein S20 [b0023]
rraA	+2.71	10.30	+1.44	9.59	0.1	11.02	0.0	0.00023687	0.00286428	A_07_P019421	b3929	cmr|menaquinone biosynthesis, unknown [b3929]
rrmJ	-3.16	12.17	-1.66	13.00	0.0	11.34	0.0	0.00009672	0.00153974	A_07_P000609	b3179	cmr|cell division protein [b3179]
rsd	+5.82	10.46	+2.54	9.19	0.1	11.73	0.1	0.00002073	0.00063877	A_07_P008637	b3995	cmr|putative transcriptional regulator [b3995]
rseA	-6.01	13.26	-2.59	14.55	0.0	11.96	0.0	0.00001067	0.00047201	A_07_P019761	b2572	cmr|sigma-E factor, negative regulatory protein [b2572]
rseB	-2.39	9.97	-1.26	10.60	0.2	9.34	0.1	0.00101769	0.00802729	A_07_P019758	b2571	cmr|regulates activity of sigma-E factor [b2571]
rseP	-2.16	12.18	-1.11	12.74	0.0	11.63	0.0	0.00075283	0.00647325	A_07_P002836	b0176	cmr|orf, hypothetical protein [b0176]
rsmE	+4.43	11.22	+2.15	10.14	0.1	12.29	0.1	0.00005163	0.00103969	A_07_P011872	b2946	cmr|orf, hypothetical protein [b2946]
rstB	-2.00	8.89	-1.00	9.39	0.1	8.39	0.1	0.00295702	0.01767474	A_07_P035086	c_2001	cmr|Sensor protein rstB [c_2001]
rstB	-2.21	8.81	-1.14	9.39	0.1	8.24	0.1	0.00184600	0.01244116	A_07_P020676	b1609	cmr|sensor histidine protein kinase [b1609]
rsuA	-2.88	12.25	-1.53	13.01	0.1	11.49	0.1	0.00018279	0.00238430	A_07_P000715	b2183	cmr|16S pseudouridylate 516 synthase [b2183]
rsxA	-18.34	10.78	-4.20	12.88	0.0	8.68	0.1	0.00000111	0.00020547	A_07_P020768	b1627	cmr|orf, hypothetical protein [b1627]
rsxB	-7.62	10.26	-2.93	11.73	0.0	8.80	0.0	0.00000659	0.00038136	A_07_P020774	b1628	cmr|orf, hypothetical protein [b1628]
rsxC	-4.07	9.75	-2.02	10.76	0.0	8.74	0.1	0.00004731	0.00098397	A_07_P020776	b1629	cmr|putative membrane protein [b1629]
rsxD	-2.54	8.10	-1.35	8.78	0.1	7.43	0.0	0.00041498	0.00423153	A_07_P020785	b1630	cmr|orf, hypothetical protein [b1630]
rtcA	-2.37	9.02	-1.24	9.64	0.4	8.40	0.0	0.00536171	0.02783211	A_07_P018126	b3420	cmr|RNA 3-terminal phosphate cyclase [b3420]
rusA	+62.89	9.87	+5.97	6.89	0.0	12.86	0.0	0.00000016	0.00019431	A_07_P016520	b0550	cmr|endodeoxyribonuclease RUS [b0550]
rutB	-2.85	11.02	-1.51	11.78	0.0	10.26	0.4	0.00427093	0.02331535	A_07_P001287	b1011	cmr|putative synthetase [b1011]
rutR	-2.11	9.40	-1.08	9.95	0.1	8.86	0.0	0.00091186	0.00745396	A_07_P001300	b1013	cmr|putative tet operon regulator [b1013]
ruvB	-2.39	11.69	-1.26	12.32	0.0	11.06	0.0	0.00037711	0.00396055	A_07_P015980	b1860	cmr|Holliday junction helicase subunit A; branch migration; repair [b1860]
rzpD	+24.13	11.25	+4.59	8.95	0.4	13.54	0.0	0.00002646	0.00072866	A_07_P010301	b0556	cmr|bacteriophage lambda endopeptidase homolog [b0556]
rzpD	+11.77	9.74	+3.56	7.96	0.2	11.52	0.0	0.00001206	0.00050646	A_07_P016543	b0556	cmr|bacteriophage lambda endopeptidase homolog [b0556]
rzpQ	-2.28	7.62	-1.19	8.21	0.4	7.02	0.0	0.00896823	0.04126118	A_07_P020510	b1573	cmr|orf, hypothetical protein [b1573]
rzpR	+2.31	7.87	+1.21	7.27	0.1	8.47	0.2	0.00121259	0.00913448	A_07_P014786	b1362	cmr|putative Rac prophage endopeptidase [b1362]
sad	-2.08	9.49	-1.06	10.02	0.2	8.96	0.0	0.00444914	0.02406294	A_07_P020272	b1525	cmr|putative aldehyde dehydrogenase [b1525]
sat	-11.02	10.44	-3.46	12.17	0.1	8.71	0.1	0.00000355	0.00030339	A_07_P036297	c_3619	cmr|Aecreted auto transpoter toxin [c_3619]
sbcB	+2.27	8.86	+1.18	8.27	0.2	9.45	0.0	0.00247431	0.01548501	A_07_P044967	Z3173	cmr|exonuclease I, 3 --> 5 specific deoxyribophosphodiesterase [Z3173]
sbcB	+2.10	9.16	+1.07	8.63	0.1	9.70	0.1	0.00120758	0.00911419	A_07_P055542	ECs2813	cmr|exonuclease I [ECs2813]
sbcB	+2.11	10.28	+1.08	9.74	0.0	10.81	0.2	0.00237912	0.01503690	A_07_P031971	c_2539	cmr|Exodeoxyribonuclease I [c_2539]
sbmA	-2.78	9.29	-1.47	10.03	0.1	8.55	0.1	0.00043202	0.00435473	A_07_P020999	b0377	cmr|sensitivity to microcin B17, possibly envelop protein [b0377]
sbp	-5.78	11.03	-2.53	12.30	0.1	9.77	0.2	0.00006029	0.00114635	A_07_P019364	b3917	cmr|periplasmic sulfate-binding protein [b3917]
sdaA	+2.77	10.58	+1.47	9.85	0.1	11.32	0.1	0.00029731	0.00335322	A_07_P015761	b1814	cmr|L-serine deaminase [b1814]
sdaC	+2.31	11.41	+1.21	10.80	0.1	12.01	0.1	0.00063562	0.00571983	A_07_P002426	b2796	cmr|probable serine transporter [b2796]
sdhA	+9.99	11.67	+3.32	10.01	0.1	13.33	0.1	0.00000559	0.00035512	A_07_P010135	b0723	cmr|succinate dehydrogenase, flavoprotein subunit [b0723]
sdhA	+10.87	10.12	+3.44	8.40	0.2	11.84	0.1	0.00001273	0.00051704	A_07_P051706	Z0877	cmr|succinate dehydrogenase, flavoprotein subunit [Z0877]
sdhA	+10.40	10.26	+3.38	8.57	0.0	11.95	0.0	0.00000323	0.00029256	A_07_P063016	ECs0748	cmr|succinate dehydrogenase flavoprotein subunit [ECs0748]
sdhB	+6.09	11.62	+2.61	10.32	0.1	12.92	0.0	0.00002023	0.00063193	A_07_P010139	b0724	cmr|succinate dehydrogenase, iron sulfur protein [b0724]
sdhC	+37.88	12.43	+5.24	9.81	0.1	15.05	0.0	0.00000050	0.00019431	A_07_P010122	b0721	cmr|succinate dehydrogenase, cytochrome b556 [b0721]
sdhD	+22.16	12.14	+4.47	9.91	0.1	14.38	0.0	0.00000109	0.00020547	A_07_P010127	b0722	cmr|succinate dehydrogenase, hydrophobic subunit [b0722]
sdiA	-6.33	9.83	-2.66	11.16	0.1	8.50	0.1	0.00001698	0.00058050	A_07_P014943	b1916	cmr|transcriptional regulator of ftsQAZ gene cluster [b1916]
sdiA	-4.92	8.16	-2.30	9.31	0.1	7.01	0.0	0.00002304	0.00067944	A_07_P035369	c_2330	cmr|Regulatory protein sdiA [c_2330]
secB	+4.53	11.12	+2.18	10.03	0.1	12.20	0.1	0.00003500	0.00083975	A_07_P016988	b3609	cmr|protein export; molecular chaperone; may bind to signel sequence [b3609]
secE	-3.53	13.72	-1.82	14.63	0.0	12.81	0.0	0.00006163	0.00115828	A_07_P008570	b3981	cmr|preprotein translocase [b3981]
secG	-2.28	11.82	-1.19	12.41	0.1	11.22	0.2	0.00227766	0.01455673	A_07_P000590	b3175	cmr|protein export - membrane protein [b3175]
secY	+2.26	14.97	+1.18	14.38	0.1	15.56	0.1	0.00093650	0.00758059	A_07_P012927	b3300	cmr|putative ATPase subunit of translocase [b3300]
selA	+2.08	10.13	+1.05	9.60	0.0	10.65	0.1	0.00103455	0.00811965	A_07_P016899	b3591	cmr|selenocysteine synthase: L-seryl-tRNA [b3591]
selA	+2.04	10.05	+1.03	9.54	0.1	10.57	0.0	0.00105798	0.00826384	A_07_P016899	b3591	cmr|selenocysteine synthase: L-seryl-tRNA [b3591]
selD	+5.36	10.36	+2.42	9.15	0.0	11.58	0.1	0.00002089	0.00063998	A_07_P018866	b1764	cmr|selenophosphate synthase, H [b1764]
serS	+4.68	8.70	+2.23	7.59	0.2	9.81	0.0	0.00006163	0.00115828	A_07_P004911	b0893	cmr|serine tRNA synthetase; also charges selenocystein tRNA with serine [b0893]
sfaB	+7.84	8.70	+2.97	7.21	0.1	10.18	0.0	0.00000712	0.00039666	A_07_P040481	c_1238	cmr|Putative F1C and S fimbrial switch Regulatory [c_1238]
sfaC	+3.80	7.91	+1.93	6.94	0.1	8.87	0.0	0.00005512	0.00108065	A_07_P040480	c_1237	cmr|Putative F1C and S fimbrial switch Regulatory [c_1237]
sfaD	+4.95	8.96	+2.31	7.81	0.0	10.12	0.1	0.00003462	0.00083595	A_07_P040493	c_1240	cmr|Putative minor F1C fimbrial subunit precursor [c_1240]
sfsA	+3.48	10.92	+1.80	10.02	0.0	11.82	0.1	0.00007566	0.00131047	A_07_P035869	c_0179	cmr|Sugar fermentation stimulation protein A [c_0179]
sfsA	+2.10	10.16	+1.07	9.63	0.1	10.70	0.0	0.00088035	0.00727980	A_07_P002692	b0146	cmr|probable regulator for maltose metabolism [b0146]
sgbH	+2.57	7.53	+1.36	6.85	0.1	8.21	0.2	0.00107145	0.00834272	A_07_P016850	b3581	cmr|probable 3-hexulose 6-phosphate synthase [b3581]
sgbU	+2.22	7.63	+1.15	7.06	0.2	8.21	0.1	0.00174831	0.01199888	A_07_P039678	c_4405	cmr|Putative hexulose-6-phosphate isomerase [c_4405]
sgcX	+2.81	7.49	+1.49	6.74	0.0	8.23	0.1	0.00019649	0.00250894	A_07_P004054	b4305	cmr|putative lyase/synthase [b4305]
sitA	-2.07	9.42	-1.05	9.95	0.1	8.90	0.1	0.00106763	0.00832527	A_07_P038676	c_1600	cmr|SitA protein [c_1600]
sitB	-2.56	8.32	-1.36	9.00	0.1	7.64	0.1	0.00047595	0.00466588	A_07_P038673	c_1599	cmr|SitB protein [c_1599]
sitC	-4.47	8.33	-2.16	9.41	0.2	7.25	0.3	0.00063612	0.00571983	A_07_P038667	c_1598	cmr|SitC protein [c_1598]
skp	+8.19	12.72	+3.03	11.20	0.0	14.24	0.0	0.00000484	0.00034614	A_07_P002847	b0178	cmr|histone-like protein, located in outer membrane or nucleoid [b0178]
slpA	+2.51	10.37	+1.33	9.70	0.5	11.03	0.0	0.00886234	0.04088152	A_07_P051860	Z0033	cmr|probable FKBX-type 16KD peptidyl-prolyl cis-trans isomerase [Z0033]
slt	+2.30	8.11	+1.20	7.51	0.3	8.71	0.0	0.00495496	0.02616938	A_07_P017645	b4392	cmr|soluble lytic murein transglycosylase [b4392]
slt	+2.34	7.90	+1.23	7.29	0.0	8.52	0.1	0.00052780	0.00502395	A_07_P017645	b4392	cmr|soluble lytic murein transglycosylase [b4392]
slt	+2.25	8.06	+1.17	7.48	0.1	8.65	0.1	0.00094559	0.00763066	A_07_P017645	b4392	cmr|soluble lytic murein transglycosylase [b4392]
slt	+2.14	8.06	+1.09	7.51	0.1	8.61	0.0	0.00083837	0.00702801	A_07_P051845	Z5994	cmr|soluble lytic murein transglycosylase [Z5994]
smg	+5.69	9.56	+2.51	8.30	0.1	10.81	0.1	0.00002521	0.00071646	A_07_P034260	c_4045	cmr|Protein smg [c_4045]
smg	+3.19	9.00	+1.67	8.17	0.2	9.84	0.1	0.00029722	0.00335322	A_07_P012853	b3284	cmr|orf, hypothetical protein [b3284]
smg	+2.41	10.98	+1.27	10.34	0.3	11.61	0.0	0.00225922	0.01447669	A_07_P045982	Z4655	cmr|orf, hypothetical protein [Z4655]
smpA	-4.85	12.12	-2.28	13.26	0.1	10.98	0.0	0.00002944	0.00076000	A_07_P019965	b2617	cmr|small membrane protein A [b2617]
smpB	-2.80	12.36	-1.48	13.10	0.0	11.61	0.1	0.00018606	0.00241091	A_07_P019980	b2620	cmr|small protein B [b2620]
sodA	+2.09	9.83	+1.06	9.30	0.0	10.36	0.0	0.00090299	0.00739560	A_07_P041367	c_4859	cmr|Superoxide dismutase [c_4859]
sodA	+2.53	7.94	+1.34	7.27	0.1	8.61	0.1	0.00070327	0.00614276	A_07_P047103	Z5453	cmr|superoxide dismutase, manganese [Z5453]
sodA	+2.04	8.38	+1.03	7.87	0.3	8.89	0.2	0.00939413	0.04259139	A_07_P019316	b3908	cmr|superoxide dismutase, manganese [b3908]
sodB	+6.67	12.61	+2.74	11.24	0.1	13.98	0.0	0.00001251	0.00051423	A_07_P018342	b1656	cmr|superoxide dismutase, iron [b1656]
sodB	+4.74	12.92	+2.25	11.80	0.0	14.05	0.1	0.00002602	0.00072493	A_07_P042333	c_2050	cmr|Superoxide dismutase [c_2050]
soxR	-2.28	8.81	-1.19	9.41	0.1	8.22	0.0	0.00086549	0.00719822	A_07_P008959	b4063	cmr|redox-sensing activator of soxS [b4063]
soxS	+2.65	11.23	+1.40	10.52	0.1	11.93	0.1	0.00059029	0.00544760	A_07_P008951	b4062	cmr|regulation of superoxide response regulon [b4062]
speB	-2.62	9.45	-1.39	10.14	0.0	8.75	0.1	0.00026764	0.00311206	A_07_P011831	b2937	cmr|agmatinase [b2937]
speD	+2.30	10.19	+1.20	9.58	0.2	10.79	0.1	0.00150225	0.01072141	A_07_P002565	b0120	cmr|S-adenosylmethionine decarboxylase [b0120]
speF	+3.33	8.42	+1.74	7.55	0.4	9.29	0.1	0.00211789	0.01377283	A_07_P009981	b0693	cmr|ornithine decarboxylase isozyme, inducible [b0693]
speG	-2.81	10.79	-1.49	11.54	0.1	10.05	0.0	0.00028659	0.00327435	A_07_P020551	b1584	cmr|spermidine N1-acetyltransferase [b1584]
spoT	-2.80	10.07	-1.49	10.81	0.1	9.33	0.1	0.00027541	0.00317893	A_07_P017193	b3650	cmr|bifunctional (p)ppGpp synthetase II and guanosine-3',5'-bis pyrophosphate 3'-pyrophosphohydrolase [b3650]
spr	+2.44	12.38	+1.29	11.73	0.1	13.02	0.1	0.00043116	0.00435418	A_07_P000674	b2175	cmr|putative lipoprotein [b2175]
srlB	+2.93	7.35	+1.55	6.58	0.2	8.13	0.0	0.00064532	0.00578255	A_07_P001966	b2704	cmr|PTS system, glucitol/sorbitol-specific enzyme IIA component [b2704]
srlE	+2.37	7.25	+1.24	6.63	0.1	7.87	0.0	0.00067470	0.00595430	A_07_P030595	c_3257	cmr|PTS system, glucitol/sorbitol-specific IIBC component [c_3257]
srlE	+2.45	7.47	+1.29	6.83	0.0	8.12	0.1	0.00049580	0.00479178	A_07_P001964	b2703	cmr|PTS system, glucitol/sorbitol-specific IIB component and second of two IIC components [b2703]
srmB	+3.91	8.93	+1.97	7.95	0.3	9.91	0.0	0.00026684	0.00310509	A_07_P042926	Z3859	cmr|ATP-dependent RNA helicase [Z3859]
srmB	+3.89	9.38	+1.96	8.40	0.0	10.36	0.0	0.00004432	0.00094837	A_07_P030217	c_3100	cmr|ATP-dependent RNA helicase srmB [c_3100]
ssb	-3.46	12.98	-1.79	13.87	0.0	12.08	0.0	0.00007147	0.00125866	A_07_P008940	b4059	cmr|ssDNA-binding protein [b4059]
ssbW	+19.42	13.85	+4.28	11.71	0.0	15.99	0.0	0.00000088	0.00019431	A_07_P051338	Z1440	cmr|putative single-stranded DNA binding protein [Z1440]
sseA	+9.67	11.65	+3.27	10.01	0.1	13.28	0.0	0.00000801	0.00041039	A_07_P013661	b2521	cmr|putative thiosulfate sulfurtransferase [b2521]
sspA	-4.34	13.57	-2.12	14.63	0.0	12.51	0.1	0.00003776	0.00087581	A_07_P012616	b3229	cmr|regulator of transcription; stringent starvation protein A [b3229]
sspB	-5.35	13.96	-2.42	15.17	0.0	12.75	0.0	0.00001630	0.00056947	A_07_P012612	b3228	cmr|stringent starvation protein B [b3228]
sstT	+2.17	8.26	+1.12	7.70	0.1	8.81	0.2	0.00228004	0.01455673	A_07_P000173	b3089	cmr|putative transport protein [b3089]
stpA	-2.16	10.67	-1.11	11.22	0.1	10.11	0.1	0.00093211	0.00756060	A_07_P020199	b2669	cmr|DNA-binding protein; H-NS-like protein; chaperone activity; RNA splicing? [b2669]
sucA	+91.76	10.65	+6.52	7.39	0.0	13.91	0.0	0.00000012	0.00019431	A_07_P010149	b0726	cmr|2-oxoglutarate dehydrogenase [b0726]
sucB	+45.69	12.07	+5.51	9.32	0.0	14.83	0.0	0.00000026	0.00019431	A_07_P010151	b0727	cmr|2-oxoglutarate dehydrogenase [b0727]
sucC	+55.82	11.22	+5.80	8.32	0.1	14.12	0.0	0.00000030	0.00019431	A_07_P010159	b0728	cmr|succinyl-CoA synthetase, beta subunit [b0728]
sucD	+36.23	10.53	+5.18	7.94	0.0	13.12	0.1	0.00000039	0.00019431	A_07_P010165	b0729	cmr|succinyl-CoA synthetase, alpha subunit [b0729]
sugE	-3.26	11.86	-1.71	12.71	0.1	11.00	0.1	0.00020118	0.00255851	A_07_P035585	c_5236	cmr|SugE protein [c_5236]
sugE	-3.41	9.53	-1.77	10.42	0.1	8.65	0.1	0.00009199	0.00148849	A_07_P048623	Z5755	cmr|suppresses groEL, may be chaperone [Z5755]
sugE	-4.10	10.25	-2.04	11.27	0.2	9.24	0.0	0.00020926	0.00262336	A_07_P010653	b4148	cmr|suppresses groEL, may be chaperone [b4148]
sugE	-12.28	8.96	-3.62	10.77	0.1	7.16	0.2	0.00000626	0.00036832	A_07_P011472	b4148	cmr|suppresses groEL, may be chaperone [b4148]
sulA	+2.65	15.01	+1.41	14.31	0.0	15.72	0.3	0.00196910	0.01302035	A_07_P005240	b0958	cmr|suppressor of lon; inhibits cell division and ftsZ ring formation [b0958]
sxy	-2.09	10.24	-1.06	10.77	0.1	9.71	0.0	0.00129644	0.00961427	A_07_P005243	b0959	cmr|orf, hypothetical protein [b0959]
tadA	-4.08	9.27	-2.03	10.29	0.0	8.26	0.1	0.00005689	0.00110173	A_07_P019700	b2559	cmr|putative deaminase [b2559]
talA	+2.22	8.13	+1.15	7.55	0.3	8.70	0.0	0.00464674	0.02485839	A_07_P013377	b2464	cmr|transaldolase A [b2464]
talB	+2.86	9.96	+1.52	9.20	0.1	10.72	0.0	0.00028694	0.00327593	A_07_P010731	b0008	cmr|transaldolase B [b0008]
tatA	-2.12	13.98	-1.09	14.53	0.0	13.44	0.0	0.00074192	0.00638990	A_07_P018990	b3836	cmr|orf, hypothetical protein [b3836]
tatB	-3.52	13.50	-1.81	14.41	0.0	12.60	0.0	0.00006673	0.00120840	A_07_P018999	b3838	cmr|orf, hypothetical protein [b3838]
tauA	-2.28	8.54	-1.19	9.14	0.3	7.95	0.0	0.00511323	0.02675396	A_07_P031067	c_0472	cmr|Taurine-binding periplasmic protein precursor [c_0472]
tdcA	+9.64	10.10	+3.27	8.46	0.2	11.73	0.4	0.00011928	0.00176667	A_07_P000316	b3118	cmr|transcriptional activator of tdc operon [b3118]
tdcB	+6.84	8.51	+2.77	7.12	0.1	9.90	0.1	0.00001321	0.00052395	A_07_P000312	b3117	cmr|threonine dehydratase, catabolic [b3117]
tdcC	+7.70	8.72	+2.94	7.24	0.3	10.19	0.1	0.00004948	0.00100904	A_07_P000306	b3116	cmr|anaerobically inducible L-threonine, L-serine permease [b3116]
tdcD	+5.18	7.46	+2.37	6.27	0.1	8.64	0.0	0.00002012	0.00063193	A_07_P000305	b3115	cmr|putative kinase [b3115]
tdcD	+13.92	9.13	+3.80	7.23	0.0	11.02	0.2	0.00000776	0.00041039	A_07_P045889	Z4467	cmr|putative kinase [Z4467]
tdcE	+2.77	9.09	+1.47	8.35	0.0	9.82	0.1	0.00032007	0.00353373	A_07_P034076	c_3872	cmr|Keto-acid formate acetyltransferase [c_3872]
tdh	+8.45	10.23	+3.08	8.69	0.0	11.77	0.0	0.00000478	0.00034614	A_07_P017024	b3616	cmr|threonine dehydrogenase [b3616]
terB	+2.21	8.59	+1.15	8.01	0.0	9.16	0.2	0.00275664	0.01676994	A_07_P046904	Z1173	cmr|putative phage inhibition, colicin resistance and tellurite [Z1173]
tfaR	-2.72	9.52	-1.45	10.25	0.0	8.80	0.1	0.00024272	0.00291707	A_07_P014841	b1373	cmr|orf, hypothetical protein [b1373]
tfaX	-2.09	7.49	-1.07	8.02	0.1	6.95	0.1	0.00154778	0.01096185	A_07_P016578	b0563	cmr|orf, hypothetical protein [b0563]
tgt	+9.05	10.62	+3.18	9.03	0.0	12.21	0.0	0.00000433	0.00033435	A_07_P021144	b0406	cmr|tRNA-guanine transglycosylase [b0406]
thiD	-5.39	10.00	-2.43	11.22	0.2	8.79	0.3	0.00033286	0.00364059	A_07_P003278	b2103	cmr|phosphomethylpyrimidine kinase [b2103]
thiG	+2.09	7.93	+1.06	7.40	0.0	8.46	0.1	0.00173298	0.01190921	A_07_P010631	b3991	cmr|thiamin biosynthesis, thiazole moiety [b3991]
thiK	+2.26	10.84	+1.17	10.25	0.0	11.42	0.1	0.00059909	0.00549159	A_07_P001731	b1106	cmr|putative beta-glucosidase [b1106]
thiM	-4.48	9.10	-2.16	10.18	0.0	8.02	0.2	0.00012725	0.00183667	A_07_P003284	b2104	cmr|hydoxyethylthiazole kinase [b2104]
thrA	+2.31	7.78	+1.21	7.18	0.1	8.38	0.1	0.00126505	0.00942593	A_07_P010704	b0002	cmr|aspartokinase I, homoserine dehydrogenase I [b0002]
thrB	+3.44	8.17	+1.78	7.27	0.2	9.06	0.1	0.00038180	0.00398874	A_07_P010710	b0003	cmr|homoserine kinase [b0003]
thrC	+3.89	9.62	+1.96	8.65	0.0	10.60	0.1	0.00009055	0.00147268	A_07_P035606	c_0005	cmr|Threonine synthase [c_0005]
thyA	+3.37	9.44	+1.75	8.56	0.1	10.31	0.1	0.00013156	0.00188305	A_07_P006119	b2827	cmr|thymidylate synthetase [b2827]
tktA	+6.81	11.60	+2.77	10.22	0.0	12.98	0.0	0.00000911	0.00043585	A_07_P032946	c_3520	cmr|Transketolase 1 [c_3520]
tktA	+3.25	8.19	+1.70	7.34	0.3	9.04	0.0	0.00100283	0.00794100	A_07_P011821	b2935	cmr|transketolase 1 isozyme [b2935]
tnaA	+185.98	10.41	+7.54	6.64	0.2	14.18	0.0	0.00000022	0.00019431	A_07_P057646	ECs4645	cmr|tryptophanase [ECs4645]
tnaA	+75.28	11.68	+6.23	8.56	0.1	14.80	0.1	0.00000037	0.00019431	A_07_P005461	b3708	cmr|tryptophanase [b3708]
tnaA	+153.65	10.56	+7.26	6.93	0.1	14.19	0.0	0.00000014	0.00019431	A_07_P049911	Z5203	cmr|tryptophanase [Z5203]
tnaB	+12.56	9.35	+3.65	7.52	0.3	11.18	0.0	0.00002526	0.00071646	A_07_P041909	c_4632	cmr|Low affinity tryptophan permease [c_4632]
tnaB	+3.98	8.02	+1.99	7.02	0.3	9.02	0.1	0.00036522	0.00389567	A_07_P005466	b3709	cmr|low affinity tryptophan permease [b3709]
tolB	+5.93	10.92	+2.57	9.64	0.2	12.20	0.0	0.00003600	0.00084763	A_07_P010216	b0740	cmr|periplasmic protein involved in the tonb-independent uptake of group A colicins [b0740]
tolC	+3.41	10.50	+1.77	9.61	0.0	11.38	0.0	0.00007176	0.00126242	A_07_P012308	b3035	cmr|outer membrane channel; specific tolerance to colicin E1; segregation of daughter chromosomes [b3035]
torD	-2.00	7.96	-1.00	8.46	0.1	7.46	0.2	0.00327607	0.01919557	A_07_P051271	Z1416	cmr|part of trimethylamine-N-oxide oxidoreductase [Z1416]
torS	-2.99	12.41	-1.58	13.20	0.1	11.62	0.0	0.00019174	0.00246301	A_07_P001197	b0993	cmr|sensor protein torS [b0993]
tpiA	+2.97	12.74	+1.57	11.95	0.0	13.53	0.1	0.00014613	0.00203963	A_07_P019375	b3919	cmr|triosephosphate isomerase [b3919]
tpx	+5.64	10.85	+2.50	9.60	0.0	12.10	0.1	0.00001575	0.00056283	A_07_P014605	b1324	cmr|thiol peroxidase [b1324]
treB	+2.35	8.19	+1.23	7.58	0.1	8.81	0.1	0.00073665	0.00635495	A_07_P003751	b4240	cmr|PTS system enzyme II, trehalose specific [b4240]
treR	-2.16	11.81	-1.11	12.36	0.1	11.26	0.0	0.00080398	0.00681264	A_07_P003760	b4241	cmr|repressor of treA,B,C [b4241]
trg	-2.08	9.75	-1.05	10.27	0.1	9.22	0.1	0.00132466	0.00972818	A_07_P009199	b1421	cmr|methyl-accepting chemotaxis protein III, ribose sensor receptor [b1421]
trkH	-2.50	8.92	-1.32	9.58	0.1	8.26	0.2	0.00092193	0.00751675	A_07_P019052	b3849	cmr|potassium uptake, requires TrkE [b3849]
trmA	-2.93	9.15	-1.55	9.93	0.1	8.38	0.2	0.00047535	0.00466588	A_07_P047177	Z5526	cmr|tRNA [Z5526]
trmD	-2.28	16.22	-1.19	16.82	0.0	15.63	0.1	0.00059234	0.00546330	A_07_P019915	b2607	cmr|tRNA methyltransferase; tRNA [b2607]
trmH	-4.16	10.12	-2.05	11.15	0.1	9.09	0.1	0.00006103	0.00115629	A_07_P017198	b3651	cmr|putative RNA methylase [b3651]
trmI	+6.22	12.78	+2.64	11.46	0.0	14.10	0.1	0.00001187	0.00050521	A_07_P011943	b2960	cmr|orf, hypothetical protein [b2960]
trmJ	-5.39	13.82	-2.43	15.04	0.0	12.61	0.0	0.00001565	0.00056283	A_07_P019564	b2532	cmr|putative ATP synthase beta subunit [b2532]
trpB	+3.84	8.62	+1.94	7.65	0.1	9.59	0.0	0.00006599	0.00120525	A_07_P014291	b1261	cmr|tryptophan synthase, beta protein [b1261]
trpB	+3.86	9.29	+1.95	8.31	0.0	10.26	0.0	0.00004525	0.00095882	A_07_P038879	c_1726	cmr|Tryptophan synthase beta chain [c_1726]
trpB	+2.65	8.63	+1.41	7.93	0.1	9.34	0.1	0.00050868	0.00488792	A_07_P044133	Z2550	cmr|tryptophan synthase, beta protein [Z2550]
trpR	+2.11	8.50	+1.08	7.96	0.0	9.04	0.0	0.00082597	0.00694666	A_07_P017646	b4393	cmr|regulator for trp operon and aroH; trp aporepressor [b4393]
trxA	-6.31	14.00	-2.66	15.33	0.0	12.67	0.0	0.00000937	0.00044530	A_07_P057729	ECs4714	cmr|thioredoxin 1 [ECs4714]
trxA	-7.73	13.63	-2.95	15.10	0.0	12.15	0.0	0.00000587	0.00036511	A_07_P005789	b3781	cmr|thioredoxin 1 [b3781]
trxA	-7.18	13.92	-2.84	15.35	0.1	12.50	0.0	0.00000758	0.00040630	A_07_P035554	c_4701	cmr|Thioredoxin 1 [c_4701]
trxB	+4.09	12.70	+2.03	11.69	0.1	13.72	0.1	0.00006174	0.00115851	A_07_P033812	c_1025	cmr|Thioredoxin reductase [c_1025]
tsgA	-3.34	8.10	-1.74	8.97	0.1	7.22	0.0	0.00009465	0.00151434	A_07_P017847	b3364	cmr|putative transport [b3364]
ttdR	-4.32	9.65	-2.11	10.71	0.1	8.60	0.2	0.00015909	0.00217908	A_07_P000033	b3060	cmr|putative transcriptional regulator LYSR-type [b3060]
tuf	+2.40	16.31	+1.26	15.67	0.1	16.94	0.0	0.00057869	0.00535939	A_07_P059760	ECs4190	cmr|protein chain elongation factor EF-Tu [ECs4190]
tuf	+2.48	16.82	+1.31	16.17	0.0	17.48	0.0	0.00029942	0.00336717	A_07_P046005	Z4697	cmr|protein chain elongation factor EF-Tu [Z4697]
tuf	+2.04	16.47	+1.03	15.96	0.0	16.99	0.0	0.00098339	0.00782734	A_07_P057936	ECs4903	cmr|protein chain elongation factor EF-Tu [ECs4903]
tufA	+2.45	16.70	+1.29	16.05	0.0	17.34	0.0	0.00032733	0.00359882	A_07_P017725	b3339	cmr|protein chain elongation factor EF-Tu [b3339]
tyrB	+2.24	8.04	+1.16	7.46	0.3	8.62	0.3	0.01011396	0.04509606	A_07_P037596	c_5031	cmr|Aromatic-amino-acid aminotransferase [c_5031]
tyrS	+3.47	8.39	+1.79	7.49	0.1	9.28	0.1	0.00009586	0.00152759	A_07_P020819	b1637	cmr|tyrosine tRNA synthetase [b1637]
ubiE	-3.77	13.74	-1.92	14.70	0.0	12.78	0.1	0.00006260	0.00116220	A_07_P018975	b3833	cmr|2-octaprenyl-6-methoxy-1,4-benzoquinone --> 2-octaprenyl-3-methyl-6-methoxy-1,4-benzoquinone [b3833]
ubiH	+2.62	11.91	+1.39	11.21	0.1	12.60	0.0	0.00029964	0.00336721	A_07_P045655	Z4244	cmr|2-octaprenyl-6-methoxyphenol--> 2-octaprenyl-6-methoxy-1, 4-benzoquinone [Z4244]
ubiH	+2.39	11.90	+1.26	11.27	0.0	12.53	0.0	0.00037546	0.00395400	A_07_P032895	c_3489	cmr|2-octaprenyl-6-methoxyphenol hydroxylase [c_3489]
ucpA	+4.17	8.83	+2.06	7.80	0.2	9.86	0.1	0.00012688	0.00183667	A_07_P013188	b2426	cmr|putative oxidoreductase [b2426]
ucpA	+5.31	11.46	+2.41	10.26	0.1	12.67	0.0	0.00002461	0.00070547	A_07_P041240	c_2960	cmr|Oxidoreductase ucpA [c_2960]
ugd	-2.62	8.97	-1.39	9.67	0.1	8.28	0.0	0.00026120	0.00308044	A_07_P015464	b2028	cmr|UDP-glucose 6-dehydrogenase [b2028]
ugd	-4.22	8.56	-2.08	9.60	0.1	7.52	0.1	0.00006241	0.00116220	A_07_P044992	Z3190	cmr|UDP-glucose 6-dehydrogenase [Z3190]
ugpB	+2.00	8.12	+1.00	7.62	0.1	8.62	0.1	0.00227880	0.01455673	A_07_P018281	b3453	cmr|sn-glycerol 3-phosphate transport system; periplasmic binding protein [b3453]
ugpC	+2.90	8.27	+1.54	7.50	0.0	9.03	0.1	0.00016049	0.00218551	A_07_P018267	b3450	cmr|ATP-binding component of sn-glycerol 3-phosphate transport system [b3450]
uhpT	-8.39	8.59	-3.07	10.12	0.0	7.05	0.0	0.00000471	0.00034354	A_07_P017270	b3666	cmr|hexose phosphate transport protein [b3666]
uhpT	-10.55	8.84	-3.40	10.54	0.0	7.14	0.1	0.00000508	0.00034758	A_07_P038972	c_4590	cmr|Hexose phosphate transport protein [c_4590]
ulaD	+2.05	9.21	+1.03	8.70	0.3	9.73	0.1	0.00561809	0.02881149	A_07_P011698	b4196	cmr|probable hexulose-6-phosphate synthase [b4196]
umuC	-2.60	11.87	-1.38	12.56	0.1	11.18	0.0	0.00026512	0.00309642	A_07_P006875	b1184	cmr|SOS mutagenesis and repair [b1184]
ung	-2.95	10.32	-1.56	11.10	0.1	9.54	0.1	0.00030249	0.00339199	A_07_P041614	c_3105	cmr|Uracil-DNA glycosylase [c_3105]
upp	+10.78	12.49	+3.43	10.78	0.2	14.21	0.1	0.00000961	0.00045183	A_07_P013547	b2498	cmr|uracil phosphoribosyltransferase [b2498]
uspA	+8.03	12.47	+3.01	10.97	0.0	13.98	0.0	0.00000508	0.00034758	A_07_P007413	b3495	cmr|universal stress protein; broad regulatory function? [b3495]
uspA	+6.82	11.53	+2.77	10.14	0.0	12.91	0.1	0.00000938	0.00044530	A_07_P049374	Z4895	cmr|universal stress protein broad regulatory function? [Z4895]
uspA	+6.92	12.00	+2.79	10.60	0.1	13.39	0.1	0.00001985	0.00062874	A_07_P034623	c_4293	cmr|Universal stress protein A [c_4293]
uspF	+17.19	11.33	+4.10	9.28	0.1	13.38	0.1	0.00000147	0.00022429	A_07_P014857	b1376	cmr|putative filament protein [b1376]
uvrA	-5.86	13.35	-2.55	14.63	0.0	12.08	0.1	0.00001396	0.00053770	A_07_P008933	b4058	cmr|excision nuclease subunit A [b4058]
uvrB	-8.71	13.26	-3.12	14.82	0.0	11.70	0.0	0.00000445	0.00033554	A_07_P033475	c_0860	cmr|Excinuclease ABC subunit B [c_0860]
uvrB	-6.34	12.69	-2.66	14.02	0.1	11.36	0.1	0.00002039	0.00063193	A_07_P004347	b0779	cmr|DNA repair; excision nuclease subunit B [b0779]
uvrY	-2.13	9.90	-1.09	10.44	0.0	9.35	0.1	0.00100322	0.00794100	A_07_P014931	b1914	cmr|putative 2-component transcriptional regulator [b1914]
uxaA	+6.48	8.24	+2.70	6.89	0.3	9.59	0.0	0.00007544	0.00130949	A_07_P000185	b3091	cmr|altronate hydrolase [b3091]
uxaA	+9.36	9.43	+3.23	7.82	0.1	11.05	0.1	0.00000455	0.00033765	A_07_P034058	c_3849	cmr|Altronate hydrolase [c_3849]
uxaC	+23.49	9.59	+4.55	7.32	0.0	11.87	0.0	0.00000070	0.00019431	A_07_P000188	b3092	cmr|uronate isomerase [b3092]
uxuB	+2.03	9.40	+1.02	8.89	0.1	9.91	0.1	0.00130641	0.00967457	A_07_P037204	c_5403	cmr|D-mannonate oxidoreductase [c_5403]
uxuB	+3.67	8.14	+1.87	7.20	0.1	9.08	0.0	0.00007440	0.00129725	A_07_P047511	Z5921	cmr|mannonate oxidoreductase [Z5921]
vacJ	+4.99	8.18	+2.32	7.02	0.1	9.34	0.0	0.00002233	0.00067002	A_07_P032512	c_2890	cmr|VacJ lipoprotein precursor [c_2890]
vacJ	+3.68	8.80	+1.88	7.86	0.3	9.74	0.2	0.00069363	0.00608327	A_07_P014018	b2346	cmr|lipoprotein precursor [b2346]
viaA	-2.01	9.24	-1.01	9.75	0.2	8.74	0.2	0.00834807	0.03900062	A_07_P005646	b3745	cmr|orf, hypothetical protein [b3745]
waaP	-4.75	10.06	-2.25	11.19	0.2	8.94	0.0	0.00006289	0.00116627	A_07_P049579	Z5054	cmr|putative LPS biosynthesis enzyme [Z5054]
waaQ	-2.00	10.96	-1.00	11.46	0.1	10.46	0.1	0.00297908	0.01777288	A_07_P049589	Z5056	cmr|putative LPS biosynthesis enzyme [Z5056]
wbbJ	+2.31	7.81	+1.21	7.20	0.1	8.41	0.0	0.00071188	0.00619557	A_07_P015485	b2033	cmr|putative O-acetyl transferase [b2033]
wbdN	-3.41	10.44	-1.77	11.32	0.1	9.55	0.0	0.00007779	0.00133123	A_07_P045051	Z3204	cmr|glycosyl transferase [Z3204]
wcaK	+2.16	7.39	+1.11	6.83	0.1	7.95	0.1	0.00101760	0.00802729	A_07_P032034	c_2570	cmr|Colanic acid biosynthesis protein wcaK [c_2570]
wrbA	+3.12	9.51	+1.64	8.69	0.1	10.33	0.1	0.00030461	0.00340122	A_07_P001254	b1004	cmr|trp repressor binding protein; affects association of trp repressor and operator [b1004]
wzyE	+2.34	8.25	+1.23	7.63	0.2	8.86	0.1	0.00132034	0.00971976	A_07_P005852	b3793	cmr|TDP-Fuc4NAc:lipidII transferase; synthesis of enterobacterial common antigen [b3793]
wzzB	-2.93	11.38	-1.55	12.15	0.0	10.60	0.0	0.00014208	0.00199905	A_07_P031985	c_2554	cmr|Chain length determinant protein [c_2554]
wzzB	-2.54	8.97	-1.34	9.64	0.2	8.30	0.1	0.00118844	0.00902162	A_07_P044990	Z3189	cmr|regulator of length of O-antigen component of [Z3189]
wzzE	-2.34	8.48	-1.22	9.10	0.2	7.87	0.0	0.00132980	0.00973786	A_07_P005801	b3785	cmr|putative transport protein [b3785]
xerC	+2.27	8.03	+1.18	7.44	0.3	8.62	0.0	0.00346557	0.01999336	A_07_P049986	Z5328	cmr|site-specific recombinase, acts on cer sequence of [Z5328]
xerC	+2.07	8.31	+1.05	7.78	0.0	8.83	0.2	0.00267201	0.01642642	A_07_P039112	c_4732	cmr|Integrase/recombinase xerC [c_4732]
xerD	-2.61	11.98	-1.38	12.68	0.0	11.29	0.1	0.00029356	0.00333465	A_07_P006436	b2894	cmr|site-specific recombinase [b2894]
xseA	-2.10	11.41	-1.07	11.95	0.3	10.88	0.1	0.00754737	0.03612822	A_07_P013602	b2509	cmr|exonuclease VII, large subunit [b2509]
xseA	-2.07	9.78	-1.05	10.30	0.1	9.25	0.1	0.00131113	0.00969583	A_07_P030157	c_3028	cmr|Exodeoxyribonuclease VII large subunit [c_3028]
xthA	+2.03	10.16	+1.02	9.65	0.0	10.67	0.1	0.00112198	0.00866326	A_07_P044436	Z2781	cmr|exonuclease III [Z2781]
yaaA	+2.35	9.18	+1.23	8.57	0.1	9.80	0.1	0.00097147	0.00775997	A_07_P010722	b0006	cmr|orf, hypothetical protein [b0006]
yaaH	-2.35	8.60	-1.23	9.21	0.1	7.98	0.0	0.00077551	0.00661768	A_07_P010741	b0010	cmr|orf, hypothetical protein [b0010]
yaaY	-3.70	8.41	-1.89	9.35	0.0	7.47	0.3	0.00034645	0.00374618	A_07_P010806	b0024	cmr|orf, hypothetical protein [b0024]
yabI	-3.45	8.36	-1.78	9.25	0.1	7.46	0.3	0.00056764	0.00528823	A_07_P035723	c_0081	cmr|Hypothetical protein yabI [c_0081]
yabI	-3.16	8.43	-1.66	9.26	0.1	7.60	0.0	0.00011198	0.00169030	A_07_P035723	c_0081	cmr|Hypothetical protein yabI [c_0081]
yabI	-3.08	8.16	-1.62	8.97	0.0	7.35	0.1	0.00014173	0.00199583	A_07_P035723	c_0081	cmr|Hypothetical protein yabI [c_0081]
yabI	-3.66	8.13	-1.87	9.07	0.0	7.20	0.2	0.00015157	0.00209512	A_07_P035723	c_0081	cmr|Hypothetical protein yabI [c_0081]
yabI	-3.24	8.31	-1.70	9.16	0.0	7.46	0.2	0.00024138	0.00291212	A_07_P035723	c_0081	cmr|Hypothetical protein yabI [c_0081]
yacL	+2.50	13.06	+1.32	12.40	0.1	13.72	0.0	0.00053770	0.00509054	A_07_P002559	b0119	cmr|orf, hypothetical protein [b0119]
yadC	-19.53	11.50	-4.29	13.64	0.0	9.35	0.0	0.00000093	0.00019431	A_07_P035826	c_0166	cmr|Hypothetical fimbrial-like protein yadC precursor [c_0166]
yadD	-2.11	10.63	-1.07	11.17	0.0	10.09	0.0	0.00076157	0.00653062	A_07_P035809	c_0162	cmr|Hypothetical protein yadD [c_0162]
yadH	-2.26	8.65	-1.17	9.23	0.1	8.06	0.1	0.00087088	0.00723162	A_07_P049187	Z0139	cmr|orf, hypothetical protein [Z0139]
yadH	-2.00	8.84	-1.00	9.34	0.0	8.34	0.1	0.00181180	0.01228992	A_07_P002602	b0128	cmr|orf, hypothetical protein [b0128]
yadS	-2.48	8.20	-1.31	8.86	0.1	7.55	0.2	0.00179934	0.01225015	A_07_P002749	b0157	cmr|orf, hypothetical protein [b0157]
yafE	+2.11	7.72	+1.08	7.18	0.0	8.26	0.1	0.00132045	0.00971976	A_07_P041461	c_0247	cmr|Hypothetical protein yafE [c_0247]
yafJ	+2.08	10.39	+1.05	9.87	0.0	10.92	0.0	0.00090310	0.00739560	A_07_P007830	b0223	cmr|putative amidotransferase [b0223]
yafK	-7.92	9.73	-2.98	11.22	0.2	8.23	0.1	0.00002622	0.00072778	A_07_P007831	b0224	cmr|orf, hypothetical protein [b0224]
yafP	-2.19	9.91	-1.13	10.48	0.1	9.35	0.1	0.00095748	0.00769113	A_07_P007881	b0234	cmr|orf, hypothetical protein [b0234]
yafY	-2.63	8.50	-1.40	9.20	0.4	7.80	0.0	0.00616345	0.03084453	A_07_P007962	b0251	cmr|orf, hypothetical protein [b0251]
yahA	-4.24	8.68	-2.08	9.73	0.1	7.64	0.0	0.00005451	0.00107551	A_07_P008268	b0315	cmr|orf, hypothetical protein [b0315]
yahM	-8.29	9.60	-3.05	11.12	0.1	8.07	0.1	0.00000583	0.00036511	A_07_P008330	b0327	cmr|orf, hypothetical protein [b0327]
yaiA	-5.86	12.02	-2.55	13.29	0.1	10.74	0.1	0.00003577	0.00084433	A_07_P021060	b0389	cmr|orf, hypothetical protein [b0389]
yaiI	+3.25	10.16	+1.70	9.32	0.5	11.01	0.0	0.00481491	0.02557557	A_07_P021047	b0387	cmr|orf, hypothetical protein [b0387]
yaiL	+2.76	7.89	+1.47	7.16	0.2	8.63	0.0	0.00088081	0.00727980	A_07_P031039	c_0462	cmr|Hypothetical protein yaiL [c_0462]
yaiO	-2.68	8.00	-1.42	8.71	0.2	7.29	0.1	0.00054648	0.00516435	A_07_P020918	b0358	cmr|orf, hypothetical protein [b0358]
yajC	+7.60	9.85	+2.93	8.39	0.3	11.32	0.1	0.00006129	0.00115791	A_07_P021148	b0407	cmr|orf, hypothetical protein [b0407]
ybaA	-2.23	8.34	-1.16	8.92	0.2	7.77	0.0	0.00181903	0.01231780	A_07_P021388	b0456	cmr|orf, hypothetical protein [b0456]
ybaB	+4.96	12.35	+2.31	11.19	0.0	13.50	0.0	0.00001976	0.00062719	A_07_P021461	b0471	cmr|orf, hypothetical protein [b0471]
ybaC	-13.32	10.54	-3.74	12.41	0.1	8.67	0.1	0.00000317	0.00029057	A_07_P031201	c_0596	cmr|Acetyl esterase [c_0596]
ybaK	+2.98	9.03	+1.58	8.24	0.1	9.82	0.0	0.00020341	0.00257851	A_07_P021513	b0481	cmr|orf, hypothetical protein [b0481]
ybaL	-3.33	10.41	-1.73	11.28	0.1	9.54	0.1	0.00020737	0.00261010	A_07_P021498	b0478	cmr|putative transport protein [b0478]
ybaQ	-9.53	10.66	-3.25	12.29	0.1	9.03	0.2	0.00001367	0.00052871	A_07_P021524	b0483	cmr|orf, hypothetical protein [b0483]
ybaR	-2.17	9.89	-1.12	10.45	0.2	9.33	0.1	0.00358689	0.02058019	A_07_P031208	c_0604	cmr|Copper-transporting P-type ATPase [c_0604]
ybbJ	-2.72	10.54	-1.45	11.26	0.0	9.82	0.0	0.00020380	0.00258139	A_07_P031218	c_0609	cmr|Hypothetical protein ybbJ [c_0609]
ybbT	+5.47	8.95	+2.45	7.72	0.3	10.18	0.0	0.00010005	0.00157212	A_07_P031224	c_0620	cmr|Ureidoglycolate hydrolase [c_0620]
ybcO	+7.19	12.25	+2.85	10.83	0.0	13.68	0.1	0.00000945	0.00044666	A_07_P016514	b0549	cmr|orf, hypothetical protein [b0549]
ybcU	+2.56	8.01	+1.36	7.33	0.1	8.69	0.1	0.00037759	0.00396055	A_07_P038504	c_1564	cmr|Bor protein homolog from lambdoid prophage DLP12 [c_1564]
ybdD	+4.73	8.64	+2.24	7.52	0.0	9.76	0.0	0.00002337	0.00068274	A_07_P010317	ABE-0285033	asap|conserved protein [b4512]
ybdM	-2.52	7.98	-1.33	8.64	0.1	7.31	0.2	0.00129500	0.00960813	A_07_P016765	b0601	cmr|orf, hypothetical protein [b0601]
ybdN	-5.58	10.63	-2.48	11.87	0.0	9.39	0.1	0.00002584	0.00072358	A_07_P016768	b0602	cmr|orf, hypothetical protein [b0602]
ybeA	-3.81	12.25	-1.93	13.22	0.0	11.29	0.0	0.00004878	0.00100402	A_07_P009747	b0636	cmr|orf, hypothetical protein [b0636]
ybeB	-3.74	13.29	-1.90	14.24	0.0	12.34	0.0	0.00004963	0.00100955	A_07_P009752	b0637	cmr|orf, hypothetical protein [b0637]
ybeL	+2.65	11.08	+1.41	10.38	0.3	11.79	0.1	0.00191148	0.01276266	A_07_P009784	b0643	cmr|putative alpha helical protein [b0643]
ybeY	+2.80	10.27	+1.49	9.52	0.1	11.01	0.2	0.00061053	0.00556489	A_07_P009856	b0659	cmr|orf, hypothetical protein [b0659]
ybeZ	+2.71	10.42	+1.44	9.71	0.0	11.14	0.1	0.00024712	0.00296089	A_07_P009865	b0660	cmr|putative ATP-binding protein in pho regulon [b0660]
ybfA	-8.86	11.00	-3.15	12.58	0.0	9.43	0.2	0.00001187	0.00050521	A_07_P010014	b0699	cmr|orf, hypothetical protein [b0699]
ybgA	-5.68	9.54	-2.51	10.80	0.1	8.29	0.1	0.00001649	0.00057297	A_07_P033376	c_0786	cmr|Hypothetical protein ybgA [c_0786]
ybgE	+3.57	8.45	+1.84	7.54	0.1	9.37	0.1	0.00010733	0.00164539	A_07_P010194	b0735	cmr|orf, hypothetical protein [b0735]
ybgO	+2.14	7.48	+1.10	6.93	0.1	8.03	0.0	0.00095513	0.00768114	A_07_P010097	b0716	cmr|orf, hypothetical protein [b0716]
ybhA	+2.80	10.14	+1.49	9.39	0.2	10.88	0.0	0.00047091	0.00463958	A_07_P004285	b0766	cmr|putative phosphatase [b0766]
ybhA	+2.55	10.03	+1.35	9.35	0.1	10.71	0.0	0.00047969	0.00468366	A_07_P046367	Z0936	cmr|putative phosphatase [Z0936]
ybhC	+3.18	8.14	+1.67	7.30	0.0	8.97	0.0	0.00009584	0.00152759	A_07_P051991	Z0943	cmr|putative pectinesterase [Z0943]

ybhI	-2.74	10.13	-1.45	10.86	0.2	9.41	0.1	0.00119085	0.00903117	A_07_P004302	b0770	cmr|putative membrane pump protein [b0770]
ybhQ	+2.02	10.28	+1.01	9.78	0.1	10.79	0.0	0.00183269	0.01238361	A_07_P004406	b0791	cmr|orf, hypothetical protein [b0791]
ybiB	+2.30	11.72	+1.20	11.12	0.1	12.32	0.1	0.00094221	0.00761113	A_07_P004455	b0800	cmr|putative enzyme [b0800]
ybiB	+2.69	10.06	+1.43	9.35	0.1	10.78	0.0	0.00024534	0.00294404	A_07_P046583	Z1021	cmr|putative enzyme [Z1021]
ybiB	+3.55	11.13	+1.83	10.21	0.1	12.04	0.0	0.00012135	0.00178598	A_07_P041584	c_0884	cmr|Hypothetical protein ybiB [c_0884]
ybiC	+3.47	8.76	+1.80	7.86	0.1	9.66	0.1	0.00013574	0.00193052	A_07_P042097	c_0885	cmr|Hypothetical oxidoreductase ybiC [c_0885]
ybiH	+2.65	7.67	+1.41	6.96	0.2	8.37	0.0	0.00112574	0.00867527	A_07_P004432	b0796	cmr|putative transcriptional regulator [b0796]
ybiJ	-4.64	9.84	-2.21	10.95	0.2	8.73	0.1	0.00010899	0.00166313	A_07_P004463	b0802	cmr|orf, hypothetical protein [b0802]
ybiN	+2.23	8.26	+1.16	7.68	0.1	8.84	0.0	0.00068183	0.00600378	A_07_P033505	c_0892	cmr|Hypothetical protein ybiN [c_0892]
ybiO	-2.94	9.82	-1.56	10.60	0.1	9.04	0.0	0.00019180	0.00246301	A_07_P004491	b0808	cmr|putative transport protein [b0808]
ybiR	-2.25	9.95	-1.17	10.54	0.1	9.37	0.1	0.00108695	0.00843837	A_07_P004542	b0818	cmr|orf, hypothetical protein [b0818]
ybiS	-2.19	10.67	-1.13	11.23	0.0	10.10	0.1	0.00073822	0.00636505	A_07_P004547	b0819	cmr|orf, hypothetical protein [b0819]
ybiS	-2.34	12.34	-1.23	12.96	0.1	11.73	0.0	0.00046052	0.00457021	A_07_P042114	c_0905	cmr|Protein ybiS precursor [c_0905]
ybiT	-13.51	10.36	-3.76	12.23	0.1	8.48	0.2	0.00000856	0.00042498	A_07_P004555	b0820	cmr|putative ATP-binding component of a transport system [b0820]
ybjG	-30.06	10.94	-4.91	13.40	0.0	8.49	0.2	0.00000161	0.00023544	A_07_P004660	b0841	cmr|orf, hypothetical protein [b0841]
ybjL	-10.93	10.15	-3.45	11.87	0.1	8.42	0.2	0.00001801	0.00059959	A_07_P004688	b0847	cmr|putative transport protein [b0847]
ybjM	-3.67	9.15	-1.87	10.08	0.1	8.21	0.0	0.00006225	0.00116220	A_07_P004692	b0848	cmr|orf, hypothetical protein [b0848]
ybjN	+3.63	10.56	+1.86	9.63	0.1	11.49	0.0	0.00007693	0.00132177	A_07_P004718	b0853	cmr|putative sensory transduction regulator [b0853]
ybjP	+2.24	9.11	+1.16	8.52	0.1	9.69	0.1	0.00123438	0.00924113	A_07_P052022	Z1095	cmr|putative enzyme [Z1095]
ybjT	+2.40	7.72	+1.26	7.09	0.0	8.35	0.0	0.00037759	0.00396055	A_07_P004800	b0869	cmr|putative dTDP-glucose enzyme [b0869]
ybjX	-4.53	10.74	-2.18	11.83	0.0	9.65	0.1	0.00003155	0.00079211	A_07_P004839	b0877	cmr|putative enzyme [b0877]
ybjX	-4.97	12.47	-2.31	13.62	0.0	11.31	0.0	0.00001916	0.00061714	A_07_P042136	c_1012	cmr|Hypothetical protein ybjX [c_1012]
ycaD	-2.22	8.25	-1.15	8.82	0.1	7.67	0.0	0.00116740	0.00891302	A_07_P033821	c_1037	cmr|Hypothetical protein ycaD [c_1037]
ycaO	+2.01	8.93	+1.01	8.43	0.0	9.44	0.1	0.00217482	0.01405686	A_07_P004973	b0905	cmr|orf, hypothetical protein [b0905]
ycbG	+3.74	9.34	+1.90	8.38	0.0	10.29	0.0	0.00005164	0.00103969	A_07_P005226	b0956	cmr|putative dehydrogenase [b0956]
ycbJ	+2.51	9.06	+1.33	8.39	0.0	9.72	0.1	0.00061142	0.00556489	A_07_P005042	b0919	cmr|orf, hypothetical protein [b0919]
yccA	+2.03	11.11	+1.02	10.60	0.1	11.62	0.1	0.00177221	0.01212591	A_07_P005300	b0970	cmr|putative carrier/transport protein [b0970]
yccM	-2.42	7.84	-1.28	8.48	0.2	7.20	0.1	0.00168022	0.01161762	A_07_P001194	b0992	cmr|orf, hypothetical protein [b0992]
yccW	+2.00	9.59	+1.00	9.09	0.0	10.09	0.1	0.00143457	0.01033203	A_07_P005282	b0967	cmr|putative oxidoreductase [b0967]
yccX	-2.53	13.24	-1.34	13.91	0.1	12.57	0.0	0.00038524	0.00401672	A_07_P005289	b0968	cmr|orf, hypothetical protein [b0968]
ycdT	-7.95	10.59	-2.99	12.08	0.0	9.09	0.1	0.00001200	0.00050646	A_07_P001352	b1025	cmr|orf, hypothetical protein [b1025]
ycdZ	-4.35	9.85	-2.12	10.91	0.1	8.79	0.1	0.00006658	0.00120840	A_07_P001391	b1036	cmr|orf, hypothetical protein [b1036]
yceH	+2.67	8.43	+1.42	7.72	0.2	9.14	0.0	0.00049233	0.00477000	A_07_P040780	c_1334	cmr|Hypothetical protein yceH [c_1334]
yceH	+2.14	8.35	+1.10	7.80	0.1	8.90	0.1	0.00114540	0.00878383	A_07_P001540	b1067	cmr|orf, hypothetical protein [b1067]
ycfJ	-7.74	9.69	-2.95	11.16	0.1	8.21	0.1	0.00000804	0.00041039	A_07_P001753	b1110	cmr|orf, hypothetical protein [b1110]
ycfL	+4.35	9.69	+2.12	8.63	0.3	10.75	0.0	0.00029772	0.00335322	A_07_P001721	b1104	cmr|orf, hypothetical protein [b1104]
ycfP	+3.19	13.84	+1.67	13.01	0.1	14.68	0.1	0.00016810	0.00224857	A_07_P001743	b1108	cmr|orf, hypothetical protein [b1108]
ycfQ	-7.73	10.97	-2.95	12.44	0.1	9.49	0.1	0.00000848	0.00042498	A_07_P001759	b1111	cmr|orf, hypothetical protein [b1111]
ycfU	-2.04	9.49	-1.03	10.01	0.1	8.98	0.0	0.00113736	0.00873918	A_07_P052403	Z1757	cmr|orf, hypothetical protein [Z1757]
ycfZ	-2.09	7.59	-1.06	8.12	0.0	7.06	0.1	0.00155417	0.01097764	A_07_P001806	b1121	cmr|homolog of virulence factor [b1121]
ycgK	+2.91	10.15	+1.54	9.38	0.1	10.92	0.0	0.00016269	0.00220238	A_07_P006843	b1178	cmr|orf, hypothetical protein [b1178]
ycgZ	+6.24	9.46	+2.64	8.14	0.2	10.78	0.0	0.00004970	0.00100963	A_07_P042226	c_1607	cmr|Hypothetical protein ycgZ [c_1607]
ychA	+3.06	10.12	+1.62	9.31	0.2	10.93	0.1	0.00036303	0.00387759	A_07_P007024	b1214	cmr|orf, hypothetical protein [b1214]
ychM	-2.28	9.13	-1.19	9.72	0.0	8.54	0.0	0.00052686	0.00502151	A_07_P038791	c_1664	cmr|Putative sulfate transporter ychM [c_1664]
ychN	+3.02	9.25	+1.59	8.45	0.3	10.04	0.1	0.00097468	0.00778163	A_07_P007047	b1219	cmr|orf, hypothetical protein [b1219]
ychN	+2.91	9.16	+1.54	8.39	0.2	9.93	0.0	0.00055626	0.00522848	A_07_P050787	Z1994	cmr|orf, hypothetical protein [Z1994]
ychO	-2.86	8.19	-1.52	8.94	0.2	7.43	0.2	0.00141589	0.01021151	A_07_P007051	b1220	cmr|putative factor [b1220]
yciG	-2.98	12.85	-1.58	13.64	0.2	12.06	0.3	0.00199382	0.01313037	A_07_P010380	b1259	cmr|orf, hypothetical protein [b1259]
yciH	+3.75	11.77	+1.91	10.82	0.1	12.73	0.1	0.00008848	0.00145271	A_07_P041123	c_1751	cmr|Protein yciH [c_1751]
yciH	+4.47	12.04	+2.16	10.96	0.0	13.12	0.0	0.00002760	0.00073830	A_07_P014394	b1282	cmr|orf, hypothetical protein [b1282]
yciI	+12.16	10.08	+3.60	8.27	0.1	11.88	0.0	0.00000463	0.00033872	A_07_P007191	b1251	cmr|orf, hypothetical protein [b1251]
yciI	+11.46	10.35	+3.52	8.59	0.1	12.11	0.0	0.00000304	0.00028634	A_07_P050796	Z2029	cmr|orf, hypothetical protein [Z2029]
yciK	+2.69	10.94	+1.43	10.23	0.1	11.66	0.0	0.00028041	0.00322248	A_07_P014337	b1271	cmr|putative oxidoreductase [b1271]
yciO	-2.56	8.82	-1.36	9.50	0.0	8.15	0.1	0.00038230	0.00399135	A_07_P044117	Z2543	cmr|orf, hypothetical protein [Z2543]
yciO	-3.53	10.60	-1.82	11.51	0.0	9.69	0.0	0.00006134	0.00115791	A_07_P038891	c_1732	cmr|Protein yciO [c_1732]
yciO	-2.67	9.67	-1.42	10.38	0.0	8.96	0.1	0.00031859	0.00352489	A_07_P014319	b1267	cmr|orf, hypothetical protein [b1267]
yciQ	-2.27	7.47	-1.18	8.06	0.0	6.88	0.3	0.00398987	0.02214967	A_07_P014324	b1268	cmr|orf, hypothetical protein [b1268]
yciW	-2.27	12.36	-1.18	12.95	0.3	11.77	0.1	0.00308684	0.01829102	A_07_P014418	b1287	cmr|putative oxidoreductase [b1287]
ycjX	-2.08	11.83	-1.05	12.36	0.0	11.31	0.2	0.00190194	0.01272597	A_07_P048461	Z2458	cmr|putative EC 2.1 enzymes [Z2458]
ydbJ	+2.50	10.45	+1.32	9.79	0.1	11.11	0.1	0.00037353	0.00394177	A_07_P010409	ABE-0285050	asap|predicted protein [b4529]
ydbK	+4.89	8.92	+2.29	7.78	0.1	10.07	0.0	0.00003337	0.00081556	A_07_P014866	b1378	cmr|putative oxidoreductase, Fe-S subunit [b1378]
ydcH	+8.43	9.06	+3.08	7.52	0.0	10.60	0.0	0.00000502	0.00034758	A_07_P009222	b1426	cmr|orf, hypothetical protein [b1426]
ydcI	-2.11	8.66	-1.08	9.20	0.1	8.12	0.0	0.00091776	0.00749052	A_07_P009204	b1422	cmr|putative transcriptional regulator LYSR-type [b1422]
ydcY	+4.68	12.07	+2.23	10.96	0.0	13.19	0.1	0.00002724	0.00073404	A_07_P009325	b1446	cmr|orf, hypothetical protein [b1446]
yddA	-2.29	7.56	-1.20	8.15	0.3	6.96	0.1	0.00362174	0.02069114	A_07_P009570	b1496	cmr|putative ATP-binding component of a transport system [b1496]
yddB	-2.27	7.54	-1.18	8.14	0.4	6.95	0.0	0.00708866	0.03438197	A_07_P048054	Z2213	cmr|orf, hypothetical protein [Z2213]
ydeA	-4.26	8.49	-2.09	9.53	0.2	7.44	0.0	0.00010327	0.00160656	A_07_P020286	b1528	cmr|putative resistance / regulatory protein [b1528]
ydfG	+2.64	8.39	+1.40	7.69	0.0	9.09	0.1	0.00033480	0.00365537	A_07_P020342	b1539	cmr|putative oxidoreductase [b1539]
ydfM	-8.19	8.69	-3.03	10.21	0.1	7.18	0.1	0.00000664	0.00038136	A_07_P031275	c_0649	cmr|Tail fiber assembly protein homolog from lambdoid [c_0649]
ydfZ	+3.13	11.45	+1.64	10.63	0.2	12.27	0.0	0.00025692	0.00304818	A_07_P020351	b1541	cmr|orf, hypothetical protein [b1541]
ydgH	+3.18	9.61	+1.67	8.78	0.2	10.45	0.0	0.00036162	0.00386772	A_07_P020654	b1604	cmr|orf, hypothetical protein [b1604]
ydgJ	+2.46	8.44	+1.30	7.79	0.2	9.09	0.2	0.00268868	0.01650314	A_07_P035111	c_2016	cmr|Hypothetical oxidoreductase ydgJ [c_2016]
ydgJ	+2.10	7.76	+1.07	7.22	0.0	8.30	0.1	0.00092859	0.00755454	A_07_P020751	b1624	cmr|orf, hypothetical protein [b1624]
ydgK	-3.13	9.21	-1.65	10.03	0.1	8.39	0.1	0.00024212	0.00291652	A_07_P020765	b1626	cmr|orf, hypothetical protein [b1626]
ydhI	-3.58	8.22	-1.84	9.14	0.2	7.31	0.0	0.00018902	0.00244038	A_07_P020850	b1643	cmr|orf, hypothetical protein [b1643]
ydhJ	-2.78	7.94	-1.48	8.68	0.1	7.20	0.1	0.00032756	0.00359886	A_07_P020852	b1644	cmr|putative membrane protein [b1644]
ydhJ	-2.41	7.81	-1.27	8.45	0.1	7.18	0.1	0.00067437	0.00595430	A_07_P020852	b1644	cmr|putative membrane protein [b1644]
ydhM	+2.20	8.12	+1.14	7.55	0.4	8.69	0.1	0.01057925	0.04681273	A_07_P042330	c_2042	cmr|Hypothetical transcriptional regulator ydhM [c_2042]
ydhM	+3.43	9.16	+1.78	8.27	0.2	10.05	0.1	0.00034389	0.00372619	A_07_P020877	b1649	cmr|orf, hypothetical protein [b1649]
ydhR	+2.39	8.97	+1.26	8.34	0.1	9.59	0.1	0.00098992	0.00786343	A_07_P018387	b1667	cmr|orf, hypothetical protein [b1667]
ydhV	+2.44	8.25	+1.29	7.61	0.1	8.89	0.1	0.00086088	0.00716707	A_07_P018419	b1673	cmr|orf, hypothetical protein [b1673]
ydhZ	+2.43	8.46	+1.28	7.82	0.1	9.10	0.1	0.00048884	0.00475369	A_07_P018430	b1675	cmr|orf, hypothetical protein [b1675]
ydiA	+4.46	8.20	+2.16	7.12	0.1	9.28	0.1	0.00003779	0.00087581	A_07_P018569	b1703	cmr|orf, hypothetical protein [b1703]
ydiI	+2.52	9.25	+1.33	8.59	0.1	9.92	0.0	0.00051760	0.00495438	A_07_P018484	b1686	cmr|orf, hypothetical protein [b1686]
ydiJ	+2.89	9.50	+1.53	8.73	0.3	10.27	0.1	0.00209469	0.01366715	A_07_P018489	b1687	cmr|putative oxidase [b1687]
ydiU	-2.38	11.27	-1.25	11.89	0.2	10.64	0.1	0.00154506	0.01094754	A_07_P018581	b1706	cmr|orf, hypothetical protein [b1706]
ydiV	-4.54	8.95	-2.18	10.04	0.1	7.86	0.1	0.00003861	0.00088510	A_07_P018587	b1707	cmr|orf, hypothetical protein [b1707]
ydjA	+7.70	10.78	+2.95	9.31	0.2	12.25	0.1	0.00003187	0.00079613	A_07_P044447	Z2798	cmr|orf, hypothetical protein [Z2798]
ydjA	+16.98	10.44	+4.09	8.40	0.1	12.49	0.1	0.00000162	0.00023544	A_07_P035242	c_2168	cmr|Protein ydjA [c_2168]
ydjA	+15.38	10.26	+3.94	8.29	0.1	12.23	0.1	0.00000222	0.00026540	A_07_P035242	c_2168	cmr|Protein ydjA [c_2168]
ydjA	+14.95	10.20	+3.90	8.25	0.1	12.15	0.1	0.00000223	0.00026540	A_07_P035242	c_2168	cmr|Protein ydjA [c_2168]
ydjA	+15.32	10.28	+3.94	8.31	0.1	12.25	0.0	0.00000258	0.00027706	A_07_P035242	c_2168	cmr|Protein ydjA [c_2168]
ydjA	+12.89	10.36	+3.69	8.51	0.2	12.20	0.0	0.00000585	0.00036511	A_07_P018872	b1765	cmr|orf, hypothetical protein [b1765]
ydjA	+14.49	10.55	+3.86	8.62	0.1	12.47	0.1	0.00000230	0.00026836	A_07_P035242	c_2168	cmr|Protein ydjA [c_2168]
ydjE	-3.90	8.18	-1.96	9.16	0.1	7.19	0.5	0.00262618	0.01620104	A_07_P041186	c_2173	cmr|Hypothetical metabolite transport protein ydjE [c_2173]
ydjE	-2.58	8.12	-1.37	8.81	0.0	7.44	0.0	0.00026679	0.00310509	A_07_P018893	b1769	cmr|putative transport protein [b1769]
ydjF	-3.91	10.03	-1.97	11.01	0.1	9.04	0.2	0.00016028	0.00218551	A_07_P018898	b1770	cmr|putative DEOR-type transcriptional regulator [b1770]
ydjM	-2.87	8.64	-1.52	9.40	0.1	7.88	0.0	0.00018693	0.00241824	A_07_P018690	b1728	cmr|orf, hypothetical protein [b1728]
ydjN	-4.43	10.82	-2.15	11.90	0.0	9.75	0.0	0.00002852	0.00074846	A_07_P018691	b1729	cmr|part of a kinase [b1729]
ydjN	-3.63	9.83	-1.86	10.76	0.0	8.90	0.1	0.00010997	0.00167356	A_07_P042351	c_2128	cmr|Hypothetical symporter ydjN [c_2128]
yeaC	+3.68	12.38	+1.88	11.44	0.1	13.32	0.1	0.00009143	0.00148396	A_07_P015578	b1777	cmr|orf, hypothetical protein [b1777]
yeaD	+4.37	9.22	+2.13	8.16	0.2	10.28	0.1	0.00012713	0.00183667	A_07_P035263	c_2185	cmr|Unknown protein from 2D-page [c_2185]
yeaD	+4.31	9.31	+2.11	8.26	0.3	10.36	0.1	0.00026229	0.00308398	A_07_P035263	c_2185	cmr|Unknown protein from 2D-page [c_2185]
yeaD	+3.88	9.54	+1.96	8.56	0.1	10.52	0.2	0.00019093	0.00245787	A_07_P035263	c_2185	cmr|Unknown protein from 2D-page [c_2185]
yeaD	+3.99	9.31	+2.00	8.31	0.0	10.31	0.0	0.00004279	0.00093353	A_07_P035263	c_2185	cmr|Unknown protein from 2D-page [c_2185]
yeaD	+3.52	8.66	+1.82	7.75	0.0	9.57	0.1	0.00007461	0.00129798	A_07_P015593	b1780	cmr|orf, hypothetical protein [b1780]
yeaD	+4.05	9.55	+2.02	8.54	0.0	10.56	0.1	0.00005425	0.00107304	A_07_P035263	c_2185	cmr|Unknown protein from 2D-page [c_2185]
yeaJ	-6.46	8.85	-2.69	10.20	0.1	7.51	0.0	0.00001290	0.00051944	A_07_P015623	b1786	cmr|orf, hypothetical protein [b1786]
'yeaJ	-2.18	9.65	-1.12	10.21	0.0	9.08	0.0	0.00066768	0.00592222	A_07_P044476	Z2826	cmr|orf Unknown function [Z2826]
yeaL	-2.42	9.33	-1.28	9.97	0.2	8.69	0.2	0.00168570	0.01164021	A_07_P015638	b1789	cmr|orf, hypothetical protein [b1789]
yeaO	+2.26	9.46	+1.18	8.87	0.1	10.05	0.1	0.00128387	0.00953902	A_07_P015655	b1792	cmr|orf, hypothetical protein [b1792]
yeaT	-3.12	7.68	-1.64	8.50	0.0	6.86	0.0	0.00010326	0.00160656	A_07_P015689	b1799	cmr|putative transcriptional regulator LYSR-type [b1799]
yeaY	-2.04	10.12	-1.03	10.63	0.1	9.60	0.1	0.00249073	0.01556729	A_07_P015721	b1806	cmr|putative outer membrane protein [b1806]
yebB	-2.20	11.10	-1.14	11.67	0.3	10.53	0.2	0.00948813	0.04290094	A_07_P035344	c_2276	cmr|Hypothetical protein yebB [c_2276]
yebE	-8.25	11.11	-3.04	12.63	0.0	9.58	0.0	0.00000523	0.00034781	A_07_P015906	b1846	cmr|orf, hypothetical protein [b1846]
yebF	-4.28	15.38	-2.10	16.43	0.0	14.34	0.0	0.00003087	0.00078408	A_07_P015914	b1847	cmr|orf, hypothetical protein [b1847]
yebG	-2.02	15.52	-1.01	16.03	0.0	15.02	0.0	0.00112270	0.00866463	A_07_P015916	b1848	cmr|orf, hypothetical protein [b1848]
yebK	+3.66	8.52	+1.87	7.58	0.1	9.46	0.2	0.00013690	0.00194533	A_07_P015941	b1853	cmr|orf, hypothetical protein [b1853]
yebN	-2.80	10.98	-1.49	11.72	0.1	10.23	0.0	0.00020675	0.00260608	A_07_P015797	b1821	cmr|orf, hypothetical protein [b1821]
yebO	-6.31	9.99	-2.66	11.32	0.0	8.66	0.1	0.00001480	0.00054604	A_07_P015812	b1825	cmr|orf, hypothetical protein [b1825]
yebR	+2.53	8.68	+1.34	8.01	0.1	9.35	0.2	0.00161855	0.01131048	A_07_P015837	b1832	cmr|orf, hypothetical protein [b1832]
yebW	-2.43	9.32	-1.28	9.96	0.1	8.68	0.3	0.00249226	0.01557068	A_07_P010475	b1837	cmr|orf, hypothetical protein [b1837]
yebY	+3.64	10.31	+1.87	9.38	0.0	11.24	0.0	0.00006165	0.00115828	A_07_P015874	b1839	cmr|orf, hypothetical protein [b1839]
yecC	-4.48	8.42	-2.16	9.50	0.1	7.34	0.0	0.00005596	0.00109042	A_07_P014947	b1917	cmr|putative ATP-binding component of a transport system [b1917]
yecH	+2.07	7.52	+1.05	7.00	0.2	8.04	0.0	0.00432253	0.02350739	A_07_P052586	Z2962	cmr|orf, hypothetical protein [Z2962]
yecH	+2.27	7.93	+1.18	7.34	0.3	8.52	0.0	0.00474457	0.02527011	A_07_P035364	c_2322	cmr|Hypothetical protein yecH [c_2322]
yecI	+3.67	10.47	+1.88	9.53	0.0	11.40	0.0	0.00006057	0.00114898	A_07_P035358	c_2315	cmr|Ferritin-like protein 2 [c_2315]
yecN	+2.11	8.81	+1.08	8.27	0.0	9.35	0.1	0.00106294	0.00829283	A_07_P016023	b1869	cmr|orf, hypothetical protein [b1869]
yecR	-3.71	7.96	-1.89	8.91	0.0	7.02	0.1	0.00006228	0.00116220	A_07_P016190	b1904	cmr|orf, hypothetical protein [b1904]
yecS	-5.67	9.08	-2.50	10.33	0.1	7.83	0.1	0.00003217	0.00079793	A_07_P014955	b1918	cmr|putative transport system permease protein [b1918]
yecS	-4.94	9.33	-2.31	10.48	0.0	8.18	0.2	0.00006188	0.00115851	A_07_P042434	c_2332	cmr|Hypothetical amino-acid ABC transporter permease protein yecS [c_2332]
yedE	+4.49	10.10	+2.17	9.01	0.0	11.18	0.0	0.00003083	0.00078408	A_07_P015006	b1929	cmr|putative transport system permease protein [b1929]
yedE	+5.23	9.80	+2.39	8.60	0.1	10.99	0.0	0.00002724	0.00073404	A_07_P052596	Z3019	cmr|putative transport system permease protein [Z3019]
yedE	+12.68	10.64	+3.66	8.81	0.1	12.47	0.0	0.00000276	0.00028062	A_07_P035376	c_2344	cmr|Hypothetical protein yedE [c_2344]
yedF	+11.11	10.15	+3.47	8.41	0.2	11.89	0.0	0.00001468	0.00054604	A_07_P015012	b1930	cmr|orf, hypothetical protein [b1930]
yedJ	-2.33	8.24	-1.22	8.85	0.0	7.63	0.1	0.00047645	0.00466781	A_07_P052607	Z3055	cmr|orf, hypothetical protein [Z3055]
yedJ	-4.63	10.21	-2.21	11.31	0.0	9.10	0.1	0.00002770	0.00073912	A_07_P041216	c_2381	cmr|Hypothetical protein yedJ [c_2381]
yedJ	-4.47	9.13	-2.16	10.21	0.0	8.05	0.1	0.00004172	0.00093045	A_07_P015168	b1962	cmr|orf, hypothetical protein [b1962]
yedR	-2.88	8.25	-1.53	9.01	0.1	7.49	0.0	0.00023553	0.00285318	A_07_P015174	b1963	cmr|orf, hypothetical protein [b1963]
yedW	-2.16	8.28	-1.11	8.84	0.1	7.73	0.1	0.00134803	0.00984389	A_07_P015203	b1969	cmr|putative 2-component transcriptional regulator [b1969]
yeeA	+3.19	8.08	+1.67	7.24	0.1	8.91	0.0	0.00018218	0.00238186	A_07_P031967	c_2536	cmr|Hypothetical protein yeeA [c_2536]
yeeO	-6.51	8.39	-2.70	9.75	0.0	7.04	0.0	0.00000906	0.00043556	A_07_P015266	b1985	cmr|orf, hypothetical protein [b1985]
yeeY	-2.28	9.83	-1.19	10.42	0.1	9.23	0.0	0.00052690	0.00502151	A_07_P015404	b2015	cmr|putative transcriptional regulator LYSR-type [b2015]
yeeZ	-2.71	12.36	-1.44	13.08	0.0	11.64	0.1	0.00027722	0.00319517	A_07_P015407	b2016	cmr|putative enzyme of sugar metabolism [b2016]
yegB	-2.00	8.06	-1.00	8.55	0.2	7.56	0.1	0.00625655	0.03120151	A_07_P042496	c_2603	cmr|Hypothetical transport protein yegB [c_2603]
yegE	-2.24	9.30	-1.16	9.88	0.1	8.72	0.3	0.00679630	0.03324044	A_07_P003112	b2067	cmr|putative sensor-type protein [b2067]
yegI	-2.11	10.11	-1.08	10.64	0.1	9.57	0.1	0.00126200	0.00941208	A_07_P003126	b2070	cmr|putative chaperonin [b2070]
yegL	-2.10	9.91	-1.07	10.45	0.1	9.38	0.0	0.00122159	0.00918208	A_07_P032081	c_2599	cmr|Hypothetical protein yegL [c_2599]
yegP	+2.16	7.87	+1.11	7.32	0.2	8.43	0.1	0.00214829	0.01391304	A_07_P032098	c_2606	cmr|Hypothetical protein yegP [c_2606]
yegQ	-5.05	10.49	-2.34	11.66	0.1	9.33	0.1	0.00002639	0.00072866	A_07_P003182	b2081	cmr|orf, hypothetical protein [b2081]
yegS	-2.17	9.57	-1.12	10.13	0.2	9.01	0.2	0.00391403	0.02191410	A_07_P032127	c_2614	cmr|Hypothetical protein yegS [c_2614]
yegW	-2.06	8.67	-1.04	9.19	0.1	8.15	0.0	0.00185675	0.01248726	A_07_P003270	b2101	cmr|putative transcriptional regulator [b2101]
yegX	-2.37	11.38	-1.24	12.00	0.1	10.75	0.1	0.00095922	0.00769519	A_07_P003271	b2102	cmr|orf, hypothetical protein [b2102]
yegX	-3.66	8.41	-1.87	9.34	0.1	7.47	0.0	0.00008650	0.00143544	A_07_P051783	Z3266	cmr|orf, hypothetical protein [Z3266]
yehD	+5.15	7.79	+2.36	6.60	0.0	8.97	0.1	0.00002448	0.00070547	A_07_P003318	b2111	cmr|putative fimbrial-like protein [b2111]
yehL	-3.25	8.25	-1.70	9.10	0.0	7.40	0.3	0.00066265	0.00588091	A_07_P003356	b2119	cmr|orf, hypothetical protein [b2119]
yehL	-5.58	9.08	-2.48	10.32	0.1	7.84	0.2	0.00004832	0.00099713	A_07_P041221	c_2649	cmr|Hypothetical protein yehL [c_2649]
yehS	-3.39	9.08	-1.76	9.96	0.0	8.20	0.0	0.00007811	0.00133518	A_07_P003385	b2124	cmr|orf, hypothetical protein [b2124]
yehX	-2.21	7.66	-1.14	8.24	0.0	7.09	0.0	0.00062542	0.00564928	A_07_P032191	c_2659	cmr|Hypothetical ABC transporter ATP-binding protein yehX [c_2659]
yeiC	+5.04	7.76	+2.33	6.60	0.3	8.93	0.1	0.00012722	0.00183667	A_07_P032264	c_2701	cmr|Hypothetical sugar kinase yeiC [c_2701]
yeiP	+4.81	9.10	+2.27	7.97	0.0	10.23	0.0	0.00002412	0.00069739	A_07_P000651	b2171	cmr|putative elongation factor [b2171]
yeiQ	+7.46	9.29	+2.90	7.84	0.0	10.74	0.1	0.00000862	0.00042621	A_07_P000660	b2172	cmr|putative oxidoreductase [b2172]
yeiT	+2.67	8.67	+1.42	7.96	0.2	9.38	0.2	0.00159737	0.01119846	A_07_P003491	b2146	cmr|putative oxidoreductase [b2146]
yejG	-4.70	12.45	-2.23	13.57	0.0	11.34	0.0	0.00002296	0.00067941	A_07_P000703	b2181	cmr|orf, hypothetical protein [b2181]
yejK	+4.18	10.28	+2.06	9.25	0.2	11.31	0.0	0.00018583	0.00240997	A_07_P000729	b2186	cmr|orf, hypothetical protein [b2186]
yejL	-2.12	12.09	-1.08	12.63	0.1	11.55	0.1	0.00119733	0.00905414	A_07_P000733	b2187	cmr|orf, hypothetical protein [b2187]
yejM	-2.28	8.55	-1.19	9.15	0.2	7.96	0.1	0.00240665	0.01516218	A_07_P000736	b2188	cmr|putative sulfatase [b2188]
yfaE	+14.19	9.86	+3.83	7.95	0.2	11.77	0.0	0.00000713	0.00039666	A_07_P000966	b2236	cmr|orf, hypothetical protein [b2236]
yfbB	+2.62	8.53	+1.39	7.83	0.0	9.22	0.1	0.00037734	0.00396055	A_07_P001104	b2263	cmr|putative enzyme [b2263]
yfbR	+2.14	7.67	+1.10	7.12	0.1	8.22	0.1	0.00147928	0.01057665	A_07_P013744	b2291	cmr|putative alpha helix protein [b2291]
yfbU	+2.00	9.98	+1.00	9.48	0.0	10.48	0.1	0.00132700	0.00973544	A_07_P013758	b2294	cmr|orf, hypothetical protein [b2294]
yfcE	+2.22	11.93	+1.15	11.35	0.1	12.50	0.0	0.00094946	0.00764622	A_07_P013789	b2300	cmr|orf, hypothetical protein [b2300]
yfcF	+2.13	8.20	+1.09	7.65	0.1	8.74	0.0	0.00095117	0.00765605	A_07_P013791	b2301	cmr|orf, hypothetical protein [b2301]
yfdE	-4.18	9.36	-2.06	10.39	0.2	8.33	0.1	0.00018448	0.00239640	A_07_P014140	b2371	cmr|putative enzyme [b2371]
yfdZ	+2.96	8.60	+1.57	7.82	0.0	9.39	0.1	0.00015009	0.00208564	A_07_P014179	b2379	cmr|putative aminotransferase [b2379]
yfeA	-2.65	8.52	-1.41	9.23	0.1	7.82	0.1	0.00047961	0.00468366	A_07_P014259	b2395	cmr|orf, hypothetical protein [b2395]
yfeN	-2.08	11.11	-1.06	11.63	0.2	10.58	0.2	0.00848145	0.03951816	A_07_P013096	b2408	cmr|putative sugar hydrolase [b2408]
yffB	-3.27	10.95	-1.71	11.81	0.0	10.10	0.1	0.00010241	0.00160236	A_07_P013411	b2471	cmr|orf, hypothetical protein [b2471]
yffL	-2.05	9.57	-1.03	10.09	0.2	9.05	0.0	0.00281837	0.01706630	A_07_P013272	b2443	cmr|orf, hypothetical protein [b2443]
yfgC	+2.14	8.50	+1.10	7.95	0.0	9.05	0.1	0.00083660	0.00702103	A_07_P013530	b2494	cmr|orf, hypothetical protein [b2494]
yfgC	+2.36	9.54	+1.24	8.92	0.2	10.16	0.1	0.00192672	0.01280417	A_07_P042608	c_3011	cmr|Hypothetical protein yfgC precursor [c_3011]
yfgD	+3.93	8.41	+1.98	7.42	0.1	9.40	0.0	0.00007451	0.00129774	A_07_P013532	b2495	cmr|putative oxidoreductase [b2495]
yfgG	+2.61	10.33	+1.38	9.63	0.1	11.02	0.1	0.00059925	0.00549159	A_07_P013578	b2504	cmr|orf, hypothetical protein [b2504]
yfgI	-2.10	10.75	-1.07	11.28	0.2	10.21	0.1	0.00230337	0.01467505	A_07_P030147	c_3025	cmr|Hypothetical protein yfgI [c_3025]
yfgM	+3.64	10.91	+1.86	9.98	0.0	11.84	0.0	0.00005736	0.00110534	A_07_P013623	b2513	cmr|orf, hypothetical protein [b2513]
yfhB	-6.78	9.92	-2.76	11.30	0.1	8.54	0.1	0.00002268	0.00067364	A_07_P019703	b2560	cmr|orf, hypothetical protein [b2560]
yfiC	+2.93	8.66	+1.55	7.88	0.2	9.43	0.0	0.00047218	0.00464624	A_07_P019777	b2575	cmr|putative enzyme [b2575]
yfiD	+5.72	11.46	+2.52	10.20	0.1	12.72	0.0	0.00001737	0.00058395	A_07_P019799	b2579	cmr|putative formate acetyltransferase [b2579]
yfiF	+7.54	11.02	+2.91	9.56	0.1	12.48	0.0	0.00000864	0.00042621	A_07_P019806	b2581	cmr|orf, hypothetical protein [b2581]
yfiQ	+3.57	9.09	+1.84	8.17	0.0	10.01	0.1	0.00007396	0.00129530	A_07_P019821	b2584	cmr|orf, hypothetical protein [b2584]
ygaA	-3.86	9.07	-1.95	10.04	0.1	8.09	0.0	0.00005897	0.00112656	A_07_P030601	c_3263	cmr|Hypothetical sigma-54-dependent transcriptional regulator ygaA [c_3263]
ygaD	+7.43	10.32	+2.89	8.88	0.0	11.77	0.1	0.00000817	0.00041270	A_07_P001946	b2700	cmr|orf, hypothetical protein [b2700]
ygaF	-3.30	8.38	-1.72	9.24	0.6	7.52	0.1	0.00900240	0.04138212	A_07_P020152	b2660	cmr|orf, hypothetical protein [b2660]
ygaF	-2.24	9.00	-1.17	9.58	0.1	8.42	0.1	0.00083875	0.00702801	A_07_P030517	c_3208	cmr|Hypothetical protein ygaF [c_3208]
ygaT	-3.03	8.34	-1.60	9.14	0.0	7.54	0.0	0.00011835	0.00175449	A_07_P041636	c_3207	cmr|Hypothetical protein ygaT [c_3207]
ygaV	+2.41	8.51	+1.27	7.88	0.2	9.15	0.2	0.00197548	0.01305157	A_07_P020189	b2667	cmr|orf, hypothetical protein [b2667]
ygaW	-6.03	11.68	-2.59	12.97	0.1	10.38	0.0	0.00001351	0.00052666	A_07_P001825	b2670	cmr|orf, hypothetical protein [b2670]
ygaZ	-2.24	9.92	-1.16	10.50	0.2	9.34	0.1	0.00203909	0.01333202	A_07_P001881	b2682	cmr|orf, hypothetical protein [b2682]
ygbE	-2.51	8.74	-1.33	9.40	0.0	8.07	0.0	0.00029639	0.00335277	A_07_P030701	c_3316	cmr|Hypothetical protein ygbE [c_3316]
ygbJ	+2.42	8.51	+1.27	7.87	0.1	9.14	0.1	0.00062520	0.00564928	A_07_P030675	c_3297	cmr|Hypothetical oxidoreductase ygbJ [c_3297]
ygcG	-4.27	9.34	-2.09	10.39	0.1	8.30	0.0	0.00004234	0.00093353	A_07_P032628	c_3342	cmr|Hypothetical protein ygcG [c_3342]
ygcN	-2.10	9.27	-1.07	9.81	0.0	8.74	0.2	0.00184697	0.01244116	A_07_P002278	b2766	cmr|orf, hypothetical protein [b2766]
ygdE	-2.03	9.07	-1.02	9.58	0.1	8.56	0.1	0.00153430	0.01089259	A_07_P006026	b2806	cmr|orf, hypothetical protein [b2806]
ygdH	+2.22	9.43	+1.15	8.85	0.1	10.00	0.2	0.00362027	0.02069114	A_07_P002424	b2795	cmr|orf, hypothetical protein [b2795]
ygdL	-2.27	10.91	-1.18	11.50	0.1	10.32	0.0	0.00057437	0.00533670	A_07_P032656	c_3383	cmr|Hypothetical protein ygdL [c_3383]
ygdQ	-2.64	8.17	-1.40	8.87	0.1	7.47	0.0	0.00026461	0.00309464	A_07_P006141	b2832	cmr|putative transport protein [b2832]
ygeK	-2.40	11.27	-1.26	11.90	0.2	10.64	0.1	0.00219770	0.01416318	A_07_P006257	b2855	cmr|putative 2-component transcriptional regulator [b2855]
ygeR	-13.56	9.89	-3.76	11.77	0.0	8.01	0.1	0.00000368	0.00030737	A_07_P006295	b2865	cmr|putative lipoprotein [b2865]
ygfA	-3.00	9.43	-1.58	10.23	0.1	8.64	0.3	0.00125004	0.00933173	A_07_P006525	b2912	cmr|putative ligase [b2912]
ygfX	-2.57	11.35	-1.36	12.04	0.0	10.67	0.0	0.00026355	0.00309415	A_07_P006446	b2896	cmr|orf, hypothetical protein [b2896]
yggD	-2.19	8.58	-1.13	9.15	0.0	8.02	0.0	0.00063391	0.00570950	A_07_P011793	b2929	cmr|putative transcriptional regulator [b2929]
yggD	-2.86	9.77	-1.52	10.53	0.0	9.01	0.1	0.00018124	0.00237586	A_07_P032921	c_3512	cmr|Hypothetical protein yggD [c_3512]
yggL	+3.82	13.00	+1.93	12.03	0.0	13.96	0.0	0.00004543	0.00095882	A_07_P011938	b2959	cmr|orf, hypothetical protein [b2959]
yggP	-2.40	8.27	-1.26	8.90	0.1	7.64	0.0	0.00045704	0.00454842	A_07_P011806	b2932	cmr|orf, hypothetical protein [b2932]
yggX	+3.15	10.78	+1.66	9.96	0.1	11.61	0.0	0.00011012	0.00167356	A_07_P011954	b2962	cmr|orf, hypothetical protein [b2962]
yghB	-7.24	11.27	-2.86	12.70	0.0	9.84	0.1	0.00000823	0.00041394	A_07_P012180	b3009	cmr|orf, hypothetical protein [b3009]
yghU	+2.33	8.06	+1.22	7.45	0.1	8.67	0.0	0.00056473	0.00527744	A_07_P012078	b2989	cmr|orf, hypothetical protein [b2989]
yghU	+3.37	8.84	+1.75	7.96	0.1	9.71	0.1	0.00009358	0.00150183	A_07_P041281	c_3726	cmr|Hypothetical GST-like protein yghU [c_3726]
yghZ	+2.83	9.51	+1.50	8.76	0.1	10.26	0.0	0.00021709	0.00269339	A_07_P012136	b3001	cmr|putative reductase [b3001]
ygiB	+2.70	11.93	+1.43	11.21	0.2	12.64	0.1	0.00050832	0.00488792	A_07_P012316	b3037	cmr|orf, hypothetical protein [b3037]
ygiC	+2.43	8.43	+1.28	7.79	0.3	9.07	0.0	0.00192703	0.01280417	A_07_P012323	b3038	cmr|putative synthetase/amidase [b3038]
ygiF	-3.99	11.43	-2.00	12.43	0.0	10.44	0.1	0.00006376	0.00117677	A_07_P000003	b3054	cmr|orf, hypothetical protein [b3054]
ygiF	-3.11	12.72	-1.64	13.54	0.0	11.90	0.0	0.00011300	0.00169761	A_07_P041286	c_3802	cmr|Hypothetical protein ygiF [c_3802]
ygiN	+13.33	10.59	+3.74	8.72	0.1	12.46	0.1	0.00000369	0.00030737	A_07_P012278	b3029	cmr|orf, hypothetical protein [b3029]
ygiP	-4.75	9.74	-2.25	10.86	0.0	8.61	0.1	0.00004191	0.00093286	A_07_P036891	c_3810	cmr|Hypothetical transcriptional regulator ygiP [c_3810]
ygjH	-2.55	12.52	-1.35	13.19	0.0	11.84	0.4	0.00572323	0.02927440	A_07_P000096	b3074	cmr|putative tRNA synthetase [b3074]
ygjO	+2.90	8.66	+1.54	7.89	0.4	9.43	0.1	0.00286514	0.01730292	A_07_P045877	Z4437	cmr|putative enzyme [Z4437]
ygjP	-5.28	9.27	-2.40	10.47	0.1	8.07	0.0	0.00002371	0.00068742	A_07_P000154	b3085	cmr|orf, hypothetical protein [b3085]
ygjP	-7.13	10.92	-2.83	12.34	0.0	9.50	0.1	0.00001063	0.00047201	A_07_P034044	c_3843	cmr|Hypothetical protein ygjP [c_3843]
ygjQ	-3.09	8.15	-1.63	8.96	0.0	7.33	0.0	0.00010538	0.00163463	A_07_P041292	c_3844	cmr|Hypothetical protein ygjQ [c_3844]
ygjR	+3.56	8.97	+1.83	8.06	0.1	9.89	0.0	0.00007139	0.00125864	A_07_P000165	b3087	cmr|orf, hypothetical protein [b3087]
ygjU	+3.12	9.26	+1.64	8.44	0.1	10.08	0.1	0.00029556	0.00334773	A_07_P034047	c_3847	cmr|Hypothetical symporter ygjU [c_3847]
yhaG	+2.22	9.35	+1.15	8.78	0.2	9.93	0.1	0.00189443	0.01269186	A_07_P034086	c_3883	cmr|D-galactarate dehydratase [c_3883]
yhaG	+4.20	9.45	+2.07	8.41	0.2	10.48	0.1	0.00014115	0.00199309	A_07_P045896	Z4480	cmr|putative hydrolase [Z4480]
yhaJ	+2.47	9.72	+1.31	9.06	0.0	10.37	0.0	0.00033044	0.00362039	A_07_P000254	b3105	cmr|putative transcriptional regulator LYSR-type [b3105]
yhaL	+2.88	10.72	+1.53	9.95	0.4	11.48	0.0	0.00345649	0.01995830	A_07_P000264	b3107	cmr|orf, hypothetical protein [b3107]
yhbU	+2.47	10.87	+1.31	10.22	0.2	11.52	0.0	0.00092482	0.00753640	A_07_P000511	b3158	cmr|putative collagenase [b3158]
yhbV	+2.02	9.32	+1.02	8.81	0.1	9.83	0.1	0.00159836	0.01119918	A_07_P000516	b3159	cmr|orf, hypothetical protein [b3159]
yhcB	+5.32	12.80	+2.41	11.60	0.0	14.01	0.1	0.00001863	0.00061218	A_07_P012640	b3233	cmr|orf, hypothetical protein [b3233]
yhcH	+3.92	8.04	+1.97	7.06	0.0	9.03	0.1	0.00005802	0.00111391	A_07_P034165	c_3975	cmr|Hypothetical protein yhcH [c_3975]
yhcH	+3.16	8.14	+1.66	7.31	0.3	8.97	0.1	0.00063371	0.00570950	A_07_P045957	Z4579	cmr|orf, hypothetical protein [Z4579]
yhcI	+3.06	7.82	+1.61	7.02	0.2	8.63	0.1	0.00085527	0.00712456	A_07_P051815	Z4580	cmr|putative NAGC-like transcriptional regulator [Z4580]
yhcJ	+5.35	8.59	+2.42	7.38	0.2	9.80	0.1	0.00007107	0.00125539	A_07_P041791	c_3977	cmr|Hypothetical protein yhcJ [c_3977]
yhcJ	+4.94	8.37	+2.31	7.22	0.1	9.53	0.2	0.00005190	0.00104364	A_07_P041304	c_3977	cmr|Hypothetical protein yhcJ [c_3977]
yhcK	-2.07	9.70	-1.05	10.22	0.0	9.17	0.0	0.00094158	0.00760999	A_07_P034168	c_3980	cmr|Hypothetical transcriptional regulator yhcK [c_3980]
yhcO	-2.26	8.25	-1.18	8.84	0.1	7.66	0.1	0.00107398	0.00835826	A_07_P012666	b3239	cmr|orf, hypothetical protein [b3239]
yhcR	-2.90	7.64	-1.54	8.41	0.1	6.87	0.2	0.00053221	0.00505894	A_07_P035544	c_3997	cmr|Hypothetical protein yhcR [c_3997]
yhcR	-3.73	8.32	-1.90	9.27	0.0	7.38	0.1	0.00006897	0.00123392	A_07_P048607	Z4601	cmr|orf, hypothetical protein [Z4601]
yhdE	+2.45	9.14	+1.29	8.49	0.2	9.79	0.1	0.00131411	0.00970876	A_07_P012715	b3248	cmr|orf, hypothetical protein [b3248]
yhdH	+7.24	9.96	+2.86	8.53	0.3	11.39	0.2	0.00007430	0.00129689	A_07_P034191	c_4009	cmr|Protein yhdH [c_4009]
yhdH	+4.97	8.61	+2.31	7.45	0.2	9.76	0.1	0.00008593	0.00143251	A_07_P012736	b3253	cmr|putative dehydrogenase [b3253]
yhdZ	+3.51	8.30	+1.81	7.39	0.1	9.20	0.1	0.00015036	0.00208675	A_07_P012823	b3271	cmr|putative ATP-binding component of a transport system [b3271]
yheF	-3.87	8.07	-1.95	9.04	0.1	7.09	0.1	0.00008903	0.00145399	A_07_P034326	c_4096	cmr|Probable general secretion pathway protein D precursor [c_4096]
yheO	-2.15	10.52	-1.11	11.08	0.0	9.97	0.0	0.00071141	0.00619497	A_07_P017760	b3346	cmr|orf, hypothetical protein [b3346]
yheS	-2.86	11.02	-1.52	11.78	0.0	10.27	0.0	0.00016158	0.00219117	A_07_P017786	b3352	cmr|putative ATP-binding component of a transport system [b3352]
yhfC	-3.95	8.50	-1.98	9.49	0.0	7.51	0.2	0.00020908	0.00262336	A_07_P041829	c_4139	cmr|Hypothetical protein yhfC [c_4139]
yhfS	-2.05	11.10	-1.03	11.61	0.0	10.58	0.0	0.00095526	0.00768114	A_07_P017907	b3376	cmr|orf, hypothetical protein [b3376]
yhfS	-2.53	8.28	-1.34	8.95	0.2	7.61	0.1	0.00149684	0.01068764	A_07_P034375	c_4146	cmr|Hypothetical protein yhfS [c_4146]
yhfU	-2.18	8.98	-1.13	9.54	0.2	8.42	0.0	0.00274830	0.01674509	A_07_P017919	b3378	cmr|orf, hypothetical protein [b3378]
yhfZ	+2.22	8.21	+1.15	7.63	0.0	8.78	0.2	0.00147284	0.01053537	A_07_P017944	b3383	cmr|orf, hypothetical protein [b3383]
yhgF	+2.06	10.02	+1.04	9.50	0.0	10.54	0.0	0.00098488	0.00783521	A_07_P018065	b3407	cmr|orf, hypothetical protein [b3407]
yhgH	+3.18	11.93	+1.67	11.09	0.0	12.76	0.0	0.00009961	0.00156674	A_07_P041315	c_4190	cmr|Hypothetical protein yhgH [c_4190]
yhhM	+2.24	7.61	+1.16	7.03	0.2	8.19	0.1	0.00231987	0.01473934	A_07_P007271	b3467	cmr|putative receptor [b3467]
yhhM	+2.04	7.72	+1.03	7.20	0.3	8.23	0.1	0.00601140	0.03031503	A_07_P007271	b3467	cmr|putative receptor [b3467]
yhhM	+2.11	7.86	+1.08	7.32	0.0	8.40	0.1	0.00139740	0.01009668	A_07_P007271	b3467	cmr|putative receptor [b3467]
yhhS	-2.22	8.33	-1.15	8.90	0.1	7.75	0.0	0.00102654	0.00807690	A_07_P007303	b3473	cmr|putative transport [b3473]
yhhW	+2.29	9.00	+1.20	8.40	0.0	9.60	0.0	0.00046068	0.00457021	A_07_P018221	b3439	cmr|orf, hypothetical protein [b3439]
yhiD	-3.37	14.27	-1.75	15.14	0.0	13.39	0.0	0.00008170	0.00138058	A_07_P007475	b3508	cmr|putative transport ATPase [b3508]
yhiN	-3.30	10.90	-1.72	11.76	0.1	10.04	0.1	0.00014561	0.00203595	A_07_P007396	b3492	cmr|orf, hypothetical protein [b3492]
yhiQ	-2.25	8.06	-1.17	8.65	0.1	7.47	0.1	0.00079704	0.00676475	A_07_P007422	b3497	cmr|orf, hypothetical protein [b3497]
yhiR	-3.89	12.59	-1.96	13.57	0.0	11.61	0.0	0.00004921	0.00100666	A_07_P007435	b3499	cmr|orf, hypothetical protein [b3499]
yhiW	-2.32	8.78	-1.21	9.39	0.0	8.17	0.1	0.00097613	0.00778927	A_07_P039549	c_4326	cmr|Hypothetical transcriptional regulator yhiW [c_4326]
yhjJ	-2.70	9.22	-1.43	9.93	0.0	8.50	0.0	0.00020640	0.00260387	A_07_P049426	Z4941	cmr|orf, hypothetical protein [Z4941]
yhjJ	-2.52	9.99	-1.33	10.65	0.0	9.32	0.1	0.00047572	0.00466588	A_07_P039556	c_4339	cmr|Protein yhjJ precursor [c_4339]
yhjQ	-4.30	8.80	-2.10	9.85	0.1	7.74	0.2	0.00017446	0.00230819	A_07_P007604	b3534	cmr|orf, hypothetical protein [b3534]
yhjR	-2.71	8.66	-1.44	9.38	0.0	7.94	0.2	0.00065454	0.00584189	A_07_P007606	b3535	cmr|orf, hypothetical protein [b3535]
yiaC	-2.17	10.24	-1.12	10.80	0.1	9.68	0.2	0.00216106	0.01398425	A_07_P007676	b3550	cmr|orf, hypothetical protein [b3550]
yiaC	-2.30	9.43	-1.20	10.03	0.1	8.83	0.0	0.00097039	0.00775788	A_07_P039621	c_4368	cmr|Hypothetical acetyltransferase yiaC [c_4368]

yiaF	+2.17	10.20	+1.12	9.65	0.0	10.76	0.0	0.00069576	0.00609231	A_07_P007698	b3554	cmr|orf, hypothetical protein [b3554]
yiaK	+2.78	8.43	+1.48	7.69	0.0	9.16	0.1	0.00028150	0.00323262	A_07_P007803	b3575	cmr|putative dehydrogenase [b3575]
yibF	+3.07	8.30	+1.62	7.49	0.0	9.11	0.1	0.00019354	0.00248131	A_07_P016905	b3592	cmr|putative S-transferase [b3592]
yibK	+2.85	9.60	+1.51	8.85	0.0	10.36	0.0	0.00015908	0.00217908	A_07_P016974	b3606	cmr|orf, hypothetical protein [b3606]
yidC	-2.50	12.63	-1.32	13.29	0.1	11.97	0.0	0.00039168	0.00405638	A_07_P005451	b3705	cmr|60 KD inner-membrane protein [b3705]
yidD	-2.73	13.42	-1.45	14.15	0.1	12.70	0.0	0.00021108	0.00263544	A_07_P021528	ABE-0285078	asap|predicted protein [b4557]
yidF	+2.73	8.79	+1.45	8.07	0.0	9.51	0.2	0.00072381	0.00627400	A_07_P017305	b3674	cmr|putative transcriptional regulator [b3674]
yidS	-3.59	8.11	-1.84	9.04	0.0	7.19	0.1	0.00010721	0.00164539	A_07_P039007	c_4611	cmr|Hypothetical protein yidS precursor [c_4611]
yidS	-4.17	7.71	-2.06	8.74	0.1	6.68	0.1	0.00006769	0.00122079	A_07_P051822	Z5186	cmr|orf, hypothetical protein [Z5186]
yieF	+2.00	11.21	+1.00	10.71	0.2	11.71	0.1	0.00313039	0.01852121	A_07_P005486	b3713	cmr|orf, hypothetical protein [b3713]
yieG	-2.01	8.45	-1.01	8.96	0.1	7.95	0.1	0.00226920	0.01451717	A_07_P005491	b3714	cmr|putative membrane / transport protein [b3714]
yieN	-2.39	10.48	-1.25	11.10	0.1	9.85	0.1	0.00068457	0.00602118	A_07_P041346	c_4674	cmr|Hypothetical protein yieN [c_4674]
yifE	+5.06	9.75	+2.34	8.58	0.2	10.92	0.0	0.00005218	0.00104650	A_07_P005711	b3764	cmr|orf, hypothetical protein [b3764]
yifK	+3.68	8.69	+1.88	7.75	0.2	9.63	0.0	0.00017860	0.00234911	A_07_P041930	c_4717	cmr|Probable transport protein yifK [c_4717]
yifL	+2.99	10.00	+1.58	9.20	0.0	10.79	0.0	0.00012138	0.00178598	A_07_P010621	ABE-0285079	asap|predicted lipoprotein [b4558]
yigI	-2.57	10.35	-1.36	11.04	0.1	9.67	0.1	0.00037688	0.00396055	A_07_P005970	b3820	cmr|orf, hypothetical protein [b3820]
yigM	-2.61	8.10	-1.38	8.79	0.1	7.41	0.1	0.00057750	0.00535466	A_07_P018941	b3827	cmr|orf, hypothetical protein [b3827]
yigP	-3.41	12.92	-1.77	13.81	0.0	12.04	0.0	0.00007244	0.00126998	A_07_P018976	b3834	cmr|orf, hypothetical protein [b3834]
yigZ	-2.07	10.56	-1.05	11.09	0.1	10.04	0.0	0.00176800	0.01210758	A_07_P041354	c_4795	cmr|Hypothetical protein yigZ [c_4795]
yihA	+4.13	9.60	+2.04	8.58	0.3	10.62	0.0	0.00046163	0.00457676	A_07_P047013	Z5400	cmr|orf, hypothetical protein [Z5400]
yihA	+3.13	10.33	+1.65	9.50	0.0	11.15	0.0	0.00010902	0.00166313	A_07_P019103	b3865	cmr|orf, hypothetical protein [b3865]
yihA	+4.69	9.94	+2.23	8.83	0.1	11.06	0.0	0.00004444	0.00094837	A_07_P039310	c_4812	cmr|Probable GTP-binding protein engB [c_4812]
yihD	+36.56	10.04	+5.19	7.44	0.3	12.63	0.0	0.00000408	0.00032474	A_07_P019075	b3858	cmr|orf, hypothetical protein [b3858]
yihI	+7.26	8.73	+2.86	7.30	0.1	10.16	0.2	0.00001919	0.00061714	A_07_P019108	b3866	cmr|orf, hypothetical protein [b3866]
yihX	+3.21	9.91	+1.68	9.06	0.1	10.75	0.1	0.00014145	0.00199367	A_07_P019205	b3885	cmr|putative phosphatase [b3885]
yiiD	+2.48	8.56	+1.31	7.91	0.2	9.22	0.1	0.00082862	0.00696146	A_07_P019216	b3888	cmr|putative acetyltransferase [b3888]
yiiD	+2.78	9.20	+1.48	8.46	0.3	9.93	0.1	0.00179341	0.01223375	A_07_P041956	c_4835	cmr|Hypothetical protein yiiD [c_4835]
yiiE	-10.17	8.93	-3.35	10.61	0.1	7.26	0.0	0.00000419	0.00032993	A_07_P019225	b3889	cmr|orf, hypothetical protein [b3889]
yiiQ	+3.55	8.39	+1.83	7.48	0.1	9.31	0.0	0.00009234	0.00148959	A_07_P019377	b3920	cmr|orf, hypothetical protein [b3920]
yiiS	+3.49	8.56	+1.80	7.65	0.1	9.46	0.1	0.00016625	0.00223475	A_07_P039426	c_4874	cmr|Hypothetical protein yiiS [c_4874]
yiiS	+3.87	8.08	+1.95	7.11	0.0	9.06	0.1	0.00005853	0.00112095	A_07_P019386	b3922	cmr|orf, hypothetical protein [b3922]
yiiS	+2.50	8.34	+1.32	7.68	0.3	9.00	0.1	0.00222932	0.01433372	A_07_P047106	Z5467	cmr|orf, hypothetical protein [Z5467]
yiiT	+2.64	9.62	+1.40	8.92	0.1	10.32	0.0	0.00032001	0.00353373	A_07_P047111	Z5468	cmr|putative regulator [Z5468]
yiiT	+2.21	9.54	+1.14	8.97	0.0	10.11	0.0	0.00059469	0.00547004	A_07_P039431	c_4875	cmr|Hypothetical protein yiiT [c_4875]
yiiU	+2.86	12.60	+1.51	11.84	0.1	13.35	0.0	0.00026306	0.00309077	A_07_P019420	b3928	cmr|orf, hypothetical protein [b3928]
yiiX	-2.76	9.64	-1.46	10.37	0.1	8.90	0.1	0.00028637	0.00327425	A_07_P052282	Z5492	cmr|orf, hypothetical protein [Z5492]
yiiX	-3.38	8.91	-1.76	9.79	0.0	8.03	0.1	0.00013007	0.00186501	A_07_P041984	c_4890	cmr|Hypothetical protein yiiX precursor [c_4890]
yiiX	-2.32	7.83	-1.21	8.44	0.0	7.22	0.2	0.00128861	0.00956524	A_07_P019465	b3937	cmr|orf, hypothetical protein [b3937]
yijF	-3.16	12.98	-1.66	13.81	0.2	12.15	0.4	0.00329507	0.01928715	A_07_P039476	c_4902	cmr|Hypothetical protein yijF precursor [c_4902]
yjaA	-3.81	10.09	-1.93	11.06	0.1	9.13	0.1	0.00012470	0.00181953	A_07_P008699	b4011	cmr|orf, hypothetical protein [b4011]
yjaB	-2.42	12.79	-1.27	13.43	0.1	12.15	0.2	0.00151648	0.01080827	A_07_P008704	b4012	cmr|orf, hypothetical protein [b4012]
yjaG	+4.98	10.37	+2.32	9.21	0.1	11.53	0.0	0.00002794	0.00073943	A_07_P008660	b3999	cmr|orf, hypothetical protein [b3999]
yjbG	-2.02	11.77	-1.01	12.28	0.1	11.26	0.1	0.00156677	0.01104171	A_07_P008783	b4028	cmr|orf, hypothetical protein [b4028]
yjbJ	-2.20	9.81	-1.14	10.38	0.0	9.24	0.1	0.00117309	0.00894178	A_07_P008870	b4045	cmr|orf, hypothetical protein [b4045]
yjbJ	-4.04	10.98	-2.02	11.99	0.1	9.97	0.0	0.00004241	0.00093353	A_07_P037555	c_5016	cmr|Protein yjbJ [c_5016]
yjbQ	+4.79	9.19	+2.26	8.06	0.2	10.32	0.0	0.00009557	0.00152759	A_07_P008923	b4056	cmr|orf, hypothetical protein [b4056]
yjcB	-13.30	9.80	-3.73	11.66	0.1	7.93	0.2	0.00001168	0.00050224	A_07_P008942	b4060	cmr|orf, hypothetical protein [b4060]
yjcB	-12.34	9.56	-3.63	11.37	0.1	7.75	0.1	0.00000544	0.00034972	A_07_P035567	c_5050	cmr|Hypothetical protein yjcB [c_5050]
yjcC	-2.74	8.07	-1.45	8.79	0.1	7.34	0.0	0.00025579	0.00303705	A_07_P052319	Z5660	cmr|orf, hypothetical protein [Z5660]
yjcC	-2.33	7.74	-1.22	8.35	0.1	7.13	0.1	0.00090055	0.00739560	A_07_P041382	c_5052	cmr|Hypothetical protein yjcC [c_5052]
yjcD	+2.58	8.75	+1.37	8.07	0.1	9.43	0.2	0.00079143	0.00672076	A_07_P008961	b4064	cmr|orf, hypothetical protein [b4064]
yjcH	+2.60	9.23	+1.38	8.54	0.1	9.92	0.0	0.00037383	0.00394212	A_07_P037683	c_5063	cmr|Hypothetical protein yjcH [c_5063]
yjcH	+2.16	9.42	+1.11	8.87	0.0	9.98	0.3	0.00377461	0.02130779	A_07_P037683	c_5063	cmr|Hypothetical protein yjcH [c_5063]
yjcH	+2.16	9.30	+1.11	8.74	0.1	9.85	0.1	0.00110963	0.00858747	A_07_P037683	c_5063	cmr|Hypothetical protein yjcH [c_5063]
yjcH	+2.17	9.32	+1.12	8.76	0.0	9.88	0.2	0.00230366	0.01467505	A_07_P037683	c_5063	cmr|Hypothetical protein yjcH [c_5063]
yjcO	-2.21	9.46	-1.14	10.03	0.0	8.89	0.1	0.00070995	0.00619249	A_07_P009034	b4078	cmr|orf, hypothetical protein [b4078]
yjcO	-2.49	9.73	-1.31	10.39	0.1	9.08	0.0	0.00037118	0.00392997	A_07_P009034	b4078	cmr|orf, hypothetical protein [b4078]
yjcO	-2.25	9.66	-1.17	10.25	0.0	9.08	0.0	0.00056055	0.00525943	A_07_P009034	b4078	cmr|orf, hypothetical protein [b4078]
yjcO	-2.02	9.58	-1.01	10.09	0.0	9.07	0.0	0.00104906	0.00821710	A_07_P009034	b4078	cmr|orf, hypothetical protein [b4078]
yjdB	+2.52	7.67	+1.33	7.01	0.2	8.34	0.1	0.00164164	0.01141493	A_07_P037782	c_5119	cmr|Hypothetical protein yjdB [c_5119]
yjdC	+4.08	9.05	+2.03	8.04	0.0	10.07	0.0	0.00003564	0.00084367	A_07_P011409	b4135	cmr|orf, hypothetical protein [b4135]
yjdJ	+2.10	8.26	+1.07	7.73	0.0	8.80	0.2	0.00315582	0.01864361	A_07_P047348	Z5729	cmr|orf, hypothetical protein [Z5729]
yjdM	+2.28	8.31	+1.19	7.71	0.2	8.90	0.0	0.00180750	0.01227664	A_07_P011276	b4108	cmr|orf, hypothetical protein [b4108]
yjdN	-2.79	8.66	-1.48	9.40	0.1	7.92	0.0	0.00025252	0.00300958	A_07_P011271	b4107	cmr|orf, hypothetical protein [b4107]
yjeI	+4.45	11.34	+2.15	10.27	0.0	12.42	0.0	0.00003207	0.00079793	A_07_P011455	b4144	cmr|orf, hypothetical protein [b4144]
yjeK	-2.23	8.85	-1.16	9.43	0.1	8.27	0.0	0.00061132	0.00556489	A_07_P011461	b4146	cmr|orf, hypothetical protein [b4146]
yjeS	-11.64	9.73	-3.54	11.50	0.0	7.96	0.1	0.00000480	0.00034614	A_07_P011550	b4166	cmr|orf, hypothetical protein [b4166]
yjfC	-2.12	7.50	-1.08	8.04	0.3	6.96	0.1	0.00523484	0.02727243	A_07_P011646	b4186	cmr|putative synthetase/amidase [b4186]
yjfN	+10.76	10.57	+3.43	8.85	0.0	12.28	0.0	0.00000296	0.00028496	A_07_P011660	b4188	cmr|orf, hypothetical protein [b4188]
yjfO	+11.70	12.32	+3.55	10.55	0.1	14.09	0.1	0.00000756	0.00040630	A_07_P035589	c_5277	cmr|Hypothetical lipoprotein yjfO precursor [c_5277]
yjfO	+10.24	10.53	+3.36	8.85	0.1	12.21	0.1	0.00000678	0.00038477	A_07_P011661	b4189	cmr|orf, hypothetical protein [b4189]
yjfO	+12.08	11.13	+3.59	9.33	0.1	12.92	0.0	0.00000294	0.00028496	A_07_P010658	b4189	cmr|orf, hypothetical protein [b4189]
yjfO	+10.13	10.77	+3.34	9.10	0.2	12.44	0.0	0.00001112	0.00048491	A_07_P048630	Z5796	cmr|orf, hypothetical protein [Z5796]
yjgA	-6.08	12.65	-2.60	13.96	0.0	11.35	0.1	0.00001171	0.00050224	A_07_P037054	c_5332	cmr|Hypothetical protein yjgA [c_5332]
yjgA	-5.05	12.54	-2.34	13.71	0.0	11.37	0.1	0.00002087	0.00063998	A_07_P003722	b4234	cmr|putative alpha helix protein [b4234]
yjgF	+35.40	11.26	+5.15	8.68	0.2	13.83	0.0	0.00000115	0.00021042	A_07_P037066	c_5342	cmr|Protein yjgF [c_5342]
yjgF	+22.20	9.99	+4.47	7.75	0.1	12.22	0.0	0.00000085	0.00019431	A_07_P003767	b4243	cmr|orf, hypothetical protein [b4243]
yjgP	-3.15	10.39	-1.66	11.22	0.1	9.56	0.1	0.00015184	0.00209697	A_07_P003851	b4261	cmr|orf, hypothetical protein [b4261]
yjgQ	-3.50	11.24	-1.81	12.15	0.0	10.34	0.0	0.00007407	0.00129569	A_07_P003856	b4262	cmr|orf, hypothetical protein [b4262]
yjgR	+5.66	8.99	+2.50	7.74	0.0	10.24	0.0	0.00001403	0.00053879	A_07_P037116	c_5364	cmr|Hypothetical protein yjgR [c_5364]
yjhD	-3.03	9.13	-1.60	9.93	0.3	8.33	0.4	0.00694566	0.03380291	A_07_P003936	b4281	cmr|orf, hypothetical protein [b4281]
yjhQ	+13.87	9.32	+3.79	7.42	0.1	11.22	0.1	0.00000257	0.00027706	A_07_P004061	b4307	cmr|orf, hypothetical protein [b4307]
yjhQ	+11.99	9.42	+3.58	7.63	0.4	11.21	0.0	0.00006636	0.00120815	A_07_P004061	b4307	cmr|orf, hypothetical protein [b4307]
yjhQ	+13.90	9.48	+3.80	7.58	0.2	11.38	0.0	0.00000856	0.00042498	A_07_P004061	b4307	cmr|orf, hypothetical protein [b4307]
yjhQ	+9.51	9.54	+3.25	7.92	0.3	11.17	0.0	0.00003209	0.00079793	A_07_P004061	b4307	cmr|orf, hypothetical protein [b4307]
yjhQ	+10.74	9.62	+3.42	7.91	0.1	11.33	0.0	0.00000334	0.00029719	A_07_P004061	b4307	cmr|orf, hypothetical protein [b4307]
yjhR	-2.64	11.85	-1.40	12.55	0.1	11.15	0.4	0.00344659	0.01992771	A_07_P004068	b4308	cmr|putative frameshift suppressor [b4308]
yjhU	-2.27	9.78	-1.18	10.37	0.1	9.19	0.1	0.00076303	0.00653952	A_07_P004004	b4295	cmr|orf, hypothetical protein [b4295]
yjhX	+9.93	10.36	+3.31	8.71	0.0	12.02	0.0	0.00000315	0.00029018	A_07_P010688	ABE-0285087	asap|conserved protein [b4566]
yjiG	+5.12	8.63	+2.36	7.45	0.0	9.81	0.1	0.00002539	0.00071770	A_07_P004174	b4329	cmr|orf, hypothetical protein [b4329]
yjiH	+3.12	7.81	+1.64	6.99	0.1	8.63	0.0	0.00016515	0.00222615	A_07_P004179	b4330	cmr|orf, hypothetical protein [b4330]
yjiL	+2.24	9.18	+1.16	8.60	0.2	9.76	0.3	0.00788191	0.03742245	A_07_P004196	b4334	cmr|putative enzyme [b4334]
yjiM	+5.00	8.80	+2.32	7.64	0.1	9.96	0.0	0.00003498	0.00083975	A_07_P004201	b4335	cmr|orf, hypothetical protein [b4335]
yjiX	+3.11	9.47	+1.64	8.66	0.1	10.29	0.0	0.00016636	0.00223475	A_07_P017462	b4353	cmr|orf, hypothetical protein [b4353]
yjjI	+4.53	10.60	+2.18	9.51	0.0	11.69	0.0	0.00002727	0.00073404	A_07_P017585	b4380	cmr|orf, hypothetical protein [b4380]
yjjK	+4.70	10.15	+2.23	9.03	0.1	11.26	0.0	0.00003527	0.00084015	A_07_P017637	b4391	cmr|putative ATP-binding component of a transport system [b4391]
yjjK	+4.48	10.11	+2.16	9.03	0.0	11.19	0.1	0.00003510	0.00083975	A_07_P017637	b4391	cmr|putative ATP-binding component of a transport system [b4391]
yjjK	+4.23	9.96	+2.08	8.92	0.0	11.00	0.1	0.00004397	0.00094686	A_07_P017637	b4391	cmr|putative ATP-binding component of a transport system [b4391]
yjjK	+4.28	10.12	+2.10	9.07	0.0	11.17	0.0	0.00003223	0.00079793	A_07_P017637	b4391	cmr|putative ATP-binding component of a transport system [b4391]
yjjK	+4.52	10.20	+2.18	9.11	0.0	11.29	0.0	0.00002582	0.00072358	A_07_P017637	b4391	cmr|putative ATP-binding component of a transport system [b4391]
yjjN	-2.32	7.47	-1.22	8.08	0.0	6.86	0.1	0.00089564	0.00737883	A_07_P017488	b4358	cmr|putative oxidoreductase [b4358]
yjjN	-2.38	7.58	-1.25	8.21	0.0	6.96	0.0	0.00041590	0.00423720	A_07_P017488	b4358	cmr|putative oxidoreductase [b4358]
yjjQ	-2.31	7.29	-1.21	7.89	0.2	6.68	0.0	0.00097819	0.00779781	A_07_P042086	c_5444	cmr|Hypothetical protein yjjQ [c_5444]
yjjQ	-3.05	7.48	-1.61	8.29	0.0	6.68	0.2	0.00060030	0.00549480	A_07_P017521	b4365	cmr|putative regulator [b4365]
ykfJ	-10.25	11.42	-3.36	13.10	0.0	9.74	0.0	0.00000350	0.00030339	A_07_P007889	b0235	cmr|orf, hypothetical protein [b0235]
ykgE	-2.05	10.89	-1.04	11.41	0.3	10.37	0.0	0.00852239	0.03965027	A_07_P008225	b0306	cmr|putative dehydrogenase subunit [b0306]
ykgJ	-3.75	8.46	-1.91	9.42	0.3	7.51	0.1	0.00077925	0.00664237	A_07_P008131	b0288	cmr|putative ferredoxin [b0288]
ykiA	-2.06	7.65	-1.05	8.17	0.2	7.13	0.0	0.00249534	0.01557755	A_07_P021074	b0392	cmr|orf, hypothetical protein [b0392]
ylaB	-2.32	11.16	-1.21	11.76	0.1	10.55	0.2	0.00146122	0.01047130	A_07_P021391	b0457	cmr|orf, hypothetical protein [b0457]
ylaC	-13.96	11.94	-3.80	13.84	0.0	10.04	0.2	0.00000400	0.00032449	A_07_P021396	b0458	cmr|orf, hypothetical protein [b0458]
yliG	+2.26	9.13	+1.17	8.54	0.1	9.71	0.1	0.00105423	0.00824530	A_07_P004626	b0835	cmr|orf, hypothetical protein [b0835]
yliG	+2.63	10.55	+1.39	9.86	0.0	11.25	0.0	0.00023226	0.00282805	A_07_P042116	c_0920	cmr|Hypothetical protein yliG [c_0920]
ymcE	+6.37	9.65	+2.67	8.31	0.0	10.98	0.0	0.00001009	0.00046432	A_07_P001189	b0991	cmr|suppresses fabA and ts growth mutation [b0991]
ymdF	-2.15	12.54	-1.11	13.09	0.0	11.98	0.0	0.00072574	0.00628152	A_07_P010350	ABE-0285039	asap|conserved protein [b4518]
ymfA	-4.66	8.59	-2.22	9.70	0.0	7.48	0.0	0.00002458	0.00070547	A_07_P040833	c_1397	cmr|Hypothetical protein ymfA [c_1397]
ymfC	-3.22	13.67	-1.69	14.52	0.0	12.83	0.0	0.00008820	0.00145271	A_07_P050485	Z1864	cmr|orf, hypothetical protein [Z1864]
ymgA	+7.02	8.08	+2.81	6.68	0.1	9.49	0.1	0.00001439	0.00054604	A_07_P006777	b1165	cmr|orf, hypothetical protein [b1165]
ymgB	+11.70	10.42	+3.55	8.65	0.2	12.20	0.1	0.00000994	0.00046030	A_07_P038703	c_1609	cmr|Hypothetical protein ymgB [c_1609]
ymgD	-3.12	8.63	-1.64	9.45	0.3	7.81	0.1	0.00103452	0.00811965	A_07_P006807	b1171	cmr|orf, hypothetical protein [b1171]
ymgG	-3.27	12.81	-1.71	13.67	0.0	11.96	0.1	0.00012847	0.00184717	A_07_P006812	b1172	cmr|orf, hypothetical protein [b1172]
ymjA	+2.31	7.96	+1.21	7.36	0.3	8.56	0.1	0.00344180	0.01990730	A_07_P014457	b1295	cmr|orf, hypothetical protein [b1295]
ynaI	-9.22	10.37	-3.20	11.97	0.1	8.77	0.1	0.00000761	0.00040630	A_07_P014632	b1330	cmr|orf, hypothetical protein [b1330]
ynbE	+2.08	7.63	+1.05	7.10	0.0	8.16	0.1	0.00150391	0.01072842	A_07_P034809	c_1829	cmr|Hypothetical protein ynbE [c_1829]
yneG	-2.00	8.08	-1.00	8.58	0.2	7.58	0.0	0.00272833	0.01664824	A_07_P035023	c_1946	cmr|Hypothetical protein yneG [c_1946]
yneH	-2.86	10.25	-1.51	11.00	0.1	9.49	0.1	0.00037056	0.00392997	A_07_P020270	b1524	cmr|putative glutaminase [b1524]
yneI	-2.15	9.54	-1.11	10.09	0.0	8.98	0.0	0.00071789	0.00623756	A_07_P035026	c_1948	cmr|Aldehyde-dehydrogenase like protein yneI [c_1948]
yneJ	+2.26	7.92	+1.17	7.33	0.1	8.50	0.0	0.00090291	0.00739560	A_07_P035034	c_1949	cmr|Hypothetical transcriptional regulator yneJ [c_1949]
ynfB	-4.43	14.07	-2.15	15.14	0.0	13.00	0.1	0.00003346	0.00081556	A_07_P020550	b1583	cmr|orf, hypothetical protein [b1583]
ynfE	+2.76	7.61	+1.46	6.88	0.3	8.34	0.0	0.00191603	0.01278216	A_07_P020568	b1587	cmr|putative oxidoreductase, major subunit [b1587]
ynfE	+4.20	8.29	+2.07	7.25	0.0	9.32	0.1	0.00004287	0.00093353	A_07_P042301	c_1977	cmr|Putative dimethyl sulfoxide reductase chain ynfE precursor [c_1977]
ynfF	+2.15	9.09	+1.10	8.54	0.3	9.64	0.1	0.00551450	0.02841910	A_07_P020575	b1588	cmr|putative oxidoreductase, major subunit [b1588]
ynfG	+5.58	8.56	+2.48	7.32	0.3	9.80	0.1	0.00012522	0.00182539	A_07_P020576	b1589	cmr|putative oxidoreductase, Fe-S subunit [b1589]
ynfM	-2.65	11.79	-1.41	12.49	0.4	11.09	0.0	0.00334249	0.01950487	A_07_P020611	b1596	cmr|putative transport protein [b1596]
yniA	+4.06	8.43	+2.02	7.42	0.0	9.44	0.1	0.00006818	0.00122531	A_07_P018674	b1725	cmr|orf, hypothetical protein [b1725]
ynjB	+2.62	7.80	+1.39	7.10	0.0	8.50	0.1	0.00027775	0.00319869	A_07_P018816	b1754	cmr|orf, hypothetical protein [b1754]
ynjE	+4.32	9.16	+2.11	8.11	0.4	10.22	0.1	0.00059507	0.00547004	A_07_P018832	b1757	cmr|putative thiosulfate sulfur transferase [b1757]
yoaB	+5.31	9.23	+2.41	8.03	0.0	10.44	0.0	0.00001686	0.00058050	A_07_P015736	b1809	cmr|orf, hypothetical protein [b1809]
yobB	+2.93	8.81	+1.55	8.04	0.1	9.59	0.0	0.00016131	0.00218930	A_07_P015892	b1843	cmr|orf, hypothetical protein [b1843]
yobH	-2.47	7.57	-1.31	8.22	0.2	6.92	0.0	0.00100920	0.00798031	A_07_P010464	ABE-0285057	asap|predicted protein [b4536]
yohK	-2.02	7.45	-1.02	7.96	0.0	6.94	0.0	0.00101102	0.00799073	A_07_P003473	b2142	cmr|putative seritonin transporter [b2142]
yohM	-2.06	10.33	-1.04	10.85	0.3	9.81	0.2	0.00833014	0.03892837	A_07_P045159	Z3274	cmr|orf, hypothetical protein [Z3274]
ypfG	-4.66	10.03	-2.22	11.14	0.0	8.92	0.0	0.00002330	0.00068274	A_07_P042601	c_2991	cmr|Hypothetical protein ypfG precursor [c_2991]
ypfG	-2.74	9.78	-1.46	10.51	0.1	9.06	0.1	0.00038817	0.00402870	A_07_P013386	b2466	cmr|orf, hypothetical protein [b2466]
ypfN	-2.22	9.64	-1.15	10.22	0.0	9.06	0.0	0.00056388	0.00527744	A_07_P010535	ABE-0285068	asap|predicted protein [b4547]
yphE	-3.23	12.98	-1.69	13.82	0.0	12.13	0.0	0.00009758	0.00154382	A_07_P019639	b2547	cmr|putative ATP-binding component of a transport system [b2547]
yphF	-2.06	8.01	-1.05	8.53	0.2	7.49	0.0	0.00359956	0.02061632	A_07_P019645	b2548	cmr|putative LACI-type transcriptional regulator [b2548]
yqaA	-2.67	10.08	-1.42	10.79	0.1	9.37	0.0	0.00034465	0.00373190	A_07_P001920	b2689	cmr|orf, hypothetical protein [b2689]
yqaB	-6.55	11.29	-2.71	12.64	0.0	9.93	0.0	0.00000939	0.00044530	A_07_P030582	c_3247	cmr|Hypothetical protein yqaB [c_3247]
yqaB	-4.89	11.00	-2.29	12.15	0.0	9.85	0.1	0.00002355	0.00068545	A_07_P001923	b2690	cmr|putative phosphatase [b2690]
yqcA	+3.73	9.63	+1.90	8.68	0.1	10.58	0.1	0.00009729	0.00154382	A_07_P002396	b2790	cmr|orf, hypothetical protein [b2790]
yqcC	+2.28	8.50	+1.19	7.91	0.1	9.10	0.1	0.00061695	0.00559838	A_07_P002409	b2792	cmr|orf, hypothetical protein [b2792]
yqeB	-2.72	8.51	-1.44	9.24	0.2	7.79	0.1	0.00080747	0.00682752	A_07_P006342	b2875	cmr|putative synthases [b2875]
yqeC	-2.54	8.69	-1.35	9.37	0.2	8.02	0.1	0.00141659	0.01021191	A_07_P006347	b2876	cmr|orf, hypothetical protein [b2876]
yqfA	+2.01	9.43	+1.01	8.93	0.1	9.94	0.0	0.00148444	0.01060874	A_07_P006461	b2899	cmr|putative oxidoreductase [b2899]
yqfB	+2.04	7.54	+1.03	7.03	0.1	8.06	0.2	0.00473002	0.02520968	A_07_P045648	Z4238	cmr|orf, hypothetical protein [Z4238]
yqfB	+2.12	7.49	+1.09	6.95	0.1	8.04	0.2	0.00255272	0.01584154	A_07_P045648	Z4238	cmr|orf, hypothetical protein [Z4238]
yqfB	+2.81	10.18	+1.49	9.43	0.1	10.92	0.1	0.00028717	0.00327619	A_07_P006468	b2900	cmr|orf, hypothetical protein [b2900]
yqfB	+2.08	7.81	+1.06	7.28	0.1	8.34	0.2	0.00334497	0.01951211	A_07_P045648	Z4238	cmr|orf, hypothetical protein [Z4238]
yqfB	+2.22	7.76	+1.15	7.19	0.1	8.34	0.2	0.00262711	0.01620104	A_07_P045648	Z4238	cmr|orf, hypothetical protein [Z4238]
yqfB	+2.72	10.50	+1.45	9.78	0.1	11.22	0.0	0.00023330	0.00283859	A_07_P032874	c_3481	cmr|Hypothetical protein yqfB [c_3481]
yqfE	-2.42	12.69	-1.27	13.33	0.2	12.05	0.0	0.00091762	0.00749052	A_07_P006538	b2915	cmr|orf, hypothetical protein [b2915]
yqgE	+2.86	10.52	+1.52	9.76	0.1	11.28	0.1	0.00048238	0.00470257	A_07_P011885	b2948	cmr|orf, hypothetical protein [b2948]
yqhA	-2.81	8.99	-1.49	9.74	0.0	8.25	0.0	0.00016060	0.00218551	A_07_P012144	b3002	cmr|orf, hypothetical protein [b3002]
yqhD	+2.81	10.37	+1.49	9.63	0.2	11.12	0.0	0.00045824	0.00455748	A_07_P012186	b3011	cmr|putative oxidoreductase [b3011]
yqjA	-9.14	11.24	-3.19	12.84	0.0	9.65	0.0	0.00000408	0.00032474	A_07_P000202	b3095	cmr|orf, hypothetical protein [b3095]
yqjA	-11.45	10.81	-3.52	12.57	0.0	9.05	0.1	0.00000264	0.00027706	A_07_P041768	c_3853	cmr|Hypothetical protein yqjA [c_3853]
yqjB	-4.07	10.37	-2.03	11.39	0.1	9.36	0.1	0.00008827	0.00145271	A_07_P000206	b3096	cmr|orf, hypothetical protein [b3096]
yqjC	+3.87	10.59	+1.95	9.62	0.1	11.57	0.0	0.00005335	0.00106045	A_07_P000212	b3097	cmr|orf, hypothetical protein [b3097]
yqjI	+5.47	11.64	+2.45	10.42	0.1	12.87	0.0	0.00001734	0.00058395	A_07_P000083	b3071	cmr|orf, hypothetical protein [b3071]
yraP	+4.02	10.23	+2.01	9.23	0.0	11.24	0.0	0.00004282	0.00093353	A_07_P000475	b3150	cmr|putative periplasmic protein [b3150]
yrbA	+3.30	10.39	+1.72	9.53	0.1	11.25	0.0	0.00011328	0.00169854	A_07_P012426	b3190	cmr|orf, hypothetical protein [b3190]
yrbB	+2.07	8.65	+1.05	8.13	0.2	9.18	0.1	0.00350282	0.02015319	A_07_P035537	c_3950	cmr|Hypothetical protein yrbB [c_3950]
yrbE	-3.86	10.98	-1.95	11.95	0.1	10.00	0.0	0.00005103	0.00103301	A_07_P012449	b3194	cmr|orf, hypothetical protein [b3194]
yrbF	-2.58	11.04	-1.37	11.73	0.2	10.36	0.2	0.00122328	0.00918860	A_07_P012451	b3195	cmr|putative ATP-binding component of a transport system [b3195]
yrbK	+2.51	12.47	+1.33	11.81	0.0	13.13	0.0	0.00031071	0.00345228	A_07_P012474	b3199	cmr|orf, hypothetical protein [b3199]
yrbL	+4.28	9.65	+2.10	8.61	0.3	10.70	0.0	0.00024195	0.00291652	A_07_P052110	Z4570	cmr|orf, hypothetical protein [Z4570]
yrbL	+4.59	10.35	+2.20	9.25	0.0	11.45	0.0	0.00002514	0.00071646	A_07_P012512	b3207	cmr|orf, hypothetical protein [b3207]
yrdD	+2.28	8.98	+1.19	8.38	0.0	9.57	0.1	0.00063065	0.00568996	A_07_P012850	b3283	cmr|putative DNA topoisomerase [b3283]
yrfF	-4.46	9.51	-2.16	10.59	0.0	8.43	0.2	0.00012662	0.00183570	A_07_P034400	c_4169	cmr|Putative membrane protein igaA homolog [c_4169]
yrfF	-3.06	8.95	-1.61	9.76	0.0	8.14	0.2	0.00037942	0.00397175	A_07_P018019	b3398	cmr|putative dehydrogenase [b3398]
ysaA	-2.28	8.54	-1.19	9.13	0.0	7.94	0.0	0.00047049	0.00463832	A_07_P007793	b3573	cmr|orf, hypothetical protein [b3573]
ytfE	+2.10	7.77	+1.07	7.23	0.0	8.30	0.1	0.00093975	0.00760301	A_07_P037039	c_5308	cmr|Hypothetical protein ytfE [c_5308]
ytfH	-3.16	10.44	-1.66	11.27	0.2	9.61	0.1	0.00039984	0.00412524	A_07_P003611	b4212	cmr|orf, hypothetical protein [b4212]
ytfH	-2.74	10.21	-1.45	10.94	0.0	9.49	0.1	0.00026556	0.00309930	A_07_P035591	c_5311	cmr|Hypothetical protein ytfH [c_5311]
ytfL	-2.01	9.08	-1.00	9.59	0.1	8.58	0.2	0.00338833	0.01968112	A_07_P003641	b4218	cmr|putative transport protein [b4218]
ytfQ	+2.39	8.95	+1.26	8.32	0.2	9.58	0.1	0.00157667	0.01109658	A_07_P037048	c_5325	cmr|ABC transporter Periplasmic binding protein ytfQ precursor [c_5325]
Z0024	-2.23	8.25	-1.16	8.83	0.3	7.67	0.1	0.00489128	0.02592874	A_07_P049126	Z0024	cmr|putative type-1 fimbrial protein [Z0024]
Z0056	-2.35	12.07	-1.24	12.69	0.1	11.45	0.0	0.00047557	0.00466588	A_07_P049148	Z0056	cmr|putative antitoxin of gyrase inhibiting toxin-antitoxin system [Z0056]
Z0202	-2.13	11.19	-1.09	11.74	0.0	10.65	0.0	0.00078870	0.00670479	A_07_P049248	Z0202	cmr|orf Unknown function [Z0202]
Z0309	-4.91	12.42	-2.30	13.56	0.0	11.27	0.0	0.00002030	0.00063193	A_07_P043395	Z0309	cmr|putative cI repressor protein for prophage CP-933H [Z0309]
Z0311	+12.08	13.77	+3.59	11.97	0.0	15.57	0.1	0.00000272	0.00028012	A_07_P043403	Z0311	cmr|partial O replication protein for prophage CP-933H [Z0311]
Z0312	+2.44	14.77	+1.29	14.12	0.0	15.41	0.1	0.00061518	0.00558557	A_07_P043406	Z0312	cmr|partial O replication protein for prophage CP-933H [Z0312]
Z0319	-2.19	9.06	-1.13	9.63	0.2	8.50	0.2	0.00265065	0.01633339	A_07_P043443	Z0319	cmr|unknown protein from prophage CP-933H [Z0319]
Z0370	+3.31	8.43	+1.73	7.56	0.2	9.29	0.0	0.00022281	0.00274273	A_07_P043596	Z0370	cmr|orf Unknown function [Z0370]
Z0395	-2.08	8.81	-1.06	9.34	0.2	8.28	0.1	0.00493578	0.02610312	A_07_P043668	Z0395	cmr|orf Unknown function [Z0395]
Z0666	+2.39	7.44	+1.26	6.81	0.0	8.07	0.1	0.00045361	0.00451997	A_07_P043951	Z0666	cmr|orf Unknown function [Z0666]
Z0949	+19.20	11.20	+4.26	9.07	0.3	13.33	0.4	0.00005135	0.00103783	A_07_P046386	Z0949	cmr|unknown protein encoded by prophage CP-933K [Z0949]
Z0950	+59.01	10.59	+5.88	7.65	0.1	13.53	0.2	0.00000090	0.00019431	A_07_P046393	Z0950	cmr|unknown protein encoded by prophage CP-933K [Z0950]
Z0951	+7.25	13.37	+2.86	11.94	0.1	14.80	0.3	0.00009771	0.00154382	A_07_P046396	Z0951	cmr|putative exonuclease encoded by prophage CP-933K [Z0951]
Z0952	+8.89	13.11	+3.15	11.53	0.1	14.68	0.0	0.00000517	0.00034758	A_07_P046403	Z0952	cmr|putative Bet recombination protein of prophage CP-933K [Z0952]
Z0960	+27.61	10.13	+4.79	7.73	0.1	12.52	0.1	0.00000137	0.00022125	A_07_P046435	Z0960	cmr|putative lysozyme protein R of prophage CP-933K [Z0960]
Z0965	-2.22	9.85	-1.15	10.43	0.1	9.28	0.0	0.00083981	0.00702923	A_07_P046451	Z0965	cmr|unknown protein encoded by prophage CP-933K [Z0965]
Z0966	-2.64	8.22	-1.40	8.92	0.1	7.52	0.1	0.00050848	0.00488792	A_07_P046460	Z0966	cmr|unknown protein encoded by prophage CP-933K [Z0966]
Z0966	-2.93	8.18	-1.55	8.96	0.1	7.40	0.1	0.00027382	0.00316517	A_07_P046460	Z0966	cmr|unknown protein encoded by prophage CP-933K [Z0966]
Z0966	-3.41	8.10	-1.77	8.98	0.0	7.21	0.1	0.00013193	0.00188652	A_07_P046460	Z0966	cmr|unknown protein encoded by prophage CP-933K [Z0966]
Z0966	-2.62	8.07	-1.39	8.77	0.0	7.38	0.2	0.00060146	0.00550224	A_07_P046460	Z0966	cmr|unknown protein encoded by prophage CP-933K [Z0966]
Z0966	-3.30	8.20	-1.72	9.06	0.1	7.34	0.1	0.00012608	0.00183113	A_07_P046460	Z0966	cmr|unknown protein encoded by prophage CP-933K [Z0966]
Z0971	+2.19	7.31	+1.13	6.75	0.0	7.88	0.1	0.00079947	0.00677807	A_07_P046483	Z0971	cmr|putative tail component of prophage CP-933K [Z0971]
Z0974	-2.30	9.81	-1.20	10.41	0.3	9.20	0.0	0.00397875	0.02211190	A_07_P046497	Z0974	cmr|putative tail component of prophage CP-933K [Z0974]
Z0977	+5.33	9.55	+2.41	8.35	0.3	10.76	0.2	0.00039883	0.00412020	A_07_P046512	Z0977	cmr|putative tail component of prophage CP-933K [Z0977]
Z0979	+4.31	8.84	+2.11	7.79	0.0	9.89	0.1	0.00003967	0.00090487	A_07_P046522	Z0979	cmr|putative tail component of prophage CP-933K [Z0979]
Z1046	+2.36	7.36	+1.24	6.74	0.0	7.98	0.0	0.00039155	0.00405638	A_07_P046587	Z1046	cmr|orf Unknown function [Z1046]
Z1051	+2.47	10.18	+1.30	9.53	0.1	10.84	0.1	0.00066107	0.00587078	A_07_P046593	Z1051	cmr|orf Unknown function [Z1051]
Z1058	-2.07	7.29	-1.05	7.81	0.0	6.76	0.0	0.00090235	0.00739560	A_07_P052018	Z1058	cmr|orf, hypothetical protein [Z1058]
Z1098	-2.16	11.48	-1.11	12.03	0.1	10.92	0.0	0.00136054	0.00990669	A_07_P046651	Z1098	cmr|orf Unknown function [Z1098]
Z1120	-2.01	10.97	-1.01	11.47	0.1	10.46	0.0	0.00167783	0.01160625	A_07_P046671	Z1120	cmr|putative P4-family integrase [Z1120]
Z1121	+2.66	8.57	+1.41	7.86	0.3	9.28	0.2	0.00271778	0.01661055	A_07_P046679	Z1121	cmr|orf Unknown function [Z1121]
Z1124	+2.19	6.96	+1.13	6.40	0.1	7.53	0.2	0.00218253	0.01408847	A_07_P046689	Z1124	cmr|putative prophage regulatory protein [Z1124]
Z1129	-2.92	13.40	-1.55	14.17	0.3	12.62	0.1	0.00095945	0.00769519	A_07_P046708	Z1129	cmr|putative helicase [Z1129]
Z1134	-2.36	7.93	-1.24	8.55	0.0	7.31	0.0	0.00042980	0.00434325	A_07_P046735	Z1134	cmr|unknown in IS600 [Z1134]
Z1150	-2.51	8.30	-1.33	8.97	0.2	7.64	0.1	0.00076977	0.00658197	A_07_P046801	Z1150	cmr|unknown in IS [Z1150]
Z1160	-3.11	9.74	-1.64	10.55	0.2	8.92	0.1	0.00045343	0.00451997	A_07_P046840	Z1160	cmr|unknown in ISEc8 [Z1160]
Z1161	-2.44	8.87	-1.29	9.51	0.0	8.22	0.1	0.00066920	0.00592567	A_07_P046841	Z1161	cmr|unknown in ISEc8 [Z1161]
Z1193	-2.09	7.80	-1.06	8.33	0.2	7.26	0.1	0.00553146	0.02846227	A_07_P046975	Z1193	cmr|orf Unknown function [Z1193]
Z1199	-2.52	9.62	-1.33	10.29	0.1	8.96	0.0	0.00045896	0.00456178	A_07_P050887	Z1199	cmr|unknown in IS [Z1199]
Z1203	-2.22	10.65	-1.15	11.23	0.2	10.08	0.1	0.00206209	0.01347675	A_07_P050909	Z1203	cmr|unknown [Z1203]
Z1204	-2.05	8.64	-1.03	9.16	0.0	8.13	0.1	0.00112179	0.00866326	A_07_P050912	Z1204	cmr|unknown [Z1204]
Z1210	-2.51	7.65	-1.33	8.32	0.1	6.99	0.2	0.00165807	0.01150422	A_07_P050942	Z1210	cmr|putative histone [Z1210]
Z1214	+2.68	9.07	+1.42	8.36	0.1	9.78	0.0	0.00026174	0.00308181	A_07_P050956	Z1214	cmr|orf Unknown function [Z1214]
Z1340	-2.42	9.94	-1.28	10.58	0.4	9.30	0.1	0.00894630	0.04122051	A_07_P051102	Z1340	cmr|unknown protein encoded by cryptic prophage CP-933M [Z1340]
Z1352	-3.58	9.17	-1.84	10.09	0.4	8.25	0.1	0.00138701	0.01003542	A_07_P051141	Z1352	cmr|putative endolysin of cryptic prophage CP-933M [Z1352]
Z1373	-2.12	11.11	-1.08	11.65	0.1	10.56	0.1	0.00151862	0.01081374	A_07_P051220	Z1373	cmr|unknown protein encoded by cryptic prophage CP-933M [Z1373]
Z1428	+45.67	10.00	+5.51	7.24	0.1	12.76	0.0	0.00000040	0.00019431	A_07_P048529	Z1428	cmr|unknown protein encoded by bacteriophage BP-933W [Z1428]
Z1429	-2.60	8.44	-1.38	9.13	0.0	7.75	0.1	0.00028377	0.00325162	A_07_P051303	Z1429	cmr|unknown protein encoded by bacteriophage BP-933W [Z1429]
Z1433	+56.21	11.60	+5.81	8.69	0.2	14.50	0.1	0.00000093	0.00019431	A_07_P051325	Z1433	cmr|unknown protein encoded by bacteriophage BP-933W [Z1433]
Z1434	+52.93	10.37	+5.73	7.50	0.3	13.23	0.2	0.00000230	0.00026836	A_07_P051326	Z1434	cmr|unknown protein encoded by bacteriophage BP-933W [Z1434]
Z1444	-3.12	12.66	-1.64	13.48	0.1	11.84	0.1	0.00016403	0.00221677	A_07_P051356	Z1444	cmr|putative serine/threonine kinase encoded by bacteriophage BP-933W [Z1444]
Z1449	+7.12	11.18	+2.83	9.77	0.2	12.60	0.0	0.00002361	0.00068568	A_07_P051385	Z1449	cmr|putative regulatory protein CII of bacteriophage BP-933W [Z1449]
Z1454	+59.98	10.27	+5.91	7.31	0.3	13.22	0.0	0.00000200	0.00025681	A_07_P051405	Z1454	cmr|putative DNA N-6-adenine-methyltransferase of bacteriophage BP-933W [Z1454]
Z1457	-2.83	11.01	-1.50	11.76	0.4	10.26	0.1	0.00326149	0.01913860	A_07_P051411	Z1457	cmr|putative DNA-binding protein Roi of bacteriophage BP-933W [Z1457]
Z1473	+15.20	9.15	+3.93	7.19	0.3	11.11	0.0	0.00001949	0.00062241	A_07_P051457	Z1473	cmr|putative endopeptidase Rz of bacteriophage BP-933W [Z1473]
Z1475	-2.39	9.26	-1.26	9.89	0.3	8.63	0.2	0.00466199	0.02493152	A_07_P051463	Z1475	cmr|putative terminase small subunit of bacteriophage BP-933W [Z1475]
Z1534	-2.12	8.80	-1.08	9.34	0.2	8.26	0.0	0.00260952	0.01613044	A_07_P051615	Z1534	cmr|putative chaperone [Z1534]
Z1660	-3.29	8.43	-1.72	9.29	0.0	7.57	0.1	0.00011484	0.00172031	A_07_P050081	Z1660	cmr|transposase for IS629 [Z1660]
Z1778	-2.09	11.81	-1.07	12.35	0.1	11.28	0.1	0.00105620	0.00825663	A_07_P050169	Z1778	cmr|unknown protein encoded by prophage CP-933N [Z1778]
Z1779	-2.10	7.61	-1.07	8.14	0.1	7.08	0.2	0.00335693	0.01956012	A_07_P050172	Z1779	cmr|unknown protein encoded by prophage CP-933N [Z1779]
Z1781	+21.31	10.13	+4.41	7.93	0.2	12.34	0.1	0.00000248	0.00027471	A_07_P050182	Z1781	cmr|unknown protein encoded by prophage CP-933N [Z1781]
Z1794	-2.67	8.82	-1.42	9.53	0.1	8.12	0.0	0.00026812	0.00311300	A_07_P050226	Z1794	cmr|putative holin protein [Z1794]
Z1805	-2.40	11.53	-1.26	12.16	0.4	10.90	0.3	0.01049221	0.04650600	A_07_P050276	Z1805	cmr|unknown protein encoded by prophage CP-933N [Z1805]
Z1819	+3.82	9.02	+1.93	8.05	0.5	9.99	0.2	0.00337643	0.01962668	A_07_P050332	Z1819	cmr|putative tail component K homolog encoded by [Z1819]
Z1856	-3.22	7.74	-1.69	8.59	0.0	6.90	0.2	0.00040565	0.00416132	A_07_P050473	Z1856	cmr|unknown protein encoded by prophage CP-933C [Z1856]
Z1866	+16.26	8.98	+4.02	6.97	0.1	10.99	0.2	0.00000783	0.00041039	A_07_P050491	Z1866	cmr|putative integrase of prophage CP-933X [Z1866]
Z1867	+104.78	10.92	+6.71	7.57	0.1	14.28	0.0	0.00000011	0.00019431	A_07_P050497	Z1867	cmr|putative integrase of prophage CP-933X [Z1867]
Z1869	+6.17	12.44	+2.63	11.13	0.1	13.76	0.0	0.00001435	0.00054604	A_07_P052425	Z1869	cmr|putative replication protein P of prophage CP-933X [Z1869]
Z1871	-2.16	8.52	-1.11	9.07	0.0	7.96	0.1	0.00094719	0.00763638	A_07_P050509	Z1871	cmr|unknown protein encoded by prophage CP-933X [Z1871]
Z1891	+24.01	10.55	+4.59	8.26	0.1	12.84	0.1	0.00000085	0.00019431	A_07_P050583	Z1891	cmr|putative tail component of prophage CP-933X [Z1891]
Z1893	+5.94	11.21	+2.57	9.92	0.1	12.49	0.1	0.00002337	0.00068274	A_07_P050588	Z1893	cmr|putative tail component of prophage CP-933X [Z1893]
Z1894	+24.34	9.70	+4.61	7.40	0.1	12.00	0.1	0.00000091	0.00019431	A_07_P050594	Z1894	cmr|putative tail component of prophage CP-933X [Z1894]
Z1895	+24.61	9.30	+4.62	6.99	0.3	11.62	0.2	0.00001694	0.00058050	A_07_P050599	Z1895	cmr|putative tail component of prophage CP-933X [Z1895]
Z1896	+5.02	8.28	+2.33	7.12	0.3	9.44	0.1	0.00019887	0.00253112	A_07_P050602	Z1896	cmr|putative tail component of prophage CP-933X [Z1896]
Z1898	+7.75	10.60	+2.95	9.12	0.4	12.07	0.1	0.00024235	0.00291707	A_07_P050610	Z1898	cmr|putative tail component of prophage CP-933X [Z1898]
Z1915	+5.05	8.94	+2.34	7.77	0.0	10.11	0.1	0.00003709	0.00087015	A_07_P050656	Z1915	cmr|putative tail protein [Z1915]
Z1919	-2.37	7.76	-1.24	8.38	0.4	7.14	0.1	0.00725740	0.03504535	A_07_P050674	Z1919	cmr|unknown protein encoded by prophage CP-933X [Z1919]
Z1957	-5.96	10.15	-2.57	11.44	0.1	8.86	0.0	0.00001412	0.00053964	A_07_P050726	Z1957	cmr|transposase for IS629 [Z1957]
Z2005	-2.67	12.53	-1.41	13.24	0.2	11.82	0.5	0.01006809	0.04494246	A_07_P050791	Z2005	cmr|orf Unknown function [Z2005]
Z2054	-2.59	15.49	-1.37	16.17	0.1	14.80	0.3	0.00155307	0.01097764	A_07_P047630	Z2054	cmr|putative killer protein encoded by prophage CP-933O [Z2054]
Z2074	-4.21	10.94	-2.07	11.98	0.1	9.90	0.0	0.00004783	0.00099032	A_07_P047687	Z2074	cmr|putative IS encoded protein within CP-933O [Z2074]
Z2076	-2.09	11.18	-1.06	11.71	0.1	10.65	0.1	0.00123192	0.00922733	A_07_P047700	Z2076	cmr|unknown protein encoded by prophage CP-933O [Z2076]
Z2080	-7.96	11.50	-2.99	13.00	0.1	10.01	0.0	0.00000625	0.00036832	A_07_P047717	Z2080	cmr|putative IS encoded protein within CP-933O [Z2080]
Z2118	+2.41	7.38	+1.27	6.74	0.1	8.01	0.0	0.00056298	0.00527744	A_07_P047862	Z2118	cmr|putative endopeptidase Rz of prophage CP-933O [Z2118]
Z2119	-4.04	8.69	-2.01	9.69	0.0	7.68	0.0	0.00004001	0.00090512	A_07_P047868	Z2119	cmr|unknown protein encoded within prophage CP-933O [Z2119]
Z2131	+3.95	9.45	+1.98	8.46	0.2	10.44	0.1	0.00016105	0.00218777	A_07_P047904	Z2131	cmr|putative terminase large subunit of prophage CP-933O [Z2131]
Z2133	+9.21	8.61	+3.20	7.01	0.1	10.22	0.0	0.00000616	0.00036832	A_07_P047906	Z2133	cmr|putative capsid assembly protein of prophage CP-933O [Z2133]
Z2136	+16.45	9.30	+4.04	7.28	0.4	11.32	0.2	0.00007196	0.00126447	A_07_P047913	Z2136	cmr|partial putative major capsid protein of prophage [Z2136]
Z2140	+3.33	7.83	+1.74	6.97	0.0	8.70	0.0	0.00007845	0.00133820	A_07_P047929	Z2140	cmr|putative tail component of prophage CP-933O [Z2140]
Z2142	-2.66	11.83	-1.41	12.54	0.2	11.12	0.3	0.00304423	0.01807256	A_07_P047939	Z2142	cmr|putative tail component of prophage CP-933O [Z2142]
Z2144	-2.53	10.81	-1.34	11.48	0.3	10.14	0.2	0.00421745	0.02312764	A_07_P047949	Z2144	cmr|putative tail component of prophage CP-933O [Z2144]
Z2181	-2.61	7.76	-1.38	8.45	0.2	7.07	0.3	0.00257129	0.01593793	A_07_P048026	Z2181	cmr|orf Unknown function [Z2181]

22297	-2.14	10.96	-1.10	11.51	0.1	10.41	0.2	0.00253752	0.01578201	A_07_P048153	22297	cmr	orf Unknown function [22297]
22298	-3.16	9.05	-1.66	9.88	0.1	8.23	0.1	0.00010782	0.00261329	A_07_P048160	22298	cmr	orf Unknown function [22298]
22360	+31.67	10.18	+6.98	7.69	0.5	12.67	0.3	0.00004287	0.00091913	A_07_P048260	22360	cmr	putative capsid protein of prophage CP-933R [22360]
22361	+43.56	11.10	+5.44	8.37	0.0	13.82	0.1	0.00000684	0.00019431	A_07_P048261	22361	cmr	putative capsid assembly protein of prophage CP-933R [22361]
22391	+52.43	9.78	+5.71	6.91	0.2	12.64	0.0	0.00000658	0.00019431	A_07_P048371	22391	cmr	unknown protein encoded within prophage CP-933R [22391]
22519	+2.31	8.16	+1.21	7.55	0.3	8.76	0.0	0.00386704	0.02171268	A_07_P049310	22519	cmr	orf Unknown function [22519]
22519	+2.12	8.41	+1.08	7.87	0.1	8.95	0.1	0.00101229	0.00799671	A_07_P049310	22519	cmr	orf Unknown function [22519]
22519	+2.15	8.30	+1.11	7.74	0.2	8.85	0.1	0.00012712	0.01850877	A_07_P049310	22519	cmr	orf Unknown function [22519]
22519	+2.11	8.23	+1.08	7.69	0.1	8.77	0.1	0.00105954	0.01139866	A_07_P049310	22519	cmr	orf Unknown function [22519]
22541	-4.24	9.04	-2.09	10.09	0.1	8.00	0.0	0.00004539	0.00095882	A_07_P049343	22541	cmr	putative transposase [22541]
22664	+2.22	9.23	+1.15	8.66	0.0	9.81	0.0	0.00050272	0.00546354	A_07_P049430	22664	cmr	orf Unknown function [22664]
22754	+2.90	8.89	+1.54	8.12	0.4	9.66	0.1	0.00389587	0.02185785	A_07_P049614	22754	cmr	orf, hypothetical protein [22754]
22804	-3.86	8.99	-1.95	9.96	0.1	8.01	0.1	0.00010204	0.00159869	A_07_P049658	22804	cmr	unknown protein encoded within i5629 [22804]
22806	-4.36	8.42	-2.13	9.48	0.2	7.36	0.0	0.00007641	0.00117571	A_07_P049661	22806	cmr	putative transposase [22806]
22836	-2.22	8.57	-1.15	9.15	0.1	7.99	0.2	0.00165870	0.00150622	A_07_P049693	22836	cmr	orf Unknown function [22836]
23083	-2.61	12.01	-1.39	12.75	0.2	11.36	0.3	0.00371235	0.02101573	A_07_P054754	23083	cmr	putative tail fiber component M of prophage [23083]
23087	-3.94	11.70	-1.98	12.69	0.6	10.71	0.2	0.00678642	0.03193372	A_07_P054772	23087	cmr	putative tail fiber component V of prophage [23087]
23099	-2.32	11.61	-1.21	12.21	0.0	11.00	0.1	0.00071096	0.00619446	A_07_P054814	23099	cmr	putative DNA packaging protein of prophage CP-933U [23099]
23108	-2.45	8.20	-1.51	8.95	0.0	7.44	0.1	0.00025321	0.00301324	A_07_P054855	23108	cmr	unknown protein encoded within prophage CP-933U [23108]
23144	-5.79	8.75	-2.53	10.02	0.0	7.49	0.1	0.00002626	0.00072778	A_07_P054923	23144	cmr	unknown function [23144]
23159	-7.91	8.59	-2.98	10.19	0.1	7.21	0.3	0.00006255	0.00116220	A_07_P054965	23159	cmr	putative outer membrane receptor for iron compound [23159]
23162	-4.07	9.38	-2.02	10.39	0.1	8.37	0.1	0.00008854	0.00145271	A_07_P054971	23162	cmr	i5629 transposase [23162]
23249	+2.14	7.93	+1.10	7.39	0.1	8.48	0.1	0.00139668	0.01606017	A_07_P055124	23249	cmr	orf, hypothetical protein [23249]
23297	-4.80	9.89	-2.26	11.02	0.0	8.76	0.1	0.00002551	0.00079867	A_07_P055211	23297	cmr	putative transposase for i5629 [23297]
23316	-2.55	14.24	-1.55	14.92	0.1	13.57	0.3	0.00008047	0.01627597	A_07_P055251	23316	cmr	unknown protein encoded within prophage CP-933V [23316]
23320	-2.26	10.61	-1.17	11.20	0.2	10.03	0.1	0.00132477	0.00972818	A_07_P055261	23320	cmr	unknown protein encoded within prophage CP-933V [23320]
23349	+29.49	9.06	+4.88	6.62	0.1	11.50	0.3	0.00005556	0.00016456	A_07_P055345	23349	cmr	putative DNA methyltransferase encoded within prophage CP-933V [23349]
23354	+8.43	13.17	+3.11	11.42	0.0	14.73	0.0	0.00004059	0.00031793	A_07_P055360	23354	cmr	putative exclusion protein rex of prophage CP-933V [23354]
23355	+7.14	14.70	+2.84	13.28	0.0	16.11	0.2	0.00002817	0.00074298	A_07_P055362	23355	cmr	putative DNA replication protein P of prophage [23355]
23356	+11.42	11.82	+3.51	10.06	0.1	13.57	0.1	0.00004031	0.00031815	A_07_P055369	23356	cmr	putative DNA replication protein O of prophage [23356]
23357	+4.65	9.75	+2.22	8.60	0.0	10.82	0.1	0.00004624	0.00097261	A_07_P055373	23357	cmr	putative regulatory protein CII of prophage CP-933V [23357]
23364	+1.96	14.02	+1.99	13.02	0.0	15.01	0.0	0.00004281	0.00069153	A_07_P055400	23364	cmr	putative host killing protein KI of prophage [23364]
23365	+25.70	11.54	+4.68	9.20	0.1	13.88	0.0	0.00000091	0.00019431	A_07_P055401	23365	cmr	putative host nuclease inhibitor protein Gam of prophage [23365]
23366	+6.97	15.19	+2.80	11.79	0.0	16.59	0.0	0.00000786	0.00061939	A_07_P055406	23366	cmr	putative recombination protein Bet of prophage CP-933V [23366]
23367	+6.78	12.28	+2.76	10.90	0.1	13.66	0.0	0.00001017	0.00046412	A_07_P055415	23367	cmr	putative exonuclease of prophage CP-933V [23367]
23390	-2.22	10.20	-1.15	10.78	0.3	9.62	0.1	0.00147715	0.02779476	A_07_P055453	23390	cmr	putative hydrolase [23390]
23603	-2.10	9.12	-1.07	9.66	0.3	8.59	0.0	0.00458362	0.02459889	A_07_P056277	23603	cmr	orf, hypothetical protein [23603]
23657	-3.54	10.50	-1.82	11.41	0.1	9.59	0.3	0.00058209	0.00539033	A_07_P056791	23657	cmr	orf, hypothetical protein [23657]
23783	-2.85	11.86	-1.51	12.61	0.1	11.10	0.1	0.00037855	0.00394677	A_07_P056960	23783	cmr	putative dimethyl sulfoxide reductase subunit C [23783]
23799	-6.29	13.75	-2.65	15.07	0.0	12.42	0.1	0.00001177	0.00056283	A_07_P056978	23799	cmr	putative ATP synthase beta subunit [23799]
23799	-5.60	13.54	-2.32	14.70	0.0	12.38	0.0	0.00001869	0.00062299	A_07_P056978	23799	cmr	putative ATP synthase beta subunit [23799]
23799	-5.34	13.80	-2.42	15.01	0.0	12.60	0.0	0.00001631	0.00059947	A_07_P056978	23799	cmr	putative ATP synthase beta subunit [23799]
23799	-5.37	14.10	-2.63	15.31	0.1	12.89	0.0	0.00002784	0.00073912	A_07_P056978	23799	cmr	putative ATP synthase beta subunit [23799]
23799	-5.60	13.80	-2.32	14.96	0.1	12.64	0.0	0.00002471	0.00070600	A_07_P056978	23799	cmr	putative ATP synthase beta subunit [23799]
23866	+2.48	7.87	+1.31	7.21	0.0	8.52	0.1	0.00014897	0.00376574	A_07_P057202	23866	cmr	orf Unknown function [23866]
23923	-4.66	10.28	-2.22	11.39	0.1	9.16	0.0	0.00001497	0.00008975	A_07_P057366	23923	cmr	orf Unknown function [23923]
23924	-6.04	10.86	-2.59	12.16	0.0	9.56	0.1	0.00001045	0.00051423	A_07_P057371	23924	cmr	partial putative transposase [23924]
23925	-4.22	9.49	-2.08	10.53	0.1	8.45	0.1	0.00007506	0.00125539	A_07_P057376	23925	cmr	partial putative transposase [23925]
23974	+3.10	8.18	+1.63	7.36	0.3	9.00	0.1	0.00113463	0.00872521	A_07_P057490	23974	cmr	orf Unknown function [23974]
24065	-3.71	9.93	-1.89	10.88	0.4	8.98	0.1	0.00164220	0.01141693	A_07_P057670	24065	cmr	orf, hypothetical protein [24065]
24105	+2.62	7.87	+1.39	7.17	0.2	8.56	0.2	0.00398500	0.01508851	A_07_P057761	24105	cmr	putative transport protein [24105]
24127	-2.66	9.51	-1.04	10.03	0.0	8.99	0.1	0.00121324	0.00914896	A_07_P057257	24127	cmr	orf, hypothetical protein [24127]
24248	+8.71	8.34	+3.12	6.78	0.3	9.90	0.2	0.00007736	0.00132538	A_07_P056573	24248	cmr	orf, hypothetical protein [24248]
24269	+6.18	8.36	+2.06	7.33	0.1	9.39	0.0	0.00003797	0.00087581	A_07_P056578	24269	cmr	orf, hypothetical protein [24269]
24270	+2.40	7.23	+1.26	6.60	0.1	7.86	0.1	0.00052686	0.00502151	A_07_P056585	24270	cmr	putative ATP-binding protein of ABC transport system [24270]
24321	-2.57	10.94	-1.36	11.62	0.2	10.26	0.2	0.00261591	0.01706455	A_07_P057744	24321	cmr	putative PagC-like membrane protein [24321]
24324	-2.45	8.64	-1.29	9.29	0.4	7.99	0.0	0.00642966	0.03186200	A_07_P057757	24324	cmr	putative transposase [24324]
24332	-2.12	9.36	-1.09	9.91	0.2	8.82	0.0	0.00301145	0.01769847	A_07_P057787	24332	cmr	putative cytotoxin [24332]
24340	-2.98	11.84	-1.58	12.63	0.0	11.05	0.1	0.00015017	0.00215104	A_07_P057803	24340	cmr	unknown protein encoded by i5618 [24340]
24385	-2.70	8.33	-1.43	9.05	0.0	7.62	0.0	0.00022281	0.00274273	A_07_P057884	24385	cmr	putative ATP-binding protein of ABC transporter family [24385]
24400	-2.62	13.23	-1.39	13.93	0.1	12.54	0.0	0.00038055	0.00397862	A_07_P057859	24400	cmr	orf Unknown function [24400]
24400	-2.52	13.78	-1.33	14.45	0.0	13.12	0.0	0.00029305	0.00331326	A_07_P057859	24400	cmr	orf Unknown function [24400]
24400	-2.64	13.50	-1.40	14.20	0.0	12.80	0.1	0.00031152	0.00345878	A_07_P057859	24400	cmr	orf Unknown function [24400]
24400	-2.47	13.67	-1.31	14.32	0.0	13.02	0.1	0.00049763	0.00480614	A_07_P057859	24400	cmr	orf Unknown function [24400]
24488	+2.01	8.21	+1.01	7.70	0.1	8.71	0.1	0.00231658	0.01475776	A_07_P057910	24488	cmr	putative phosphotransferase system enzyme subunit [24488]
24495	+2.29	8.04	+1.20	7.45	0.3	8.64	0.2	0.00702396	0.03412869	A_07_P057911	24495	cmr	putative galactosamine-6-phosphate isomerase [24495]
24501	-25.09	11.99	-4.65	14.32	0.0	9.67	0.2	0.00000164	0.00022629	A_07_P057934	24501	cmr	orf, hypothetical protein [24501]
24854	-2.96	10.26	-1.57	11.04	0.0	9.47	0.1	0.00019627	0.00250894	A_07_P061157	24854	cmr	putative acyl carrier protein [24854]
24856	-2.22	7.62	-1.15	8.20	0.1	7.05	0.2	0.00577327	0.01187519	A_07_P061161	24856	cmr	putative enzyme [24856]
24862	+2.21	7.40	+1.16	6.83	0.0	7.97	0.1	0.00074516	0.00641985	A_07_P061200	24862	cmr	orf Unknown function [24862]
24863	+2.00	7.37	+1.00	6.87	0.1	7.87	0.0	0.00150613	0.00966221	A_07_P061205	24863	cmr	putative 3-oxoacyl- [24863]
24866	-2.06	9.10	-1.04	9.63	0.1	8.58	0.1	0.00162319	0.01175546	A_07_P061220	24866	cmr	putative beta-ketoacyl-ACP synthase [24866]
24878	-3.15	8.77	-1.66	9.60	0.1	7.94	0.1	0.00051563	0.00190760	A_07_P061946	24878	cmr	putative xylulose kinase [24878]
24950	-3.83	9.96	-1.94	10.93	0.2	8.99	0.2	0.00034745	0.00195414	A_07_P049440	24950	cmr	orf Unknown function [24950]
24999	-2.38	8.08	-1.25	8.70	0.1	7.45	0.1	0.00085060	0.00746840	A_07_P049684	24999	cmr	orf Unknown function [24999]
25122	-2.13	12.02	-1.09	12.56	0.1	11.47	0.3	0.00768718	0.03743065	A_07_P047570	25122	cmr	putative hippuricase [25122]
25123	-2.47	12.06	-1.30	12.73	0.1	11.41	0.1	0.00119816	0.00606366	A_07_P047573	25123	cmr	putative citrate permease [25123]
25418	-2.14	7.54	-1.10	8.09	0.1	6.99	0.1	0.00111754	0.00862748	A_07_P047247	25418	cmr	D-gluconate-6-phosphate dehydrogenase [25418]
25852	-18.99	14.23	-4.25	16.16	0.0	12.30	0.0	0.00000033	0.00010091	A_07_P047387	25852	cmr	orf Unknown function [25852]
25940	+2.77	7.96	+1.47	7.23	0.0	8.70	0.0	0.00017957	0.00235985	A_07_P047549	25940	cmr	orf Unknown function [25940]
25987	+2.39	8.58	+1.26	7.95	0.0	9.21	0.1	0.00046682	0.00461378	A_07_P050868	25987	cmr	orf Unknown function [25987]
25988	+4.99	8.80	+2.12	7.64	0.0	9.96	0.1	0.00003020	0.00077353	A_07_P050871	25988	cmr	putative lipase-protein ligase A [25988]
25988	+6.75	8.56	+2.75	7.18	0.2	9.93	0.1	0.00005733	0.00110534	A_07_P050871	25988	cmr	putative lipase-protein ligase A [25988]
25988	+4.61	8.66	+2.20	7.55	0.1	9.76	0.1	0.00005459	0.00107563	A_07_P050871	25988	cmr	putative lipase-protein ligase A [25988]
25988	+5.60	8.82	+2.68	7.58	0.1	10.06	0.0	0.00001800	0.00061693	A_07_P050871	25988	cmr	putative lipase-protein ligase A [25988]
25988	+4.73	8.80	+2.24	7.68	0.1	9.93	0.1	0.00003315	0.00081556	A_07_P050871	25988	cmr	putative lipase-protein ligase A [25988]
26030	+6.39	8.60	+2.67	7.27	0.3	9.94	0.1	0.00010875	0.00142231	A_07_P049936	26030	cmr	putative tail component of cryptic prophage CP-933P [26030]
26036	-2.29	10.54	-1.19	11.13	0.0	9.94	0.0	0.00047521	0.00466588	A_07_P049215	26036	cmr	putative tail assembly protein of cryptic prophage [26036]
26060	-4.25	8.02	-2.09	9.06	0.4	6.98	0.0	0.00112312	0.00866111	A_07_P049262	26060	cmr	putative Q antiterminator encoded by prophage CP-933P [26060]
zapA	+2.08	11.41	+1.06	10.88	0.1	11.94	0.0	0.00096608	0.00783803	A_07_P006520	b2910	cmr	orf, hypothetical protein [b2910]
zntA	+3.08	9.39	+1.62	8.58	0.0	10.20	0.1	0.00020523	0.00195429	A_07_P014561	c_4262	cmr	Lead, cadmium, zinc and mercury transporting ATPase [c_4262]
zntR	-2.62	11.29	-1.39	11.99	0.1	10.60	0.0	0.00037081	0.00302997	A_07_P052121	28662	cmr	putative transcriptional regulator [28662]
zruC	-2.88	9.03	-1.53	9.80	0.0	8.27	0.0	0.00016756	0.00224522	A_07_P017968	b1858	cmr	putative ATP-binding component of a transport system [b1858]

E. coli ATCC 25922 ΔmarR pBK-QnrS1 (EC19) versus *E. coli* ATCC 25922 pBK-CMV | Significant differential expression (greater than or equal to two-fold, P value <0,05)

Gene Name (ProbeID)	Fold Change	logSignal (A)	logRatio (M)	logControl	StdErr (logControl)	logExperiment	StdErr (logExperiment)	pval (limma)	FDR (limma)	pval (RankProd)	FDR (RankProd)	Oligo	Systematic Name	Description
aaeA	-22.98	9.57	-4.52	11.83	0.1	7.31	0.1	0.00000025	0.00004211	0.00000889	0.00777778	A_07_P012680	b3241	cmr|putative membrane protein [b3241]
aaeB	-4.76	8.06	-2.25	9.18	0.1	6.93	0.2	0.00002685	0.00047665	0.00372586	0.20297578	A_07_P012673	b3240	cmr|orf, hypothetical protein [b3240]
aaeX	-4.49	8.06	-2.17	9.15	0.0	6.98	0.0	0.00001461	0.00031702	0.00448742	0.21873065	A_07_P010572	b3242	cmr|orf, hypothetical protein [b3242]
ABE-0285085	-3.66	8.47	-1.87	9.40	0.1	7.53	0.1	0.00006973	0.00093397	0.00973641	0.31737060	A_07_P010678	ABE-0285085	asap|IS1 transposase InsAB', C-ter fragment (pseudogene) [b4564]
ABH-0247453	-34.16	11.39	-5.09	13.94	0.0	8.84	0.1	0.00000009	0.00003427	0.00000254	0.00400000	A_07_P048654	ABH-0247453	asap|predicted protein []
ABH-0285233	-2.20	9.08	-1.14	9.65	0.1	8.51	0.4	0.00588241	0.02592801	0.05585175	0.61107019	A_07_P048532	ABH-0285233	asap|non-LEE-encoded type III secreted effector []
ABR-0081747	-5.03	12.51	-2.33	13.67	0.0	11.34	0.2	0.00001612	0.00034029	0.00301575	0.18403101	A_07_P035421	ABR-0081747	asap|toxic membrane protein []
ABR-0081751	-4.70	8.67	-2.23	9.79	0.1	7.56	0.2	0.00005011	0.00074154	0.00390180	0.20614094	A_07_P041043	ABR-0081751	asap|predicted ferredoxin []
ABR-0081753	+12.78	11.45	+3.68	9.61	0.1	13.29	0.1	0.00000077	0.00006301	0.00154789	0.11772947	A_07_P041110	ABR-0081753	asap|predicted protein []
ABR-0081754	+3.77	7.79	+1.91	6.84	0.4	8.75	0.1	0.00056011	0.00422026	0.01763211	0.35139241	A_07_P041114	ABR-0081754	asap|predicted protein []
ACA-0244204	-2.12	8.62	-1.08	9.17	0.2	8.08	0.1	0.00215976	0.01173970	0.06152439	0.63600788	A_07_P059059	ACA-0244204	asap|Hemolysin C []
ACA-0244210	-3.64	11.40	-1.86	12.33	0.1	10.46	0.3	0.00018526	0.00189276	0.01012576	0.32534694	A_07_P059088	ACA-0244210	asap|predicted protein []
ACA-0285117	-3.43	11.73	-1.78	12.62	0.2	10.84	0.1	0.00009614	0.00116257	0.01227325	0.33840630	A_07_P062850	ACA-0285117	asap|toxic polypeptide, small []
accB	+4.00	10.72	+2.00	9.72	0.1	11.72	0.2	0.00007675	0.00099210	0.01556911	0.33716644	A_07_P012745	b3255	cmr|acetylCoA carboxylase, BCCP subunit; carrier of biotin [b3255]
accC	+2.63	10.71	+1.40	10.02	0.1	11.41	0.2	0.00049052	0.00384788	0.03520325	0.47738157	A_07_P012747	b3256	cmr|acetyl CoA carboxylase, biotin carboxylase subunit [b3256]
aceA	+8.39	9.35	+3.07	7.82	0.0	10.88	0.1	0.00000227	0.00010914	0.00360264	0.17345566	A_07_P008720	b4015	cmr|isocitrate lyase [b4015]
aceA	+7.98	9.14	+3.00	7.64	0.3	10.64	0.5	0.00009455	0.00114776	0.00393102	0.18096491	A_07_P037462	c_4972	cmr|Isocitrate lyase [c_4972]
aceB	+38.05	9.85	+5.25	7.23	0.0	12.48	0.1	0.00000008	0.00003427	0.00007050	0.02265306	A_07_P008715	b4014	cmr|malate synthase A [b4014]
aceE	+47.02	11.63	+5.56	8.85	0.0	14.40	0.1	0.00000005	0.00003344	0.00002731	0.01228571	A_07_P002535	b0114	cmr|pyruvate dehydrogenase [b0114]
aceF	+10.21	11.88	+3.35	10.20	0.1	13.55	0.2	0.00000343	0.00013521	0.00251080	0.14695167	A_07_P002536	b0115	cmr|pyruvate dehydrogenase [b0115]
ackA	+6.30	12.97	+2.66	11.64	0.1	14.30	0.0	0.00000479	0.00016636	0.00640307	0.22911364	A_07_P013766	b2296	cmr|acetate kinase [b2296]
acnA	+4.95	9.45	+2.31	8.29	0.1	10.60	0.2	0.00001857	0.00037436	0.01037729	0.28072165	A_07_P014361	b1276	cmr|aconitate hydrase 1 [b1276]
acnB	+8.79	10.39	+3.14	8.82	0.0	11.96	0.1	0.00000165	0.00009590	0.00336573	0.16929712	A_07_P002554	b0118	cmr|aconitate hydrase B [b0118]
acpD	+3.67	8.69	+1.88	7.76	0.1	9.63	0.0	0.00004370	0.00066995	0.01875826	0.35928224	A_07_P052470	Z2315	cmr|acyl carrier protein phosphodiesterase [Z2315]
acpD	+3.58	9.31	+1.84	8.39	0.2	10.23	0.1	0.00007575	0.00098524	0.01962525	0.36827175	A_07_P063175	ECs2014	cmr|acyl carrier protein phosphodiesterase [ECs2014]
acpP	+2.57	16.20	+1.36	15.52	0.0	16.88	0.1	0.00025930	0.00240996	0.03660950	0.48394626	A_07_P001671	b1094	cmr|acyl carrier protein [b1094]
acpS	+4.35	8.74	+2.12	7.68	0.1	9.80	0.1	0.00003894	0.00061546	0.01372332	0.31680352	A_07_P019720	b2563	cmr|CoA:apo- [b2563]
acpS	+5.45	8.87	+2.45	7.65	0.0	10.10	0.2	0.00001266	0.00029313	0.00850737	0.25609943	A_07_P053485	ECs3429	cmr|CoA:apo- [ECs3429]
acpS	+3.75	8.79	+1.91	7.83	0.1	9.74	0.2	0.00009050	0.00111579	0.01810595	0.35455224	A_07_P042915	Z3844	cmr|CoA:apo- [Z3844]
acpT	-2.48	10.46	-1.31	11.11	0.0	9.80	0.2	0.00082641	0.00565446	0.03864456	0.53323401	A_07_P007313	b3475	cmr|orf, hypothetical protein [b3475]
acrE	-2.02	9.62	-1.01	10.13	0.0	9.11	0.2	0.00209626	0.01146076	0.07281250	0.66960280	A_07_P012792	b3265	cmr|transmembrane protein affects septum formation and cell membrane permeability [b3265]
acrF	-2.68	9.63	-1.42	10.34	0.4	8.92	0.3	0.00368600	0.01778149	0.02742696	0.47399561	A_07_P012796	b3266	cmr|integral transmembrane protein; acridine resistance [b3266]
acs	+11.92	8.70	+3.58	6.91	0.1	10.49	0.4	0.00000951	0.00024416	0.00173209	0.12283784	A_07_P052329	Z5668	cmr|acetyl-CoA synthetase [Z5668]
acs	+13.77	9.02	+3.78	7.13	0.2	10.91	0.1	0.00000204	0.00010341	0.00130208	0.11081081	A_07_P008986	b4069	cmr|acetyl-CoA synthetase [b4069]
actP	+2.88	7.86	+1.53	7.10	0.2	8.62	0.2	0.00069270	0.00489273	0.02942645	0.44249284	A_07_P063696	ECs5049	cmr|putative transport protein [ECs5049]
actP	+3.38	7.73	+1.76	6.85	0.1	8.61	0.1	0.00008779	0.00109090	0.02139482	0.38672790	A_07_P052321	Z5666	cmr|putative transport protein [Z5666]
actP	+3.06	8.23	+1.62	7.42	0.4	9.03	0.2	0.00159375	0.00924197	0.02689278	0.42767677	A_07_P008980	b4067	cmr|putative transport protein [b4067]
ade	+4.38	8.58	+2.13	7.52	0.0	9.65	0.1	0.00001771	0.00036352	0.01337081	0.31325893	A_07_P017261	b3665	cmr|probable adenine deaminase [b3665]
adhE	+3.60	8.55	+1.85	7.62	0.1	9.47	0.1	0.00005783	0.00081514	0.01941247	0.36646283	A_07_P007143	b1241	cmr|CoA-linked acetaldehyde dehydrogenase and iron-dependent alcohol dehydrogenase; pyruvate-formate-lyase deactivase [b1241]
aefA	-2.43	8.83	-1.28	9.47	0.0	8.19	0.1	0.00043708	0.00355256	0.04018547	0.54307296	A_07_P031187	c_0584	cmr|Potassium efflux system kefA [c_0584]
aes	-19.09	10.64	-4.25	12.77	0.1	8.51	0.0	0.00000029	0.00004211	0.00002223	0.01346154	A_07_P021486	b0476	cmr|putative lipase [b0476]
agaB	+2.33	7.41	+1.22	6.80	0.0	8.02	0.4	0.00518647	0.02346429	0.04667619	0.53445091	A_07_P000415	b3138	cmr|PTS system, cytoplasmic, N-acetylgalactosamine-specific IIB component 1 [b3138]
agaS	+19.45	8.98	+4.28	6.84	0.1	11.12	0.1	0.00000050	0.00005264	0.00053862	0.06784000	A_07_P034110	c_3893	cmr|Putative tagatose-6-phosphate ketose/aldose isomerase [c_3893]
agaS	+14.85	8.95	+3.89	7.01	0.1	10.90	0.1	0.00000069	0.00006127	0.00107025	0.09970414	A_07_P000404	b3136	cmr|putative tagatose-6-phosphate aldose/ketose isomerase [b3136]
agaV	+13.38	8.37	+3.74	6.50	0.1	10.24	0.4	0.00000687	0.00020075	0.00139799	0.11523560	A_07_P000390	b3133	cmr|PTS system, cytoplasmic, N-acetylgalactosamine-specific IIB component 2 [b3133]
agaW	+10.61	9.22	+3.41	7.52	0.3	10.92	0.2	0.00000668	0.00019764	0.00224403	0.13747082	A_07_P000391	b3134	cmr|PTS system N-acetylgalactosameine-specific IIC component 2 [b3134]
agp	+4.78	10.08	+2.26	8.95	0.3	11.21	0.1	0.00005168	0.00075483	0.01115600	0.28840722	A_07_P033935	c_1137	cmr|Glucose-1-phosphatase precursor [c_1137]
agp	+6.03	10.00	+2.59	8.71	0.1	11.30	0.1	0.00000897	0.00023724	0.00698933	0.23869848	A_07_P001241	b1002	cmr|periplasmic glucose-1-phosphatase [b1002]
ahpC	+4.16	15.76	+2.06	14.73	0.1	16.79	0.0	0.00002118	0.00040971	0.01469004	0.32712871	A_07_P016781	b0605	cmr|alkyl hydroperoxide reductase, C22 subunit; detoxification of hydroperoxides [b0605]
aidB	-3.49	9.13	-1.80	10.03	0.3	8.23	0.0	0.00036704	0.00311187	0.01149835	0.33277574	A_07_P011655	b4187	cmr|putative acyl coenzyme A dehydrogenase [b4187]
aldA	+5.54	8.70	+2.47	7.46	0.1	9.93	0.0	0.00000745	0.00021277	0.00823742	0.25085106	A_07_P009166	b1415	cmr|aldehyde dehydrogenase, NAD-linked [b1415]
allA	+2.71	8.84	+1.44	8.12	0.5	9.56	0.2	0.00448159	0.02087519	0.03530678	0.47755155	A_07_P016314	b0505	cmr|orf, hypothetical protein [b0505]
allB	+5.22	9.54	+2.38	8.34	0.2	10.73	0.1	0.00001849	0.00037316	0.00925368	0.26781250	A_07_P016349	b0512	cmr|putative hydrolase [b0512]
allD	+8.19	8.51	+3.03	6.99	0.0	10.03	0.1	0.00000197	0.00010186	0.00376524	0.17801802	A_07_P016372	b0517	cmr|putative malate dehydrogenase [b0517]
alr	-2.72	9.96	-1.44	10.68	0.0	9.24	0.0	0.00015799	0.00168751	0.02803163	0.47557112	A_07_P008909	b4053	cmr|alanine racemase 1 [b4053]
alsB	+18.77	9.82	+4.23	7.70	0.1	11.93	0.1	0.00000035	0.00004756	0.00058626	0.07210938	A_07_P011177	b4088	cmr|putative LACI-type transcriptional regulator [b4088]
alsC	+2.24	9.70	+1.16	9.12	0.4	10.28	0.1	0.00749382	0.03128686	0.05345465	0.56864189	A_07_P011170	b4086	cmr|putative transport system permease protein [b4086]
alsE	+2.67	10.11	+1.42	9.40	0.1	10.82	0.0	0.00021456	0.00210860	0.03380462	0.46974404	A_07_P011164	b4085	cmr|putative epimerase [b4085]
alsK	+2.56	9.48	+1.36	8.80	0.2	10.16	0.3	0.00123580	0.00761208	0.03760925	0.48694079	A_07_P011158	b4084	cmr|putative NAGC-like transcriptional regulator [b4084]
amiA	-7.62	12.09	-2.93	13.56	0.0	10.63	0.0	0.00000214	0.00010587	0.00068534	0.08174242	A_07_P042594	c_2969	cmr|Probable N-acetylmuramoyl-L-alanine amidase amiA precursor [c_2969]
amiA	-7.28	12.10	-2.86	13.53	0.0	10.67	0.0	0.00000250	0.00011564	0.00081936	0.08896552	A_07_P052703	Z3700	cmr|N-acetylmuramoyl-l-alanine amidase I [Z3700]
amiA	-6.27	11.65	-2.65	12.97	0.0	10.33	0.1	0.00000674	0.00019841	0.00140943	0.12536723	A_07_P013234	b2435	cmr|N-acetylmuramoyl-l-alanine amidase I [b2435]
amiB	-2.47	10.68	-1.30	11.33	0.1	10.02	0.1	0.00040250	0.00334584	0.03762132	0.52743544	A_07_P011563	b4169	cmr|N-acetylmuramoyl-l-alanine amidase II; a murein hydrolase [b4169]
amn	+6.98	9.13	+2.80	7.73	0.4	10.53	0.2	0.00007407	0.00096772	0.00525089	0.20823678	A_07_P015257	b1982	cmr|AMP nucleosidase [b1982]
ampD	+2.73	12.09	+1.45	11.36	0.1	12.81	0.2	0.00040718	0.00336868	0.03256733	0.46109712	A_07_P041423	c_0129	cmr|AmpD protein [c_0129]
ampD	+3.96	10.96	+1.98	9.97	0.0	11.95	0.1	0.00002787	0.00048979	0.01631669	0.34297730	A_07_P002511	b0110	cmr|regulates ampC [b0110]
ampE	+2.56	9.30	+1.36	8.62	0.0	9.97	0.1	0.00032013	0.00280126	0.03703887	0.48514143	A_07_P002518	b0111	cmr|regulates ampC [b0111]
amtB	-2.19	10.84	-1.13	11.41	0.0	10.28	0.3	0.00318791	0.01587041	0.05572980	0.61058455	A_07_P031178	c_0570	cmr|Probable ammonium transporter [c_0570]
amyA	-2.72	9.17	-1.44	9.89	0.2	8.45	0.1	0.00078279	0.00539515	0.02792492	0.47529730	A_07_P014999	b1927	cmr|cytoplasmic alpha-amylase [b1927]
anmK	+2.06	10.26	+1.04	9.74	0.1	10.78	0.0	0.00157484	0.00914241	0.05988504	0.59710576	A_07_P052526	Z2654	cmr|orf, hypothetical protein [Z2654]
anmK	+2.12	10.13	+1.08	9.59	0.1	10.67	0.1	0.00122976	0.00758080	0.05584858	0.57923584	A_07_P063211	ECs2349	cmr|hypothetical protein [ECs2349]
ansB	+40.81	12.89	+5.35	10.22	0.1	15.57	0.2	0.00000011	0.00003545	0.00005526	0.02071429	A_07_P011926	b2957	cmr|periplasmic L-asparaginase II [b2957]
apaG	-2.17	9.47	-1.12	10.03	0.1	8.91	0.2	0.00239039	0.01268674	0.05722497	0.61624487	A_07_P010939	b0050	cmr|orf, hypothetical protein [b0050]
apbA	+2.76	9.57	+1.46	8.84	0.1	10.30	0.0	0.00017638	0.00182810	0.03157393	0.45647383	A_07_P031138	c_0536	cmr|2-dehydropantoate 2-reductase [c_0536]
aphA	+4.59	8.77	+2.20	7.67	0.2	9.87	0.1	0.00003992	0.00062694	0.01223260	0.29905280	A_07_P008919	b4055	cmr|diadenosine tetraphosphatase [b4055]
aphA	+3.93	10.59	+1.98	9.60	0.1	11.58	0.1	0.00004822	0.00071961	0.01641895	0.34329349	A_07_P042001	c_5045	cmr|Class B acid phosphatase precursor [c_5045]
apt	+4.05	11.86	+2.02	10.85	0.0	12.87	0.0	0.00002125	0.00040998	0.01541667	0.33664355	A_07_P021451	b0469	cmr|adenine phosphoribosyltransferase [b0469]
araA	+8.57	8.81	+3.10	7.26	0.1	10.36	0.0	0.00000202	0.00010341	0.00348006	0.17121875	A_07_P010999	b0062	cmr|L-arabinose isomerase [b0062]
araB	+2.58	7.98	+1.37	7.29	0.0	8.66	0.3	0.00125678	0.00771115	0.03669017	0.48419950	A_07_P011001	b0063	cmr|L-ribulokinase [b0063]
araC	+2.42	11.14	+1.27	10.50	0.0	11.78	0.1	0.00052484	0.00401973	0.04166349	0.50770124	A_07_P011010	b0064	cmr|transcriptional regulator for ara operon [b0064]
araF	+2.44	8.27	+1.29	7.63	0.1	8.92	0.1	0.00055073	0.00416662	0.04054433	0.50025862	A_07_P016171	b1901	cmr|L-arabinose-binding periplasmic protein [b1901]
argE	+3.86	8.77	+1.95	7.80	0.2	9.75	0.1	0.00006300	0.00086859	0.01686420	0.34571615	A_07_P039521	c_4916	cmr|Acetylornithine deacetylase [c_4916]
argE	+3.36	7.87	+1.75	6.99	0.2	8.74	0.0	0.00012698	0.00142599	0.02151423	0.38799542	A_07_P008486	b3957	cmr|acetylornithine deacetylase [b3957]
argG	+2.45	8.07	+1.29	7.42	0.2	8.71	0.0	0.00067428	0.00481225	0.04081491	0.50007004	A_07_P000576	b3172	cmr|argininosuccinate synthetase [b3172]
argG	+2.48	8.67	+1.31	8.01	0.1	9.32	0.1	0.00042246	0.00347138	0.03963224	0.49482157	A_07_P045946	Z4534	cmr|argininosuccinate synthetase [Z4534]
argG	+2.45	8.69	+1.29	8.04	0.1	9.33	0.0	0.00035096	0.00299810	0.04055069	0.49994518	A_07_P041781	c_3929	cmr|Argininosuccinate synthase [c_3929]
argI	-2.06	9.98	-1.04	10.50	0.1	9.46	0.1	0.00181650	0.01024317	0.06816565	0.65599022	A_07_P003818	b4254	cmr|ornithine carbamoyltransferase 1 [b4254]
argR	-3.68	11.14	-1.88	12.08	0.0	10.21	0.2	0.00007539	0.00098262	0.00975419	0.31729339	A_07_P012656	b3237	cmr|repressor of arg regulon; cer-mediated site specific recombination [b3237]
ariR	+2.13	9.91	+1.09	9.36	0.2	10.45	0.1	0.00262182	0.01363658	0.05684642	0.58419713	A_07_P006784	b1166	cmr|orf, hypothetical protein [b1166]
arnC	+2.76	9.64	+1.46	8.91	0.2	10.37	0.0	0.00031384	0.00276655	0.03214558	0.45883953	A_07_P001060	b2254	cmr|putative sugar transferase [b2254]
arnF	-2.67	8.30	-1.42	9.01	0.1	7.60	0.3	0.00091094	0.00609775	0.02993585	0.48638803	A_07_P010515	b2258	cmr|putative transport/receptor protein [b2258]
arnT	+2.69	8.39	+1.43	7.67	0.2	9.10	0.1	0.00052333	0.00401527	0.03403392	0.46961437	A_07_P001072	b2257	cmr|orf, hypothetical protein [b2257]
aroA	+2.44	8.93	+1.29	8.28	0.1	9.57	0.2	0.00078560	0.00540818	0.04108295	0.50296267	A_07_P033835	c_1046	cmr|3-phosphoshikimate 1-carboxyvinyltransferase [c_1046]
aroD	+2.51	7.52	+1.33	6.86	0.1	8.19	0.0	0.00035602	0.00303253	0.03812055	0.48715097	A_07_P018517	b1693	cmr|3-dehydroquinate dehydratase [b1693]
aroG	+2.54	8.09	+1.35	7.42	0.2	8.76	0.0	0.00045177	0.00362894	0.03729040	0.48641259	A_07_P010251	b0754	cmr|3-deoxy-D-arabinoheptulosonate-7-phosphate synthase [b0754]
aroH	+2.32	9.43	+1.21	8.82	0.4	10.04	0.3	0.01297006	0.04853831	0.05324886	0.56914460	A_07_P018571	b1704	cmr|3-deoxy-D-arabinoheptulosonate-7-phosphate synthase [b1704]
aroK	-2.56	11.72	-1.36	12.39	0.0	11.04	0.1	0.00026313	0.00243694	0.03396024	0.50920952	A_07_P017976	b3390	cmr|shikimate kinase I [b3390]
arrD	+12.76	9.80	+3.67	7.96	0.1	11.63	0.1	0.00000074	0.00006247	0.00150279	0.11771144	A_07_P016536	b0555	cmr|bacteriophage lambda lysozyme homolog [b0555]
artI	+5.39	8.96	+2.43	7.75	0.1	10.18	0.2	0.00001698	0.00035267	0.00867060	0.25903226	A_07_P004766	b0863	cmr|arginine 3rd transport system periplasmic binding protein [b0863]
artP	+7.65	9.33	+2.94	7.87	0.2	10.80	0.1	0.00000750	0.00021366	0.00413872	0.18564103	A_07_P004773	b0864	cmr|ATP-binding component of 3rd arginine transport system [b0864]
artQ	+2.41	8.23	+1.27	7.59	0.2	8.87	0.1	0.00117340	0.00730198	0.04268674	0.51146119	A_07_P033780	c_0995	cmr|Arginine transport system permease protein artQ [c_0995]
asd	+4.90	9.74	+2.29	8.59	0.1	10.88	0.2	0.00002307	0.00043145	0.01059769	0.28327674	A_07_P018194	b3433	cmr|aspartate-semialdehyde dehydrogenase [b3433]
asnA	-7.40	11.20	-2.89	12.65	0.0	9.76	0.2	0.00000511	0.00017328	0.00076029	0.08673913	A_07_P005641	b3744	cmr|asparagine synthetase A [b3744]
aspA	+6.78	15.53	+2.76	14.15	0.0	16.91	0.1	0.00000457	0.00016295	0.00552782	0.21435961	A_07_P011426	b4139	cmr|aspartate ammonia-lyase [b4139]
aspC	+6.20	9.60	+2.63	8.28	0.2	10.91	0.3	0.00002887	0.00050012	0.00666921	0.23230088	A_07_P052047	Z1275	cmr|aspartate aminotransferase [Z1275]
aspC	+9.42	11.20	+3.24	9.58	0.1	12.82	0.1	0.00000237	0.00011227	0.00290904	0.15631399	A_07_P005088	b0928	cmr|aspartate aminotransferase [b0928]
asr	-7.25	10.30	-2.86	11.73	0.0	8.87	0.2	0.00000880	0.00023401	0.00081364	0.08958042	A_07_P020616	b1597	cmr|acid shock protein [b1597]
astA	+4.40	8.58	+2.14	7.51	0.0	9.64	0.2	0.00005468	0.00078482	0.01328506	0.31171386	A_07_P018783	b1747	cmr|orf, hypothetical protein [b1747]
atoC	+3.42	8.56	+1.77	7.67	0.2	9.44	0.0	0.00010509	0.00124498	0.02133384	0.38651323	A_07_P000888	b2220	cmr|response regulator of ato, ornithine decarboxylase antizyme [b2220]
atoS	+2.52	9.15	+1.33	8.48	0.1	9.81	0.0	0.00027150	0.00249826	0.03804688	0.48660439	A_07_P000883	b2219	cmr|sensor protein AtoS for response regulator AtoC [b2219]
atpA	+4.43	15.25	+2.15	14.18	0.0	16.32	0.1	0.00001621	0.00034168	0.01302337	0.30786787	A_07_P005591	b3734	cmr|membrane-bound ATP synthase, F1 sector, alpha-subunit [b3734]
atpB	+2.29	12.56	+1.19	11.96	0.0	13.15	0.1	0.00070636	0.00496691	0.04692391	0.53495293	A_07_P005614	b3738	cmr|membrane-bound ATP synthase, F0 sector, subunit a [b3738]
atpD	+4.42	11.51	+2.14	10.44	0.0	12.58	0.1	0.00002036	0.00039679	0.01308498	0.30839820	A_07_P005582	b3732	cmr|membrane-bound ATP synthase, F1 sector, beta-subunit [b3732]
atpE	+5.00	12.71	+2.32	11.55	0.0	13.87	0.2	0.00002599	0.00046542	0.01005399	0.27673077	A_07_P005607	b3737	cmr|membrane-bound ATP synthase, F0 sector, subunit c [b3737]
atpG	+5.72	12.40	+2.52	11.14	0.0	13.66	0.3	0.00002725	0.00048212	0.00772612	0.24623482	A_07_P005587	b3733	cmr|membrane-bound ATP synthase, F1 sector, gamma-subunit [b3733]
atpH	+9.02	13.18	+3.17	11.60	0.1	14.77	0.1	0.00000193	0.00010107	0.00319741	0.16559211	A_07_P005596	b3735	cmr|membrane-bound ATP synthase, F1 sector, delta-subunit [b3735]
azoR	+2.90	8.96	+1.54	8.19	0.2	9.73	0.2	0.00042576	0.00349110	0.02904726	0.44057803	A_07_P009153	b1412	cmr|acyl carrier protein phosphodiesterase [b1412]
b0255	-2.54	10.98	-1.34	11.65	0.2	10.31	0.0	0.00052323	0.00401527	0.03547891	0.51577101	A_07_P007981	b0255	cmr|IS911 hypothetical protein, variant [b0255]
b0257	-2.72	15.79	-1.44	16.51	0.0	15.07	0.1	0.00025491	0.00238178	0.02762005	0.47524590	A_07_P007992	b0257	cmr|putative transposase [b0257]
b0322	-5.51	9.20	-2.46	10.43	0.1	7.96	0.1	0.00001156	0.00027749	0.00227261	0.15831858	A_07_P008305	b0322	cmr|orf, hypothetical protein [b0322]
b0359	-2.31	8.58	-1.21	9.18	0.3	7.97	0.1	0.00213642	0.01164156	0.04744538	0.57681853	A_07_P020924	b0359	cmr|putative transferase [b0359]
b0359	-2.21	7.81	-1.14	8.38	0.1	7.24	0.1	0.00111960	0.00707343	0.05482914	0.60833686	A_07_P010289	b0359	cmr|putative transferase [b0359]
b0362	-2.14	7.13	-1.10	7.68	0.3	6.58	0.1	0.00310301	0.01553432	0.05892658	0.62348118	A_07_P020932	b0362	cmr|orf, hypothetical protein [b0362]
b0374	-6.91	8.20	-2.79	9.60	0.1	6.81	0.1	0.00000411	0.00015128	0.00100927	0.10121019	A_07_P020983	b0374	cmr|putative flagellin structural protein [b0374]
b0395	+2.20	7.44	+1.14	6.87	0.0	8.01	0.0	0.00066382	0.00475922	0.05072980	0.55852448	A_07_P021086	b0395	cmr|orf, hypothetical protein [b0395]
b0501	-2.55	9.23	-1.35	9.90	0.5	8.56	0.0	0.00560317	0.02495386	0.03376842	0.50826960	A_07_P016291	b0501	cmr|orf, hypothetical protein [b0501]
b0663	-2.19	7.53	-1.13	8.09	0.0	6.96	0.4	0.00682664	0.02911120	0.05415777	0.60515259	A_07_P009880	b0663	cmr|putative RNA [b0663]
b0671	-4.12	7.96	-2.04	8.98	0.0	6.94	0.2	0.00003803	0.00060518	0.00620300	0.25767810	A_07_P009885	b0671	cmr|putative RNA [b0671]
b0725	+11.48	8.67	+3.52	6.91	0.0	10.43	0.4	0.00001790	0.00036590	0.00186547	0.12938326	A_07_P010142	b0725	cmr|orf, hypothetical protein [b0725]
b1170	-3.72	8.14	-1.89	9.09	0.1	7.19	0.2	0.00008955	0.00110664	0.00901931	0.30537634	A_07_P006805	b1170	cmr|putative part of putative ATP-binding component of a transport system [b1170]
b1364	-2.28	10.02	-1.19	10.62	0.0	9.43	0.0	0.00050192	0.00391007	0.04930259	0.58538462	A_07_P014798	b1364	cmr|orf, hypothetical protein [b1364]
b1543	-2.52	7.43	-1.33	8.09	0.0	6.76	0.2	0.00055653	0.00420042	0.03496888	0.51118849	A_07_P020361	b1543	cmr|putative transport protein [b1543]
b1995	-4.11	8.32	-2.04	9.34	0.0	7.30	0.1	0.00002553	0.00046151	0.00630907	0.25733161	A_07_P015310	b1995	cmr|orf, hypothetical protein [b1995]
b2680	-2.13	7.80	-1.09	8.34	0.2	7.25	0.1	0.00338037	0.01658994	0.05928417	0.62684352	A_07_P001871	b2680	cmr|orf, hypothetical protein [b2680]
b3000	-2.17	7.77	-1.12	8.33	0.2	7.21	0.1	0.00232079	0.01240276	0.05753874	0.61667120	A_07_P012133	b3000	cmr|orf, hypothetical protein [b3000]
b3016	-2.58	9.42	-1.37	10.11	0.0	8.74	0.0	0.00022417	0.00217051	0.03279980	0.50577865	A_07_P012215	b3016	cmr|orf, hypothetical protein [b3016]
b3111	+30.92	10.28	+4.95	7.80	0.0	12.75	0.1	0.00000011	0.00003548	0.00012894	0.03274194	A_07_P000282	b3111	cmr|putative L-serine dehydratase [b3111]
b3112	+21.78	9.54	+4.44	7.31	0.1	11.76	0.1	0.00000027	0.00004211	0.00037983	0.05588785	A_07_P000290	b3112	cmr|putative L-serine dehydratase [b3112]
b3436	-2.01	7.38	-1.01	7.88	0.1	6.88	0.1	0.00225257	0.01211220	0.07350610	0.67205575	A_07_P018209	b3436	cmr|low-affinity gluconate transport permease protein, interrupted [b3436]
b3695	+2.35	8.19	+1.23	7.57	0.1	8.81	0.2	0.00114620	0.00718671	0.04469957	0.52323420	A_07_P005410	b3695	cmr|regulator protein for dgo operon [b3695]
b3762	+2.40	7.80	+1.26	7.17	0.1	8.44	0.2	0.00076000	0.00527345	0.04244411	0.51049656	A_07_P005705	b3762	cmr|orf, hypothetical protein [b3762]
b3763	+2.89	8.60	+1.53	7.83	0.0	9.37	0.2	0.00033969	0.00292453	0.02939723	0.44247610	A_07_P005708	b3763	cmr|regulator of pssA [b3763]
b3814	+2.06	9.28	+1.04	8.76	0.1	9.80	0.1	0.00135218	0.00813168	0.05996824	0.59717900	A_07_P005938	b3814	cmr|orf, hypothetical protein [b3814]
b3837	-2.86	12.15	-1.51	12.91	0.0	11.40	0.1	0.00013328	0.00148186	0.02378303	0.44470309	A_07_P018994	b3837	cmr|putative histone [b3837]
b3841	-3.00	10.25	-1.58	11.05	0.0	9.46	0.1	0.00010142	0.00121246	0.02001778	0.40665806	A_07_P019013	b3841	cmr|orf, hypothetical protein [b3841]
b3914	-2.11	12.29	-1.07	12.83	0.0	11.76	0.1	0.00116466	0.00727060	0.06327109	0.64433376	A_07_P019349	b3914	cmr|orf, hypothetical protein [b3914]
b4285	-4.76	14.79	-2.25	15.92	0.0	13.67	0.2	0.00002895	0.00050086	0.00383575	0.20402027	A_07_P003953	b4285	cmr|putative transposase [b4285]
basR	+2.49	9.81	+1.32	9.15	0.1	10.47	0.0	0.00044064	0.00356882	0.03898247	0.49296386	A_07_P037777	c_5118	cmr|Transcriptional Regulatory protein basR/pmrA [c_5118]
basS	-3.73	12.36	-1.90	13.31	0.5	11.41	0.4	0.00254753	0.01335163	0.00958905	0.31386694	A_07_P011296	b4112	cmr|sensor protein for basR [b4112]
bax	-8.14	12.01	-3.02	13.53	0.0	10.50	0.0	0.00000177	0.00009825	0.00052210	0.07210526	A_07_P007778	b3570	cmr|putative ATP-binding protein [b3570]
bcp	+12.99	10.13	+3.70	8.28	0.1	11.98	0.3	0.00000271	0.00012064	0.00143229	0.11505102	A_07_P013456	b2480	cmr|bacterioferritin comigratory protein [b2480]
bcsA	-2.37	8.85	-1.25	9.48	0.1	8.23	0.2	0.00070282	0.00494641	0.04290460	0.55871795	A_07_P007596	b3533	cmr|putative cellulose synthase [b3533]
bcsF	-2.16	8.24	-1.11	8.80	0.1	7.69	0.1	0.00090114	0.00605586	0.05860836	0.62304524	A_07_P007618	b3537	cmr|orf, hypothetical protein [b3537]
betA	+3.38	9.28	+1.76	8.41	0.0	10.16	0.1	0.00008598	0.00108038	0.02164126	0.38806378	A_07_P043676	Z0398	cmr|choline dehydrogenase, a flavoprotein [Z0398]
betA	+5.19	9.89	+2.38	8.70	0.2	11.08	0.1	0.00003470	0.00056726	0.00941883	0.26864130	A_07_P008247	b0311	cmr|choline dehydrogenase, a flavoprotein [b0311]
betA	+4.95	10.47	+2.31	9.31	0.2	11.62	0.1	0.00002784	0.00048967	0.01040015	0.28037671	A_07_P030984	c_0431	cmr|Choline dehydrogenase [c_0431]
betB	+2.79	12.11	+1.48	11.37	0.1	12.85	0.0	0.00015409	0.00165376	0.03074568	0.44903525	A_07_P008251	b0312	cmr|NAD+-dependent betaine aldehyde dehydrogenase [b0312]
betT	-2.72	10.97	-1.44	11.69	0.4	10.25	0.0	0.00175767	0.00998653	0.02735963	0.47387239	A_07_P051906	Z0401	cmr|high-affinity choline transport [Z0401]
bfr	-2.38	9.58	-1.25	10.21	0.1	8.96	0.0	0.00045092	0.00362761	0.04319995	0.55932566	A_07_P017709	b3336	cmr|bacterioferrin, an iron storage homoprotein [b3336]
bglJ	-2.03	7.89	-1.02	8.40	0.1	7.38	0.0	0.00124532	0.00765274	0.07175940	0.66732428	A_07_P017526	b4366	cmr|2-component transcriptional regulator [b4366]
bhsA	-21.35	10.52	-4.42	12.73	0.1	8.31	0.2	0.00000049	0.00005264	0.00001651	0.01300000	A_07_P001765	b1112	cmr|orf, hypothetical protein [b1112]
birA	-4.20	10.91	-2.07	11.94	0.0	9.87	0.1	0.00002185	0.00041549	0.00585938	0.25136240	A_07_P008550	b3973	cmr|biotin- [b3973]
bolA	+14.34	10.05	+3.84	8.13	0.0	11.98	0.0	0.00000040	0.00004930	0.00116679	0.10497143	A_07_P021288	b0435	cmr|possible regulator of murein genes [b0435]
bssS	-9.90	13.15	-3.31	14.80	0.0	11.49	0.1	0.00000134	0.00008557	0.00021977	0.04739726	A_07_P001504	b1060	cmr|orf, hypothetical protein [b1060]
btuB	-6.14	11.19	-2.62	12.49	0.0	9.88	0.5	0.00019524	0.00196595	0.00150597	0.12679144	A_07_P008533	b3966	cmr|outer membrane receptor for transport of vitamin B12, E colicins, and bacteriophage BF23 [b3966]
btuE	+2.18	9.05	+1.13	8.48	0.1	9.61	0.1	0.00099628	0.00650846	0.05235772	0.56421629	A_07_P044422	Z2739	cmr|vitamin B12 transport [Z2739]
btuE	+2.47	8.96	+1.30	8.31	0.1	9.62	0.1	0.00050733	0.00393662	0.03991679	0.49719146	A_07_P044422	Z2739	cmr|vitamin B12 transport [Z2739]
btuE	-2.60	10.63	-1.38	11.31	0.1	9.94	0.3	0.00108716	0.00692964	0.03133003	0.49623742	A_07_P035160	c_2106	cmr|Vitamin B12 transport periplasmic protein btuE [c_2106]
c_0036	+3.33	8.96	+1.74	8.10	0.2	9.83	0.1	0.00012296	0.00139175	0.02203316	0.39329932	A_07_P035658	c_0036	cmr|Hypothetical protein [c_0036]
c_0059	-2.30	11.81	-1.20	12.41	0.1	11.21	0.1	0.00087529	0.00591949	0.04761369	0.57663846	A_07_P035683	c_0059	cmr|Putative antitoxin of gyrase inhibiting toxin-antitoxin system [c_0059]
c_0062	-2.73	7.76	-1.45	8.48	0.1	7.03	0.1	0.00024126	0.00228540	0.02708206	0.47270510	A_07_P035698	c_0062	cmr|Hypothetical protein [c_0062]
c_0086	-2.50	10.51	-1.32	11.17	0.2	9.84	0.4	0.00394398	0.01878789	0.03470719	0.51307981	A_07_P035735	c_0086	cmr|Transposase [c_0086]
c_0088	-3.43	8.98	-1.78	9.87	0.1	8.09	0.1	0.00007290	0.00095734	0.01216527	0.33839223	A_07_P035738	c_0088	cmr|Hypothetical protein [c_0088]
c_0100	-2.44	11.39	-1.28	12.03	0.0	10.75	0.5	0.00618393	0.02696945	0.03980818	0.54029310	A_07_P041416	c_0100	cmr|S-adenosyl-methyltransferase mraW [c_0100]
c_0120	-5.23	9.78	-2.39	10.97	0.0	8.59	0.2	0.00002764	0.00048679	0.00267276	0.16967742	A_07_P035766	c_0120	cmr|Hypothetical protein [c_0120]
c_0138	-3.61	9.01	-1.85	9.94	0.0	8.09	0.2	0.00006491	0.00088731	0.01037729	0.32224852	A_07_P035783	c_0138	cmr|Unknown protein of IS629 encoded within prophage [c_0138]
c_0163	-2.02	9.74	-1.01	10.24	0.1	9.23	0.2	0.00303078	0.01527901	0.07138974	0.66664294	A_07_P035811	c_0163	cmr|Hypothetical protein [c_0163]
c_0192	-2.02	7.58	-1.01	8.08	0.0	7.07	0.1	0.00182749	0.01029029	0.07292175	0.66904429	A_07_P035893	c_0192	cmr|Hypothetical protein [c_0192]
c_0226	-2.83	9.21	-1.50	9.96	0.1	8.47	0.1	0.00016170	0.00171435	0.02430323	0.44962397	A_07_P035924	c_0226	cmr|Putative cell cycle protein mesJ [c_0226]
c_0253	-2.49	8.63	-1.32	9.28	0.0	7.97	0.0	0.00027668	0.00253932	0.03706682	0.52480216	A_07_P035949	c_0253	cmr|Hypothetical protein [c_0253]
c_0256	-2.78	7.98	-1.47	8.72	0.1	7.25	0.0	0.00018424	0.00188477	0.02624111	0.46735294	A_07_P035961	c_0256	cmr|Hypothetical protein [c_0256]
c_0257	-7.52	10.56	-2.91	12.02	0.0	9.11	0.1	0.00000321	0.00013128	0.00072218	0.08299270	A_07_P035967	c_0257	cmr|Unknown in ISEc8 [c_0257]
c_0258	-4.31	11.20	-2.11	12.25	0.2	10.14	0.2	0.00005496	0.00078754	0.00558435	0.24354571	A_07_P035972	c_0258	cmr|Unknown in ISEc8 [c_0258]
c_0260	-2.96	7.69	-1.57	8.47	0.1	6.90	0.1	0.00017223	0.00179690	0.02099784	0.41636020	A_07_P035978	c_0260	cmr|Hypothetical protein [c_0260]
c_0261	-2.23	7.85	-1.16	8.43	0.0	7.27	0.0	0.00056367	0.00423782	0.05310340	0.59846815	A_07_P035987	c_0261	cmr|Hypothetical protein [c_0261]
c_0264	-3.43	8.02	-1.78	8.91	0.0	7.13	0.0	0.00004644	0.00069738	0.01219639	0.33746924	A_07_P036004	c_0264	cmr|Hypothetical protein [c_0264]
c_0274	-2.53	8.24	-1.34	8.91	0.1	7.57	0.0	0.00030480	0.00271268	0.03498158	0.51089981	A_07_P036041	c_0274	cmr|Hypothetical protein [c_0274]
c_0277	-2.08	7.47	-1.05	8.00	0.0	6.94	0.0	0.00100507	0.00654555	0.06666413	0.64988235	A_07_P036056	c_0277	cmr|Hypothetical protein [c_0277]
c_0279	-3.49	7.75	-1.80	8.65	0.2	6.85	0.1	0.00015065	0.00162457	0.01164888	0.33467153	A_07_P036068	c_0279	cmr|Hypothetical protein ykfF [c_0279]
c_0280	-2.65	10.32	-1.40	11.02	0.4	9.62	0.1	0.00172723	0.00984915	0.02991997	0.48663223	A_07_P036072	c_0280	cmr|Hypothetical protein [c_0280]
c_0281	-2.83	10.32	-1.50	11.07	0.0	9.57	0.3	0.00048711	0.00383450	0.02360010	0.44286055	A_07_P036079	c_0281	cmr|Hypothetical protein [c_0281]
c_0284	-3.58	9.80	-1.84	10.72	0.1	8.88	0.1	0.00005273	0.00076604	0.01069931	0.32456647	A_07_P036095	c_0284	cmr|Conserved hypothetical protein [c_0284]
c_0286	-4.61	9.72	-2.20	10.82	0.1	8.62	0.1	0.00002215	0.00041939	0.00416984	0.21177419	A_07_P036101	c_0286	cmr|Conserved hypothetical protein [c_0286]
c_0287	-6.35	12.32	-2.67	13.65	0.1	10.98	0.0	0.00000553	0.00017942	0.00138402	0.12522989	A_07_P036106	c_0287	cmr|Hypothetical protein [c_0287]
c_0289	-4.47	8.40	-2.16	9.48	0.1	7.32	0.1	0.00002464	0.00045104	0.00462589	0.22272171	A_07_P036114	c_0289	cmr|Hypothetical protein [c_0289]
c_0297	-2.08	10.37	-1.05	10.90	0.3	9.85	0.1	0.00552769	0.02470981	0.06644499	0.65178193	A_07_P036146	c_0297	cmr|Hypothetical protein [c_0297]
c_0301	-2.43	7.55	-1.28	8.18	0.0	6.91	0.1	0.00044254	0.00358038	0.04041349	0.54335611	A_07_P036159	c_0301	cmr|Hypothetical protein [c_0301]
c_0304	-2.31	7.60	-1.21	8.21	0.1	7.00	0.1	0.00071095	0.00498360	0.04688707	0.57581123	A_07_P036164	c_0304	cmr|Hypothetical protein [c_0304]
c_0305	-4.56	9.71	-2.19	10.80	0.3	8.61	0.5	0.00093184	0.00618762	0.00453506	0.22037037	A_07_P036170	c_0305	cmr|Hypothetical protein [c_0305]
c_0309	-2.75	8.38	-1.46	9.11	0.1	7.66	0.0	0.00018821	0.00191593	0.02711446	0.47222345	A_07_P036181	c_0309	cmr|Conserved hypothetical protein [c_0309]
c_0310	-2.21	8.11	-1.15	8.68	0.2	7.54	0.2	0.00264500	0.01373901	0.05425432	0.60537208	A_07_P036189	c_0310	cmr|Hypothetical protein [c_0310]
c_0313	-4.30	12.67	-2.10	13.72	0.3	11.61	0.3	0.00018503	0.00189159	0.00572218	0.24886740	A_07_P036201	c_0313	cmr|Hypothetical protein [c_0313]
c_0315	-3.25	10.37	-1.70	11.22	0.2	9.52	0.0	0.00020045	0.00200247	0.01505018	0.36908100	A_07_P036212	c_0315	cmr|Hypothetical protein [c_0315]
c_0316	-2.51	8.68	-1.33	9.34	0.1	8.02	0.3	0.00131852	0.00797966	0.03669207	0.52278733	A_07_P036219	c_0316	cmr|Hypothetical protein [c_0316]
c_0319	+2.86	8.93	+1.52	8.17	0.1	9.68	0.0	0.00013868	0.00152367	0.02953697	0.44373092	A_07_P036230	c_0319	cmr|Putative oligogalacturonide lyase [c_0319]
c_0328	-2.92	8.13	-1.55	8.91	0.0	7.36	0.1	0.00017324	0.00180391	0.02153138	0.42215442	A_07_P036267	c_0328	cmr|Hypothetical protein [c_0328]
c_0331	+4.01	8.60	+2.00	7.60	0.0	9.60	0.1	0.00002381	0.00044188	0.01586319	0.33933424	A_07_P036277	c_0331	cmr|Putative ribokinase [c_0331]
c_0332	+2.13	9.16	+1.09	8.61	0.0	9.70	0.2	0.00202682	0.01116916	0.05452807	0.57118430	A_07_P030713	c_0332	cmr|Putative L-fucose permease [c_0332]
c_0337	-7.17	10.57	-2.84	11.99	0.0	9.15	0.1	0.00000355	0.00013789	0.00085366	0.09142857	A_07_P030738	c_0337	cmr|Putative conserved protein [c_0337]
c_0339	-4.21	9.07	-2.07	10.10	0.1	8.03	0.1	0.00002571	0.00046319	0.00584286	0.25133880	A_07_P030741	c_0339	cmr|Hypothetical protein [c_0339]
c_0340	-3.21	8.66	-1.68	9.51	0.0	7.82	0.2	0.00015661	0.00167393	0.01541159	0.37271889	A_07_P030749	c_0340	cmr|Conserved hypothetical protein [c_0340]
c_0348	-2.52	9.12	-1.34	9.79	0.0	8.45	0.0	0.00025679	0.00239370	0.03552020	0.51541935	A_07_P030761	c_0348	cmr|Hypothetical protein [c_0348]
c_0349	-3.84	7.91	-1.94	8.88	0.2	6.93	0.3	0.00024648	0.00232227	0.00842607	0.29878378	A_07_P030767	c_0349	cmr|Putative Transposase within prophage [c_0349]
c_0352	-5.51	9.67	-2.46	10.90	0.1	8.44	0.1	0.00000834	0.00022675	0.00222370	0.15699552	A_07_P030781	c_0352	cmr|Partial Transposase [c_0352]
c_0355	-5.06	9.08	-2.34	10.25	0.2	7.91	0.2	0.00005434	0.00078198	0.00318534	0.19214559	A_07_P030788	c_0355	cmr|Hypothetical protein [c_0355]
c_0357	-2.86	8.09	-1.52	8.85	0.1	7.33	0.3	0.00085615	0.00581755	0.02242251	0.43368550	A_07_P030794	c_0357	cmr|Hypothetical protein [c_0357]
c_0358	-2.80	8.47	-1.49	9.21	0.1	7.73	0.1	0.00023864	0.00227020	0.02486090	0.45512791	A_07_P030798	c_0358	cmr|Hypothetical protein [c_0358]
c_0361	-2.65	12.28	-1.41	12.98	0.3	11.57	0.0	0.00107460	0.00687464	0.02999555	0.48685567	A_07_P030810	c_0361	cmr|Putative cytoplasmic membrane export protein [c_0361]
c_0365	-4.37	8.31	-2.13	9.37	0.1	7.24	0.1	0.00002131	0.00041024	0.00506669	0.23054913	A_07_P030828	c_0365	cmr|Hypothetical protein [c_0365]
c_0385	-3.39	8.31	-1.76	9.19	0.0	7.43	0.0	0.00005502	0.00078754	0.01290968	0.34332770	A_07_P030859	c_0385	cmr|Hypothetical protein [c_0385]
c_0393	-2.21	7.98	-1.14	8.55	0.2	7.41	0.1	0.00156232	0.00908314	0.05506733	0.60883427	A_07_P030878	c_0393	cmr|Haemoglobin protease [c_0393]
c_0396	-2.07	7.77	-1.05	8.29	0.0	7.24	0.1	0.00117271	0.00730198	0.06704395	0.65116595	A_07_P030886	c_0396	cmr|Insertion element IS1 1/2/3/5/6 protein insA [c_0396]
c_0397	-3.28	7.87	-1.71	8.73	0.0	7.02	0.0	0.00006032	0.00084197	0.01437881	0.35990461	A_07_P030892	c_0397	cmr|InsB protein [c_0397]
c_0410	+5.09	8.81	+2.35	7.64	0.0	9.99	0.0	0.00000859	0.00022953	0.00969830	0.27120782	A_07_P030916	c_0410	cmr|Hypothetical protein ycjY [c_0410]
c_0413	+3.30	7.51	+1.72	6.65	0.2	8.37	0.4	0.00118945	0.00738206	0.02354294	0.40911700	A_07_P030931	c_0413	cmr|Putative aldo/keto reductase [c_0413]
c_0414	+5.59	8.66	+2.48	7.42	0.0	9.91	0.2	0.00001298	0.00029667	0.00811230	0.24945312	A_07_P030940	c_0414	cmr|2,5-diketo-D-gluconic acid reductase A [c_0414]
c_0427	-2.80	8.23	-1.49	8.97	0.3	7.49	0.2	0.00186327	0.01045079	0.02455602	0.45164720	A_07_P030962	c_0427	cmr|Conserved hypothetical protein [c_0427]
c_0429	-2.37	9.17	-1.25	9.79	0.0	8.55	0.0	0.00037936	0.00319396	0.04368585	0.56054605	A_07_P030975	c_0429	cmr|Conserved hypothetical protein [c_0429]
c_0467	-2.27	8.58	-1.18	9.17	0.1	7.99	0.0	0.00067174	0.00479850	0.05040015	0.58647450	A_07_P031049	c_0467	cmr|Hypothetical protein yaiO [c_0467]
c_0481	-2.67	8.82	-1.41	9.52	0.0	8.11	0.1	0.00020382	0.00202457	0.02941374	0.48138254	A_07_P031085	c_0481	cmr|Hypothetical protein [c_0481]
c_0487	-3.05	11.70	-1.61	12.51	0.0	10.90	0.0	0.00009069	0.00111721	0.01873666	0.39437166	A_07_P041502	c_0487	cmr|D-alanine--D-alanine ligase A [c_0487]
c_0503	+2.38	9.40	+1.25	8.77	0.1	10.02	0.1	0.00082600	0.00565414	0.04257241	0.51047982	A_07_P031097	c_0503	cmr|Hypothetical protein yajF [c_0503]
c_0550	+2.32	7.26	+1.21	6.65	0.1	7.86	0.1	0.00060068	0.00443370	0.04538364	0.52849112	A_07_P031150	c_0550	cmr|Hypothetical protein [c_0550]
c_0583	-4.16	10.48	-2.06	11.51	0.1	9.45	0.1	0.00003293	0.00054976	0.00607342	0.25430851	A_07_P031182	c_0583	cmr|Hypothetical protein [c_0583]
c_0608	-3.15	10.41	-1.66	11.24	0.1	9.58	0.3	0.00059751	0.00442070	0.01697917	0.38025605	A_07_P031211	c_0608	cmr|Hypothetical protein [c_0608]
c_0608	-2.25	9.73	-1.17	10.32	0.3	9.15	0.1	0.00222208	0.01199330	0.05124936	0.59198092	A_07_P031211	c_0608	cmr|Hypothetical protein [c_0608]
c_0638	-2.35	8.43	-1.24	9.05	0.1	7.82	0.1	0.00092723	0.00617004	0.04334604	0.55846154	A_07_P031250	c_0638	cmr|Hypothetical protein [c_0638]
c_0640	+2.79	7.84	+1.48	7.10	0.1	8.58	0.2	0.00034627	0.00296932	0.03103277	0.45071956	A_07_P031257	c_0640	cmr|Conserved hypothetical protein [c_0640]
c_0697	-3.19	8.68	-1.67	9.52	0.1	7.85	0.2	0.00016621	0.00175269	0.01571646	0.37377644	A_07_P031357	c_0697	cmr|Conserved hypothetical protein [c_0697]
c_0719	-2.56	8.09	-1.36	8.77	0.1	7.41	0.1	0.00028991	0.00262169	0.03331428	0.50676329	A_07_P033287	c_0719	cmr|Conserved hypothetical protein [c_0719]
c_0761	+2.45	7.64	+1.29	6.99	0.0	8.28	0.0	0.00031134	0.00275220	0.04068153	0.50077404	A_07_P033336	c_0761	cmr|Putative dihydrodipicolinate synthase [c_0761]
c_0778	+37.34	9.34	+5.22	6.73	0.0	11.95	0.1	0.00000006	0.00003344	0.00007431	0.02340000	A_07_P033361	c_0778	cmr|Hypothetical protein [c_0778]
c_0784	-6.07	8.62	-2.60	9.92	0.0	7.31	0.3	0.00002007	0.00039347	0.00157965	0.12886010	A_07_P033375	c_0784	cmr|Hypothetical protein [c_0784]
c_0795	+2.06	7.63	+1.04	7.11	0.0	8.15	0.0	0.00108489	0.00692357	0.05897866	0.59370844	A_07_P033384	c_0795	cmr|Putative conserved protein [c_0795]
c_0813	-2.27	8.19	-1.18	8.78	0.4	7.59	0.2	0.00820557	0.03364282	0.05014355	0.58695911	A_07_P033406	c_0813	cmr|Hypothetical protein [c_0813]
c_0897	+24.35	13.44	+4.61	11.14	0.1	15.74	0.4	0.00000264	0.00011947	0.00025978	0.04595506	A_07_P033506	c_0897	cmr|Hypothetical protein [c_0897]
c_0938	-2.73	7.70	-1.45	8.42	0.3	6.97	0.0	0.00125915	0.00772048	0.02683498	0.47100334	A_07_P033552	c_0938	cmr|Hypothetical protein [c_0938]
c_0940	-2.33	7.63	-1.22	8.24	0.0	7.02	0.1	0.00056673	0.00425291	0.04630843	0.57317610	A_07_P033562	c_0940	cmr|Hypothetical protein ybiI [c_0940]
c_0947	-2.54	11.84	-1.35	12.51	0.2	11.17	0.3	0.00165643	0.00952130	0.03368839	0.50755024	A_07_P033599	c_0947	cmr|Probable capsid portal protein [c_0947]
c_1005	-2.46	7.84	-1.30	8.49	0.1	7.19	0.1	0.00051927	0.00399580	0.03902503	0.53473455	A_07_P041077	c_1005	cmr|NADH oxidoreductase hcr [c_1005]
c_1020	-2.71	9.18	-1.44	9.90	0.1	8.46	0.0	0.00019111	0.00193740	0.02758511	0.47568456	A_07_P033805	c_1020	cmr|Hypothetical protein [c_1020]
c_1094	-2.35	10.72	-1.23	11.33	0.3	10.10	0.0	0.00160038	0.00927702	0.04361852	0.56059592	A_07_P033878	c_1094	cmr|Hypothetical protein [c_1094]
c_1111	-2.71	9.54	-1.44	10.26	0.3	8.82	0.1	0.00100463	0.00654555	0.02764672	0.47466739	A_07_P033904	c_1111	cmr|Hypothetical protein [c_1111]
c_1138	+2.66	9.26	+1.41	8.56	0.3	9.97	0.1	0.00166841	0.00957964	0.03534489	0.47724700	A_07_P033937	c_1138	cmr|Hypothetical protein [c_1138]
c_1166	+5.44	9.21	+2.44	7.99	0.2	10.43	0.1	0.00002390	0.00044210	0.00861725	0.25841905	A_07_P033974	c_1166	cmr|Conserved hypothetical protein [c_1166]
c_1172	-4.54	8.08	-2.18	9.17	0.1	6.99	0.1	0.00002339	0.00043630	0.00440930	0.21761755	A_07_P034010	c_1172	cmr|Hypothetical protein [c_1172]
c_1173	-6.18	11.14	-2.63	12.46	0.1	9.83	0.5	0.00017393	0.00180865	0.00147485	0.12551351	A_07_P034004	c_1173	cmr|Hypothetical protein [c_1173]
c_1174	-3.47	9.81	-1.80	10.70	0.2	8.91	0.3	0.00042433	0.00348135	0.01215257	0.33863717	A_07_P040226	c_1174	cmr|Hypothetical protein [c_1174]
c_1174	-3.15	9.67	-1.65	10.50	0.1	8.84	0.2	0.00022394	0.00216966	0.01685785	0.37969957	A_07_P040226	c_1174	cmr|Hypothetical protein [c_1174]
c_1174	-2.21	9.96	-1.14	10.53	0.2	9.39	0.4	0.00728257	0.03058331	0.05183943	0.59099203	A_07_P040226	c_1174	cmr|Hypothetical protein [c_1174]
c_1174	-2.42	9.90	-1.27	10.54	0.2	9.27	0.3	0.00439179	0.02054201	0.03869792	0.53303587	A_07_P040226	c_1174	cmr|Hypothetical protein [c_1174]
c_1175	+5.89	8.15	+2.56	6.87	0.1	9.43	0.2	0.00000996	0.00025049	0.00714685	0.24145923	A_07_P040232	c_1175	cmr|Putative aminotransferase [c_1175]
c_1186	-2.29	9.00	-1.19	9.60	0.1	8.41	0.0	0.00059276	0.00438964	0.04907711	0.58447050	A_07_P040258	c_1186	cmr|Putative beta-ketoacyl-ACP synthase [c_1186]

c_1187	+3.06	7.17	+1.61	6.36	0.4	7.98	0.0	0.00080370	0.00552067	0.02663173	0.42741081	A_07_P040261	c_1187	cmr|3-oxoacyl- [c_1187]
c_1189	+2.03	7.61	+1.02	7.10	0.0	8.12	0.1	0.00142754	0.00844932	0.06099149	0.60128366	A_07_P040271	c_1189	cmr|Putative 3-oxoacyl- [c_1189]
c_1190	+2.69	7.72	+1.43	7.01	0.0	8.44	0.1	0.00022453	0.00217267	0.03303100	0.46556849	A_07_P040280	c_1190	cmr|Conserved hypothetical protein [c_1190]
c_1198	-2.42	8.81	-1.27	9.45	0.0	8.18	0.1	0.00041749	0.00343417	0.04053227	0.54356048	A_07_P040314	c_1198	cmr|Conserved hypothetical protein [c_1198]
c_1199	-3.52	10.50	-1.81	11.41	0.0	9.59	0.3	0.00032643	0.00283787	0.01158981	0.33419414	A_07_P040317	c_1199	cmr|Putative acyl carrier protein [c_1199]
c_1202	-2.35	7.66	-1.24	8.28	0.0	7.05	0.1	0.00060450	0.00445358	0.04425749	0.56238095	A_07_P040334	c_1202	cmr|Conserved hypothetical protein [c_1202]
c_1203	-2.20	9.70	-1.14	10.27	0.1	9.13	0.2	0.00134273	0.00809032	0.05487170	0.60795215	A_07_P040338	c_1203	cmr|Putative O-methyltransferase [c_1203]
c_1204	-2.39	10.13	-1.26	10.76	0.1	9.50	0.1	0.00060308	0.00444514	0.04185722	0.54962469	A_07_P040344	c_1204	cmr|Conserved hypothetical protein [c_1204]
c_1204	-3.25	10.37	-1.70	11.22	0.0	9.52	0.1	0.00008818	0.00109403	0.01506733	0.36892691	A_07_P040344	c_1204	cmr|Conserved hypothetical protein [c_1204]
c_1204	-2.52	10.41	-1.33	11.07	0.1	9.74	0.1	0.00043739	0.00355327	0.03520262	0.51270120	A_07_P040344	c_1204	cmr|Conserved hypothetical protein [c_1204]
c_1204	-3.60	9.98	-1.85	10.90	0.1	9.05	0.3	0.00021800	0.00213179	0.01049035	0.32320939	A_07_P040344	c_1204	cmr|Conserved hypothetical protein [c_1204]
c_1204	-3.24	10.19	-1.69	11.04	0.1	9.34	0.0	0.00008226	0.00104105	0.01516387	0.36956656	A_07_P040344	c_1204	cmr|Conserved hypothetical protein [c_1204]
c_1206	-2.14	9.06	-1.10	9.61	0.0	8.51	0.2	0.00146660	0.00862539	0.05980501	0.62855140	A_07_P040351	c_1206	cmr|Hypothetical protein [c_1206]
c_1209	-2.56	9.55	-1.36	10.23	0.2	8.87	0.2	0.00117909	0.00733158	0.03263910	0.50627586	A_07_P040366	c_1209	cmr|Hypothetical protein [c_1209]
c_1214	+2.95	12.45	+1.56	11.67	0.1	13.23	0.0	0.00011486	0.00132092	0.02767658	0.43314115	A_07_P040383	c_1214	cmr|Cea protein [c_1214]
c_1215	-4.52	12.58	-2.18	13.67	0.0	11.49	0.0	0.00001356	0.00030459	0.00445185	0.21767081	A_07_P040390	c_1215	cmr|Entry exclusion protein 2 [c_1215]
c_1219	-2.53	8.21	-1.34	8.88	0.0	7.54	0.2	0.00045928	0.00367611	0.03612424	0.51750682	A_07_P040407	c_1219	cmr|Putative Transposase [c_1219]
c_1220	-3.07	8.93	-1.62	9.74	0.2	8.12	0.1	0.00032254	0.00281803	0.01770389	0.38658807	A_07_P040413	c_1220	cmr|Phospho-2-dehydro-3-deoxyheptonate aldolase, Trp-sensitive [c_1220]
c_1225	-2.46	10.08	-1.30	10.73	0.1	9.43	0.1	0.00054184	0.00411349	0.03768674	0.52741333	A_07_P040430	c_1225	cmr|Transposase insE for insertion sequence IS3A/B/C/D/E/fA/fB [c_1225]
c_1235	-11.05	8.78	-3.47	10.51	0.0	7.04	0.1	0.00000101	0.00007407	0.00012513	0.03862745	A_07_P040469	c_1235	cmr|Conserved hypothetical protein [c_1235]
c_1236	-7.06	8.88	-2.82	10.29	0.0	7.47	0.0	0.00000273	0.00012064	0.00097307	0.10013072	A_07_P040474	c_1236	cmr|Conserved hypothetical protein [c_1236]
c_1249	-2.70	7.87	-1.43	8.58	0.1	7.15	0.1	0.00030899	0.00273608	0.02850165	0.47839019	A_07_P040540	c_1249	cmr|Hypothetical protein [c_1249]
c_1253	-4.66	9.61	-2.22	10.72	0.1	8.49	0.2	0.00003365	0.00055720	0.00404535	0.20813725	A_07_P040560	c_1253	cmr|ATP binding cassette [c_1253]
c_1257	-23.00	11.03	-4.52	13.29	0.1	8.77	0.1	0.00000022	0.00004002	0.00000921	0.00878788	A_07_P040573	c_1257	cmr|Putative conserved protein [c_1257]
c_1258	-2.96	7.57	-1.57	8.35	0.4	6.78	0.4	0.00361801	0.01758082	0.02067200	0.41302030	A_07_P040577	c_1258	cmr|Hypothetical protein [c_1258]
c_1267	-3.44	8.50	-1.78	9.39	0.5	7.61	0.4	0.00460613	0.02137938	0.01185658	0.33694946	A_07_P040614	c_1267	cmr|Hypothetical protein [c_1267]
c_1268	-2.75	8.25	-1.46	8.98	0.0	7.52	0.0	0.00015475	0.00165961	0.02664444	0.46975364	A_07_P040616	c_1268	cmr|Hypothetical protein [c_1268]
c_1271	-2.03	8.61	-1.02	9.12	0.1	8.10	0.1	0.00148001	0.00869077	0.07131987	0.66638576	A_07_P040631	c_1271	cmr|Hypothetical protein [c_1271]
c_1272	-4.68	8.02	-2.23	9.13	0.1	6.90	0.0	0.00001406	0.00031050	0.00395135	0.20736667	A_07_P040636	c_1272	cmr|Hypothetical protein yeeP [c_1272]
c_1273	+2.75	11.16	+1.46	10.43	0.1	11.89	0.1	0.00023131	0.00222327	0.03210747	0.45912807	A_07_P040643	c_1273	cmr|Antigen 43 precursor [c_1273]
c_1284	-5.17	11.07	-2.37	12.26	0.2	9.89	0.0	0.00002188	0.00041549	0.00276994	0.17444000	A_07_P040687	c_1284	cmr|Hypothetical protein yeeT [c_1284]
c_1286	-7.64	9.98	-2.93	11.45	0.0	8.51	0.2	0.00000488	0.00016794	0.00063961	0.07992063	A_07_P040696	c_1286	cmr|Hypothetical protein [c_1286]
c_1294	-3.93	7.65	-1.97	8.64	0.0	6.66	0.1	0.00002816	0.00049161	0.00740218	0.27550827	A_07_P040732	c_1294	cmr|Hypothetical protein [c_1294]
c_1323	+2.05	7.81	+1.04	7.29	0.1	8.32	0.1	0.00121835	0.00753406	0.06002731	0.59663510	A_07_P040769	c_1323	cmr|Cytochrome b561 homolog 2 [c_1323]
c_1337	-2.65	7.64	-1.41	8.34	0.0	6.94	0.0	0.00019136	0.00193876	0.02981263	0.48538780	A_07_P040785	c_1337	cmr|Hypothetical protein [c_1337]
c_1406	-3.06	8.35	-1.62	9.16	0.1	7.55	0.1	0.00010397	0.00123441	0.01831809	0.38867925	A_07_P040862	c_1406	cmr|Hypothetical protein [c_1406]
c_1413	-2.13	10.13	-1.09	10.68	0.2	9.59	0.2	0.00378201	0.01815367	0.06169906	0.63531066	A_07_P040889	c_1413	cmr|Unknown protein encoded within prophage [c_1413]
c_1413	-3.01	10.02	-1.59	10.82	0.1	9.23	0.1	0.00012169	0.00137842	0.01963097	0.40191157	A_07_P040889	c_1413	cmr|Unknown protein encoded within prophage [c_1413]
c_1413	-2.33	10.11	-1.22	10.72	0.3	9.50	0.1	0.00161992	0.00936961	0.04660506	0.57458888	A_07_P040889	c_1413	cmr|Unknown protein encoded within prophage [c_1413]
c_1417	-2.37	9.30	-1.25	9.92	0.4	8.67	0.1	0.00514141	0.02328724	0.04317772	0.55949794	A_07_P040905	c_1417	cmr|Hypothetical protein [c_1417]
c_1421	-12.97	9.49	-3.70	11.34	0.1	7.64	0.0	0.00000065	0.00005973	0.00005653	0.02282051	A_07_P040925	c_1421	cmr|Hypothetical protein [c_1421]
c_1436	-2.74	8.77	-1.45	9.50	0.2	8.04	0.0	0.00049589	0.00387652	0.02710938	0.47265781	A_07_P042220	c_1436	cmr|Probable lysozyme from lambdoid prophage Qin [c_1436]
c_1444	-2.32	10.95	-1.21	11.56	0.2	10.34	0.1	0.00106656	0.00683435	0.04648247	0.57397647	A_07_P041004	c_1444	cmr|Prophage Qin DNA packaging protein NU1 homolog [c_1444]
c_1445	+2.19	10.55	+1.13	9.98	0.2	11.11	0.1	0.00167289	0.00959142	0.05271977	0.56540872	A_07_P041010	c_1445	cmr|Putative DNA packaging protein of prophage terminase [c_1445]
c_1446	+2.35	10.70	+1.23	10.09	0.3	11.32	0.0	0.00304880	0.01533556	0.04514863	0.52653333	A_07_P041015	c_1446	cmr|Putative DNA packaging protein of prophage [c_1446]
c_1448	+16.87	11.09	+4.08	9.05	0.1	13.13	0.2	0.00000064	0.00005892	0.00077299	0.08278912	A_07_P041021	c_1448	cmr|Putative capsid assembly protein of prophage [c_1448]
c_1453	+9.76	11.28	+3.29	9.64	0.1	12.93	0.1	0.00000208	0.00010447	0.00272612	0.15328571	A_07_P038108	c_1453	cmr|Putative head-tail joining protein of prophage [c_1453]
c_1457	-2.39	8.87	-1.26	9.50	0.5	8.24	0.2	0.00963082	0.03810697	0.04156822	0.54857502	A_07_P038133	c_1457	cmr|Hypothetical protein [c_1457]
c_1484	-2.70	8.98	-1.43	9.70	0.4	8.26	0.2	0.00217741	0.01181128	0.02720655	0.47278146	A_07_P038229	c_1484	cmr|Unknown protein encoded by prophage [c_1484]
c_1487	-2.72	10.26	-1.44	10.98	0.1	9.54	0.0	0.00023244	0.00223011	0.02765879	0.47435730	A_07_P038235	c_1487	cmr|Hypothetical protein [c_1487]
c_1496	-2.34	9.52	-1.23	10.13	0.5	8.90	0.0	0.00827161	0.03384310	0.04448107	0.56385668	A_07_P038279	c_1496	cmr|Unknown protein encoded by prophage [c_1496]
c_1501	+2.81	8.91	+1.49	8.17	0.0	9.66	0.1	0.00018131	0.00186421	0.03066057	0.44945996	A_07_P038305	c_1501	cmr|Hypothetical protein [c_1501]
c_1506	-2.98	8.04	-1.58	8.83	0.0	7.25	0.2	0.00018609	0.00190000	0.02009972	0.40779639	A_07_P038330	c_1506	cmr|Unknown protein encoded by prophage [c_1506]
c_1514	-2.35	12.13	-1.24	12.75	0.0	11.52	0.2	0.00110264	0.00699719	0.04430132	0.56203062	A_07_P038334	c_1514	cmr|Hypothetical protein [c_1514]
c_1519	+11.52	8.78	+3.53	7.02	0.3	10.54	0.2	0.00001253	0.00029182	0.00186547	0.12881579	A_07_P038347	c_1519	cmr|Prophage lambda integrase [c_1519]
c_1522	+49.53	10.48	+5.63	7.66	0.4	13.30	0.3	0.00000116	0.00007956	0.00001842	0.00935484	A_07_P038354	c_1522	cmr|Hypothetical protein [c_1522]
c_1523	+45.54	12.01	+5.51	9.26	0.1	14.77	0.2	0.00000009	0.00003427	0.00003303	0.01405405	A_07_P035459	c_1523	cmr|Unknown protein encoded by bacteriophage [c_1523]
c_1524	+25.47	10.45	+4.67	8.12	0.0	12.79	0.8	0.00003460	0.00056633	0.00021087	0.04000000	A_07_P038365	c_1524	cmr|Hypothetical protein [c_1524]
c_1525	+37.38	12.05	+5.22	9.44	0.0	14.66	0.2	0.00000022	0.00003960	0.00006098	0.02181818	A_07_P038369	c_1525	cmr|Hypothetical protein [c_1525]
c_1526	+47.56	10.55	+5.57	7.76	0.1	13.33	0.2	0.00000014	0.00003548	0.00002414	0.01187500	A_07_P038374	c_1526	cmr|Hypothetical protein [c_1526]
c_1527	+30.29	10.11	+4.92	7.65	0.3	12.57	0.1	0.00000084	0.00006592	0.00013148	0.03234375	A_07_P038377	c_1527	cmr|Hypothetical protein [c_1527]
c_1528	+37.02	10.26	+5.21	7.65	0.3	12.86	0.9	0.00004461	0.00067949	0.00006098	0.02133333	A_07_P038381	c_1528	cmr|Hypothetical protein [c_1528]
c_1531	+71.59	11.14	+6.16	8.06	0.0	14.22	0.2	0.00000006	0.00003344	0.00000635	0.00666667	A_07_P038395	c_1531	cmr|Hypothetical protein [c_1531]
c_1532	+18.33	11.09	+4.20	8.99	0.3	13.19	0.1	0.00000171	0.00009748	0.00065358	0.07566176	A_07_P038400	c_1532	cmr|Unknown protein encoded within prophage [c_1532]
c_1533	+2.08	12.34	+1.06	11.81	0.3	12.87	0.1	0.00387837	0.01854039	0.05993140	0.59718987	A_07_P038402	c_1533	cmr|Hypothetical protein [c_1533]
c_1536	+3.08	13.79	+1.62	12.98	0.1	14.60	0.2	0.00015546	0.00166500	0.02576855	0.42437238	A_07_P038406	c_1536	cmr|Putative recombination protein Bet of prophage [c_1536]
c_1538	+20.85	12.87	+4.38	10.67	0.0	15.06	0.1	0.00000027	0.00004211	0.00043445	0.06107143	A_07_P038419	c_1538	cmr|Hypothetical protein [c_1538]
c_1540	+4.72	14.52	+2.24	13.40	0.1	15.64	0.0	0.00001264	0.00029313	0.01157203	0.29290997	A_07_P038423	c_1540	cmr|Lambda Regulatory protein CIII [c_1540]
c_1541	+8.94	13.82	+3.16	12.24	0.0	15.41	0.5	0.00005442	0.00078251	0.00319614	0.16662252	A_07_P038427	c_1541	cmr|Putative single-stranded DNA binding protein of prophage [c_1541]
c_1542	-2.71	15.17	-1.44	15.89	0.0	14.45	0.1	0.00018152	0.00186421	0.02827426	0.47558761	A_07_P038431	c_1542	cmr|Lambda ant-restriction protein [c_1542]
c_1546	-4.02	12.42	-2.01	13.42	0.0	11.41	0.1	0.00003119	0.00053034	0.00700330	0.26762136	A_07_P038451	c_1546	cmr|Repressor protein [c_1546]
c_1547	+4.32	12.87	+2.11	11.82	0.1	13.93	0.1	0.00002376	0.00044169	0.01368839	0.31646109	A_07_P038456	c_1547	cmr|Hypothetical protein [c_1547]
c_1548	+2.73	12.03	+1.45	11.30	0.2	12.75	0.3	0.00130654	0.00793298	0.03314914	0.46639857	A_07_P038465	c_1548	cmr|Putative Regulatory protein CII of bacteriophage [c_1548]
c_1549	+6.95	13.27	+2.80	11.87	0.0	14.67	0.0	0.00000285	0.00012365	0.00521913	0.20855330	A_07_P038470	c_1549	cmr|Putative replication protein O of bacteriophage [c_1549]
c_1550	+4.05	14.64	+2.02	13.63	0.1	15.65	0.2	0.00005542	0.00079029	0.01558244	0.33699176	A_07_P038471	c_1550	cmr|Putative replication protein P of bacteriophage [c_1550]
c_1554	+41.30	10.62	+5.37	7.93	0.2	13.30	0.1	0.00000012	0.00003548	0.00005399	0.02073171	A_07_P038485	c_1554	cmr|Unknown protein encoded within prophage [c_1554]
c_1555	+23.29	9.62	+4.54	7.35	0.1	11.89	0.3	0.00000068	0.00006127	0.00031949	0.05239583	A_07_P038490	c_1555	cmr|Putative DNA N-6-adenine-methyltransferase of bacteriophage [c_1555]
c_1556	+100.86	10.61	+6.66	7.28	0.2	13.94	0.1	0.00000003	0.00003344	0.00000064	0.00125000	A_07_P038492	c_1556	cmr|Hypothetical protein [c_1556]
c_1565	+3.99	12.51	+2.00	11.51	0.2	13.51	0.3	0.00024458	0.00230877	0.01545351	0.33604972	A_07_P038514	c_1565	cmr|Partial tonB-like membrane protein encoded within prophage [c_1565]
c_1567	+4.74	9.98	+2.25	8.86	0.1	11.10	0.3	0.00009809	0.00118435	0.01105945	0.28732673	A_07_P038518	c_1567	cmr|Hypothetical protein [c_1567]
c_1570	+2.93	10.99	+1.55	10.21	0.4	11.76	0.0	0.00153853	0.00896468	0.02936484	0.44325983	A_07_P038532	c_1570	cmr|Putative DNA packaging protein of prophage [c_1570]
c_1571	+7.02	9.51	+2.81	8.10	0.0	10.91	0.1	0.00000326	0.00013195	0.00517467	0.20836317	A_07_P038538	c_1571	cmr|Putative capsid protein of prophage [c_1571]
c_1572	+42.15	10.55	+5.40	7.86	0.1	13.25	0.2	0.00000016	0.00003548	0.00004764	0.01973684	A_07_P038541	c_1572	cmr|Putative capsid assembly protein of prophage [c_1572]
c_1574	+18.06	10.41	+4.17	8.32	0.1	12.50	0.2	0.00000062	0.00005819	0.00063199	0.07481203	A_07_P038551	c_1574	cmr|Putative capsid protein of prophage [c_1574]
c_1575	+17.97	9.42	+4.17	7.34	0.2	11.51	0.3	0.00000248	0.00011555	0.00064533	0.07582090	A_07_P038556	c_1575	cmr|Putative capsid protein of prophage [c_1575]
c_1576	+11.05	9.38	+3.47	7.65	0.2	11.11	0.1	0.00000395	0.00014758	0.00202553	0.13177686	A_07_P038564	c_1576	cmr|Hypothetical protein [c_1576]
c_1577	+12.51	8.85	+3.65	7.03	0.1	10.68	0.2	0.00000158	0.00009392	0.00153709	0.11804878	A_07_P038569	c_1577	cmr|Putative head-tail joining protein of prophage [c_1577]
c_1579	+8.11	11.06	+3.02	9.55	0.1	12.57	0.3	0.00001003	0.00025069	0.00375127	0.17842900	A_07_P038580	c_1579	cmr|Putative tail component of prophage [c_1579]
c_1580	+37.55	9.64	+5.23	7.03	0.0	12.26	0.2	0.00000015	0.00003548	0.00007685	0.02372549	A_07_P038581	c_1580	cmr|Tail protein [c_1580]
c_1583	+8.95	9.47	+3.16	7.89	0.0	11.05	0.1	0.00000175	0.00009825	0.00322980	0.16672131	A_07_P038594	c_1583	cmr|Putative tail component of prophage [c_1583]
c_1585	+3.11	9.71	+1.64	8.89	0.2	10.53	0.2	0.00048931	0.00384271	0.02537221	0.42315678	A_07_P038605	c_1585	cmr|Putative tail component of prophage [c_1585]
c_1587	+2.49	9.62	+1.32	8.96	0.1	10.28	0.1	0.00061776	0.00452296	0.03910696	0.49334936	A_07_P038615	c_1587	cmr|Putative tail component of prophage [c_1587]
c_1590	+2.12	9.51	+1.08	8.97	0.1	10.06	0.1	0.00143197	0.00846284	0.05630081	0.58200919	A_07_P038626	c_1590	cmr|Putative tail component of prophage [c_1590]
c_1591	+2.28	9.31	+1.19	8.72	0.3	9.90	0.1	0.00334406	0.01643911	0.04963415	0.55500000	A_07_P038637	c_1591	cmr|Hypothetical protein [c_1591]
c_1593	+3.12	7.99	+1.64	7.17	0.2	8.81	0.2	0.00031656	0.00278278	0.02523183	0.42126193	A_07_P038645	c_1593	cmr|Hypothetical protein [c_1593]
c_1596	-3.17	8.87	-1.66	9.70	0.0	8.04	0.2	0.00012656	0.00142224	0.01622586	0.37789941	A_07_P038656	c_1596	cmr|Hypothetical protein [c_1596]
c_1605	-4.16	11.49	-2.06	12.52	0.1	10.47	0.0	0.00002668	0.00047513	0.00608105	0.25395225	A_07_P038687	c_1605	cmr|Hypothetical protein [c_1605]
c_1611	-2.22	8.36	-1.15	8.93	0.3	7.78	0.1	0.00301130	0.01521009	0.05223069	0.59330447	A_07_P038708	c_1611	cmr|Hypothetical protein [c_1611]
c_1640	-4.00	11.85	-2.00	12.85	0.1	10.85	0.1	0.00005581	0.00079521	0.00699441	0.26793187	A_07_P038726	c_1640	cmr|Putative Na [c_1640]
c_1657	+5.23	8.38	+2.39	7.19	0.1	9.58	0.1	0.00001317	0.00029928	0.00919970	0.26822222	A_07_P038777	c_1657	cmr|Protein ycgS [c_1657]
c_1660	-3.62	9.45	-1.85	10.38	0.0	8.53	0.2	0.00011571	0.00132585	0.01034045	0.32365805	A_07_P038788	c_1660	cmr|Hypothetical protein [c_1660]
c_1714	-6.19	10.94	-2.63	12.25	0.1	9.62	0.1	0.00000833	0.00022675	0.00152376	0.12760638	A_07_P038863	c_1714	cmr|Hypothetical protein [c_1714]
c_1755	+2.21	8.98	+1.14	8.41	0.0	9.55	0.0	0.00060575	0.00445856	0.05038554	0.55864085	A_07_P038912	c_1755	cmr|Conserved hypothetical protein [c_1755]
c_1766	-2.33	8.65	-1.22	9.26	0.4	8.04	0.2	0.00587739	0.02592801	0.04396913	0.56234768	A_07_P034731	c_1766	cmr|Putative membrane transport protein [c_1766]
c_1800	+2.51	8.75	+1.33	8.09	0.1	9.42	0.1	0.00034988	0.00299377	0.03848831	0.48907183	A_07_P034765	c_1800	cmr|Conserved hypothetical protein [c_1800]
c_1812	-3.41	9.49	-1.77	10.38	0.2	8.61	0.2	0.00020074	0.00200374	0.01278519	0.34232993	A_07_P034785	c_1812	cmr|Hypothetical protein [c_1812]
c_1819	+2.49	8.91	+1.32	8.25	0.2	9.57	0.2	0.00087652	0.00592275	0.03952680	0.49428912	A_07_P034790	c_1819	cmr|Putative conserved protein [c_1819]
c_1825	+5.12	10.43	+2.36	9.25	0.3	11.60	0.1	0.00004019	0.00062962	0.00965638	0.27099822	A_07_P034801	c_1825	cmr|Hypothetical protein [c_1825]
c_1935	-3.84	8.68	-1.94	9.65	0.2	7.71	0.3	0.00019392	0.00195589	0.00839050	0.29819413	A_07_P034987	c_1935	cmr|Chaperone protein fimC precursor [c_1935]
c_1956	-4.17	10.91	-2.06	11.94	0.2	9.88	0.1	0.00010381	0.00123350	0.00629192	0.25864230	A_07_P035043	c_1956	cmr|Putative outer membrane protein yieC precursor [c_1956]
c_1989	-9.66	10.59	-3.27	12.23	0.1	8.95	0.1	0.00000187	0.00009959	0.00022929	0.04878378	A_07_P035078	c_1989	cmr|Putative acid shock protein [c_1989]
c_2059	+2.01	9.26	+1.00	8.76	0.1	9.76	0.1	0.00274436	0.01410089	0.06430831	0.61886919	A_07_P035140	c_2059	cmr|Protein ydhR precursor [c_2059]
c_2148	+4.02	8.24	+2.01	7.24	0.4	9.24	0.2	0.00050248	0.00391058	0.01544398	0.33677285	A_07_P035198	c_2148	cmr|Succinylornithine transaminase [c_2148]
c_2155	+4.66	9.39	+2.22	8.28	0.2	10.50	0.1	0.00003590	0.00058029	0.01174733	0.29450637	A_07_P042371	c_2155	cmr|Protein ynjB [c_2155]
c_2158	+9.34	9.95	+3.22	8.34	0.0	11.56	0.1	0.00000134	0.00008557	0.00296557	0.15720539	A_07_P041171	c_2158	cmr|Putative thiosulfate sulfurtransferase ynjE precursor [c_2158]
c_2225	-2.11	7.62	-1.08	8.16	0.2	7.08	0.3	0.00556420	0.02483072	0.06394309	0.64574727	A_07_P035300	c_2225	cmr|Hypothetical protein [c_2225]
c_2255	-20.20	10.18	-4.34	12.35	0.0	8.01	0.1	0.00000019	0.00003706	0.00001651	0.01238095	A_07_P035318	c_2255	cmr|Hypothetical protein [c_2255]
c_2273	-2.31	9.94	-1.21	10.54	0.0	9.33	0.0	0.00048258	0.00381030	0.04759019	0.57724191	A_07_P035336	c_2273	cmr|High-affinity zinc uptake system membrane protein znuB [c_2273]
c_2348	+30.03	9.90	+4.91	7.45	0.4	12.36	0.3	0.00000413	0.00015132	0.00013211	0.03200000	A_07_P035389	c_2348	cmr|Outer membrane porin protein nmpC precursor [c_2348]
c_2405	+2.26	8.03	+1.18	7.44	0.1	8.62	0.1	0.00093493	0.00620521	0.04854611	0.54750000	A_07_P031475	c_2405	cmr|Hypothetical protein [c_2405]
c_2409	+2.73	7.81	+1.45	7.09	0.1	8.54	0.0	0.00017747	0.00183705	0.03250889	0.46151488	A_07_P031493	c_2409	cmr|Hypothetical protein [c_2409]
c_2412	-3.78	9.16	-1.92	10.12	0.4	8.20	0.1	0.00034373	0.00295415	0.00871507	0.30222467	A_07_P031509	c_2412	cmr|Hypothetical protein [c_2412]
c_2418	-3.32	8.95	-1.73	9.82	0.3	8.09	0.2	0.00039369	0.00329173	0.01338161	0.34765677	A_07_P031531	c_2418	cmr|Prophage P4 integrase [c_2418]
c_2423	-2.32	7.93	-1.21	8.54	0.1	7.33	0.0	0.00064284	0.00464471	0.04700775	0.57505051	A_07_P031557	c_2423	cmr|Putataive AraC type regulator [c_2423]
c_2450	+2.90	12.01	+1.53	11.24	0.0	12.77	0.1	0.00015643	0.00167317	0.02872269	0.43946550	A_07_P031648	c_2450	cmr|Hypothetical protein [c_2450]
c_2451	+3.16	10.58	+1.66	9.75	0.0	11.41	0.1	0.00008787	0.00109097	0.02422066	0.41314193	A_07_P031651	c_2451	cmr|Putative thioesterase [c_2451]
c_2454	+3.87	8.55	+1.95	7.57	0.0	9.52	0.1	0.00003748	0.00059842	0.01700394	0.34677461	A_07_P031667	c_2454	cmr|Hypothetical protein [c_2454]
c_2455	-4.46	12.89	-2.16	13.96	0.1	11.81	0.2	0.00003130	0.00053044	0.00488122	0.22804154	A_07_P031671	c_2455	cmr|Putative peptide synthetase [c_2455]
c_2458	-2.86	9.61	-1.52	10.37	0.1	8.85	0.1	0.00015379	0.00165162	0.02339304	0.44160671	A_07_P031686	c_2458	cmr|Putative peptide synthetase [c_2458]
c_2460	+6.80	7.92	+2.76	6.54	0.2	9.31	0.1	0.00000817	0.00022493	0.00539825	0.21089330	A_07_P031697	c_2460	cmr|Putative polyketide synthase [c_2460]
c_2461	+4.69	8.78	+2.23	7.67	0.1	9.90	0.1	0.00001959	0.00038789	0.01173844	0.29475279	A_07_P031704	c_2461	cmr|Hypothetical protein [c_2461]
c_2463	+2.61	8.18	+1.39	7.49	0.1	8.87	0.1	0.00043918	0.00356045	0.03575203	0.47863946	A_07_P031708	c_2463	cmr|Putative transacylase [c_2463]
c_2466	+2.59	9.29	+1.37	8.60	0.4	9.97	0.2	0.00333375	0.01641745	0.03717099	0.48646717	A_07_P031725	c_2466	cmr|Hypothetical protein [c_2466]
c_2467	+3.40	9.54	+1.76	8.66	0.1	10.42	0.0	0.00006399	0.00087841	0.02122523	0.38498848	A_07_P031728	c_2467	cmr|Putative 3-hydroxyacyl-CoA dehydrogenase [c_2467]
c_2467	+2.39	9.72	+1.26	9.09	0.4	10.35	0.0	0.00341103	0.01672999	0.04467988	0.52339286	A_07_P031728	c_2467	cmr|Putative 3-hydroxyacyl-CoA dehydrogenase [c_2467]
c_2467	+2.93	9.83	+1.55	9.06	0.3	10.61	0.3	0.00174661	0.00994168	0.02936484	0.44283525	A_07_P031728	c_2467	cmr|Putative 3-hydroxyacyl-CoA dehydrogenase [c_2467]
c_2467	+2.50	9.60	+1.32	8.94	0.3	10.26	0.0	0.00103688	0.00669591	0.03944995	0.49490040	A_07_P031728	c_2467	cmr|Putative 3-hydroxyacyl-CoA dehydrogenase [c_2467]
c_2467	+3.10	9.91	+1.63	9.09	0.4	10.72	0.1	0.00103523	0.00669352	0.02627096	0.42684211	A_07_P031728	c_2467	cmr|Putative 3-hydroxyacyl-CoA dehydrogenase [c_2467]
c_2468	+4.26	8.24	+2.09	7.20	0.1	9.29	0.2	0.00003656	0.00058730	0.01414190	0.32174855	A_07_P031733	c_2468	cmr|Putative polyketide synthase [c_2468]
c_2470	+3.07	8.98	+1.62	8.17	0.2	9.79	0.0	0.00016819	0.00176652	0.02577807	0.42408568	A_07_P031741	c_2470	cmr|Putative peptide/polyketide synthase [c_2470]
c_2481	-6.22	8.07	-2.64	9.39	0.0	6.75	0.2	0.00000912	0.00023883	0.00148310	0.12553763	A_07_P031773	c_2481	cmr|Hypothetical protein [c_2481]
c_2482	-6.86	8.34	-2.78	9.73	0.1	6.95	0.0	0.00000334	0.00013377	0.00104548	0.10287500	A_07_P031779	c_2482	cmr|Putative outer membrane receptor for iron compound [c_2482]
c_2484	-5.20	11.62	-2.38	12.80	0.0	10.43	0.1	0.00000858	0.00022953	0.00268483	0.16975904	A_07_P031782	c_2484	cmr|Hypothetical protein ybdM [c_2484]
c_2485	-2.08	10.61	-1.06	11.14	0.1	10.08	0.2	0.00269736	0.01391457	0.06613885	0.65121326	A_07_P031787	c_2485	cmr|Hypothetical protein ybdN [c_2485]
c_2489	-2.40	7.84	-1.26	8.47	0.1	7.21	0.1	0.00059604	0.00441187	0.04160633	0.54861809	A_07_P031799	c_2489	cmr|Putative transferase [c_2489]
c_2492	+2.21	8.13	+1.14	7.56	0.0	8.70	0.1	0.00086261	0.00585134	0.05107215	0.55916551	A_07_P031808	c_2492	cmr|Putative carbohydrate kinase [c_2492]
c_2494	+2.99	7.95	+1.58	7.16	0.2	8.74	0.0	0.00017949	0.00185302	0.02703633	0.42779899	A_07_P031818	c_2494	cmr|Hypothetical protein [c_2494]
c_2496	-2.48	9.91	-1.31	10.57	0.0	9.25	0.1	0.00039822	0.00332076	0.03720020	0.52527354	A_07_P031827	c_2496	cmr|Hypothetical protein [c_2496]
c_2497	-2.33	10.28	-1.22	10.89	0.0	9.66	0.1	0.00046278	0.00369283	0.04620173	0.57275591	A_07_P031834	c_2497	cmr|Transposase [c_2497]
c_2500	-5.71	8.47	-2.51	9.72	0.1	7.21	0.3	0.00003357	0.00055697	0.00203061	0.14732719	A_07_P031846	c_2500	cmr|Hypothetical protein [c_2500]
c_2501	-2.26	8.94	-1.18	9.53	0.0	8.35	0.2	0.00091596	0.00611315	0.05105056	0.59055107	A_07_P031851	c_2501	cmr|Hypothetical protein [c_2501]
c_2512	+2.71	8.42	+1.44	7.70	0.2	9.14	0.1	0.00042714	0.00349708	0.03343750	0.46753108	A_07_P031888	c_2512	cmr|Transposase [c_2512]
c_2514	+6.46	9.09	+2.69	7.74	0.1	10.43	0.0	0.00000413	0.00015132	0.00608041	0.22577830	A_07_P031900	c_2514	cmr|Hypothetical protein [c_2514]
c_2522	-3.06	10.00	-1.61	10.80	0.0	9.19	0.0	0.00008684	0.00108440	0.01829713	0.38875843	A_07_P031916	c_2522	cmr|Conserved hypothetical protein [c_2522]
c_2528	-3.24	8.95	-1.70	9.80	0.1	8.10	0.1	0.00010763	0.00126648	0.01476435	0.36548742	A_07_P031949	c_2528	cmr|Hypothetical protein [c_2528]
c_2558	+5.88	10.83	+2.55	9.56	0.2	12.11	0.1	0.00001683	0.00035043	0.00737741	0.24452632	A_07_P031994	c_2558	cmr|Mannose-1-phosphate guanylyltransferase [c_2558]
c_2562	-2.79	12.85	-1.48	13.58	0.0	12.11	0.1	0.00020273	0.00201497	0.02537411	0.45918391	A_07_P032014	c_2562	cmr|Glycosyl transferase [c_2562]
c_2566	-2.61	11.56	-1.39	12.25	0.0	10.87	0.1	0.00022964	0.00221673	0.03186992	0.49876740	A_07_P032030	c_2566	cmr|Hypothetical protein [c_2566]
c_2669	-4.15	9.35	-2.05	10.38	0.5	8.32	0.1	0.00088812	0.00598822	0.00639926	0.25701531	A_07_P032221	c_2669	cmr|Hypothetical protein [c_2669]
c_2670	-3.08	9.30	-1.62	10.11	0.2	8.49	0.3	0.00057666	0.00430688	0.01764101	0.38628651	A_07_P032229	c_2670	cmr|Putative conserved protein [c_2670]
c_2729	-3.58	8.71	-1.84	9.63	0.1	7.79	0.1	0.00005426	0.00078198	0.01045859	0.32286275	A_07_P032291	c_2729	cmr|Hypothetical protein [c_2729]
c_2755	-3.08	10.50	-1.62	11.31	0.1	9.69	0.1	0.00011952	0.00135862	0.01817772	0.38831750	A_07_P032344	c_2755	cmr|Hypothetical protein [c_2755]
c_2891	-2.68	10.90	-1.42	11.61	0.0	10.18	0.3	0.00131114	0.00794857	0.02933753	0.48163712	A_07_P032517	c_2891	cmr|Hypothetical protein [c_2891]
c_2895	-3.40	10.54	-1.77	11.43	0.0	9.66	0.2	0.00014103	0.00154404	0.01283473	0.34307301	A_07_P032532	c_2895	cmr|yapH homolog [c_2895]
c_2896	-2.01	11.16	-1.01	11.66	0.1	10.65	0.2	0.00323869	0.01605494	0.07252096	0.67005282	A_07_P032539	c_2896	cmr|Hypothetical protein [c_2896]
c_2897	+2.72	7.60	+1.44	6.88	0.2	8.32	0.0	0.00042845	0.00350235	0.03318407	0.46647321	A_07_P032543	c_2897	cmr|Type 1 fimbriae Regulatory protein fimB [c_2897]
c_2911	-2.14	8.05	-1.10	8.60	0.0	7.50	0.0	0.00077416	0.00535752	0.06056593	0.63274718	A_07_P042574	c_2911	cmr|YfdX protein precursor [c_2911]
c_3030	-2.36	8.21	-1.24	8.83	0.1	7.59	0.1	0.00078222	0.00539515	0.04420922	0.56313107	A_07_P030168	c_3030	cmr|SinI homolog [c_3030]
c_3031	-5.45	8.77	-2.45	9.99	0.0	7.54	0.1	0.00000834	0.00022675	0.00227134	0.15893333	A_07_P030171	c_3031	cmr|SinH homolog [c_3031]
c_3053	-5.05	12.02	-2.34	13.19	0.2	10.85	0.1	0.00002101	0.00040692	0.00296684	0.18246094	A_07_P041244	c_3053	cmr|Protein yfhF [c_3053]
c_3116	-3.61	11.11	-1.85	12.03	0.0	10.18	0.0	0.00003741	0.00059799	0.01019309	0.32485830	A_07_P030232	c_3116	cmr|Ribosomal large subunit pseudouridine synthase D [c_3116]
c_3156	+2.13	8.21	+1.09	7.67	0.1	8.76	0.1	0.00124606	0.00765430	0.05540079	0.57610964	A_07_P030311	c_3156	cmr|Putative tail fiber component K of prophage [c_3156]
c_3158	+4.18	8.07	+2.06	7.04	0.1	9.10	0.3	0.00010760	0.00126648	0.01427337	0.32194842	A_07_P030320	c_3158	cmr|Putative tail component of prophage [c_3158]
c_3159	+2.91	10.16	+1.54	9.39	0.5	10.93	0.4	0.00677485	0.02892955	0.03122269	0.45264273	A_07_P030328	c_3159	cmr|Putative tail component of prophage [c_3159]
c_3161	+6.64	8.26	+2.73	6.90	0.2	9.63	0.2	0.00001118	0.00027255	0.00570567	0.21909756	A_07_P030336	c_3161	cmr|Putative tail component of prophage [c_3161]
c_3163	+10.03	8.60	+3.33	6.94	0.2	10.26	0.2	0.00000516	0.00017391	0.00248666	0.14773585	A_07_P030350	c_3163	cmr|Putative tail component of prophage [c_3163]
c_3164	+20.63	9.16	+4.37	6.98	0.1	11.34	0.3	0.00000198	0.00010186	0.00045668	0.06252174	A_07_P030353	c_3164	cmr|Putative tail component of prophage [c_3164]
c_3165	+5.50	9.21	+2.46	7.98	0.6	10.44	0.1	0.00075642	0.00525554	0.00820122	0.25120623	A_07_P030358	c_3165	cmr|Putative tail fiber component Z of prophage [c_3165]
c_3170	-2.16	7.50	-1.11	8.06	0.0	6.95	0.0	0.00076961	0.00533070	0.05935976	0.62722148	A_07_P030384	c_3170	cmr|Putative capsid protein of prophage [c_3170]
c_3176	+22.85	11.92	+4.51	9.67	0.1	14.18	0.0	0.00000021	0.00003960	0.00034045	0.05360000	A_07_P030411	c_3176	cmr|GnsB protein [c_3176]
c_3214	-2.01	8.52	-1.01	9.02	0.0	8.02	0.0	0.00129101	0.00785683	0.07301004	0.66946418	A_07_P030524	c_3214	cmr|Hypothetical protein [c_3214]
c_3224	-2.10	8.90	-1.07	9.43	0.2	8.36	0.0	0.00191708	0.01066141	0.06408981	0.64598592	A_07_P030537	c_3224	cmr|Conserved hypothetical protein [c_3224]
c_3225	+2.36	8.40	+1.24	7.78	0.0	9.02	0.1	0.00057437	0.00429996	0.04342543	0.51599245	A_07_P030542	c_3225	cmr|Conserved hypothetical protein [c_3225]
c_3242	-2.91	8.94	-1.54	9.71	0.1	8.17	0.5	0.00427627	0.02010921	0.02241425	0.43405904	A_07_P030574	c_3242	cmr|Hypothetical protein [c_3242]
c_3243	-2.03	9.09	-1.02	9.60	0.1	8.58	0.1	0.00207985	0.01140546	0.06978023	0.65904019	A_07_P030576	c_3243	cmr|Hypothetical protein [c_3243]
c_3252	-8.38	11.80	-3.07	13.33	0.0	10.26	0.0	0.00000159	0.00009392	0.00047764	0.06899083	A_07_P041659	c_3252	cmr|Regulatory protein recX [c_3252]
c_3270	-3.57	8.34	-1.84	9.26	0.0	7.42	0.0	0.00003805	0.00060518	0.01065485	0.32446809	A_07_P030625	c_3270	cmr|Hypothetical protein [c_3270]
c_3273	-4.72	12.93	-2.24	14.05	0.1	11.81	0.2	0.00002388	0.00044210	0.00379637	0.20539519	A_07_P030635	c_3273	cmr|Hypothetical protein ygjM [c_3273]
c_3274	-2.08	12.69	-1.05	13.22	0.0	12.17	0.1	0.00111221	0.00704458	0.06662093	0.65026658	A_07_P030642	c_3274	cmr|Hypothetical protein [c_3274]
c_3276	-2.19	8.35	-1.13	8.92	0.0	7.79	0.0	0.00066923	0.00478490	0.05632241	0.61281272	A_07_P030650	c_3276	cmr|Hypothetical protein [c_3276]
c_3292	+2.51	11.24	+1.33	10.58	0.3	11.90	0.1	0.00115979	0.00724307	0.03897167	0.49322347	A_07_P030663	c_3292	cmr|Potential molybdenum-pterin-binding-protein [c_3292]
c_3305	-3.08	7.70	-1.62	8.51	0.1	6.89	0.0	0.00009945	0.00119708	0.01825521	0.38839189	A_07_P030690	c_3305	cmr|Hypothetical protein [c_3305]
c_3309	-2.73	10.63	-1.45	11.36	0.2	9.91	0.1	0.00047759	0.00378609	0.02758321	0.47617325	A_07_P030697	c_3309	cmr|Hypothetical protein [c_3309]
c_3343	-2.43	7.49	-1.28	8.14	0.1	6.85	0.2	0.00095926	0.00633003	0.03898310	0.53462544	A_07_P032631	c_3343	cmr|Hypothetical protein [c_3343]
c_3379	-2.10	9.50	-1.07	10.04	0.1	8.96	0.1	0.00171857	0.00981186	0.06390244	0.64658098	A_07_P032655	c_3379	cmr|Hypothetical protein [c_3379]
c_3391	+2.09	7.90	+1.07	7.37	0.1	8.44	0.0	0.00111780	0.00707056	0.05746697	0.58560518	A_07_P032689	c_3391	cmr|Secreted protein Hcp [c_3391]
c_3391	+2.05	7.76	+1.04	7.24	0.3	8.28	0.1	0.00644007	0.02780162	0.06277248	0.60743085	A_07_P032689	c_3391	cmr|Secreted protein Hcp [c_3391]
c_3394	-5.33	8.17	-2.41	9.37	0.1	6.96	0.2	0.00002462	0.00045104	0.00259400	0.17159664	A_07_P032706	c_3394	cmr|Hypothetical protein [c_3394]
c_3395	-2.09	7.59	-1.07	8.12	0.1	7.06	0.2	0.00229506	0.01228192	0.06476372	0.64780178	A_07_P032713	c_3395	cmr|Hypothetical protein [c_3395]
c_3396	-4.26	8.78	-2.09	9.82	0.0	7.73	0.1	0.00002534	0.00045915	0.00548780	0.24338028	A_07_P032716	c_3396	cmr|Hypothetical protein [c_3396]
c_3397	-2.87	7.73	-1.52	8.49	0.0	6.97	0.0	0.00012170	0.00137842	0.02339240	0.44212485	A_07_P032722	c_3397	cmr|Hypothetical protein [c_3397]
c_3398	-2.62	10.75	-1.39	11.44	0.2	10.05	0.0	0.00058751	0.00436104	0.03092988	0.49437563	A_07_P032729	c_3398	cmr|Hypothetical protein [c_3398]
c_3432	-2.76	11.40	-1.46	12.13	0.1	10.67	0.3	0.00088897	0.00599144	0.02554116	0.46061856	A_07_P032816	c_3432	cmr|Transposase [c_3432]
c_3506	+6.16	10.60	+2.62	9.29	0.1	11.91	0.2	0.00001088	0.00026728	0.00665079	0.23268889	A_07_P032900	c_3506	cmr|Hypothetical protein [c_3506]
c_3507	+11.47	9.24	+3.52	7.48	0.3	11.00	0.3	0.00001392	0.00030904	0.00186039	0.12960177	A_07_P032905	c_3507	cmr|Hypothetical protein [c_3507]
c_3508	+6.17	9.09	+2.63	7.78	0.0	10.40	0.0	0.00000440	0.00015907	0.00662348	0.23328859	A_07_P032907	c_3508	cmr|Hypothetical protein [c_3508]
c_3509	+2.38	7.40	+1.25	6.77	0.0	8.02	0.1	0.00060729	0.00446453	0.04291603	0.51264795	A_07_P032913	c_3509	cmr|Putative ATP-binding protein of ABC transport system [c_3509]
c_3513	-3.35	12.42	-1.74	13.29	0.1	11.54	0.2	0.00011025	0.00128478	0.01352388	0.34847791	A_07_P032930	c_3513	cmr|Putative conserved protein [c_3513]
c_3518	-3.74	8.47	-1.90	9.42	0.1	7.52	0.1	0.00004421	0.00067646	0.00913681	0.30671642	A_07_P032938	c_3518	cmr|Hypothetical protein [c_3518]
c_3523	-2.00	7.17	-1.00	7.67	0.2	6.67	0.0	0.00301865	0.01524235	0.07454205	0.67564191	A_07_P032958	c_3523	cmr|Conserved hypothetical protein [c_3523]
c_3557	-4.29	9.41	-2.10	10.46	0.1	8.36	0.2	0.00003607	0.00058187	0.00556784	0.24350000	A_07_P032997	c_3557	cmr|ShiA homolog [c_3557]
c_3560	-4.02	8.17	-2.01	9.17	0.1	7.16	0.0	0.00003642	0.00058676	0.00692835	0.26735294	A_07_P033008	c_3560	cmr|Unknown protein encoded by ISEc8 within prophage [c_3560]
c_3564	-3.54	9.71	-1.82	10.62	0.4	8.80	0.0	0.00068068	0.00483817	0.01085683	0.32434535	A_07_P033028	c_3564	cmr|Hypothetical protein [c_3564]
c_3565	-4.98	10.28	-2.32	11.43	0.2	9.12	0.2	0.00004521	0.00068369	0.00324060	0.18966543	A_07_P033031	c_3565	cmr|Putative response regulator [c_3565]
c_3566	-2.01	7.83	-1.01	8.33	0.2	7.32	0.1	0.00244758	0.01291377	0.07278646	0.67014620	A_07_P033036	c_3566	cmr|Hypothetical protein [c_3566]
c_3575	-2.59	8.44	-1.37	9.13	0.2	7.75	0.0	0.00056631	0.00425177	0.03234502	0.50270484	A_07_P033084	c_3575	cmr|Transposase insF for insertion sequence IS3A/B/C/D/E/fA [c_3575]
c_3576	-2.29	8.99	-1.20	9.59	0.0	8.40	0.0	0.00050822	0.00393965	0.04881034	0.58261562	A_07_P033087	c_3576	cmr|Unknown in IS [c_3576]
c_3579	-4.43	10.25	-2.15	11.32	0.0	9.18	0.1	0.00002033	0.00039679	0.00475102	0.22598187	A_07_P033108	c_3579	cmr|Hypothetical protein [c_3579]
c_3580	-10.36	11.59	-3.37	13.28	0.0	9.90	0.1	0.00000110	0.00007696	0.00016324	0.04015625	A_07_P033102	c_3580	cmr|Hypothetical protein [c_3580]
c_3581	-4.39	11.71	-2.13	12.78	0.0	10.65	0.1	0.00001863	0.00037505	0.00488059	0.22869048	A_07_P033112	c_3581	cmr|Hypothetical protein [c_3581]
c_3594	-11.74	10.87	-3.55	12.64	0.1	9.09	0.0	0.00000069	0.00006127	0.00008003	0.03000000	A_07_P033172	c_3594	cmr|Putative Transposase [c_3594]
c_3595	-10.24	10.51	-3.36	12.19	0.0	8.84	0.3	0.00000628	0.00019141	0.00019118	0.04560606	A_07_P033176	c_3595	cmr|Transposase [c_3595]
c_3596	-8.68	11.41	-3.12	12.96	0.1	9.85	0.1	0.00000210	0.00010502	0.00040333	0.06350000	A_07_P033185	c_3596	cmr|Hypothetical protein in IS [c_3596]
c_3597	-5.43	9.92	-2.44	11.15	0.0	8.70	0.1	0.00000985	0.00024973	0.00232470	0.16052632	A_07_P033190	c_3597	cmr|Transposase [c_3597]
c_3598	-5.38	9.37	-2.43	10.58	0.0	8.15	0.1	0.00000810	0.00022454	0.00239139	0.16369565	A_07_P033191	c_3598	cmr|Hypothetical protein [c_3598]
c_3598	-6.60	9.55	-2.72	10.92	0.1	8.19	0.1	0.00000554	0.00017942	0.00116743	0.11139394	A_07_P033191	c_3598	cmr|Hypothetical protein [c_3598]
c_3598	-6.28	9.50	-2.65	10.82	0.1	8.17	0.1	0.00000546	0.00017880	0.00142785	0.12351648	A_07_P033191	c_3598	cmr|Hypothetical protein [c_3598]
c_3598	-8.02	9.44	-3.00	10.94	0.0	7.94	0.0	0.00000182	0.00009954	0.00056847	0.07649573	A_07_P033191	c_3598	cmr|Hypothetical protein [c_3598]
c_3598	-6.96	9.41	-2.80	10.81	0.1	8.02	0.0	0.00000302	0.00012594	0.00098450	0.10000000	A_07_P033191	c_3598	cmr|Hypothetical protein [c_3598]
c_3600	-2.57	9.96	-1.36	10.64	0.0	9.27	0.2	0.00047920	0.00379316	0.03409108	0.51068506	A_07_P033203	c_3600	cmr|Hypothetical protein [c_3600]
c_3601	-9.08	9.66	-3.18	11.25	0.1	8.07	0.0	0.00000157	0.00009392	0.00034045	0.05583333	A_07_P033207	c_3601	cmr|Hypothetical protein [c_3601]
c_3602	-4.05	11.94	-2.02	12.94	0.2	10.93	0.1	0.00006046	0.00084243	0.00675940	0.26341584	A_07_P033212	c_3602	cmr|Hypothetical protein [c_3602]
c_3603	-3.05	10.13	-1.61	10.93	0.1	9.32	0.4	0.00173790	0.00989906	0.01901677	0.39550859	A_07_P033216	c_3603	cmr|Hypothetical protein [c_3603]
c_3604	-2.40	8.32	-1.26	8.95	0.0	7.68	0.2	0.00066439	0.00476110	0.04135671	0.54900506	A_07_P033222	c_3604	cmr|Hypothetical protein [c_3604]
c_3606	+4.79	9.86	+2.26	8.73	0.1	10.99	0.1	0.00001500	0.00032347	0.01117759	0.28801964	A_07_P033231	c_3606	cmr|Hypothetical protein [c_3606]
c_3609	-2.80	8.79	-1.48	9.53	0.1	8.05	0.3	0.00076433	0.00529881	0.02561738	0.46146453	A_07_P033238	c_3609	cmr|Hypothetical protein [c_3609]
c_3612	-2.60	10.87	-1.38	11.56	0.2	10.18	0.2	0.00082584	0.00565414	0.03170160	0.49811377	A_07_P033247	c_3612	cmr|Transposase insC for insertion element IS2A/D/F/H/I/K [c_3612]
c_3614	-3.59	9.36	-1.84	10.28	0.1	8.43	0.1	0.00007989	0.00101674	0.01030615	0.32322709	A_07_P033257	c_3614	cmr|Hypothetical protein [c_3614]
c_3616	-2.76	10.96	-1.47	11.70	0.1	10.23	0.0	0.00024430	0.00230872	0.02642149	0.46897407	A_07_P033266	c_3616	cmr|Unknown in ISEc8 [c_3616]
c_3617	-2.48	8.34	-1.31	8.99	0.1	7.68	0.1	0.00040646	0.00336751	0.03800114	0.52899204	A_07_P036281	c_3617	cmr|Unknown in putative ISEc8 [c_3617]
c_3618	-9.26	9.58	-3.21	11.19	0.1	7.98	0.1	0.00000151	0.00009241	0.00029662	0.05367816	A_07_P036289	c_3618	cmr|Hypothetical protein [c_3618]
c_3618	-9.33	9.67	-3.22	11.29	0.1	8.06	0.1	0.00000177	0.00009825	0.00029281	0.05423529	A_07_P036289	c_3618	cmr|Hypothetical protein [c_3618]
c_3618	-8.38	9.32	-3.07	10.86	0.1	7.79	0.0	0.00000184	0.00009954	0.00047891	0.06854545	A_07_P036289	c_3618	cmr|Hypothetical protein [c_3618]
c_3618	-10.39	9.68	-3.38	11.37	0.1	7.99	0.1	0.00000112	0.00007798	0.00016133	0.04031746	A_07_P036289	c_3618	cmr|Hypothetical protein [c_3618]
c_3618	-8.55	9.31	-3.10	10.86	0.0	7.76	0.0	0.00000154	0.00009303	0.00041603	0.06421569	A_07_P036289	c_3618	cmr|Hypothetical protein [c_3618]
c_3620	-6.54	10.60	-2.71	11.95	0.1	9.24	0.2	0.00000801	0.00022294	0.00122015	0.11434524	A_07_P036293	c_3620	cmr|Hypothetical protein [c_3620]
c_3630	-3.64	9.42	-1.86	10.35	0.1	8.48	0.1	0.00004213	0.00064958	0.01004129	0.32395492	A_07_P036335	c_3630	cmr|Hypothetical protein yjhS precursor [c_3630]
c_3631	-3.68	9.31	-1.88	10.25	0.1	8.37	0.2	0.00012020	0.00136440	0.00925749	0.30879237	A_07_P036340	c_3631	cmr|Hypothetical protein [c_3631]
c_3636	+2.35	8.18	+1.23	7.56	0.0	8.80	0.0	0.00041120	0.00339303	0.04414380	0.52138035	A_07_P036358	c_3636	cmr|Hypothetical protein [c_3636]
c_3638	+2.51	8.60	+1.32	7.93	0.1	9.26	0.2	0.00100411	0.00654555	0.03895960	0.49346742	A_07_P036368	c_3638	cmr|Hypothetical protein yhcI [c_3638]
c_3639	+5.94	9.41	+2.57	8.12	0.0	10.69	0.0	0.00000490	0.00016801	0.00709604	0.24129590	A_07_P036375	c_3639	cmr|N-acetylneuraminate lyase subunit [c_3639]
c_3641	-4.06	9.38	-2.02	10.39	0.2	8.37	0.3	0.00014757	0.00159788	0.00698298	0.26814634	A_07_P036385	c_3641	cmr|Unknown in ISEc8 [c_3641]
c_3643	-2.31	10.88	-1.21	11.48	0.0	10.27	0.1	0.00066705	0.00477580	0.04809705	0.58070552	A_07_P036391	c_3643	cmr|Unknown in ISEc8 [c_3643]
c_3646	-4.18	12.18	-2.06	13.21	0.3	11.15	0.2	0.00018976	0.00192999	0.00594703	0.25237197	A_07_P036409	c_3646	cmr|Hypothetical protein [c_3646]
c_3648	-2.23	7.64	-1.15	8.21	0.0	7.06	0.0	0.00059978	0.00443275	0.05385480	0.60434070	A_07_P036418	c_3648	cmr|Hypothetical protein [c_3648]
c_3652	-2.73	9.32	-1.45	10.04	0.1	8.59	0.1	0.00021834	0.00213217	0.02730882	0.47351322	A_07_P036440	c_3652	cmr|Hypothetical protein yfjI [c_3652]
c_3654	-3.20	8.29	-1.68	9.13	0.0	7.45	0.1	0.00007783	0.00100024	0.01572917	0.37351433	A_07_P036449	c_3654	cmr|Hypothetical protein yeeP [c_3654]
c_3655	+4.53	11.35	+2.18	10.26	0.1	12.44	0.2	0.00004593	0.00069200	0.01248539	0.30148773	A_07_P036451	c_3655	cmr|Antigen 43 precursor [c_3655]
c_3658	-35.74	14.04	-5.16	16.62	0.0	11.46	0.0	0.00000006	0.00003344	0.00000254	0.00500000	A_07_P036466	c_3658	cmr|Hypothetical protein [c_3658]
c_3659	-36.27	9.91	-5.18	12.50	0.0	7.32	0.2	0.00000012	0.00003548	0.00000191	0.00428571	A_07_P036474	c_3659	cmr|Unknown protein encoded by ISEc8 [c_3659]
c_3660	-40.62	9.86	-5.34	12.53	0.0	7.19	0.1	0.00000006	0.00003344	0.00000127	0.00400000	A_07_P036480	c_3660	cmr|Unknown protein encoded by ISEc8 [c_3660]
c_3661	-2.14	8.79	-1.10	9.34	0.0	8.24	0.2	0.00222082	0.01199062	0.05936484	0.62685446	A_07_P036481	c_3661	cmr|Hypothetical protein [c_3661]
c_3662	-3.47	11.44	-1.79	12.33	0.1	10.54	0.1	0.00006923	0.00092999	0.01185023	0.33737794	A_07_P036488	c_3662	cmr|Unknown protein encoded by ISEc8 [c_3662]
c_3663	-4.84	8.68	-2.27	9.82	0.1	7.54	0.0	0.00001315	0.00029912	0.00343242	0.19369176	A_07_P036493	c_3663	cmr|Hypothetical protein [c_3663]
c_3666	-2.70	7.96	-1.43	8.68	0.0	7.24	0.1	0.00026573	0.00245372	0.02813897	0.47585392	A_07_P036509	c_3666	cmr|Hypothetical protein ykfF [c_3666]
c_3668	-2.41	9.03	-1.27	9.66	0.1	8.39	0.1	0.00042903	0.00350320	0.04201220	0.55120000	A_07_P036519	c_3668	cmr|Hypothetical protein yafZ [c_3668]

c_3670	-3.58	9.05	-1.84	9.97	0.0	8.13	0.1	0.00003973	0.00062482	0.01053481	0.32331384	A_07_P036530	c_3670
c_3675	-3.66	9.05	-1.54	10.36	0.0	8.82	0.1	0.00003159	0.00146726	0.02238694	0.43408404	A_07_P036540	c_3675
c_3681	-11.23	11.94	-3.49	10.48	0.0	10.20	0.1	0.00000378	0.00006333	0.00093544	0.03688889	A_07_P036563	c_3681
c_3682	-15.53	10.81	-3.96	12.78	0.0	8.83	0.1	0.00000041	0.00004972	0.00000176	0.01666667	A_07_P036581	c_3682
c_3683	-48.00	12.07	-5.59	14.86	0.0	9.28	0.2	0.00000007	0.00003344	0.00000004	0.00333333	A_07_P036593	c_3683
c_3686	+7.73	10.15	+2.95	8.68	0.1	11.63	0.0	0.00000126	0.00013195	0.00436766	0.18873596	A_07_P036604	c_3686
c_3689	+4.66	9.55	+2.22	8.04	0.1	10.26	0.0	0.00001795	0.00004652	0.01379717	0.29561129	A_07_P036619	c_3689
c_3693	+3.76	9.09	+1.95	8.14	0.2	10.05	0.5	0.01122096	0.00754130	0.01575812	0.35276046	A_07_P036636	c_3693
c_3693	+4.14	9.68	+2.05	8.66	0.3	10.75	0.3	0.00020649	0.00248118	0.01431720	0.32247496	A_07_P036636	c_3693
c_3693	+4.69	9.53	+2.23	8.42	0.0	10.65	0.0	0.00001154	0.00027747	0.01161331	0.29348315	A_07_P036636	c_3693
c_3693	+5.19	9.59	+2.38	8.41	0.0	10.78	0.0	0.00001246	0.00029182	0.01178294	0.26826401	A_07_P036636	c_3693
c_3693	+5.64	9.69	+2.50	8.44	0.1	10.94	0.1	0.00001282	0.00029422	0.00792302	0.24980000	A_07_P036636	c_3693
c_3694	-2.61	11.34	+1.38	10.64	0.0	12.03	0.2	0.00037046	0.00316432	0.01554433	0.47707587	A_07_P036641	c_3694
c_3695	+6.32	10.28	+2.66	8.95	0.2	11.61	0.1	0.00001787	0.00034585	0.00635673	0.22901602	A_07_P036649	c_3695
c_3703	-2.63	10.69	-1.40	11.38	0.4	9.94	0.3	0.00415636	0.01962154	0.08984308	0.49368744	A_07_P036678	c_3703
c_3712	-2.84	9.51	-1.51	9.86	0.5	8.35	0.1	0.00365790	0.01771453	0.02258622	0.44309069	A_07_P036681	c_3712
c_3766	-2.04	10.18	-1.03	10.69	0.0	9.67	0.0	0.00118679	0.00737365	0.07088351	0.66407540	A_07_P036765	c_3766
c_3772	-2.00	7.80	-1.00	8.30	0.3	7.42	0.3	0.01000337	0.03922098	0.07631669	0.67959842	A_07_P036806	c_3772
c_3774	-2.13	7.96	-1.09	8.51	0.2	7.42	0.3	0.00541979	0.03841630	0.06136638	0.61631283	A_07_P036820	c_3774
c_3819	-7.63	14.84	-2.93	16.30	0.0	13.37	0.3	0.00002140	0.00041080	0.00067010	0.08178295	A_07_P036906	c_3819
c_3873	+85.55	10.54	+6.42	7.31	0.0	13.75	0.4	0.00000025	0.00004211	0.00000254	0.00363636	A_07_P036983	c_3873
c_3890	+4.35	8.96	+2.12	7.90	0.7	10.02	0.3	0.00354636	0.01728069	0.03145084	0.31373333	A_07_P034096	c_3890
c_3891	+5.95	8.72	+2.57	7.43	0.3	10.00	0.1	0.00300764	0.00071298	0.00703566	0.24107066	A_07_P034105	c_3891
c_3928	+2.90	7.53	+1.26	6.90	0.0	8.16	0.1	0.00056498	0.00424382	0.04212452	0.51090761	A_07_P034139	c_3928
c_3976	+7.03	8.38	+2.81	6.97	0.1	9.79	0.0	0.00000290	0.00012554	0.00509909	0.20746186	A_07_P041030	c_3976
c_4010	+2.37	9.35	+1.25	8.71	0.1	9.97	0.1	0.00009663	0.00409357	0.04556136	0.51727179	A_07_P034196	c_4010
c_4013	-2.87	11.12	-1.52	11.88	0.0	10.37	0.3	0.00050293	0.00391210	0.02266514	0.43623472	A_07_P034204	c_4013
c_4014	-9.53	8.60	-3.25	10.22	0.1	6.97	0.1	0.00000165	0.00009590	0.00026931	0.05435897	A_07_P034207	c_4014
c_4015	-3.21	8.27	-1.68	9.11	0.1	7.42	0.3	0.00320327	0.00280126	0.01334488	0.37245658	A_07_P034215	c_4015
c_4016	-8.91	8.31	-3.15	9.88	0.0	6.72	0.0	0.00000133	0.00008557	0.00034239	0.05550701	A_07_P034216	c_4016
c_4064	-2.34	8.70	-1.23	9.31	0.0	8.09	0.2	0.00088345	0.00645412	0.04692248	0.57275454	A_07_P034279	c_4064
c_4074	-2.05	7.50	-1.04	8.02	0.1	6.98	0.1	0.00160014	0.00653567	0.04835386	0.65131498	A_07_P034295	c_4074
c_4088	-2.89	8.64	-1.53	9.40	0.0	7.87	0.3	0.00064316	0.00464494	0.02282903	0.43725061	A_07_P034318	c_4088
c_4209	-2.31	10.19	-1.01	10.80	0.0	9.59	0.1	0.00001957	0.00418282	0.04745109	0.57247904	A_07_P034572	c_4209
c_4223	+2.58	8.60	+1.37	7.91	0.0	9.28	0.1	0.00282083	0.00254758	0.03627819	0.48078283	A_07_P034506	c_4223
c_4277	+2.94	8.05	+1.56	7.27	0.3	8.83	0.0	0.00067879	0.00483352	0.02892756	0.44006681	A_07_P034581	c_4277
c_4284	-3.38	10.35	-1.76	11.23	0.1	9.47	0.0	0.00006186	0.00085663	0.01295795	0.34345118	A_07_P034612	c_4284
c_4352	-3.08	7.91	-1.05	8.43	0.0	7.38	0.0	0.00006313	0.00024695	0.00066277	0.16266227	A_07_P034674	c_4352
c_4360	-4.39	9.19	-2.04	10.16	0.1	8.03	0.5	0.00070340	0.00484828	0.00549543	0.24303371	A_07_P034692	c_4360
c_4422	-2.84	12.23	-1.51	12.58	0.2	11.47	0.2	0.00021976	0.00224334	0.00404345	0.44797633	A_07_P034723	c_4422
c_4437	+3.89	7.74	+1.96	6.76	0.1	8.72	0.1	0.00003111	0.00052951	0.01682454	0.34650195	A_07_P034756	c_4437
c_4437	+3.56	7.90	+1.83	6.98	0.1	8.81	0.1	0.00005920	0.00083145	0.01982914	0.36980336	A_07_P034756	c_4437
c_4437	+3.46	7.88	+1.79	6.98	0.1	8.78	0.0	0.00005088	0.00074789	0.01862311	0.37808140	A_07_P034756	c_4437
c_4437	+3.27	7.81	+1.71	6.95	0.1	8.66	0.1	0.00009916	0.00119443	0.02034417	0.40564877	A_07_P034756	c_4437
c_4437	+3.04	7.69	+1.60	7.13	0.1	8.24	0.2	0.00056730	0.00425363	0.02477846	0.42845528	A_07_P034756	c_4437
c_4481	-2.21	10.32	-1.15	10.89	0.1	9.75	0.2	0.00147108	0.00864850	0.05102340	0.59889685	A_07_P034839	c_4481
c_4486	+2.47	11.97	+1.30	8.65	0.1	7.95	0.0	0.00073605	0.00014135	0.00432662	0.12266224	A_07_P034865	c_4486
c_4486	+2.43	7.32	+1.28	6.68	0.1	7.96	0.1	0.00064617	0.00463377	0.04135988	0.50478295	A_07_P034865	c_4486
c_4486	+2.44	7.27	+1.29	6.63	0.0	7.90	0.1	0.00011262	0.00075733	0.04068280	0.50039844	A_07_P034865	c_4486
c_4486	+2.41	7.37	+1.27	6.73	0.2	8.00	0.3	0.00242815	0.01238651	0.04392658	0.51959429	A_07_P034865	c_4486
c_4487	+3.08	7.97	+1.62	7.16	0.1	8.78	0.0	0.00010830	0.00127097	0.02163115	0.42432228	A_07_P034867	c_4487
c_4488	+2.21	7.38	+1.14	6.81	0.0	7.95	0.2	0.01103158	0.00761804	0.05146659	0.55997927	A_07_P034873	c_4488
c_4493	-2.24	8.45	-1.16	9.03	0.0	7.87	0.2	0.00099344	0.00602848	0.05178544	0.59209150	A_07_P034886	c_4493
c_4523	-3.33	8.49	-1.74	9.36	0.2	7.62	0.2	0.00033643	0.00260553	0.01389155	0.35398822	A_07_P040008	c_4523
c_4548	-4.41	8.95	-2.14	10.02	0.2	7.88	0.3	0.00018843	0.00152298	0.00917534	0.22413793	A_07_P040129	c_4548
c_4580	-3.99	8.91	-2.00	9.91	0.2	7.92	0.1	0.00006641	0.00090442	0.00738686	0.27134393	A_07_P038963	c_4580
c_4688	+3.08	8.08	+1.62	7.27	0.6	8.89	0.2	0.00152571	0.02397730	0.04972617	0.42968034	A_07_P039023	c_4688
c_4735	+2.46	9.16	+1.30	8.51	0.1	9.81	0.1	0.00065548	0.00364940	0.03986664	0.49727488	A_07_P039123	c_4735
c_4758	-2.15	8.38	-1.23	7.66	0.4	8.90	0.1	0.01235420	0.01253409	0.04575521	0.53908530	A_07_P039181	c_4758
c_4762	-2.21	8.10	-1.14	8.67	0.2	7.53	0.3	0.00484344	0.02226426	0.05144863	0.60802521	A_07_P039201	c_4762
c_4769	+2.09	7.47	+1.06	8.52	0.2	8.00	0.1	0.00204941	0.01127391	0.05831803	0.58936830	A_07_P039231	c_4769
c_4770	+2.81	8.07	+1.49	7.53	0.0	8.81	0.1	0.00021347	0.00209925	0.01860991	0.44986952	A_07_P039236	c_4770
c_4776	+6.51	8.82	+2.17	7.74	0.3	9.91	0.1	0.00006881	0.00092591	0.01261751	0.30128244	A_07_P039258	c_4776
c_4777	+7.86	8.43	+2.97	6.94	0.0	9.92	0.2	0.00000415	0.00015177	0.00461650	0.18307246	A_07_P039263	c_4777
c_4778	+3.29	8.28	+1.72	7.43	0.1	9.71	0.1	0.00110378	0.00123152	0.03981344	0.39983344	A_07_P039269	c_4778
c_4779	+3.83	8.48	+1.94	7.51	0.1	9.45	0.1	0.00004185	0.00064800	0.01728468	0.34796233	A_07_P039274	c_4779
c_4780	+3.44	12.89	+1.78	12.00	0.0	13.78	0.1	0.00005899	0.00082929	0.02016069	0.38251179	A_07_P039276	c_4780
c_4836	+8.89	11.73	+3.11	10.08	0.0	13.38	0.2	0.00000262	0.00015964	0.00138728	0.14800725	A_07_P039365	c_4836
c_4837	-24.91	12.42	-4.64	14.74	0.0	10.10	0.1	0.00000015	0.00003548	0.00000609	0.00733333	A_07_P039369	c_4837
c_4838	-3.51	12.45	-1.81	13.35	0.1	11.54	0.1	0.00006439	0.00088167	0.01129192	0.33197910	A_07_P039373	c_4838
c_4839	-23.26	11.28	-4.54	13.55	0.1	9.01	0.1	0.00000019	0.00003706	0.00009921	0.00878788	A_07_P039376	c_4839
c_4858	-2.08	7.19	-1.06	8.66	0.0	7.72	0.2	0.00139138	0.00873732	0.07267312	0.58520107	A_07_P039424	c_4858
c_4924	-3.00	7.91	-1.59	8.70	0.0	7.11	0.1	0.00129378	0.00192678	0.03167276	0.40315175	A_07_P039536	c_4924
c_4925	-2.28	8.42	-1.25	9.05	0.1	7.80	0.2	0.00110936	0.00703689	0.04366423	0.56072594	A_07_P039541	c_4925
c_4926	-3.60	8.75	-1.85	9.67	0.1	7.82	0.2	0.00009887	0.00119375	0.01052083	0.32315562	A_07_P037396	c_4926
c_4986	-2.35	7.54	-1.23	8.16	0.1	6.93	0.3	0.00016898	0.00421682	0.04622675	0.56918465	A_07_P037506	c_4986
c_5019	-2.46	8.81	-2.31	9.96	0.0	7.65	0.2	0.00003008	0.00051644	0.00320884	0.18992481	A_07_P035565	c_5019
c_5029	-2.55	7.66	-1.35	8.33	0.0	6.98	0.1	0.00001110	0.00225320	0.02498538	0.51598193	A_07_P037590	c_5029
c_5033	-2.13	8.29	-1.09	8.84	0.1	7.75	0.1	0.00133635	0.00854492	0.06027980	0.63319868	A_07_P037610	c_5033
c_5035	+2.51	8.14	+1.35	7.47	0.1	8.83	0.0	0.00040108	0.00033578	0.03748984	0.48039522	A_07_P037619	c_5035
c_5055	-2.60	8.34	-1.38	7.65	0.0	9.03	0.2	0.00041565	0.00362042	0.03964884	0.47927782	A_07_P037658	c_5055
c_5058	-2.60	8.93	-1.38	9.62	0.2	8.24	0.2	0.00115467	0.00721967	0.03234502	0.50120158	A_07_P037663	c_5058
c_5061	-3.07	8.87	-1.62	9.68	0.7	8.06	0.3	0.00846565	0.03408004	0.01778011	0.38664365	A_07_P037671	c_5061
c_5063	-1.98	8.57	-1.58	9.36	0.2	7.78	0.1	0.00021106	0.00208075	0.01992691	0.40586028	A_07_P037671	c_5063
c_5062	-6.38	8.85	-2.67	7.52	0.1	10.19	0.1	0.00000761	0.00021549	0.00431542	0.22920138	A_07_P037679	c_5062
c_5088	-2.64	7.54	-1.40	8.24	0.0	6.84	0.0	0.00020171	0.00020865	0.01005569	0.49017436	A_07_P037733	c_5088
c_5135	-4.18	7.30	-1.12	7.86	0.4	6.74	0.3	0.00267622	0.01383164	0.05706745	0.61665752	A_07_P037796	c_5135
c_5153	-4.45	9.69	-2.15	10.77	0.0	8.62	0.2	0.00002800	0.00049142	0.00473450	0.22650135	A_07_P037845	c_5153
c_5154	-3.12	9.07	-1.64	9.89	0.1	8.25	0.2	0.00003125	0.00277437	0.01680471	0.37983557	A_07_P037850	c_5154
c_5166	-3.19	9.68	-1.67	10.52	0.0	8.85	0.2	0.00016398	0.00173498	0.01609557	0.37641902	A_07_P037902	c_5166
c_5207	-2.43	11.47	-1.28	12.11	0.0	10.84	0.3	0.00245124	0.01294373	0.04021341	0.54251928	A_07_P038018	c_5207
c_5233	-2.23	8.53	-1.15	9.10	0.1	7.95	0.0	0.00009560	0.00490746	0.05403709	0.60462240	A_07_P038033	c_5233
c_5265	-6.31	10.49	-2.66	11.82	0.0	9.16	0.1	0.00000514	0.00037372	0.00009037	0.12437500	A_07_P038094	c_5265
c_5296	-15.98	12.12	-4.00	14.12	0.0	10.12	0.1	0.00000049	0.00005264	0.00003174	0.01724138	A_07_P037000	c_5296
c_5297	-3.27	9.07	-1.70	9.87	0.2	8.16	0.2	0.00002632	0.00244187	0.01644444	0.35746783	A_07_P037001	c_5297
c_5321	-2.87	8.97	-1.52	9.73	0.2	8.21	0.5	0.00328103	0.01622380	0.02365573	0.44268351	A_07_P037042	c_5321
c_5334	-2.63	8.46	-1.40	7.76	0.1	8.16	0.2	0.00769324	0.02368166	0.04381374	0.48511686	A_07_P037056	c_5334
c_5341	-78.91	11.78	-6.30	14.93	0.1	8.63	0.1	0.00000002	0.00003344	0.00000000	0.00000000	A_07_P042071	c_5341
c_5343	-80.00	9.66	-5.32	12.10	0.1	7.00	0.2	0.00000010	0.00003427	0.00000127	0.00033333	A_07_P037072	c_5343
c_5350	-2.56	7.76	-1.36	8.43	0.1	7.08	0.2	0.00029383	0.00264683	0.03331872	0.55585452	A_07_P037109	c_5350
c_5375	-2.56	9.79	-1.36	10.41	0.4	9.05	0.3	0.00442881	0.02866605	0.03202109	0.50362555	A_07_P037145	c_5375
c_5376	-2.71	10.49	-1.44	11.21	0.2	9.77	0.3	0.00145624	0.00654356	0.02832190	0.47758407	A_07_P037149	c_5376
c_5416	-2.30	8.46	-1.20	7.86	0.2	9.06	0.1	0.00113202	0.00726015	0.04697091	0.53180130	A_07_P037222	c_5416
c_5455	-4.16	8.80	-2.06	7.77	0.1	9.83	0.4	0.00209057	0.00267978	0.04226843	0.52714849	A_07_P037341	c_5455
cshA	-9.51	11.78	-3.25	13.41	0.0	10.16	0.4	0.00001880	0.00037681	0.00027947	0.05410099	A_07_P010884	b0039
csiC	+2.59	8.16	+1.38	7.87	0.1	9.25	0.1	0.00033281	0.00287739	0.04612487	0.48936318	A_07_P037675	c_5064
cstA	-2.10	8.27	-1.07	6.29	0.0	7.90	0.2	0.00370676	0.01818085	0.05607720	0.58473836	A_07_P010887	b0040
carA	+4.97	8.86	+2.31	7.59	0.2	10.01	0.3	0.00366654	0.00806540	0.01843165	0.28089501	A_07_P010840	b0032
carB	+15.05	10.55	+3.91	8.60	0.2	12.51	0.1	0.00000141	0.00008809	0.00102579	0.09076559	A_07_P010855	b0033
cbl	5.81	12.96	2.54	14.23	0.0	13.68	0.1	0.00000348	0.00052217	0.00184894	0.10203008	A_07_P012271	b0367
cbpA	+5.66	8.58	+2.50	7.33	0.2	9.83	0.6	0.00068225	0.00484496	0.08046512	0.24968442	A_07_P012135	b1000
cbpM	+7.60	8.70	+2.93	7.23	0.0	10.16	0.1	0.00000295	0.00012541	0.00438135	0.18892549	A_07_P012126	b0999
ccmD	+2.20	7.94	+1.13	7.37	0.0	8.90	0.2	0.00087096	0.00590290	0.05162411	0.56034473	A_07_P033305	c_2735
cdaR	-2.39	9.46	-1.26	10.08	0.0	8.83	0.1	0.00089505	0.00604647	0.01816542	0.54979047	A_07_P002772	b0562
cdh	-2.40	8.13	-1.26	8.76	0.1	7.12	0.2	0.00081298	0.00557469	0.04210429	0.51948838	A_07_P033970	b3918
cdsA	-2.46	11.17	-1.30	11.83	0.0	10.52	0.4	0.00377216	0.01811930	0.03746881	0.52435502	A_07_P033981	b0175
cesA	-4.67	11.19	-2.22	12.30	0.1	10.08	0.2	0.00002948	0.00058857	0.00402249	0.20900990	A_07_P018702	b1731
chaA	-7.76	9.45	-2.46	10.68	0.0	8.23	0.3	0.00000152	0.00015776	0.02483244	0.47148408	A_07_P037032	b1216
chaB	-3.08	8.93	-1.66	9.46	0.0	8.40	0.1	0.00103857	0.00653968	0.06602229	0.65195715	A_07_P037036	b1217
chbC	-2.04	8.78	-1.03	9.29	0.2	8.26	0.3	0.00804993	0.03420749	0.06736598	0.65268308	A_07_P018731	b1737
chcA	-3.62	11.63	-1.86	12.56	0.1	10.70	0.1	0.00005155	0.00095836	0.00768291	0.33126430	A_07_P018084	b1881
chpB	-2.03	10.86	-1.02	11.27	0.0	10.35	0.0	0.00116813	0.00798215	0.07096102	0.66508333	A_07_P003680	b4225
chuS	-2.45	8.13	-1.29	7.48	0.2	8.77	0.1	0.00066807	0.00473877	0.04035823	0.49910590	A_07_P018657	c_4307
cipA	+5.44	10.17	+2.44	8.95	0.0	11.39	0.1	0.00000941	0.00024118	0.00595057	0.25811069	A_07_P004862	b0882
cipB	+2.51	9.46	+1.12	8.79	0.0	10.12	0.2	0.00068863	0.00487553	0.01910556	0.49417717	A_07_P004845	b0532
cipF	+3.14	11.92	+1.65	11.01	0.1	12.74	0.5	0.01158294	0.00916269	0.02509210	0.41981934	A_07_P021300	b0437
cipS	-9.12	10.36	-4.64	9.51	0.1	11.18	0.2	0.00019965	0.00199656	0.02350677	0.41942605	A_07_P004856	b0881
cirr	-2.62	8.04	-1.39	8.73	0.1	7.34	0.3	0.00023333	0.00223585	0.03105310	0.49433771	A_07_P004661	b0842
cobB	-2.10	8.76	-1.07	8.23	0.0	9.29	0.2	0.00216169	0.01112176	0.05055139	0.58307771	A_07_P024609	2761
cobS	-2.87	8.87	-1.52	9.63	0.1	8.11	0.1	0.00022282	0.00216294	0.02133079	0.44255422	A_07_P015292	b1992
cobT	-2.03	10.00	-1.02	10.51	0.3	9.49	0.3	0.01214682	0.04584142	0.07191754	0.66741203	A_07_P011288	b1991
cobU	-2.55	9.40	-1.35	10.08	0.0	8.73	0.3	0.00033358	0.00282047	0.03461954	0.51173348	A_07_P015296	b1993
codA	+6.62	9.14	+2.73	7.77	0.0	9.87	0.1	0.00000258	0.00007942	0.00238436	0.12836158	A_07_P008878	b0337
codB	+5.22	8.05	+2.37	6.84	0.2	9.24	0.2	0.00001606	0.00033988	0.00934070	0.26888826	A_07_P010022	c_0455
coeBB	-2.43	7.83	-1.28	7.19	0.1	8.47	0.5	0.00164068	0.00863553	0.04104403	0.50517428	A_07_P003871	b0336
cpdA	-2.35	12.63	-1.23	13.24	0.1	12.01	0.4	0.00404772	0.01920077	0.04463163	0.56485331	A_07_P012295	b3032
cpdR	+3.95	10.90	+1.98	9.91	0.0	11.88	0.1	0.00002594	0.00006663	0.01843037	0.34315104	A_07_P010340	b0932
cpdR1	+2.71	11.29	+1.89	10.34	0.0	12.23	0.2	0.00006663	0.01777566	0.35325516	0.54043979	c_4864	
cmD	-4.05	9.98	-2.02	10.09	0.1	8.07	0.0	0.00002503	0.00045582	0.00663681	0.26386364	A_07_P017684	b4400
crp	-2.20	10.02	-1.13	10.59	0.0	12.45	0.1	0.00095151	0.00611315	0.05659398	0.61270083	A_07_P017815	b3357
crr	+3.70	10.48	+1.89	9.54	0.0	11.42	0.1	0.00003538	0.00057410	0.01873525	0.35453431	A_07_P013145	b2417
csdA	-3.46	13.22	-1.79	12.11	0.0	10.32	0.1	0.00006549	0.00089423	0.01180577	0.33672101	A_07_P015050	b2810
cspA	+2.25	8.96	+1.17	7.48	0.3	8.65	0.1	0.00297198	0.01507177	0.05052655	0.55823860	A_07_P040743	c_1306
cspB	+2.08	7.62	+1.06	7.09	0.1	8.15	0.1	0.00145995	0.00812449	0.05434797	0.58949131	A_07_P040743	b0041
cspG	-2.16	9.69	-1.11	10.24	0.3	9.13	0.1	0.00351460	0.01716843	0.05702553	0.61705155	A_07_P001396	b0337
cstD	-2.79	9.28	-1.48	10.02	0.1	8.54	0.2	0.00088795	0.00224823	0.02370553	0.42514329	A_07_P020146	b2659
csiE	+5.07	8.38	+2.34	7.01	0.1	9.35	0.1	0.00001216	0.00028817	0.00869079	0.27337394	A_07_P019579	b2535
cspC	+4.40	14.27	+2.14	10.20	0.1	15.34	0.3	0.00011363	0.00114163	0.00187475	0.30575152	A_07_P015859	b3223
cspD	+51.91	10.78	+5.70	7.94	0.1	13.63	0.1	0.00000005	0.00003344	0.00001842	0.01035714	A_07_P004854	b0880
cspE	-6.64	12.07	-2.73	11.61	0.1	14.34	0.1	0.00000008	0.00015128	0.00370227	0.21859223	A_07_P014444	c_0714
cspF	+6.47	12.77	+2.69	11.43	0.1	14.12	0.0	0.00000046	0.00016034	0.00084738	0.22561611	A_07_P009684	b0623
cspF	-2.05	9.10	-1.04	9.62	0.4	8.27	0.3	0.00485591	0.02268007	0.04604859	0.60001859	A_07_P009435	b0158
cstA	+11.23	10.57	+3.49	8.82	0.4	12.31	0.0	0.00000975	0.00024676	0.00203633	0.13193416	A_07_P010748	b0598
cusA	-2.26	8.54	-1.18	9.13	0.1	7.95	0.1	0.00106472	0.00683365	0.05408568	0.58651214	A_07_P013031	c_0661
cusF	-2.29	9.60	-1.19	10.20	0.3	9.01	0.2	0.00467191	0.02160826	0.04792810	0.57910975	A_07_P016630	b0573
cvpA	+4.38	12.67	+2.13	11.60	0.1	13.73	0.1	0.00002579	0.00004669	0.00145128	0.31327378	A_07_P013853	b2213
cvpA	+3.91	10.80	+1.97	9.82	0.1	11.79	0.1	0.00001646	0.00016808	0.01663808	0.34512516	A_07_P042620	23575
cwrA	-3.84	12.52	-1.94	13.49	0.2	11.55	0.4	0.00075194	0.00523164	0.00884140	0.32283938	A_07_P008906	b1191
cyaY	-10.78	10.53	-4.42	9.72	0.0	11.34	0.1	0.00001528	0.00124621	0.00524234	0.42466116	A_07_P008897	b1827
cyaR	+2.64	11.58	+1.40	10.87	0.1	12.28	0.1	0.00012188	0.00275682	0.03466011	0.47218651	A_07_P043940	c_4726
cyaC	+2.75	11.70	+1.46	10.97	0.1	12.43	0.0	0.00003279	0.00282385	0.01600159	0.40998177	A_07_P017663	c_5315
cybC	+3.51	10.61	+1.83	9.71	0.0	11.52	0.1	0.00006700	0.00090852	0.02028819	0.37397887	A_07_P003731	b4236
cydA	+36.33	12.60	+4.72	10.24	0.0	14.96	0.1	0.00000016	0.00003348	0.00000152	0.00457174	A_07_P018853	b0733
cydB	+34.44	12.42	+4.61	10.11	0.1	14.72	0.0	0.00000013	0.00003548	0.00036105	0.04566667	A_07_P010187	b0734
cydC	+2.05	9.55	+1.03	8.63	0.2	9.67	0.1	0.00102157	0.01627796	0.06186865	0.60575871	A_07_P008879	b1866
cysA	+2.08	11.89	+1.05	11.27	0.0	12.42	0.2	0.00169423	0.01054400	0.05665447	0.59668632	A_07_P021271	b0432
cysB	+4.95

dsdX	+3.74	7.90	+1.90	6.95	0.3	8.85	0.2	0.00306062	0.00272199	0.01893658	0.35412422	A_07_P014107	b2565	cmr/transport system permease [b2365]
dtd	+4.22	10.05	+2.08	9.02	0.3	13.00	0.2	0.00037668	0.00183002	0.01427020	0.32280172	A_07_P010312	b3887	cmr/orf, hypothetical protein [b3887]
dusA	-2.04	8.81	-1.03	9.33	0.1	8.00	0.2	0.00401449	0.01906612	0.07009895	0.66125824	A_07_P008886	b4849	cmr/orf, hypothetical protein [b4849]
dusB	+2.52	11.61	+1.33	10.94	0.1	12.20	0.4	0.00279614	0.01491532	0.04019981	0.49930031	A_07_P012768	b2160	cmr/putative dehydrogenase [b2160]
E1A_r60_s104	-3.24	10.45	-1.17	11.08	0.3	9.87	0.3	0.02556985	0.02659485	0.01149708	0.59268813	(+)E1A_r60_s104	E1A_r60_s104	
E1A_r60_s104	-2.48	9.33	-1.31	9.99	0.4	8.68	0.0	0.02287579	0.01462208	0.02674289	0.52303797	(+)E1A_r60_s104	E1A_r60_s104	
E1A_r60_s104	-3.12	10.05	-1.08	10.59	0.0	9.51	0.2	0.01707084	0.01014814	0.06197027	0.63685379	(+)E1A_r60_s104	E1A_r60_s104	
E1A_r60_s104	-2.29	9.60	-1.19	10.19	0.5	9.00	0.0	0.00920517	0.03680429	0.04685396	0.57474178	(+)E1A_r60_s104	E1A_r60_s104	
E1A_r60_s104	-4.50	9.92	-2.17	11.01	0.3	8.84	0.1	0.00906152	0.00085136	0.04470284	0.22564024	(+)E1A_r60_s104	E1A_r60_s104	
E1A_r60_s104	-3.35	9.45	-1.74	10.32	0.1	8.57	0.1	0.00307119	0.00094658	0.01347693	0.34835796	(+)E1A_r60_s104	E1A_r60_s104	
E1A_r60_s104	-2.79	9.65	-1.48	10.39	0.6	8.91	0.1	0.00880790	0.03228368	0.01939329	0.44790971	(+)E1A_r60_s104	E1A_r60_s104	
E1A_r60_s104	-2.50	9.74	-1.32	10.40	0.4	9.08	0.4	0.00918236	0.03674987	0.03418445	0.51111111	(+)E1A_r60_s104	E1A_r60_s104	
E1A_r60_s104	-2.14	10.02	-1.10	10.57	0.1	9.48	0.5	0.01343664	0.04984015	0.05805511	0.61925474	(+)E1A_r60_s104	E1A_r60_s104	
E1A_r60_s104	-2.41	10.06	-1.27	10.70	0.3	9.43	0.4	0.00765333	0.03116738	0.03976230	0.54103036	(+)E1A_r60_s104	E1A_r60_s104	
E1A_r60_s107	-3.38	9.63	-1.76	10.51	0.3	8.70	0.2	0.00035734	0.00303184	0.01306974	0.34525168	(+)E1A_r60_s107	E1A_r60_s107	
E1A_r60_s107	-2.08	8.70	-1.06	9.21	0.2	8.18	0.1	0.00180672	0.01003897	0.06546875	0.65303915	(+)E1A_r60_s107	E1A_r60_s107	
E1A_r60_s107	-2.28	9.30	-1.19	9.89	0.5	8.70	0.1	0.01081189	0.00024147	0.04849412	0.58121189	(+)E1A_r60_s107	E1A_r60_s107	
E1A_r60_s107	-2.30	8.69	-1.20	9.29	0.5	8.09	0.0	0.00791262	0.03271972	0.04737170	0.57363785	(+)E1A_r60_s107	E1A_r60_s107	
E1A_r60_s107	-2.12	8.95	-1.15	9.52	0.4	8.37	0.3	0.01305239	0.04874212	0.05164444	0.59302120	(+)E1A_r60_s107	E1A_r60_s107	
E1A_r60_s107	-2.18	9.09	-1.12	9.65	0.3	8.52	0.2	0.00415479	0.01962000	0.05154736	0.60843728	(+)E1A_r60_s107	E1A_r60_s107	
E1A_r60_s135	-2.29	8.92	-1.20	9.52	0.4	8.32	0.0	0.00368350	0.00848533	0.04869347	0.58288859	(+)E1A_r60_s135	E1A_r60_s135	
E1A_r60_s135	-2.34	9.12	-1.23	9.73	0.1	8.50	0.1	0.00606055	0.00446243	0.04521083	0.56879393	(+)E1A_r60_s135	E1A_r60_s135	
E1A_r60_s135	-3.42	9.41	-1.78	10.30	0.7	8.52	0.0	0.00533795	0.02401652	0.01233549	0.33038579	(+)E1A_r60_s135	E1A_r60_s135	
E1A_r60_s135	-3.11	9.48	-1.64	10.30	0.1	8.66	0.3	0.00042917	0.00050320	0.01703252	0.37975706	(+)E1A_r60_s135	E1A_r60_s135	
E1A_r60_s135	-2.78	9.02	-1.47	9.76	0.2	8.28	0.0	0.00032175	0.00281267	0.02548590	0.46014908	(+)E1A_r60_s135	E1A_r60_s135	
E1A_r60_s135	-3.00	9.16	-1.60	10.47	0.3	8.66	0.2	0.00848185	0.03439917	0.07508117	0.67764806	(+)E1A_r60_s135	E1A_r60_s135	
E1A_r60_s20	-2.87	10.11	-1.52	10.87	0.3	9.35	0.2	0.01000870	0.00655968	0.02315611	0.44060533	(+)E1A_r60_s20	E1A_r60_s20	
E1A_r60_s20	-2.31	10.11	-1.07	10.64	0.1	9.57	0.1	0.00179503	0.01051122	0.06156899	0.64611362	(+)E1A_r60_s20	E1A_r60_s20	
E1A_r60_s20	-3.35	9.79	-1.23	10.41	0.1	9.18	0.1	0.00088937	0.00384275	0.04747784	0.56587149	(+)E1A_r60_s20	E1A_r60_s20	
E1A_r60_s20	-2.18	9.81	-1.12	10.39	0.2	9.27	0.0	0.00186498	0.01065585	0.05736079	0.61598070	(+)E1A_r60_s20	E1A_r60_s20	
E1A_r60_s20	-2.15	9.95	-1.10	10.50	0.1	9.40	0.3	0.00195537	0.01750326	0.05592267	0.62935333	(+)E1A_r60_s20	E1A_r60_s20	
E1A_r60_s20	-2.57	10.21	-1.36	10.89	0.1	9.53	0.5	0.00469711	0.02170570	0.03138351	0.55581441	(+)E1A_r60_s20	E1A_r60_s20	
E1A_r60_s20	-2.58	9.96	-1.37	10.64	0.3	9.28	0.1	0.00091569	0.00611315	0.03266037	0.55579724	(+)E1A_r60_s20	E1A_r60_s20	
E1A_r60_s20	-2.58	10.13	-1.37	10.82	0.3	9.45	0.0	0.00002607	0.00619134	0.03266037	0.55630708	(+)E1A_r60_s20	E1A_r60_s20	
E1A_r60_s20	-2.62	10.18	-1.39	10.88	0.0	9.49	0.2	0.00048598	0.00382757	0.03088288	0.49412602	(+)E1A_r60_s20	E1A_r60_s20	
E1A_r60_s22	-2.11	10.92	-1.08	11.46	0.1	10.38	0.2	0.00280006	0.01467889	0.02316168	0.43889074	(+)E1A_r60_s22	E1A_r60_s22	
E1A_r60_s22	-2.14	10.70	-1.10	11.24	0.0	10.15	0.0	0.00078308	0.00539515	0.06889177	0.63404762	(+)E1A_r60_s22	E1A_r60_s22	
E1A_r60_s22	-2.66	10.80	-1.41	11.50	0.4	10.09	0.1	0.00232371	0.01328758	0.02302370	0.48082550	(+)E1A_r60_s22	E1A_r60_s22	
E1A_r60_s22	-2.55	10.87	-1.35	11.54	0.3	10.19	0.1	0.00106688	0.00682964	0.03470704	0.51207865	(+)E1A_r60_s22	E1A_r60_s22	
E1A_r60_s22	-2.68	10.56	-1.31	11.21	0.1	9.90	0.1	0.00049826	0.00386116	0.03885575	0.52872792	(+)E1A_r60_s22	E1A_r60_s22	
E1A_r60_s22	-2.33	10.73	-1.22	11.34	0.2	10.12	0.2	0.00169325	0.00936916	0.04618585	0.57301024	(+)E1A_r60_s22	E1A_r60_s22	
E1A_r60_s22	-3.75	10.78	-1.46	11.51	0.0	10.05	0.1	0.00113185	0.00712615	0.02657457	0.46906709	(+)E1A_r60_s22	E1A_r60_s22	
E1A_r60_s22	-3.35	10.65	-1.23	11.26	0.0	10.03	0.2	0.00115015	0.00722086	0.04519346	0.56879916	(+)E1A_r60_s22	E1A_r60_s22	
E1A_r60_s22	-2.43	10.63	-1.28	11.27	0.1	9.99	0.1	0.00057885	0.00431914	0.04037221	0.54126496	(+)E1A_r60_s22	E1A_r60_s22	
E1A_r60_s22	-2.31	10.65	-1.21	11.26	0.2	10.05	0.1	0.00153628	0.00896468	0.04747989	0.57632999	(+)E1A_r60_s22	E1A_r60_s22	
E1A_r60_s22	-2.68	10.60	-1.42	11.31	0.2	9.89	0.0	0.00051447	0.00386851	0.02912919	0.47971757	(+)E1A_r60_s22	E1A_r60_s22	
E1A_r60_s22	-3.85	10.59	-1.51	11.31	0.1	9.83	0.0	0.00180056	0.00188075	0.02169724	0.44415476	(+)E1A_r60_s22	E1A_r60_s22	
E1A_r60_s22	-3.92	10.71	-1.54	11.49	0.1	9.94	0.1	0.00020795	0.00205389	0.02156504	0.42176398	(+)E1A_r60_s22	E1A_r60_s22	
E1A_r60_s22	-2.23	10.66	-1.16	11.24	0.1	10.08	0.3	0.02218366	0.01183450	0.06408343	0.69491130	(+)E1A_r60_s22	E1A_r60_s22	
E1A_r60_s22	-2.03	10.73	-1.02	11.24	0.2	10.22	0.0	0.00207812	0.01509091	0.07065739	0.66413691	(+)E1A_r60_s22	E1A_r60_s22	
E1A_r60_s22	-2.10	10.65	-1.07	11.19	0.0	10.12	0.2	0.00163574	0.00941319	0.06346209	0.64535229	(+)E1A_r60_s22	E1A_r60_s22	
E1A_r60_s22	-2.57	10.65	-1.36	11.33	0.1	9.97	0.1	0.00028436	0.00258935	0.03269445	0.55587317	(+)E1A_r60_s22	E1A_r60_s22	
E1A_r60_s22	-2.23	7.83	-1.16	8.41	0.3	7.28	0.3	0.00422149	0.01988127	0.05278124	0.59785612	(+)E1A_r60_s97	E1A_r60_s97	
E1A_r60_s97	-2.08	7.99	-1.06	8.52	0.1	7.46	0.1	0.00133391	0.00804129	0.06547200	0.65150599	(+)E1A_r60_s97	E1A_r60_s97	
E1A_r60_s97	-2.18	8.09	-1.42	8.81	0.2	7.28	0.0	0.00022493	0.00401973	0.02835279	0.47910577	(+)E1A_r60_s97	E1A_r60_s97	
E1A_r60_s11	+2.22	7.76	+1.15	7.19	0.2	8.32	0.3	0.01030309	0.00664690	0.05605549	0.55809657	(+)E1A_r60_s11	E1A_r60_s11	
E1A_r60_s11	+2.84	8.12	+1.51	7.37	0.2	8.87	0.4	0.00305345	0.01544424	0.06090953	0.65050259	(+)E1A_r60_s11	E1A_r60_s11	
E1A_r60_s11	-3.29	8.15	-1.72	9.01	0.2	7.29	0.2	0.00220690	0.00262909	0.01407139	0.35676718	(+)E1A_r60_s11	E1A_r60_s11	
eae0	-2.58	12.20	-1.37	12.89	0.1	11.52	0.1	0.00010854	0.00360434	0.01209842	0.55150878	A_07_P008177	b0287	cmr/attaching and effacing protein, pathogenesis factor [b0297]
eagR	+2.22	9.20	+1.15	8.62	0.3	9.77	0.1	0.00325172	0.01608894	0.05212779	0.56362758	A_07_P041749	c_3832	cmr/Eag operon repressor [c_3832]
eco	+2.19	9.98	+1.13	8.61	0.2	9.61	0.0	0.00061364	0.00853589	0.05135519	0.55990857	A_07_P000801	b2209	cmr/ecotin, a serine protease inhibitor [b2208]
eco	+2.30	12.92	+1.20	12.32	0.4	13.53	0.2	0.00755325	0.01484848	0.01135291	0.55990305	A_07_P045511	Z4667	cmr/ecotin, a serine protease inhibitor [Z4667]
eco	+2.61	13.08	+1.39	12.39	0.1	13.78	0.2	0.00464385	0.00358698	0.03561095	0.47732021	A_07_P032326	c_2750	cmr/Ecotin precursor [c_2750]
EcO016	-3.69	12.49	-1.88	13.44	0.0	11.54	0.0	0.00060878	0.00073942	0.00509942	0.11355987	A_07_P042852	EcO016	cmr/Cell protein [EcO016]
EcO031	+2.51	10.03	+1.33	9.37	0.2	10.70	0.0	0.00061364	0.00449774	0.03887869	0.49284219	A_07_P042890	EcO031	cmr/putative FMN-type NAD(P)-dependent cis-trans isomerase [EcO031]
EcO052	-3.25	11.92	-1.17	12.50	0.0	11.33	0.0	0.00053382	0.00406992	0.01165396	0.33230381	A_07_P039413	EcO052	cmr/Cell-like protein [EcO052]
EcO127	-2.40	9.81	-1.26	10.44	0.2	9.18	0.2	0.00126149	0.00772497	0.04097434	0.54530854	A_07_P042900	EcO127	cmr/hypothetical protein [EcO127]
EcO132	-2.64	8.51	-1.40	9.27	0.3	7.82	0.0	0.00162192	0.00242251	0.03840473	0.49049130	A_07_P042912	EcO132	cmr/hypothetical protein [EcO132]
EcO192	-2.06	11.00	-1.04	11.24	0.2	10.48	0.1	0.00183856	0.01004164	0.06703951	0.65153469	A_07_P035513	EcO192	cmr/hypothetical protein [EcO192]
EcO211	-2.19	9.24	-1.17	8.56	0.0	9.93	0.1	0.00033756	0.00203550	0.03683556	0.47996613	A_07_P042916	EcO211	cmr/DNA polymerase III epsilon subunit [EcO211]
EcO218	-2.23	8.39	-1.16	8.97	0.4	7.81	0.2	0.00466527	0.02867161	0.05280587	0.59838362	A_07_P045547	EcO218	cmr/cmf-like protein [EcO218]
EcO228	-2.37	10.15	-1.24	10.77	0.3	9.52	0.2	0.00246307	0.01428613	0.05268043	0.59806512	A_07_P045567	EcO228	cmr/hypothetical protein [EcO228]
EcO290	-2.14	11.38	-1.10	11.93	0.1	10.83	0.1	0.00120662	0.00747030	0.05995935	0.62849534	A_07_P043647	EcO290	cmr/hypothetical protein [EcO290]
EcO296	-3.35	9.76	-1.75	10.63	0.2	8.89	0.1	0.00016130	0.00171124	0.01232844	0.34540947	A_07_P043677	EcO296	cmr/putative Dpr family transcription activator [EcO296]
EcO325	-3.75	8.20	-1.46	8.93	0.2	7.47	0.0	0.00228487	0.00259096	0.02626239	0.46921348	A_07_P053765	EcO325	cmr/hypothetical protein [EcO325]
EcO326	-2.27	8.12	-1.18	8.72	0.0	7.53	0.1	0.00146881	0.00453175	0.04698398	0.58588806	A_07_P053768	EcO326	cmr/hypothetical protein [EcO326]
EcO330	-3.24	8.73	-1.70	9.58	0.1	7.88	0.0	0.00007365	0.00046448	0.01512195	0.36911628	A_07_P053789	EcO330	cmr/hypothetical protein [EcO330]
EcO332	+4.88	8.71	+2.29	7.57	0.3	9.86	0.2	0.00010694	0.00128313	0.01076605	0.28486668	A_07_P053796	EcO332	cmr/hypothetical protein [EcO332]
EcO335	+2.16	7.48	+1.11	6.92	0.1	8.03	0.1	0.00101159	0.00657578	0.05130348	0.56934193	A_07_P053815	EcO335	cmr/putative oxidoreductase [EcO335]
EcO357	+3.07	9.34	+1.63	8.43	0.0	10.05	0.2	0.00030398	0.00270694	0.02650407	0.42732038	A_07_P053871	EcO357	cmr/choline dehydrogenase [EcO357]
EcO453	-2.04	10.39	-1.03	10.90	0.0	9.87	0.1	0.00170368	0.00973655	0.06494761	0.67476338	A_07_P053991	EcO453	cmr/5-aminolevulinate dehydratase [EcO453]
EcO449	-7.63	11.38	-2.93	12.85	0.0	9.92	0.0	0.00000215	0.00010587	0.00069106	0.08119403	A_07_P054018	EcO449	cmr/positive response regulator for phn regulon PhoB [EcO449]
EcO483	+3.49	8.73	+1.80	7.83	0.0	9.64	0.7	0.00068276	0.00267779	0.02148077	0.38462514	A_07_P054083	EcO483	cmr/cytochrome c-dihydroxyl oxidase subunit IV [EcO483]
EcO547	-2.18	10.24	-1.13	10.80	0.1	9.68	0.3	0.00327481	0.01619812	0.07329978	0.61568895	A_07_P054119	EcO547	cmr/hypothetical protein [EcO547]
EcO551	-3.55	10.80	-1.35	11.48	0.1	10.13	0.0	0.00028746	0.00260312	0.01508338	0.35196338	A_07_P054138	EcO551	cmr/hypothetical protein [EcO551]
EcO573	+2.60	7.60	+1.38	6.92	0.0	8.29	0.1	0.00031892	0.00279411	0.03900066	0.47940628	A_07_P054146	EcO573	cmr/allantoinase [EcO573]
EcO679	-2.20	10.45	-1.13	11.01	0.0	9.88	0.0	0.00036522	0.00461444	0.04230700	0.61265089	A_07_P054223	EcO679	cmr/minor lipoprotein [EcO679]
EcO694	+2.83	11.27	+1.50	10.52	0.2	12.02	0.2	0.00030216	0.00269224	0.03031885	0.44652947	A_07_P054560	EcO694	cmr/putative periplasmic binding transport protein [EcO694]
EcO711	-3.61	9.89	-1.85	10.81	0.1	8.96	0.2	0.00016645	0.00175383	0.00958570	0.32205708	A_07_P054574	EcO711	cmr/hypothetical protein [EcO711]
EcO742	+2.13	7.17	+1.09	6.63	0.1	7.72	0.1	0.00109917	0.00685512	0.05462779	0.57188840	A_07_P054583	EcO742	cmr/putative chaperone [EcO742]
EcO778	-3.20	8.66	-1.68	9.50	0.1	7.82	0.1	0.00144646	0.00155282	0.01573202	0.37422601	A_07_P054671	EcO778	cmr/putative synthetase A protein [EcO778]
EcO794	+2.04	9.94	+1.03	9.42	0.1	10.45	0.1	0.00202955	0.01117636	0.06136751	0.60347908	A_07_P054677	EcO794	cmr/putative phosphatase [EcO794]
EcO805	+107.44	11.01	+6.75	7.63	0.0	14.38	0.2	0.00000004	0.00003344	0.00000004	0.00166647	A_07_P054700	EcO805	cmr/hypothetical C4-type zinc finger protein TraR-family [EcO805]
EcO806	+5.73	11.19	+2.52	9.93	0.3	12.45	0.2	0.00005770	0.00081407	0.00775915	0.24620032	A_07_P054701	EcO806	cmr/hypothetical protein [EcO806]
EcO807	+17.00	9.90	+4.09	7.85	0.0	11.94	0.2	0.00000108	0.00003677	0.00041597	0.08470199	A_07_P054708	EcO807	cmr/hypothetical protein [EcO807]
EcO808	+4.67	11.63	+2.22	10.52	0.2	12.74	0.2	0.00160542	0.00124701	0.01769556	0.29459459	A_07_P054712	EcO808	cmr/hypothetical protein [EcO808]
EcO809	+3.57	12.72	+1.84	11.80	0.1	13.63	0.1	0.00004771	0.00071332	0.01927754	0.36424350	A_07_P054720	EcO809	cmr/exonuclease [EcO809]
EcO810	+16.70	10.18	+4.06	8.15	0.1	12.21	0.1	0.00000046	0.00005132	0.00080285	0.08426667	A_07_P054725	EcO810	cmr/NinE protein [EcO810]
EcO816	+22.16	12.92	+4.47	8.45	0.2	17.39	0.1	0.00000052	0.00005341	0.00058604	0.05508804	A_07_P054765	EcO816	cmr/endonuclease [EcO816]
EcO820	+12.89	8.70	+3.69	6.85	0.1	10.54	0.1	0.00000077	0.00006501	0.00142721	0.11582474	A_07_P054766	EcO820	cmr/putative endopeptidase [EcO820]
EcO821	-1.54	10.13	-1.35	10.80	0.2	9.45	0.0	0.00058367	0.00434242	0.03403763	0.53148621	A_07_P054771	EcO821	cmr/putative lipoprotein Rci precursor [EcO821]
EcO825	-3.52	8.74	-1.34	9.41	0.2	8.07	0.0	0.00048784	0.00383643	0.03159798	0.51532528	A_07_P054775	EcO825	cmr/putative terminase large subunit [EcO825]
EcO827	-2.26	9.83	-1.18	10.42	0.1	9.24	0.3	0.00286751	0.01463408	0.04838923	0.58155725	A_07_P054801	EcO827	cmr/putative portal protein [EcO827]
EcO828	-3.64	8.30	-1.40	8.90	0.1	7.69	0.1	0.00027739	0.00254324	0.00854146	0.24740741	A_07_P054809	EcO828	cmr/hypothetical protein [EcO828]
EcO836	-3.53	9.75	-1.82	10.66	0.6	8.84	0.0	0.00324174	0.01606236	0.01506009	0.32792844	A_07_P054847	EcO836	cmr/putative minor tail protein [EcO836]
EcO840	+5.47	9.34	+2.45	8.11	0.1	10.57	0.1	0.00022544	0.00042174	0.00462111	0.25492337	A_07_P054856	EcO840	cmr/putative minor tail protein [EcO840]
EcO841	+2.61	8.57	+1.38	7.28	0.2	9.26	0.2	0.00071962	0.00503543	0.03611535	0.48364243	A_07_P054872	EcO841	cmr/putative tail assembly protein [EcO841]
EcO878	+4.28	10.42	+2.10	9.38	0.0	11.47	0.1	0.00003939	0.00038447	0.00186279	0.19192015	A_07_P054933	EcO878	cmr/putative enzyme [EcO878]
EcO901	+2.36	7.24	+1.24	6.62	0.1	7.87	0.2	0.00153812	0.00864468	0.04455094	0.52260021	A_07_P054937	EcO901	cmr/hypothetical protein [EcO901]
EcO906	+2.17	10.55	+1.12	9.99	0.2	11.10	0.1	0.00188334	0.00105161	0.01394754	0.56852736	A_07_P054943	EcO906	cmr/hypothetical protein [EcO906]
EcO950	-2.69	11.30	-1.43	12.02	0.1	10.59	0.0	0.00018626	0.00100047	0.02909489	0.48015723	A_07_P054991	EcO950	cmr/hypothetical protein [EcO950]
EcO952	+2.13	8.69	+1.09	8.15	0.1	9.24	0.1	0.00164716	0.00948135	0.05138888	0.57647059	A_07_P054994	EcO952	cmr/hypothetical protein [EcO952]
EcO981	+5.37	8.44	+2.43	7.23	0.2	9.66	0.1	0.00002006	0.00019347	0.00875826	0.25967985	A_07_P055053	EcO981	cmr/anaerobic dimethyl sulfoxide reductase subunit C [EcO981]
EcO11	+6.41	9.93	+2.68	8.59	0.1	11.27	0.1	0.00000701	0.00020342	0.00104055	0.22561033	A_07_P055067	EcO11	cmr/aspartate aminotransferase [EcO11]
EcO15	+7.70	9.51	+2.94	8.04	0.0	10.98	0.3	0.00001331	0.00030070	0.00433181	0.18891967	A_07_P055074	EcO15	cmr/aminopeptidase N [EcO15]
EcO161	+2.11	7.61	+1.07	6.87	0.1	7.95	0.1	0.00111380	0.00764458	0.05658885	0.58324820	A_07_P055088	EcO161	cmr/hypothetical protein [EcO161]
EcO171	-2.88	10.40	-1.52	11.16	0.4	9.64	0.0	0.00200255	0.01055861	0.02267712	0.43345558	A_07_P055126	EcO171	cmr/hypothetical protein [EcO171]
EcO181	-4.64	9.93	-2.21	10.10	0.1	9.76	0.1	0.00001605	0.00033988	0.00396786	0.20724713	A_07_P055173	EcO181	cmr/hypothetical protein [EcO181]
EcO182	-5.26	11.25	-2.40	10.65	0.0	11.85	0.3	0.00000217	0.00013011	0.00020541	0.06925461	A_07_P055221	EcO182	cmr/putative lipoprotein Rci protein precursor [EcO182]
EcO183	+2.05	7.13	+1.04	6.61	0.0	7.65	0.0	0.00108047	0.00809376	0.05904622	0.59401278	A_07_P055227	EcO183	cmr/putative endopeptidase [EcO183]
EcO198	-2.10	7.51	-1.07	8.05	0.4	6.98	0.2	0.00861171	0.00483819	0.06180589	0.63607546	A_07_P055241	EcO198	cmr/hypothetical protein [EcO198]
EcO105	-4.69	11.90	-2.17	12.98	0.1	10.82	0.2	0.00004518	0.00008369	0.00475483	0.22548193	A_07_P055269	EcO105	cmr/putative terminase small subunit [EcO105]
EcO106	+3.07	8.96	+1.62	8.15	0.0	9.76	0.0	0.00008139	0.00103195	0.02316163	0.42491543	A_07_P055274	EcO106	cmr/putative terminase large subunit [EcO106]
EcO107	+5.81	8.51	+2.54	7.24	0.0	9.79	0.2	0.00000996	0.00025049	0.00742315	0.24501048	A_07_P055276	EcO107	cmr/putative portal protein [EcO107]
EcO108	+27.96	10.47	+4.81	8.66	0.0	12.27	0.0	0.00000023	0.00004002	0.00017276	0.03720027	A_07_P055281	EcO108	cmr/putative head-tail preconnector protein [EcO108]
EcO109	+37.99	10.12	+4.91	7.67	0.3	12.57	0.1	0.00000040	0.00000450	0.00013656	0.03257576	A_07_P055290	EcO109	cmr/putative head decoration protein [EcO109]
EcO110	+18.81	8.96	+4.23	6.84	0.0	11.07	0.1	0.00000022	0.00004002	0.00060722	0.07242424	A_07_P055293	EcO110	cmr/putative major head protein [EcO110]
EcO112	+3.22	8.28	+1.15	7.71	0.1	8.86	0.0	0.00071315	0.00489460	0.05005611	0.55769122	A_07_P055302	EcO112	cmr/putative minor tail protein [EcO112]
EcO116	-2.65	10.61	-1.41	11.31	0.1	9.90	0.4	0.00131375	0.01527904	0.02486648	0.47691955	A_07_P055316	EcO116	cmr/putative terminase large subunit [EcO116]
EcO125	-2.09	7.37	-1.06	7.90	0.1	6.84	0.1	0.00153063	0.00834653	0.06416611	0.65136192	A_07_P055404	EcO125	cmr/hypothetical protein [EcO125]
EcO156	-6.16	9.66	-2.62	10.97	0.0	8.35	0.8	0.00119179	0.00753702	0.00145516	0.11401587	A_07_P055921	EcO156	cmr/hypothetical protein [EcO156]
EcO160	-3.74	10.26	-1.45	10.99	0.0	9.53	0.1	0.00017415	0.00180973	0.02679942	0.47143017	A_07_P055927	EcO160	cmr/putative integrase [EcO160]
EcO161	-2.28	9.60	-1.10	10.09	0.1	9.41	0.1	0.00068153	0.00484612	0.04891457	0.58581587	A_07_P055928	EcO161	cmr/putative integrase [EcO161]
EcO163	+22.95	9.39	+4.52	7.13	0.0	11.65	0.0	0.00000104	0.00003548	0.00022393	0.05204082	A_07_P055944	EcO163	cmr/hypothetical protein [EcO163]
EcO170	+39.78	10.11	+4.90	7.66	0.0	12.56	0.2	0.00000073	0.00006202	0.00010634	0.03208955	A_07_P055980	EcO170	cmr/C4-type zinc finger protein [EcO170]
EcO173	+3.12	9.73	+1.64	8.91	0.6	10.55	0.3	0.00512656	0.02323331	0.02682546	0.42740964	A_07_P055991	EcO173	cmr/hypothetical protein [EcO173]
EcO174	+10.13	12.17	+3.34	10.50	0.3	13.84	0.1	0.00000674	0.00015281	0.00066276	0.14682347	A_07_P055992	EcO174	cmr/exonuclease [EcO174]
EcO175	+4.86	14.83	+2.28	13.69	0.0	15.97	0.1	0.00001725	0.00035688	0.00076617	0.28466643	A_07_P056005	EcO175	cmr/recombination protein Bet [EcO175]
EcO176	+18.15

EC02771	-2.45	8.10	-1.29	8.75	0.3	7.46	0.0	0.00190255	0.01101912	0.03836573	0.53078207	A_07_P055443	EC02771	cmr	hypothetical protein [EC02771]
EC02773	-3.27	10.95	-1.71	11.81	0.0	10.10	0.1	0.00090303	0.00113624	0.01485847	0.30157729	A_07_P055453	EC02773	cmr	putative integrase [EC02773]
EC02782	-7.90	8.67	-2.98	10.16	0.1	7.18	0.0	0.00000023	0.00010855	0.00569843	0.07733333	A_07_P055462	EC02782	cmr	hypothetical protein [EC02782]
EC02792	-7.36	8.62	-2.88	10.06	0.0	7.18	0.0	0.00000240	0.00011310	0.00078443	0.08758865	A_07_P055475	EC02792	cmr	hypothetical protein [EC02792]
EC02793	-3.49	8.70	-1.80	9.60	0.1	7.80	0.5	0.01572565	0.00777312	0.01696418	0.32631180	A_07_P055479	EC02793	cmr	hypothetical protein [EC02793]
EC02795	-8.48	10.56	-3.08	12.10	0.1	9.02	0.2	0.00000487	0.00016794	0.00043318	0.06621359	A_07_P055487	EC02795	cmr	putative transposase OrfB protein of insertion sequence ISG29 [EC02795]
EC02796	-6.27	11.79	-2.65	13.11	0.0	10.46	0.0	0.00000413	0.00015128	0.00142403	0.12455556	A_07_P055493	EC02796	cmr	hypothetical protein [EC02796]
EC02797	-2.91	9.98	-1.54	10.76	0.1	9.21	0.2	0.00023492	0.00224565	0.02153228	0.42166667	A_07_P055498	EC02797	cmr	hypothetical protein [EC02797]
EC02798	-2.18	10.70	-1.12	11.26	0.1	10.14	0.1	0.00099124	0.00689804	0.05737661	0.61600000	A_07_P055501	EC02798	cmr	hypothetical protein [EC02798]
EC02814	+2.34	7.50	+1.23	6.88	0.0	9.01	0.3	0.02030613	0.01233699	0.04516260	0.53630644	A_07_P055548	EC02814	cmr	hypothetical protein [EC02814]
EC02825	-8.14	8.79	-3.03	7.28	0.2	10.30	0.1	0.00000503	0.00023570	0.00376524	0.11455556	A_07_P058351	EC02825	cmr	N- [EC02825]
EC02827	+2.39	7.39	+1.26	6.76	0.1	8.02	0.1	0.00050057	0.00380530	0.04286616	0.51288099	A_07_P055553	EC02827	cmr	phosphorothioyl-amp cyclohydrolase [EC02827]
EC02828	-2.13	8.98	-1.09	9.52	0.1	8.43	0.2	0.02193798	0.01271122	0.06145789	0.61581633	A_07_P055560	EC02828	cmr	regulator of length of O-antigen component of lipopolysaccharide chains [EC02828]
EC02829	-3.42	8.85	-1.77	9.73	0.0	10.01	0.0	0.00010834	0.00127097	0.01232025	0.13739913	A_07_P055562	EC02829	cmr	UDP-glucose 6-dehydrogenase [EC02829]
EC02845	-3.26	10.37	-1.70	11.22	0.1	9.51	0.1	0.00060495	0.00093061	0.01488832	0.36601256	A_07_P055592	EC02845	cmr	putative glycosyl transferase [EC02845]
EC02905	-3.13	8.55	-1.65	9.38	0.1	7.73	0.3	0.00034892	0.00268717	0.01658028	0.37771135	A_07_P062818	EC02905	cmr	hypothetical protein [EC02905]
EC02907	-2.21	8.94	-1.14	9.52	0.1	8.37	0.3	0.00303648	0.01750326	0.05222752	0.59412572	A_07_P062822	EC02907	cmr	hydroxyethylthiazole kinase [EC02907]
EC02910	-2.08	8.32	-1.04	8.84	0.2	7.90	0.2	0.00228787	0.01224763	0.06844766	0.65669714	A_07_P055739	EC02910	cmr	putative outer membrane protein [EC02910]
EC02912	-3.06	9.97	-1.04	10.49	0.0	9.45	0.2	0.00180318	0.01051561	0.05278593	0.65490781	A_07_P055744	EC02912	cmr	hypothetical protein [EC02912]
EC02918	-2.48	8.90	-1.31	9.55	0.1	8.25	0.1	0.00040664	0.00336751	0.03817518	0.52861038	A_07_P055764	EC02918	cmr	hypothetical protein [EC02918]
EC02923	-4.42	9.08	-2.14	10.11	0.1	7.96	0.1	0.00002219	0.00061938	0.00489051	0.22726727	A_07_P055792	EC02923	cmr	putative transposase OrfB protein of insertion sequence ISG29 [EC02923]
EC02966	-2.50	10.64	-1.32	11.30	0.6	9.98	0.0	0.01098888	0.04543883	0.03587072	0.51140674	A_07_P055824	EC02966	cmr	putative tail assembly protein [EC02966]
EC02963	-2.88	11.31	-1.53	12.08	0.0	10.55	0.1	0.00018346	0.00187806	0.02265561	0.43058507	A_07_P055840	EC02963	cmr	putative terminase large subunit [EC02963]
EC02975	-2.52	10.08	-1.33	10.75	0.1	9.42	0.0	0.00030608	0.00272199	0.01607215	0.41185715	A_07_P055866	EC02975	cmr	antitermination protein [EC02975]
EC02978	-2.54	8.46	-1.35	9.14	0.1	7.79	0.0	0.00028576	0.00259753	0.03464240	0.51308561	A_07_P055883	EC02978	cmr	hypothetical protein [EC02978]
EC02981	+10.07	8.36	+3.71	6.50	0.0	10.21	0.7	0.00080407	0.00109678	0.00141832	0.11569948	A_07_P055891	EC02981	cmr	putative DNA methylase [EC02981]
EC02985	+6.42	12.82	+2.68	11.47	0.0	14.16	0.2	0.00001043	0.00025872	0.00602071	0.22569048	A_07_P055912	EC02985	cmr	lien protein [EC02985]
EC02986	+4.12	14.13	+2.04	13.11	0.0	15.15	0.0	0.00002245	0.00042379	0.01510752	0.33179916	A_07_P055916	EC02986	cmr	phage replication protein P [EC02986]
EC02987	+5.92	10.74	+2.57	9.45	0.2	12.02	0.3	0.00004676	0.00068082	0.00725165	0.24239915	A_07_P055921	EC02987	cmr	phage replication protein O [EC02987]
EC02988	+3.25	9.25	+1.70	8.39	0.2	10.10	0.2	0.00027822	0.00245413	0.02104179	0.40512661	A_07_P055928	EC02988	cmr	regulatory protein CI [EC02988]
EC02996	+10.03	13.37	+3.33	11.71	0.1	15.04	0.0	0.00000104	0.00007542	0.00258702	0.14866964	A_07_P055967	EC02996	cmr	putative single-stranded DNA binding protein [EC02996]
EC02997	+5.88	13.10	+2.56	11.82	0.1	14.38	0.4	0.00002617	0.00087056	0.00742621	0.24466127	A_07_P055972	EC02997	cmr	regulatory protein cII [EC02997]
EC02999	+11.27	12.02	+3.49	10.27	0.2	13.77	0.6	0.00000347	0.00113992	0.00196519	0.13110169	A_07_P055981	EC02999	cmr	host-nuclease inhibitor protein gam [EC02999]
EC03000	+13.36	11.01	+3.74	9.14	0.1	12.88	0.1	0.00000060	0.00005729	0.00139037	0.11521053	A_07_P056989	EC03000	cmr	putative host-nuclease inhibitor protein Gam [EC03000]
EC03001	+3.79	14.00	+1.92	12.08	0.1	14.00	0.1	0.00005067	0.00074622	0.01738023	0.34879487	A_07_P052993	EC03001	cmr	recombination protein Bet [EC03001]
EC03002	+2.72	11.79	+1.45	11.06	0.0	12.51	0.1	0.00022114	0.00215178	0.01558493	0.41138614	A_07_P053000	EC03002	cmr	exonuclease [EC03002]
EC03003	+21.83	11.53	+4.45	9.31	0.1	13.76	0.2	0.00000042	0.00004998	0.00036014	0.05504854	A_07_P053004	EC03003	cmr	hypothetical protein [EC03003]
EC03004	+21.07	9.93	+4.40	7.73	0.1	12.13	0.3	0.00000043	0.00006145	0.00036046	0.06078646	A_07_P053006	EC03004	cmr	hypothetical protein [EC03004]
EC03005	+21.70	11.25	+4.45	9.03	0.3	13.47	0.3	0.00000369	0.00014246	0.00036522	0.05426528	A_07_P053011	EC03005	cmr	hypothetical protein [EC03005]
EC03006	+38.28	9.18	+4.82	6.77	0.1	11.59	0.2	0.00000033	0.00006520	0.00016859	0.03768563	A_07_P053018	EC03006	cmr	putative CA type phic Gpor protein [EC03006]
EC03042	+27.58	10.54	+4.79	8.15	0.1	12.93	0.2	0.00000025	0.00004211	0.00017721	0.03671053	A_07_P053100	EC03042	cmr	glucitose-binding transport protein [EC03042]
EC03094	+2.26	13.08	+1.18	12.50	0.1	13.67	0.2	0.00006434	0.00635518	0.04751778	0.53979912	A_07_P053126	EC03094	cmr	ecotin, a serine protease inhibitor [EC03094]
EC03104	+2.33	10.39	+1.22	9.78	0.0	11.00	0.1	0.00075538	0.00450357	0.04496888	0.52560505	A_07_P053132	EC03104	cmr	outer membrane protein C OmpC [EC03104]
EC03152	+2.19	8.75	+1.13	8.18	0.0	9.32	0.0	0.00066086	0.00470229	0.05142276	0.55988935	A_07_P053169	EC03152	cmr	2-oxoglutarate decarboxylase [EC03152]
EC03152	+2.46	8.69	+1.30	8.04	0.0	9.34	0.2	0.00032606	0.00484739	0.03988729	0.49680929	A_07_P053169	EC03152	cmr	2-oxoglutarate decarboxylase [EC03152]
EC03152	+2.52	8.82	+1.33	8.15	0.2	9.48	0.2	0.00081632	0.00559521	0.03839113	0.48902104	A_07_P053169	EC03152	cmr	2-oxoglutarate decarboxylase [EC03152]
EC03160	+5.73	8.03	+2.52	6.77	0.1	9.28	0.1	0.00000849	0.00022916	0.00703989	0.24702648	A_07_P052826	EC03160	cmr	NADH dehydrogenase I chain H [EC03160]
EC03163	+36.31	9.46	+4.72	7.10	0.1	11.82	0.1	0.00000016	0.00003548	0.00003325	0.03950617	A_07_P053173	EC03163	cmr	NADH dehydrogenase I chain K [EC03163]
EC03167	+12.09	10.09	+3.67	8.26	0.1	11.91	0.1	0.00000585	0.00003859	0.00148133	0.11601000	A_07_P053176	EC03167	cmr	NADH dehydrogenase I chain G [EC03167]
EC03169	+7.42	11.86	+2.89	10.41	0.2	13.30	0.0	0.00000796	0.00022222	0.00470227	0.19071571	A_07_P053350	EC03169	cmr	NADH dehydrogenase I chain E [EC03169]
EC03179	+4.11	10.25	+1.77	9.37	0.0	11.14	0.2	0.00008388	0.00105814	0.02139990	0.38617615	A_07_P053181	EC03179	cmr	hypothetical protein [EC03179]
EC03189	-2.78	8.58	-1.47	9.32	0.3	7.85	0.1	0.00090774	0.00608664	0.02258651	0.45940023	A_07_P053190	EC03189	cmr	hypothetical protein [EC03189]
EC03190	+2.48	7.49	+1.31	6.83	0.0	8.14	0.2	0.00146151	0.00411468	0.03184815	0.49490019	A_07_P053195	EC03190	cmr	ATP-binding component of heptidine transport [EC03190]
EC03196	+4.57	9.00	+2.19	7.90	0.0	10.10	0.1	0.00001777	0.00036419	0.01230691	0.29947450	A_07_P053197	EC03196	cmr	aminophosphorbosylbisnitrafenase [EC03196]
EC03197	+4.22	10.73	+2.08	9.69	0.0	11.77	0.1	0.00002886	0.00050012	0.01464594	0.32469330	A_07_P053205	EC03197	cmr	membrane protein required for colicin V production [EC03197]
EC03226	-2.63	8.95	-1.40	9.65	0.4	8.25	0.0	0.02208897	0.01194579	0.03019293	0.48719424	A_07_P053303	EC03226	cmr	putative replication protein [EC03226]
EC03243	-2.08	8.33	-1.06	8.86	0.1	7.80	0.2	0.00190570	0.01060487	0.05238198	0.65168438	A_07_P053317	EC03243	cmr	succinic-6-phosphate hydrolase [EC03243]
EC03296	-6.26	10.97	-2.65	12.30	0.1	9.65	0.0	0.00000473	0.00016577	0.00142403	0.12521140	A_07_P053399	EC03296	cmr	thiosulfate binding protein [EC03296]
EC03306	-5.75	11.72	-2.52	12.98	0.0	10.46	0.0	0.00000583	0.00018375	0.00192247	0.14546894	A_07_P053373	EC03306	cmr	N-acetylmuramyl-l-alanine amidase [EC03306]
EC03311	+2.14	7.36	+1.10	6.81	0.0	7.91	0.1	0.00090470	0.00607145	0.05451269	0.56990642	A_07_P053415	EC03311	cmr	ethanolamine ammonia-lyase light chain [EC03311]
EC03370	+4.75	11.35	+2.25	10.21	0.1	12.37	0.1	0.00002874	0.00049935	0.01535453	0.29337641	A_07_P053630	EC03370	cmr	IMP dehydrogenase [EC03370]
EC03382	-3.65	11.39	-1.41	12.10	0.1	10.69	0.1	0.00025197	0.00203847	0.02469212	0.44644560	A_07_P053440	EC03382	cmr	putative anaerobic dimethyl sulfoxide reductase chain C [EC03382]
EC03398	-6.71	13.17	-3.28	14.81	0.0	11.53	0.3	0.00001067	0.00026319	0.00025989	0.05128870	A_07_P053458	EC03398	cmr	putative ATP synthase beta subunit [EC03398]
EC03462	+3.25	8.51	+1.70	7.68	0.3	9.38	0.1	0.00056128	0.00422450	0.02232508	0.40987221	A_07_P053492	EC03462	cmr	ATP-dependent RNA helicase [EC03462]
EC03450	+2.89	9.49	+1.53	8.73	0.0	10.26	0.5	0.00103463	0.01553432	0.02996126	0.44459001	A_07_P053496	EC03450	cmr	hypothetical protein [EC03450]
EC03489	-2.44	11.79	-1.29	12.44	0.3	11.15	0.2	0.00189486	0.01054400	0.03842907	0.53972318	A_07_P053872	EC03489	cmr	hypothetical protein [EC03489]
EC03492	-3.98	8.60	-1.99	9.60	0.0	7.61	0.1	0.00002814	0.00049161	0.00700384	0.27122010	A_07_P053876	EC03492	cmr	hypothetical protein [EC03492]
EC03535	+3.02	8.59	+1.59	7.59	0.0	9.59	0.1	0.00019251	0.00194954	0.02481720	0.42777102	A_07_P053525	EC03535	cmr	hypothetical protein [EC03535]
EC03569	-3.46	8.00	-1.79	8.90	0.1	7.11	0.0	0.00000502	0.00079754	0.01185658	0.33634234	A_07_P053593	EC03569	cmr	electron transport protein HyaN [EC03569]
EC03586	-2.16	11.30	+1.21	10.69	0.0	11.90	0.1	0.00109295	0.00854946	0.04620173	0.53904891	A_07_P054010	EC03586	cmr	HypE protein [EC03586]
EC03591	+3.70	8.74	+1.89	7.79	0.0	9.68	0.5	0.00132479	0.00861289	0.01786268	0.35286073	A_07_P054017	EC03591	cmr	hypothetical protein [EC03591]
EC03594	-2.40	9.60	-1.29	10.04	0.1	9.15	0.5	0.00050645	0.00394855	0.01399455	0.54079566	A_07_P054024	EC03594	cmr	transcriptional regulator [EC03594]
EC03610	-2.42	9.02	-1.27	9.66	0.3	8.38	0.1	0.00102266	0.01027329	0.04647393	0.54123956	A_07_P054055	EC03610	cmr	hypothetical protein [EC03610]
EC03622	-2.31	8.40	-1.21	9.00	0.5	7.80	0.1	0.01026192	0.04008828	0.04617748	0.77467200	A_07_P054090	EC03622	cmr	hypothetical protein [EC03622]
EC03649	-2.47	7.88	-1.30	7.23	0.1	8.53	0.2	0.00367812	0.00483092	0.04016672	0.49769291	A_07_P054311	EC03649	cmr	putative transport protein [EC03649]
EC03663	-5.74	11.79	-2.52	10.53	0.0	13.05	0.1	0.00000832	0.00022675	0.00760513	0.24794679	A_07_P054319	EC03663	cmr	tRNA-fucosilidrome [EC03663]
EC03670	-2.42	9.27	-1.28	9.91	0.1	8.64	0.1	0.00064505	0.00359144	0.04680221	0.54393734	A_07_P054142	EC03670	cmr	hypothetical protein [EC03670]
EC03680	-2.87	7.98	-1.52	7.22	0.2	8.75	0.0	0.00037752	0.00254324	0.02395313	0.44287081	A_07_P054146	EC03680	cmr	prepilin peptidase dependent protein A [EC03680]
EC03734	-2.15	8.88	-1.10	9.43	0.2	8.33	0.1	0.00277533	0.01423748	0.05326601	0.62063306	A_07_P054259	EC03734	cmr	type III secretion protein EivE [EC03734]
EC03758	-3.11	8.76	-1.64	9.58	0.2	7.95	0.1	0.00018059	0.00186075	0.01706491	0.37681627	A_07_P054278	EC03758	cmr	putative oxidoreductase Fe-S subunit [EC03758]
EC03764	-3.46	9.28	-1.79	10.37	0.2	8.38	0.1	0.00011662	0.00132344	0.01186991	0.33551167	A_07_P054285	EC03764	cmr	ispDH4 monooxygenase Rev2 [EC03764]
EC03771	+3.03	9.27	+1.60	8.47	0.2	10.07	0.1	0.00025789	0.00229826	0.02665142	0.42685656	A_07_P054349	EC03771	cmr	putative oxidoreductase [EC03771]
EC03772	+2.07	7.77	+1.05	7.25	0.1	8.29	0.0	0.00122246	0.00469157	0.03273128	0.49205468	A_07_P054352	EC03772	cmr	hypothetical protein [EC03772]
EC03774	+6.98	9.11	+2.80	7.71	0.1	10.52	0.1	0.00000441	0.00015967	0.00512211	0.20771208	A_07_P054354	EC03774	cmr	glycine dearylase [EC03774]
EC03778	+2.26	11.88	+1.18	11.29	0.0	12.47	0.0	0.00054130	0.00411349	0.04788844	0.54393808	A_07_P054265	EC03778	cmr	2-octaprenyl-6-methoxyphenol 4-monooxygenase [EC03778]
EC03792	-2.01	7.30	-1.00	7.80	0.2	6.80	0.3	0.00688415	0.02501845	0.07213605	0.66845792	A_07_P054301	EC03792	cmr	putative transcriptional regulator LYSR-type [EC03792]
EC03799	-2.12	7.28	-1.08	6.74	0.1	7.82	0.1	0.00144275	0.00851195	0.05324012	0.57528847	A_07_P054312	EC03799	cmr	hypothetical protein [EC03799]
EC03800	+10.08	8.50	+3.23	6.83	0.1	10.16	0.1	0.00008723	0.00215524	0.01466667	0.37018518	A_07_P054318	EC03800	cmr	putative transporter [EC03800]
EC03801	+4.85	8.67	+2.28	7.53	0.1	9.81	0.1	0.00001637	0.00034464	0.01090638	0.28523256	A_07_P054323	EC03801	cmr	hypothetical lipoprotein [EC03801]
EC03802	+2.19	7.30	+1.13	6.74	0.0	7.87	0.0	0.00065923	0.00473490	0.05099221	0.55945554	A_07_P054330	EC03802	cmr	putative ABC transporter ATP-binding subunit [EC03802]
EC03810	+3.19	8.76	+1.67	7.94	0.0	9.62	0.1	0.00130656	0.01165692	0.02468113	0.41576471	A_07_P054340	EC03810	cmr	transmeletase 1 isozyme [EC03810]
EC03844	-5.27	9.62	-2.40	10.82	0.0	8.42	0.0	0.00000751	0.00021366	0.00262449	0.17216667	A_07_P054361	EC03844	cmr	hypothetical protein [EC03844]
EC03850	-2.00	7.41	-1.00	7.91	0.4	6.91	0.1	0.01131864	0.04894311	0.07188168	0.66574063	A_07_P054394	EC03850	cmr	putative virulence-related membrane protein [EC03850]
EC03860	-3.02	9.33	-1.59	10.13	0.3	8.53	0.0	0.00050219	0.00391025	0.01923844	0.39801577	A_07_P054442	EC03860	cmr	putative adherence factor [EC03860]
EC03869	-3.13	11.68	-1.65	12.50	0.1	10.86	0.0	0.00007988	0.00101674	0.01706283	0.37926863	A_07_P054468	EC03869	cmr	hypothetical protein [EC03869]
EC03870	-3.39	9.01	-1.76	9.89	0.3	8.13	0.1	0.00018870	0.00337775	0.01247849	0.33750614	A_07_P054475	EC03870	cmr	hypothetical protein [EC03870]
EC03874	+2.19	9.70	+1.26	9.07	0.2	10.33	0.1	0.00190314	0.00854496	0.04425711	0.51476067	A_07_P054483	EC03874	cmr	hypothetical protein [EC03874]
EC03878	+2.82	11.55	+1.50	10.80	0.0	12.30	0.3	0.00068376	0.00381767	0.03669360	0.44860081	A_07_P054488	EC03878	cmr	hydrogenase 2 maturation protein HybD [EC03878]
EC03916	-2.54	8.66	-1.34	8.85	0.1	8.47	0.1	0.00025664	0.00264625	0.03448233	0.51275701	A_07_P054524	EC03916	cmr	putative ABC-type iron-siderophore transport system ATP-binding protein [EC03916]
EC03950	-2.62	13.09	-1.39	13.78	0.3	12.40	0.0	0.00033533	0.00224666	0.01133093	0.49675716	A_07_P054634	EC03950	cmr	hypothetical protein [EC03950]
EC03995	+78.34	10.40	+6.29	7.25	0.2	13.54	0.1	0.00000006	0.00003344	0.00008508	0.00571429	A_07_P054659	EC03995	cmr	putative kinase [EC03995]
EC04006	+4.58	9.21	+2.20	8.11	0.1	10.31	0.0	0.00002383	0.00044168	0.01238404	0.29380498	A_07_P054708	EC04006	cmr	putative hydrolase [EC04006]
EC04013	+3.79	7.80	+1.92	6.84	0.2	8.76	0.2	0.00011648	0.00174012	0.01763402	0.35098609	A_07_P054671	EC04013	cmr	N-acetylglucosamine-specific PTS system enzyme IID component [EC04013]
EC04014	+6.62	8.47	+2.73	7.10	0.1	9.83	0.2	0.00001275	0.00029373	0.00573806	0.23874052	A_07_P054680	EC04014	cmr	N-acetyl-galactosamine / galactosamine PTS system enzyme IIA component [EC04014]
EC04018	+3.59	8.68	+1.64	7.76	0.1	9.60	0.2	0.00009339	0.00111982	0.01970528	0.36801898	A_07_P054680	EC04014	cmr	N-acetyl-galactosamine / galactosamine PTS system enzyme IIA component [EC04014]
EC04014	+4.18	8.18	+2.06	7.15	0.1	9.21	0.3	0.00010708	0.00229787	0.04148822	0.32516070	A_07_P054680	EC04014	cmr	N-acetyl-galactosamine / galactosamine PTS system enzyme IIA component [EC04014]
EC04014	+2.89	8.52	+1.53	7.76	0.1	9.29	0.4	0.00160761	0.00810508	0.02966146	0.44348528	A_07_P054680	EC04014	cmr	N-acetyl-galactosamine / galactosamine PTS system enzyme IIA component [EC04014]
EC04014	+4.27	8.61	+2.16	7.51	0.1	9.65	0.1	0.00003950	0.00062195	0.01380018	0.31764620	A_07_P054680	EC04014	cmr	N-acetyl-galactosamine / galactosamine PTS system enzyme IIA component [EC04014]
EC04023	-32.65	11.78	-5.03	14.29	0.1	9.27	0.1	0.00000009	0.00003427	0.00000318	0.00454545	A_07_P054688	EC04023	cmr	truncated putative fimbrial protein [EC04023]
EC04052	+2.83	8.49	+1.50	7.74	0.1	9.24	0.0	0.00019626	0.00184642	0.02802541	0.44428571	A_07_P054701	EC04052	cmr	organosuccinamine synthetase [EC04052]
EC04086	+3.51	9.65	+1.81	8.74	0.0	10.55	0.1	0.00004735	0.00070931	0.02028709	0.37356725	A_07_P054500	EC04086	cmr	hypothetical protein [EC04086]
EC04094	+4.24	8.11	+2.08	7.07	0.0	9.16	0.0	0.00001848	0.00037316	0.01423136	0.32241655	A_07_P054712	EC04094	cmr	hypothetical protein [EC04094]
EC04098	+2.99	7.94	+1.58	7.15	0.0	8.73	0.1	0.00014144	0.00154753	0.02700140	0.42767606	A_07_P054716	EC04098	cmr	N-acetylneuraminate lyase [EC04098]
EC04115	+4.50	8.11	+2.17	7.20	0.1	9.02	0.1	0.00004911	0.00049931	0.01298419	0.28224300	A_07_P054737	EC04115	cmr	hypothetical protein [EC04115]
EC04150	+2.53	10.80	+1.34	10.13	0.0	11.47	0.2	0.00085313	0.00580363	0.03798145	0.48735126	A_07_P054737	EC04150	cmr	hypothetical protein [EC04150]
EC04196	-2.24	9.85	-1.16	10.44	0.2	9.27	0.1	0.00184277	0.01053794	0.05238786	0.59325559	A_07_P054765	EC04196	cmr	hypothetical protein [EC04196]
EC04227	+2.39	7.30	+1.26	6.67	0.1	7.92	0.0	0.00061156	0.00339421	0.04241108	0.51087988	A_07_P054765	EC04227	cmr	hypothetical protein [EC04227]
EC04253	-3.86	9.37	-1.53	9.94	0.1	8.81	0.5	0.00318230	0.01585126	0.02280805	0.43791463	A_07_P054156	EC04253	cmr	hypothetical protein [EC04253]
EC04260	+4.40	8.29	+2.14	7.23	0.2	9.36	0.5	0.00098195	0.00386646	0.01168158	0.35511195	A_07_P054542	EC04260	cmr	positive regulator of mal regulon [EC04260]
EC04282	+2.73	8.55	+1.45	7.83	0.0	9.28	0.1	0.00028755	0.00260232	0.03279644	0.46280072	A_07_P054833	EC04282	cmr	putative ATP-dependent DNA helicase [EC04282]
EC04292	-2.60	10.69	-1.43	11.41	0.5	9.98	0.2	0.00767107	0.03252107	0.07839473	0.47427489	A_07_P054864	EC04292	cmr	hypothetical membrane protein [EC04292]
EC04325	-2.04	8.58	-1.03	9.09	0.0	8.06	0.1	0.00126043	0.00772450	0.06965701	0.65956250	A_07_P054892	EC04325	cmr	putative O-methyltransferase [EC04325]
EC04329	-3.93	10.32	-1.97	11.30	0.0	9.33	0.0	0.00002480	0.00045357	0.00747586	0.27564403	A_07_P054912	EC04329	cmr	putative acyl carrier protein [EC04329]
EC04331	-2.05	7.94	-1.03	8.46	0.2	7.42	0.2	0.00435358	0.02039497	0.06708779	0.65118989	A_07_P054921	EC04331	cmr	putative surfactin synthetase [EC04331]
EC04332	-2.47	7.47	-1.31	8.12	0.1	6.82	0.2	0.00096625	0.00603846	0.03715289	0.52516622	A_07_P054928	EC04332	cmr	hypothetical protein [EC04332]
EC04334	+2.04	8.47	+1.03	7.96	0.1	8.98	0.1	0.00267386	0.01381863	0.06230246	0.60623609	A_07_P054939	EC04334	cmr	hypothetical protein [EC04334]
EC04335	-2.09	7.92	+1.06	7.39	0.0	8.45	0.1	0.00100237	0.00614014	0.05378831	0.64498691	A_07_P054941	EC04335	cmr	hypothetical protein [EC04335]
EC04337	+2.15	7.51	+1.10	6.96	0.0	8.06	0.4	0.00577740	0.02558586	0.05491140	0.57388188	A_07_P054955	EC04337	cmr	hypothetical lipoprotein [EC04337]
EC04338	-2.12	7.71	-1.13	7.65	0.1	7.77	0.1	0.00468056	0.00880008	0.01883100	0.48676675	A_07_P054960	EC04338	cmr	putative 3-oxoacyl- [EC04338]
EC04339	+2.54	7.18	+1.35	6.51	0.2	7.85	0.3	0.02118849	0.01155702	0.03847524	0.48931341	A_07_P054965	EC04339	cmr	putative beta-hydroxydecanoyl-ACP dehydrase [EC04339]
EC04341	-2.10	8.79	-1.07	9.52	0.0	8.25	0.0	0.00090872	0.00609665	0.04449437	0.64738354	A_07_P054973	EC04341	cmr	putative 3-oxoacyl- [EC04341]
EC04350	+2.86	7.59	+1.52	6.83	0.2	8.35	0.0	0.00030736	0.00272536	0.02976517	0.44391469	A_07_P054987	EC04350	cmr	putative phosphotransferase system enzyme IIA [EC04350]
EC04367	+2.34	8.52	+1.62	10.53	0.1	6.51	0.1	0.00000105	0.00007379	0.00126625	0.12041667	A_07_P060029	EC04367	cmr	universal stress protein UspA [EC04367]
EC04407	-2.78	9.30	-1.47	10.03	0.1	8.56

fis	+2.89	10.18	+1.53	9.41	0.1	10.94	0.3	0.00048743	0.00383512	0.02931911	0.44290424	A_07_P012272	b3261
fkbB	+2.76	11.70	+1.46	11.08	0.1	12.51	0.1	0.00018158	0.00186421	0.01434329	0.45487132	A_07_P011753	b4207
fkpA	+4.66	10.57	+2.22	9.46	0.0	11.68	0.0	0.00002055	0.00008896	0.01100273	0.29555906	A_07_P010828	b0928
flgK	-2.70	9.28	-1.43	9.99	0.1	8.56	0.2	0.00045681	0.00363587	0.02880892	0.47995772	A_07_P001612	b1082
flhD	+2.52	8.50	+1.34	7.83	0.0	9.17	0.3	0.00095948	0.00605156	0.03833651	0.48872065	A_07_P014140	b1892
fliA	-4.51	7.85	-2.17	8.94	0.1	6.77	0.1	0.00002524	0.00045780	0.00449106	0.21850000	A_07_P014973	b1922
fliE	-3.89	7.73	-1.96	8.71	0.3	6.75	0.1	0.00019642	0.00178076	0.00936842	0.28078276	A_07_P014949	b1937
fliI	-2.60	12.47	-1.38	13.16	0.3	11.78	0.1	0.00119865	0.00742973	0.02215130	0.50217262	A_07_P004091	Z3031
fliJ	-3.16	12.40	-1.66	13.23	0.2	11.57	0.2	0.00129527	0.00787670	0.01456789	0.37757971	A_07_P015201	ECs2880
fliM	-2.56	11.95	-1.36	12.63	0.4	11.27	0.0	0.00265915	0.01378518	0.03316682	0.50631274	A_07_P015566	b1941
fliN	-2.71	11.81	-1.44	12.53	0.2	11.09	0.1	0.00033156	0.00286975	0.01472864	0.47346241	A_07_P014959	c2358
fliY	-8.70	12.59	-3.12	14.15	0.0	11.02	0.3	0.00000664	0.00019716	0.00041286	0.06435644	A_07_P041209	c2335
flx	-7.14	11.50	-2.88	12.93	0.0	10.06	0.0	0.00000262	0.00011934	0.00089334	0.08958333	A_07_P014664	b3520
fls	-3.21	8.68	-1.68	9.52	0.2	7.84	0.3	0.00052930	0.00404719	0.01509614	0.36906832	A_07_P013891	b2321
fku	+2.34	10.31	+1.23	9.73	0.0	10.92	0.0	0.01299494	0.04882604	0.11620079	0.55830413	A_07_P000326	b0300
fmt	-2.42	12.05	-1.28	12.69	0.0	11.41	0.1	0.00032296	0.00401527	0.04018039	0.54347079	A_07_P012874	b3288
fnr	-0.86	13.83	-3.01	15.33	0.0	12.32	0.1	0.00000271	0.00012864	0.00054498	0.07268142	A_07_P014367	b1334
focA	+4.99	10.96	+2.32	9.80	0.1	12.12	0.1	0.00001449	0.00031589	0.01022167	0.27939236	A_07_P004969	b0904
focA	+69.57	13.05	+6.12	9.99	0.0	16.11	0.0	0.00000003	0.00000104	0.00003611	0.00625003	A_07_P004686	c_1239
focB	-2.65	12.99	-1.40	13.69	0.1	12.28	0.2	0.00043046	0.00358857	0.03098514	0.49475659	A_07_P013519	b2492
focC	+8.38	9.70	+3.07	8.16	0.1	11.23	0.3	0.00000380	0.00014395	0.00342614	0.17352584	A_07_P004500	c_1241
focD	+5.73	10.78	+2.52	9.52	0.3	12.04	0.2	0.00005259	0.00076528	0.00761687	0.24725773	A_07_P004505	c_1242
focF	+7.07	10.31	+2.82	8.90	0.2	11.72	0.1	0.00005578	0.00081187	0.00512968	0.20778351	A_07_P004507	c_1243
focG	+6.51	10.66	+2.70	9.31	0.8	12.01	0.1	0.00151105	0.00794857	0.04616425	0.22569767	A_07_P004512	c_1244
focH	+5.76	10.08	+2.53	8.82	0.1	11.34	0.2	0.00001555	0.00031216	0.00764990	0.24731006	A_07_P004520	c_1245
focA	+2.10	9.10	+0.97	8.56	0.1	10.03	0.3	0.01004138	0.03622686	0.09700013	0.53843192	A_07_P002929	b0048
fokA	+2.03	10.24	+1.02	9.73	0.1	10.75	0.1	0.01098825	0.01100668	0.06193514	0.60603480	A_07_P015679	c_0058
folA	+2.34	9.21	+1.23	8.60	0.0	9.82	0.2	0.00073522	0.00513543	0.04478659	0.52382330	A_07_P014609	ECs0551
folX	+2.15	9.41	+1.10	8.86	0.1	9.96	0.1	0.01004063	0.00671463	0.05405140	0.57128495	A_07_P013803	b2303
fpr	+3.21	9.39	+1.68	8.54	0.1	10.23	0.1	0.00012566	0.00141116	0.02348577	0.40947951	A_07_P019438	c_4676
fpr	+5.11	9.99	+2.35	7.91	0.1	10.26	0.1	0.00001826	0.00037077	0.00965142	0.27137746	A_07_P019996	b3924
frdA	+2.40	14.78	+1.26	14.14	0.0	15.41	0.0	0.00036212	0.00307507	0.04231668	0.51509663	A_07_P015155	b4154
frdB	+4.28	12.64	+2.10	11.59	0.1	13.69	0.0	0.00002162	0.00041206	0.01397548	0.31934688	A_07_P011497	b4153
frdC	+3.82	11.76	+1.93	10.79	0.2	12.73	0.0	0.00007141	0.00094701	0.01719258	0.34836551	A_07_P011498	b4152
frdD	+3.90	10.04	+1.96	9.06	0.2	11.03	0.1	0.00004983	0.00073949	0.01655991	0.34441215	A_07_P011487	b4151
frmR	+6.88	10.68	+2.78	9.29	0.1	12.07	0.1	0.00005518	0.00082746	0.00527626	0.20767500	A_07_P015951	b0957
frr	-2.96	13.28	-1.57	14.07	0.0	12.50	0.3	0.00005689	0.00393517	0.02097815	0.41649433	A_07_P059928	ECs0174
frr	-2.64	13.95	-1.40	14.60	0.0	13.25	0.0	0.00000306	0.00020181	0.00110068	0.14973178	A_07_P049243	b0161
frr	-2.21	13.81	-1.14	14.38	0.0	13.24	0.1	0.00007045	0.00479144	0.05117785	0.60746650	A_07_P035911	c_0208
frr	-2.84	13.30	-1.51	14.05	0.0	12.55	0.0	0.00013523	0.00141122	0.01398944	0.44675355	A_07_P003818	b0172
frsA	-2.20	8.98	-1.14	9.55	0.0	8.41	0.1	0.00066535	0.00480746	0.05646225	0.60882927	A_07_P000634	b2167
frsA	-2.11	9.18	-1.08	9.72	0.1	8.64	0.1	0.00124030	0.00763383	0.06383003	0.64623067	A_07_P042526	c_2702
fruR	+3.41	10.15	+1.77	9.26	0.1	11.04	0.1	0.00008685	0.00108440	0.01902147	0.38765108	A_07_P013076	b0080
fsaA	+2.15	7.85	+1.11	7.30	0.1	8.41	0.0	0.00066005	0.00638357	0.05138034	0.56861976	A_07_P004579	b0825
fteA	+18.92	10.17	+4.24	8.05	0.0	12.29	0.1	0.00000206	0.00002411	0.00022292	0.07158730	A_07_P011693	b1905
fteB	+5.95	10.40	+2.57	9.11	0.1	11.69	0.1	0.00000820	0.00002525	0.00017058	0.24155983	A_07_P011680	b1902
fteE	4.98	10.99	3.17	12.57	0.0	9.40	0.1	0.00000102	0.00009455	0.00033155	0.05553191	A_07_P027353	b3463
fts.	-3.32	10.80	-1.22	11.41	0.2	10.19	0.3	0.00403942	0.02252231	0.04691502	0.57570538	A_07_P011094	b0083
ftsN	-2.25	11.52	-1.17	12.10	0.1	10.93	0.1	0.00074840	0.00521165	0.01578925	0.59170537	A_07_P011663	b3013
ftsQ	-2.31	11.46	-1.21	12.06	0.0	10.85	0.1	0.00052068	0.00400770	0.04720274	0.57520124	A_07_P002438	b0093
ftsW	+2.23	8.79	+1.16	8.21	0.1	9.36	0.2	0.00170326	0.00853948	0.05069554	0.55820774	A_07_P011122	b0089
ftsY	-6.05	12.94	-2.60	14.24	0.1	11.64	0.3	0.00002835	0.00049426	0.00140694	0.12908163	A_07_P002556	b3464
fucA	+3.92	10.97	+1.96	10.00	0.2	11.94	0.0	0.00002525	0.00045142	0.00148898	0.34452298	A_07_P000969	b3800
fucK	+4.23	9.54	+2.08	8.50	0.1	10.58	0.1	0.00003138	0.00051308	0.01427337	0.32241033	A_07_P000014	b2803
fucK	-5.42	11.94	-2.44	10.72	0.3	13.16	0.1	0.00005615	0.00079813	0.00862231	0.23927757	A_07_P042154	b2180
fucO	+5.90	10.05	+2.56	8.77	0.0	11.33	0.2	0.00000914	0.00023912	0.00732180	0.24243070	A_07_P005991	b2799
fucP	-2.98	10.15	-1.57	10.93	0.3	9.36	0.3	0.00118379	0.00797666	0.04206932	0.43809957	A_07_P000961	b2801
fucR	+5.40	8.47	+2.43	7.26	0.1	9.69	0.1	0.00000977	0.00024876	0.00827213	0.25973535	A_07_P000824	b2805
fucU	+4.58	11.40	+2.20	10.30	0.1	12.50	0.0	0.00001344	0.00032073	0.01122116	0.29923795	A_07_P000818	b2804
fumA	+22.52	10.85	+4.49	8.60	0.0	13.10	0.0	0.00000015	0.00003548	0.00035188	0.05485149	A_07_P020691	b1612
fumB	+13.58	10.48	+3.84	9.56	0.4	11.40	0.1	0.00066255	0.00836283	0.01956395	0.36762266	A_07_P011347	b4122
fumC	+7.45	8.91	+2.90	7.46	0.0	10.36	0.0	0.00000051	0.00013758	0.00460203	0.19627346	A_07_P043312	c_2003
fumC	+12.73	9.15	+3.67	7.32	0.1	10.99	0.1	0.00000085	0.00006436	0.00154027	0.11771845	A_07_P020689	b1611
fur	-2.20	12.61	-1.14	13.18	0.0	12.04	0.0	0.00007670	0.00496708	0.02166829	0.41118829	A_07_P000683	b0683
gabT	-2.93	10.66	-1.55	11.43	0.6	9.88	0.1	0.00055660	0.03821185	0.02809968	0.41428768	A_07_P041262	c_3210
gabP	-3.18	10.30	-1.67	9.46	0.1	11.13	0.0	0.00011003	0.00128322	0.02306034	0.41311148	A_07_P015526	b0962
gabR	+9.65	11.79	+3.27	10.15	0.1	13.42	0.0	0.00000119	0.00008082	0.00234554	0.15122665	A_07_P004240	b0757
gabM	+10.84	11.40	+3.44	9.38	0.2	12.82	0.1	0.00000119	0.00008082	0.00234554	0.15122665	A_07_P004231	b0756
gabP	-2.21	7.40	-1.15	7.97	0.0	6.83	0.1	0.00068725	0.00486692	0.05408473	0.60476562	A_07_P011856	b2943
gabS	+3.06	9.61	+1.61	8.80	0.0	10.42	0.0	0.00029845	0.00267394	0.01603873	0.42094301	A_07_P012245	c_2165
galT	+2.13	10.26	+1.09	9.72	0.0	10.81	0.4	0.00712342	0.03010768	0.05683873	0.58282353	A_07_P004241	b0758
galactin	+31.76	12.99	+4.78	11.10	0.0	14.88	0.0	0.00000157	0.00000969	0.00125445	0.10972222	A_07_P018614	c_1537
galE	+27.39	11.10	+4.78	8.71	0.1	13.49	0.1	0.00000014	0.00003548	0.00018293	0.03740260	A_07_P015590	b1779
galF	-2.13	7.88	-1.09	8.43	0.1	7.34	0.1	0.00014805	0.00118504	0.04129573	0.63699010	A_07_P000857	b3327
galI	-2.87	8.66	-1.52	9.42	0.2	7.90	0.0	0.00029158	0.00263253	0.02946275	0.43836165	A_07_P002585	b0124
galK	+177.19	11.61	+7.47	7.88	0.0	15.34	0.1	0.00000000	0.00000000	0.00000000	0.00000000	A_07_P047711	c_3484
galM	+92.40	10.75	+6.53	7.49	0.2	14.02	0.1	0.00000005	0.00003344	0.00000318	0.00416667	A_07_P004489	b2904
galR	+103.63	11.91	+6.68	8.57	0.0	15.25	0.1	0.00000008	0.00003344	0.00000564	0.00542857	A_07_P042275	c_3484
galS	+8.12	9.37	+3.02	7.86	0.1	10.88	0.1	0.00000320	0.00013126	0.00375635	0.17813253	A_07_P032879	c_3483
gcvP	+8.51	9.19	+3.09	7.65	0.2	10.74	0.0	0.00000180	0.00012501	0.00346926	0.17122257	A_07_P002779	Z4240
gcvP	+12.70	8.87	+3.67	7.04	0.0	10.71	0.0	0.00000051	0.00005264	0.00155159	0.11848039	A_07_P004681	b2903
gcvH	+7.59	9.24	+2.92	7.78	0.1	10.70	0.1	0.00000409	0.00015128	0.00442280	0.19068306	A_07_P013453	b2479
gcvT	-66.83	10.98	-6.06	7.95	0.0	14.01	0.2	0.00000007	0.00003344	0.00008826	0.00722222	A_07_P004691	b2905
gdhA	+2.75	9.19	+1.46	8.08	0.0	9.54	0.1	0.00102228	0.00201310	0.03188115	0.45921147	A_07_P052546	Z2793
gdhA	-2.13	9.59	-1.09	8.65	0.3	9.74	0.3	0.00869728	0.02904896	0.05866169	0.59278552	A_07_P018851	b1761
gef	-3.75	12.69	-1.91	13.65	0.0	11.74	0.1	0.00003371	0.00055746	0.00879700	0.30240175	A_07_P004882	Z0016
gefA	-2.63	10.66	-1.40	11.36	0.0	9.96	0.2	0.00016692	0.00132485	0.01424849	0.49679719	A_07_P004878	Z0016
gfcA	-3.41	11.94	-1.77	12.83	0.0	11.05	0.0	0.00004950	0.00073662	0.01248412	0.33713551	A_07_P005179	b0987
gfcD	-5.39	14.44	-2.43	15.66	0.0	13.23	0.5	0.00010674	0.00193615	0.00249832	0.13679145	A_07_P013364	b0984
gjt	-2.03	7.65	-1.02	8.16	0.0	7.14	0.0	0.01119368	0.00740477	0.07110772	0.66519311	A_07_P034524	c_4216
gldB	-2.21	10.46	-1.14	11.08	0.1	9.89	0.2	0.00167502	0.00610209	0.03132099	0.60852203	A_07_P000745	b0740
gldI	+4.89	9.23	+1.80	8.33	0.1	10.14	0.1	0.00007734	0.00096640	0.02642255	0.37536756	A_07_P012016	b2976
gldB	+4.89	11.23	+2.29	10.09	0.1	12.38	0.2	0.00003145	0.00053123	0.01661166	0.28316949	A_07_P047726	c_3705
gltF	+8.59	9.13	+3.10	7.58	0.1	10.68	0.1	0.00000288	0.00012407	0.00338034	0.16895238	A_07_P012026	b2978
gltG	+35.14	9.58	+5.13	7.01	0.0	12.15	0.2	0.00000011	0.00003344	0.00008253	0.02650445	A_07_P012024	b2977
gltA	+9.40	12.35	+3.23	10.74	0.2	13.97	0.1	0.00000285	0.00012365	0.00281377	0.15435540	A_07_P019501	b3945
glgA	+6.94	10.82	+2.79	9.42	0.1	12.22	0.1	0.00000558	0.00017943	0.00420906	0.20179371	A_07_P011671	b3429
glgB	+5.09	9.68	+2.35	8.50	0.1	10.85	0.1	0.00003176	0.00028105	0.00978341	0.27101284	A_07_P011689	b3432
glgC	+9.85	10.23	+3.30	8.57	0.1	11.89	0.1	0.00000192	0.00005899	0.00242286	0.14859177	A_07_P011679	b3430
glgP	-2.02	8.35	-1.59	7.46	0.3	9.05	0.3	0.00153327	0.01724670	0.07239977	0.42861723	A_07_P016166	b3926
glgS	+7.24	10.22	+2.86	8.79	0.0	11.65	0.1	0.00000290	0.00012407	0.00480501	0.20173333	A_07_P012366	b3049
glgX	+7.05	11.28	+2.82	9.87	0.1	12.69	0.0	0.00000112	0.00004197	0.00166911	0.10483333	A_07_P012431	b3411
glmM	+3.70	11.27	+1.89	10.32	0.1	12.21	0.2	0.00006809	0.00091941	0.01841115	0.35117748	A_07_P000591	b3176
glnA	-3.46	13.41	-1.79	14.30	0.0	12.51	0.1	0.00005038	0.00074420	0.01942061	0.33518034	A_07_P012829	b0870
glnB	+3.09	10.93	+1.63	10.12	0.1	11.74	0.2	0.00017203	0.00179690	0.02585652	0.43491561	A_07_P019668	b2553
glnD	+2.25	8.47	+1.17	7.89	0.1	9.06	0.1	0.00098728	0.00584673	0.04960689	0.55173448	A_07_P012971	b3657
glnA	+3.80	9.43	+1.93	8.47	0.2	10.39	0.1	0.00008625	0.00108122	0.01728849	0.34762452	A_07_P020890	b3651
glpB	-2.25	11.39	-1.17	11.97	0.0	10.80	0.1	0.00064682	0.00514345	0.05423577	0.59232577	A_07_P041234	c_2793
glpB	-2.53	10.35	-1.34	11.02	0.1	9.68	0.3	0.00030110	0.00268893	0.03576156	0.51654128	A_07_P000998	b2242
glpE	-2.04	9.84	-1.03	10.36	0.0	9.33	0.1	0.00168846	0.00967008	0.05234194	0.66176098	A_07_P013513	b3235
glpF	+13.78	9.94	+3.79	8.05	0.1	11.83	0.1	0.00000061	0.00005601	0.00125889	0.10950276	A_07_P019412	b3927
glpK	+3.91	10.38	+1.97	9.40	0.1	11.36	0.1	0.00003456	0.00056413	0.01676764	0.34538697	A_07_P000990	b3926
glpQ	+2.54	8.30	+1.35	7.63	0.2	8.97	0.1	0.00051156	0.00365777	0.03790396	0.48794767	A_07_P000882	b2239
glpT	+16.35	9.52	+3.37	7.63	0.1	11.00	0.2	0.00000271	0.00012664	0.00372424	0.14321839	A_07_P043326	ECs3125
glpT	+6.77	9.25	+2.76	7.87	0.1	10.63	0.0	0.00000032	0.00013758	0.00546939	0.21261728	A_07_P052656	Z3698
glpT	+5.57	9.63	+2.48	8.39	0.1	10.87	0.1	0.00000185	0.00012664	0.00386784	0.20399641	A_07_P000990	b2240
glnA	+34.23	13.59	+5.10	11.04	0.1	16.14	0.1	0.00000013	0.00003548	0.00009337	0.02625000	A_07_P056596	ECs0745
glnA	+20.30	11.36	+4.34	9.19	0.2	13.53	0.1	0.00000046	0.00005132	0.00047254	0.06148760	A_07_P010018	b0720
glnA	+31.28	14.21	+4.97	11.72	0.0	16.69	0.1	0.00000016	0.00003548	0.00001941	0.01313333	A_07_P046286	Z0873
gltD	+2.09	8.94	+1.06	8.11	0.1	9.17	0.1	0.00115693	0.00722808	0.05796550	0.58788623	A_07_P012545	b3213
gltB	+2.46	11.54	+1.30	10.89	0.1	12.19	0.2	0.00093106	0.00609795	0.05608741	0.55018735	A_07_P008841	b0655
gltK	+4.46	8.64	+2.16	7.56	0.1	9.72	0.1	0.00003641	0.00045661	0.01797789	0.30575114	A_07_P008831	b0653
gltL	+4.17	9.00	+2.06	7.97	0.1	10.03	0.2	0.00003717	0.00055471	0.02475156	0.32741636	A_07_P008852	b0652
gltP	+3.01	8.61	+1.59	7.82	0.2	9.42	0.1	0.01020146	0.07744423	0.02784489	0.43162018	A_07_P009026	b4077
gltJ	-4.06	9.29	-2.02	10.30	0.1	8.28	0.0	0.00003635	0.00205415	0.00682831	0.26809863	A_07_P047711	AAC-Q85377
glyA	+8.77	11.80	+3.13	10.23	0.1	13.36	0.2	0.00000659	0.00019656	0.00331936	0.16833859	A_07_P019657	b2551
gmhA	-4.44	9.29	-1.78	8.40	0.0	10.18	0.2	0.00013279	0.00147358	0.02564497	0.37650413	A_07_P035336	ECs0249
gmhA	+3.87	9.37	+1.95	8.39	0.2	10.35	0.0	0.00007725	0.00096606	0.01674162	0.34500000	A_07_P043366	Z0280
gmhA	+5.75	11.58	+2.52	10.32	0.1	12.84	0.0	0.00000015	0.00003548	0.00157780	0.10482222	A_07_P018845	c_0372
gmk	-13.38	12.61	-3.74	14.48	0.0	10.74	0.1	0.00000055	0.00005504	0.00005145	0.02250000	A_07_P017181	b3648
gnd	+5.21	8.98	+2.38	7.79	0.4	10.17	0.2	0.00001152	0.00129577	0.02878618	0.26894053	A_07_P015470	b3029
gnd	+4.80	10.48	+2.26	9.35	0.1	11.61	0.2	0.00002730	0.00048247	0.01160044	0.28809918	A_07_P042888	c_2556
gnaA	-2.31	10.99	-1.21	11.59	0.1	10.39	0.1	0.00006351	0.00461448	0.05816881	0.52922644	A_07_P015043	AAC-Q85038
gnaB	+18.04	10.15	+4.17	8.07	0.5	12.24	0.0	0.00000939	0.00024309	0.00602213	0.07236641	A_07_P020994	b1550
gntR	-2.68	11.69	-1.42	10.98	0.1	12.40	0.1	0.00004524	0.00033603	0.00412232	0.47004047	A_07_P013091	b3413
gntT	-3.26	11.02	-1.70	11.87	0.1	10.16	0.1	0.00007988	0.00101674	0.01490536	0.36782132	A_07_P013896	b3414
gntT	-3.39	11.24	-1.76	12.12	0.1	10.36	0.0	0.00007977	0.00101674	0.01288864	0.34032330	A_07_P013896	b3414
gntT	-3.17	11.14	-1.66	11.97	0.1	10.31	0.1	0.00011484	0.00132092	0.01634782	0.37683748	A_07_P013896	b3414
gntT	-3.78	11.06	-1.92	12.02	0.1	10.10	0.1	0.00004499	0.00068369	0.00848704	0.29959641	A_07_P013896	b3414
gntT	-3.36	11.05	-1.75	11.93	0.1	10.38	0.3	0.00008375	0.00105675	0.01388834	0.34602329	A_07_P013896	b3414
gor	-2.21	11.32	-1.14	11.89	0.1	10.75	0.0	0.01105222	0.04251391	0.05435595	0.60564756	A_07_P007636	b3580
gpmA	+6.44	10.06	+2.69	8.72	0.1	11.40	0.2	0.00000778	0.00021851	0.00687797	0.22617349	A_07_P017954	b3385
gpmA	+5.81	8.28	+2.54	7.01	0.2	9.54	0.1	0.00001879	0.00037681	0.00750635	0.24628833	A_07_P004227	b0755
gpsA	+3.16	10.80	+1.66	9.97	0.1	11.63	0.1	0.00007188	0.00126841	0.01408154	0.31411828	A_07_P018918	b3608
gnsB	-2.85	10.84	-1.51	11.59	0.1	10.08	0.1	0.00001289	0.00180865	0.02332444	0.44296743	A_07_P018057	b3406
grcA	+7.75	13.07	+2.95	11.59	0.0	14.54	0.2	0.00000836	0.00022376	0.00430894	0.11890936	A_07_P011446	b4143
grcS	+10.27	12.85	+3.36	12.17	0.1	15.53	0.2	0.00000380	0.00014395	0.00236652	0.14330769	A_07_P011443	b4142
grdB	+17.75	10.15	+4.15	8.08	0.0	12.23	0.1	0.00000002	0.00000548	0.00071837	0.07946799	A_07_P011251	b3564
gshA	-3.35	10.34	-1.74	11.21	0.0	9.47	0.1	0.00005868	0.00082629	0.01238887	0.34639073	A_07_P009912	b2688
gshB	-2.73	11.41	-1.45	10.68	0.1	12.13	0.1	0.00023932	0.00227157	0.03206391	0.46031022	A_07_P011876	b2947
gspD	-2.82	7.82	-1.50	8.57	0.0	7.08	0.1	0.00017886	0.00184898	0.02485010	0.45545984	A_07_P013055	b3325
gspE	-3.44	7.85	-1.78	8.74	0.4	6.96	0.1	0.00013125	0.00262895	0.05160192	0.33516286	A_07_P013056	b3326
gspF	-2.25	7.91	-1.17	8.42	0.2	7.25	0.1	0.00019736	0.00242466	0.05133003	0.59269366	A_07_P013076	b3330
gspL	-3.20	9.76	-1.68	10.40	0.1	9.12	0.1	0.00011352	0.00131450	0.01604797	0.37360003	A_07_P013091	b3333
gspM	-3.76	7.77	-1.91	8.72	0.1	6.81	0.1	0.00004779	0.00071390	0.00882008	0.30191721	A_07_P017669	b3334
gsP	+7.52	10.91	+2.91	8.66	0.4	11.58	0.3	0.00000619	0.00015223	0.00188058	0.19188059	A_07_P000883	b2338
guaA	+3.01	10.85	+1.59	10.11	0.1	11.64	0.1	0.00001766	0.00076640	0.02676688	0.42383174	A_07_P013594	b2507
guaB	+3.18	11.17	+1.76	10.29	0.0	12.05	0.1	0.00000958	0.00063316	0.02385533	0.39101136	A_07_P010513	c_3027
guaB	+3.78	11.19	+1.92	10.23	0.1	12.15	0.2	0.00000115	0.00034344	0.01742267	0.34918575	A_07_P004928	Z3772
gyrA	-5.76	12.78	-2.53	14.04	0.0	11.52	0.4	0.00006573	0.00089669	0.00192391	0.14492823	A_07_P000942	b2231
gyrB	-4.86	12.64	-2.28	13.78	0.0	11.50	0.1	0.00001385	0.00030876	0.00139621	0.09449436	A_07_P000929	b3699
hchA	+3.17	10.52	+1.67	9.69	0.3	11.35	0.4	0.00032926	0.00285769	0.02464431	0.41580281	A_07_P015194	b1967
hda	-4.10	10.66	-2.04	11.68	0.1	9.64	0.2	0.00004237	0.00064958	0.00430801	0.25833333	A_07_P013136	b3496
hdeA	+5.27	8.61	+2.40	7.41	0.1	9.81	0.1	0.00001327	0.00033123	0.00988882	0.36452336	A_07_P007483	b3510
hdeB	+2.82	7.90	+1.62	6.79	0.0	9.01	0.0	0.00110906	0.00802484	0.02007381	0.40525931	A_07_P007487	b3509
hdhA	+2.98	9.89	+1.57	9.11	0.1	10.66	0.1	0.00013756	0.00151663	0.02716209	0.42892678	A_07_P035106	c_2011
hemB	-2.25	12.24	-1.17	10.82	0.0	13.66	0.1	0.00015290	0.00152884	0.01509025	0.33260664	A_07_P000966	b0451
hemC	-3.72	11.42	-1.89	10.47	0.1	12.37	0.5	0.00012625	0.00801741	0.01782139	0.35248744	A_07_P000937	c_4724
hemD	-3.72	9.83	-1.90	8.88	0.1	10.78	0.2	0.00012928	0.00146554	0.01788962	0.35207880	A_07_P000952	b

IscA	-4.38	11.47	-2.13	12.53	0.1	0.40	0.00040036	0.00063161	0.00492696	0.22814706	A_07_P019544	b2528	cmr/putative regulator [b2528]
IscR	-3.66	10.55	-1.99	11.91	0.6	1.1	0.00003098	0.00052867	0.00731119	0.26928573	A_07_P019560	b2531	cmr/orf, hypothetical protein [b2531]
IscS	-2.32	12.13	-1.21	12.79	0.6	1.1	0.00051379	0.00398651	0.04698514	0.57522551	A_07_P019553	b2530	cmr/putative aminotransferase [b2530]
IscX	-2.94	12.26	-1.56	13.08	0.4	1.1	0.00116660	0.00727690	0.02163872	0.42267990	A_07_P019576	b2524	cmr/orf, hypothetical protein [b2524]
IsiA	-2.06	8.61	-1.04	8.93	0.0	7.89	0.01047745	0.00882272	0.06881122	0.65765573	A_07_P019302	c_3623	cmr/isiA protein [c_3623]
KatG	-7.65	10.78	-2.94	9.31	0.1	12.24	0.00000229	0.00010966	0.00431339	0.18862889	A_07_P019988	b3942	cmr/catalase; hydroperoxidase HPI [b3942]
KbaZ	-4.81	8.14	-2.27	7.01	0.1	9.28	0.01003298	0.00061238	0.01097752	0.28614238	A_07_P020381	b3132	cmr/putative tagatose-6-phosphate kinase 2 [b3132]
kdtA	-24.09	11.37	-4.59	9.07	0.1	13.66	0.44	0.00000152	0.00013758	0.00261005	0.04516684	b1617	cmr/2-amino-3-ketobutyrate CoA ligase [b1617]
kdpA	-3.09	8.58	-1.63	9.40	0.1	7.77	0.1	0.00010038	0.00120402	0.01785315	0.38602999	A_07_P010006	b0698
kdsA	-2.28	11.92	-1.19	12.51	0.0	11.32	0.0	0.00050169	0.00391007	0.04955621	0.58499624	A_07_P007028	b1215
kdsC	-2.44	12.93	-1.29	13.57	0.0	12.29	0.1	0.00016652	0.00296466	0.03939738	0.54561260	A_07_P012468	b3198
kefA	-2.71	8.68	-1.44	9.40	0.0	7.95	0.1	0.00017255	0.00179905	0.02807545	0.47580194	A_07_P021413	b0465
kefB	-2.27	8.58	-1.18	9.17	0.0	7.99	0.0	0.00051064	0.00355448	0.05353026	0.58718819	A_07_P017779	b3350
kefC	-2.38	11.25	-1.25	11.87	0.1	10.62	0.1	0.00047497	0.00377105	0.04329425	0.55930978	A_07_P017784	b3351
KpsC	-2.15	7.54	-1.23	6.92	0.0	8.15	0.0	0.00039951	0.00232976	0.04387057	0.52190441	A_07_P020265	c_3690
KpsE	+3.76	9.41	+1.91	8.46	0.1	10.37	0.1	0.00006641	0.00090442	0.01792556	0.35277500	A_07_P036606	c_3687
KpsT	+3.61	10.15	+1.85	9.23	0.1	11.08	0.1	0.00004092	0.00063841	0.01090853	0.29236658	A_07_P036618	c_3697
kqsA	-4.25	11.44	-2.09	12.48	0.0	10.39	0.5	0.00075986	0.00527345	0.06243682	0.25881579	A_07_P010844	b0051
L7002	-2.68	12.74	-1.42	13.45	0.4	12.03	0.5	0.00324432	0.01656409	0.02816553	0.47578326	ABH-0243999	asap[unknown:L7002]
L7009	-2.06	7.37	-1.18	8.26	0.5	6.48	0.7	0.01087705	0.04204475	0.05093369	0.58962235	ABH-0246019	asap[replication protein:L7009]
L7015	-1.77	10.77	-1.91	11.73	0.1	9.81	0.0	0.00003333	0.00053152	0.00879256	0.30357456	ABH-0246096	asap[replication protein:L7015]
L7073	-2.06	10.26	-1.04	10.78	0.1	9.74	0.2	0.00217767	0.01181128	0.06767213	0.65323728	ABH-0248663	asap[unknown:L7073]
L7079	-1.18	11.31	-1.67	12.15	0.0	10.48	0.0	0.00008844	0.00092248	0.01601753	0.37638806	ABH-0248148	asap[unknown:L7079]
L7082	-4.98	9.80	-2.32	10.46	0.3	9.15	0.1	0.00007552	0.00069348	0.01031687	0.19380074	ABH-0246151	asap[unknown:L7082]
lacI	+3.48	8.55	+1.80	7.65	0.1	9.45	0.1	0.00007462	0.00097352	0.02076649	0.38027875	A_07_P008419	b0345
lacZ	+4.50	8.14	+2.17	7.05	0.6	9.22	0.5	0.00005746	0.00061349	0.01270008	0.30419790	A_07_P008421	cmr/beta-galactosidase [b0344]
lacZ	+2.47	7.48	+1.30	6.83	0.3	8.13	0.2	0.00009759	0.00151170	0.04237424	0.51082695	A_07_P008412	b0344
lamB	+36.70	10.38	+5.12	7.82	0.1	12.94	0.3	0.00000036	0.00004777	0.00007679	0.02396615	A_07_P008822	b4036
lamB	+40.48	10.00	+5.34	7.33	0.0	12.67	0.2	0.00000010	0.00003427	0.00005018	0.00205641	A_07_P037538	c_5006
lbhA	-2.41	8.97	-1.27	8.34	0.2	9.61	0.1	0.00095931	0.00633093	0.04250826	0.51005909	A_07_P014878	b1380
leuE	-10.83	8.86	-3.44	10.57	0.1	7.14	0.1	0.00000209	0.00010461	0.00012767	0.03792453	A_07_P015685	b1798
lfer	-2.27	9.42	-1.18	10.01	0.3	8.82	0.1	0.02466112	0.01266781	0.04664494	0.53916454	A_07_P018933	b1653
lgB	-2.45	8.18	-1.30	8.83	0.0	7.53	0.2	0.01006605	0.00683382	0.03790015	0.52992805	A_07_P017180	b3647
lgT	-2.79	10.46	-1.48	11.20	0.1	9.72	0.2	0.00017125	0.00179167	0.02912120	0.45870670	A_07_P020865	b0147
lipA	+2.49	12.92	+1.31	12.26	0.0	13.57	0.1	0.00038188	0.00321037	0.03932121	0.49395850	A_07_P009709	b0628
lipB	-8.20	12.41	-3.04	13.93	0.0	10.89	0.0	0.00000168	0.00006634	0.00050114	0.02046643	A_07_P009718	b0630
livE	-6.12	8.15	-2.04	9.17	0.1	7.13	0.1	0.00004613	0.00067579	0.00630399	0.25779221	A_07_P034548	c_4248
lldD	+4.52	8.68	+1.54	7.56	0.5	9.79	0.4	0.00000615	0.00009168	0.00132787	0.29952160	A_07_P008851	b3603
llsP	+3.24	7.37	+1.70	6.52	0.1	8.22	0.2	0.00006416	0.00114522	0.02193275	0.40954796	A_07_P018959	b3603
lldR	+5.03	8.51	+2.33	7.55	0.1	9.68	0.1	0.00001905	0.00038105	0.00102731	0.12567986	A_07_P018965	b3604
lolA	+2.82	9.55	+1.50	8.80	0.0	10.30	0.0	0.00013537	0.00150088	0.03010553	0.44488285	A_07_P004904	b0891
lolC	-2.34	12.92	-1.16	10.54	0.2	9.37	0.0	0.00009714	0.00651142	0.05222879	0.59371119	A_07_P040818	c_1391
lon	+2.23	11.00	+1.16	10.42	0.0	11.58	0.2	0.00145789	0.01065789	0.05662278	0.55839734	A_07_P043874	20545
lpcA	+3.91	10.52	+1.97	9.54	0.0	11.51	0.4	0.00045155	0.00362894	0.01882288	0.33929444	A_07_P007824	b0222
lpxA	-3.74	11.63	-1.46	12.36	0.0	10.91	0.1	0.00018207	0.00188867	0.02192092	0.47213808	A_07_P002865	b0181
lpxB	-2.21	10.65	-1.15	11.22	0.1	10.08	0.1	0.00008148	0.00092945	0.05438262	0.60551627	A_07_P002870	b0182
lpxC	-7.54	14.30	-2.91	15.76	0.0	12.84	0.2	0.00000763	0.00021562	0.00372011	0.08281481	A_07_P002853	b0096
lpxK	-3.03	9.36	-1.60	10.16	0.3	8.56	0.3	0.00056024	0.00422026	0.01885036	0.39517976	A_07_P016456	b0524
lpxK	-5.26	9.96	-2.39	11.36	0.0	8.77	0.0	0.00008015	0.00022461	0.00264634	0.11709624	A_07_P002859	b0915
lpxL	-4.19	11.59	-2.07	12.62	0.0	10.55	0.1	0.00030109	0.00052951	0.00518491	0.25082192	A_07_P001680	b3554
lpxP	-3.17	11.31	-1.66	12.14	0.0	10.48	0.0	0.00007275	0.00055677	0.01426510	0.17727941	A_07_P014174	b2378
lrhA	-4.49	11.82	-2.17	12.90	0.0	10.73	0.0	0.00001382	0.00030876	0.00458079	0.22190769	A_07_P013734	b2389
lrp	+4.93	10.06	+2.30	8.90	0.0	11.21	0.0	0.00001257	0.00023413	0.00248324	0.27990242	A_07_P018008	b0889
lsrA	-2.06	8.12	-1.05	8.64	0.4	7.60	0.0	0.00755613	0.01148853	0.06427094	0.65210625	A_07_P020212	b1513
lsrK	-3.56	8.87	-1.83	9.79	0.3	7.95	0.0	0.00022092	0.00221785	0.02308376	0.42836600	A_07_P020203	b1511
ltaE	+3.41	9.15	+1.77	8.26	0.0	10.03	0.2	0.00009602	0.00116203	0.02104357	0.38257506	A_07_P004805	b0870
lysC	-2.31	7.51	-1.21	6.91	0.1	8.12	0.1	0.00005134	0.00611165	0.04638910	0.51937756	A_07_P000885	b0928
lysS	-3.66	11.48	-1.79	12.38	0.1	10.58	0.3	0.00038475	0.00322860	0.01287550	0.33781690	A_07_P004616	b2890
lysU	+4.68	10.53	+2.23	9.41	0.2	11.64	0.1	0.00003330	0.00054981	0.01179052	0.29460079	A_07_P013361	b4129
lysK	+3.86	7.85	+1.95	6.87	0.1	8.82	0.1	0.00003218	0.00054058	0.01701220	0.34606651	A_07_P019671	c_4403
maa	-11.27	9.26	-3.49	11.05	0.1	7.51	0.4	0.00000852	0.00002936	0.00001115	0.03500000	A_07_P021405	b0619
maeB	-2.63	8.51	-1.46	9.21	0.0	7.81	0.0	0.00003535	0.00203026	0.03869398	0.49452229	A_07_P004848	b0879
MaeA	+6.15	8.90	+2.05	7.87	0.1	9.92	0.1	0.00004876	0.00072623	0.01475864	0.32726761	A_07_P009486	b1479
maeB	+3.21	10.86	+1.68	10.02	0.2	11.70	0.1	0.00015900	0.00169372	0.02402693	0.41072747	A_07_P019179	b0843
malE	+25.22	11.18	+4.66	8.85	0.1	13.50	0.2	0.00000028	0.00001211	0.00023849	0.04103345	A_07_P008811	b4034
malF	+2.39	7.93	+1.26	7.30	0.0	8.56	0.1	0.00004051	0.00318264	0.04250645	0.51040241	A_07_P008806	b4033
malI	-2.25	10.12	-1.17	10.70	0.1	9.53	0.3	0.00085717	0.00582084	0.05160104	0.59266958	A_07_P020735	b3620
malS	-2.27	10.12	-1.18	10.91	0.0	9.33	0.1	0.00010882	0.00076048	0.01479543	0.38547099	A_07_P020732	c_2012
malK	+5.28	7.79	+2.40	6.59	0.0	8.99	0.2	0.00002092	0.00005129	0.00055234	0.26540037	A_07_P008816	b4035
MalP	-4.29	8.32	+1.20	7.72	0.1	8.92	0.2	0.01054575	0.00060319	0.04802341	0.54331416	A_07_P008827	b4037
malP	+13.88	9.74	+3.79	7.85	0.1	11.64	0.1	0.00000087	0.00006750	0.00123730	0.10948320	A_07_P018111	b3417
malQ	+3.92	9.21	+1.97	8.25	0.0	10.17	0.1	0.00006407	0.00088750	0.01912723	0.34631217	A_07_P018108	b3416
malT	+4.22	8.29	+2.08	7.25	0.0	9.33	0.1	0.00015321	0.00071138	0.01373519	0.31661786	A_07_P034638	c_4196
malT	+4.42	8.24	+2.14	7.17	0.0	9.31	0.1	0.00002419	0.00044487	0.01008388	0.30816469	A_07_P018118	b3418
malT	+5.21	8.63	+2.38	7.44	0.1	9.82	0.1	0.00001546	0.00033209	0.00937182	0.26925182	A_07_P012557	24774
malX	+3.06	9.62	+1.61	8.81	0.0	10.43	0.2	0.00005124	0.00611315	0.04638910	0.51937756	A_07_P007920	b1621
malY	+3.01	9.27	+1.59	8.48	0.1	10.07	0.0	0.00014279	0.00155578	0.02660515	0.42720388	A_07_P042322	c_2014
mamA	+2.59	8.89	+1.37	8.20	0.0	9.57	0.0	0.00009327	0.00086563	0.01603391	0.28809003	A_07_P010700	b1613
mamA	+3.07	8.83	+1.62	8.02	0.1	9.64	0.1	0.00011710	0.00133575	0.02569930	0.42434874	A_07_P004397	22616
mamA	+3.01	8.92	+1.59	8.12	0.0	9.71	0.0	0.00009281	0.00119135	0.02659932	0.42711951	A_07_P019266	c_2005
mamB	-2.20	8.51	-1.46	9.21	0.0	7.81	0.0	0.00003530	0.01762833	0.02534629	0.56479945	A_07_P019386	c_2157
mamB	+6.15	8.90	+2.05	7.87	0.1	9.92	0.1	0.00004876	0.00072623	0.01475864	0.32726761	A_07_P009486	b1479
mamB	+3.21	10.86	+1.68	10.02	0.2	11.70	0.1	0.00015900	0.00169372	0.02402693	0.41072747	A_07_P019179	b0843
mamB	+25.22	11.18	+4.66	8.85	0.1	13.50	0.2	0.00000028	0.00001211	0.00023849	0.04103345	A_07_P008811	b4034
mamF	+2.39	7.93	+1.26	7.30	0.0	8.56	0.1	0.00004051	0.00318264	0.04250645	0.51040241	A_07_P008806	b4033
mamI	-2.25	10.12	-1.17	10.70	0.1	9.53	0.3	0.00085717	0.00582084	0.05160104	0.59266958	A_07_P020735	b3620
mamS	-2.27	10.12	-1.18	10.91	0.0	9.33	0.1	0.00010882	0.00076048	0.01479543	0.38547099	A_07_P020732	c_2012
mamK	+5.28	7.79	+2.40	6.59	0.0	8.99	0.2	0.00002092	0.00005129	0.00055234	0.26540037	A_07_P008816	b4035
MamP	-4.29	8.32	+1.20	7.72	0.1	8.92	0.2	0.01054575	0.00060319	0.04802341	0.54331416	A_07_P008827	b4037
mamP	+13.88	9.74	+3.79	7.85	0.1	11.64	0.1	0.00000087	0.00006750	0.00123730	0.10948320	A_07_P018111	b3417
mamQ	+3.92	9.21	+1.97	8.25	0.0	10.17	0.1	0.00006407	0.00088750	0.01912723	0.34631217	A_07_P018108	b3416
mamT	+4.22	8.29	+2.08	7.25	0.0	9.33	0.1	0.00015321	0.00071138	0.01373519	0.31661786	A_07_P034638	c_4196
mamT	+4.42	8.24	+2.14	7.17	0.0	9.31	0.1	0.00002419	0.00044487	0.01008388	0.30816469	A_07_P018118	b3418
mamT	+5.21	8.63	+2.38	7.44	0.1	9.82	0.1	0.00001546	0.00033209	0.00937182	0.26925182	A_07_P012557	24774
mamX	+3.06	9.62	+1.61	8.81	0.0	10.43	0.2	0.00005124	0.00611315	0.04638910	0.51937756	A_07_P007920	b1621
mamY	+3.01	9.27	+1.59	8.48	0.1	10.07	0.0	0.00014279	0.00155578	0.02660515	0.42720388	A_07_P042322	c_2014
mamA	+2.59	8.89	+1.37	8.20	0.0	9.57	0.0	0.00009327	0.00086563	0.01603391	0.28809003	A_07_P010700	b1613
mamA	+3.07	8.83	+1.62	8.02	0.1	9.64	0.1	0.00011710	0.00133575	0.02569930	0.42434874	A_07_P004397	22616
mamA	+3.01	8.92	+1.59	8.12	0.0	9.71	0.0	0.00009281	0.00119135	0.02659932	0.42711951	A_07_P019266	c_2005
mamB	-2.20	8.51	-1.46	9.21	0.0	7.81	0.0	0.00003530	0.01762833	0.02534629	0.56479945	A_07_P019386	c_2157
mamB	+10.16	9.96	+3.34	8.29	0.0	11.63	0.1	0.00000128	0.00008337	0.00240601	0.14705882	A_07_P015778	b1817
mamF	+4.62	9.59	+2.21	8.48	0.1	10.69	0.1	0.00001405	0.00016972	0.01203032	0.29773437	A_07_P015818	b1818
mamZ	+1.92	9.54	+1.97	8.56	0.2	10.53	0.1	0.00007393	0.00096669	0.01627160	0.34296511	A_07_P015786	b1819
marR	+16.77	11.14	+4.07	9.10	0.1	13.17	0.3	0.00000327	0.00013195	0.00085439	0.08434211	A_07_P020303	b1531
marR	+8.31	9.69	+3.06	8.16	0.1	11.22	0.1	0.00000232	0.00010802	0.00305091	0.17418182	A_07_P020307	b1532
marR	+5.24	8.78	+2.39	7.59	0.0	9.98	0.2	0.00002157	0.00061171	0.02049387	0.36891521	A_07_P004853	22169
marR	+10.74	12.62	+3.42	10.91	0.2	14.33	0.1	0.00000337	0.00013444	0.00227924	0.13615079	A_07_P020299	b1530
marA	2.24	9.68	-1.16	10.26	0.4	9.10	0.2	0.00617115	0.02882859	0.05145756	0.59307427	A_07_P020294	b1529
marA	-2.09	9.38	-1.07	9.91	0.3	8.84	0.2	0.00719933	0.03034706	0.06236019	0.63838878	A_07_P014579	c_0405
marC	-3.00	9.06	-1.58	9.85	0.1	8.27	0.1	0.00021844	0.00201317	0.02026701	0.48811054	A_07_P020305	b1532
mchD	-2.01	11.79	-1.01	12.44	0.0	11.29	0.0	0.00918280	0.03674987	0.07327680	0.67073837	A_07_P004645	c_1230
mchF	-2.10	10.62	-1.07	11.16	0.1	10.08	0.3	0.00030426	0.01712857	0.06282489	0.64423848	A_07_P004653	c_1232
mdaB	+6.24	9.87	+2.64	8.55	0.2	11.19	0.1	0.00001114	0.00027193	0.00641070	0.22886621	A_07_P012273	b3028
mdh	+11.12	12.00	+3.53	10.34	0.0	13.67	0.0	0.00000371	0.00003576	0.00015241	0.01267305	A_07_P018361	b3236
mdoC	-2.12	8.19	-1.09	8.73	0.0	7.64	0.5	0.00007590	0.00064480	0.06168139	0.63607190	A_07_P001448	b1047
mdoG	-2.00	11.12	-1.00	11.62	0.0	10.62	0.0	0.00019918	0.00832840	0.07446677	0.67349570	A_07_P001451	b1048
mdtI	+2.16	7.74	+1.11	7.18	0.1	8.29	0.3	0.00112968	0.01563754	0.05596735	0.57922281	A_07_P020626	b1599
mdtK	+1.70	11.06	-1.89	12.01	0.0	10.12	0.0	0.00003356	0.00054981	0.00939016	0.30882759	A_07_P018376	b1663
mdtL	2.27	7.97	-1.16	8.56	0.3	7.38	0.2	0.00588058	0.02592805	0.04986058	0.58550060	A_07_P005475	b3710
mdtQ	-2.07	7.30	-1.05	7.62	0.0	6.57	0.1	0.00119988	0.00751494	0.06686710	0.65122298	A_07_P003459	b2139
mdtQ	-2.42	8.46	-1.27	9.10	0.1	7.82	0.0	0.00045128	0.00363886	0.04891115	0.54910058	A_07_P003458	b2139
mesB	+3.20	8.92	+1.68	8.08	0.1	9.76	0.1	0.00015918	0.00169054	0.02376711	0.41076643	A_07_P011333	b4119
mesB	+8.69	9.99	+3.12	8.43	0.1	11.55	0.2	0.00000275	0.00012089	0.00330475	0.16783871	A_07_P001030	b2262
mesC	-2.12	12.61	-1.08	13.15	0.1	12.07	0.4	0.01300041	0.04861721	0.06415664	0.64779974	A_07_P001094	b2261
mesD	+10.05	8.84	+3.11	8.03	0.1	9.64	0.1	0.00016493	0.00174946	0.02463651	0.42680655	A_07_P001093	b2264
mesD	+2.11	8.91	+1.08	8.37	0.2	9.45	0.2	0.00318024	0.01585490	0.05734502	0.61473093	A_07_P021889	c_2808
mesE	-2.83	8.97	+1.50	8.22	0.2	9.72	0.2	0.00066435	0.00462327	0.03079932	0.44939759	A_07_P019374	b1919
metH	+3.58	8.38	+1.84	7.46	0.3	9.30	0.3	0.00046664	0.00362003	0.01942771	0.36631138	A_07_P017969	EC4837
metH	+4.52	8.78	+2.18	7.69	0.0	9.86	0.0	0.00001405	0.00010409	0.00251461	0.10370547	A_07_P047219	b2987
metH	+2.77	7.94	+1.47	7.20	0.1	8.68	0.2	0.00082562	0.00565414	0.02325038	0.45908680	A_07_P008740	b4019
metH	+4.75	9.57	+2.25	8.44	0.1	10.69	0.1	0.00002075	0.00060158	0.01145071	0.29238001	A_07_P017967	c_4979
metH	-4.73	10.54	-2.24	11.66	0.1	9.42	0.2	0.00003812	0.00049161	0.00183003	0.20406678	A_07_P002955	b0199
mgfA	+11.66	8.95	+3.54	7.17	0.1	10.72	0.2	0.00000426	0.00015341	0.00178428	0.12848869	A_07_P005027	b2499
mgfB	+21.58	9.54	+4.43	7.32	0.3	11.75	0.1	0.00000092	0.00006969	0.00040587	0.05756757	A_07_P003515	b2150
mgfB	-28.71	10.62	-4.84	8.19	0.1	13.06	0.1	0.00000012	0.00003537	0.00003133	0.00428571	A_07_P003519	c_2684
mgfB	-39.48	10.87	-5.30	8.22	0.1	13.52	0.2	0.00000020	0.00003706	0.00006152	0.02127660	A_07_P045485	23405
mgfC	+8.64	9.42	+3.11	7.86	0.0	10.97	0.1	0.00000188	0.00006480	0.00348956	0.16889358	A_07_P003504	b2148
mgsA	-6.96	10.52	-2.89	9.12	0.2	10.50	0.2	0.00000048	0.00002416	0.00509954	0.20811518	A_07_P005264	b0963
mgsA	-69.36	11.32	-6.12	14.38	0.0	8.26	0.1	0.00000002	0.00003344	0.00000964	0.00500000	A_07_P003761	b4242
miaA	+2.65	12.96	+1.40	12.26	0.0	13.66	0.2	0.00006922	0.00447365	0.04469179	0.47223678	A_07_P011571	b4171
minD	+13.01	7.44	+3.11	9.65	0.2	12.24	0.1	0.00002715	0.00250274	0.02721585	0.42879514	A_07_P008827	b1175
minC	-6.68	12.35	+2.50	11.09	0.0	13.60	0.1	0.00000792	0.00022158	0.00780234	0.24666607	A_07_P008821	b1174
minC	-7.11	13.65	-2.83	15.07	0.0	12.24	0.1	0.00000458	0.00016295	0.00807081	0.09263514	A_07_P005634	b3742
mipA	+4.08	11.75	+2.03	10.73	0.1	12.77	0.1	0.00003080	0.00052169	0.01158928	0.33976027	A_07_P015602	b1762
mlc	-2.10	10.53	-1.07	11.07	0.1	9.99	0.0	0.00143944	0.00812449	0.06357088	0.64571613	A_07_P000061	b2813
mlrD	-2.17	10.44	-1.24	9.82	0.2	11.07	0.3	0.00241629	0.01278684	0.04410921	0.51278010	A_07_P002982	b0243
mnmA	-2.53	11.94	-1.34	12.61	0.0	11.27	0.1	0.00036765	0.00311361	0.03578760	0.51646363	A_07_P006616	b1133
mntH	-7.68	9.81	-2.94	11.28	0.2	8.34	0.0	0.00000536	0.00017381	0.00050701	0.08122077	A_07_P018491	b3202
mobA	+3.35	10.46	+1.74	9.59	0.1	11.33	0.2	0.00011308	0.00131105	0.02269132	0.39183259	A_07_P004361	b0782
mobB	-2.12	11.23	+1.08	10.69	0.0	11.77	0.1	0.00428750	0.02014998	0.05836669	0.59039178	A_07_P004363	b0783
MoeC	+2.37	10.98	+1.24	10.36	0.0	11.60	0.2	0.00008054	0.00483817	0.04606455	0.51733986	A_07_P041580	c_0867
moeA	+3.86	8.28	+1.95	7.30	0.0	9.26	0.1	0.00004252	0.00036288	0.01444644	0.34483243	A_07_P015693	c_4801
moeA	+2.02	9.19	+1.01	8.68	0.1	9.69	0.1	0.01645224	0.00853373	0.06231834	0.60601606	A_07_P041574	c_0840
moeA	-2.10	11.36	-1.07	11.90	0.0	10.83	0.0	0.00019185	0.00854496	0.06449988	0.64599616	A_07_P004356	b0827
moeB	-3.20	8.85	-1.68	9.69	0.1	8.01	0.4	0.00073704	0.00514135	0.01600102	0.37656203	A_07_P004583	b0826
moeC	-4.48	12.19	-2.16	13.27	0.1	11.11	0.5	0.00000808	0.00024823	0.00408274	0.12325264	A_07_P003056	b0918
moeC	-2.53	11.86	-1.28	12.51	0.0	11.21	0.2	0.00056081	0.00422257	0.03622650	0.51802906	A_07_P010779	b0918
moeB_C	+2.87	7.81	+1.52	7.05	0.2	8.57	0.6	0.00804445	0.03420749	0.03098877	0.45280130	A_07_P045591	23285
mscA	-2.08	7.47	-1.06	8.00	0.0	6.94	0.1	0.00110016	0.00707411	0.04349191	0.51121571	A_07_P014130	b1890
msbB	-3.70	8.26	-1.89	9.20	0.0	7.31	0.0	0.00003416	0.00056195	0.00971711	0.30721277	A_07_P014121	b1889
msyB	-2.23	12.34	-1.16	12.92	0.0	11.76	0.0	0.00060018	0.00442275	0.03309338	0.50893441	A_07_P004214	b4243
mtnZ	-3.50	12.24	-1.81	13.15	0.0	11.34	0.1	0.00005529	0.00078914	0.01461705	0.33164207	A_07_P011082	b0881
mrcA	-2.11	10.16	-1.08	10.70	0.1	9.62	0.1	0.00019124	0.00763615	0.06250572	0.63969348	A_07_P003852	b0149
mrcB	-3.15	11.08	-1.65	11.90	0.5	10.25	0.5	0.00082650	0.02945729	0.01596766	0.37588826	A_07_P014431	c_0183
mskA	-5.28	10.13	-2.40	11.33	0.0	8.93	0.0	0.00000730	0.00020980	0.00235511	0.17172996	A_07_P005017	b0914
msrA	+3.62	8.71	+1.86	7.78	0.1	9.64	0.1	0.00006711	0.00090923	0.01908791	0.36250905	A_07_P003647	b4219
msrB	+7.19	10.51	+2.85	12.09	0.1	8.93	0.1	0.00000297	0.00012541	0.00149558	0.09263514	A_07_P003648	b4220

pcnB	-2.11	11.59	-1.08	12.13	0.1	11.05	0.0	0.00101963	0.00661709	0.06291667	0.64197019	A_07_P02676	1043
pdaB	+2.76	10.62	+1.47	9.89	0.0	11.35	0.2	0.00039651	0.00282187	0.03197048	0.45730025	A_07_P01888	1232
pdxJ	+5.51	9.31	+2.46	8.08	0.0	10.54	0.1	0.00005551	0.00024416	0.00869043	0.25196452	A_07_P019721	1056
pdxK	+2.15	9.96	+1.10	9.40	0.1	10.51	0.0	0.00085505	0.00582155	0.05384654	0.56858684	A_07_P013150	1261
pdxT	+2.37	8.74	+1.24	8.22	0.3	9.36	0.1	0.02129265	0.01160110	0.64437754	0.52218236	A_07_P028811	1636
pepB	+6.76	9.68	+2.25	8.56	0.0	10.81	0.2	0.00002036	0.00039679	0.01125762	0.28913540	A_07_P013674	1052
pepD	+11.98	10.67	+2.81	8.76	0.1	12.57	0.0	0.00000507	0.00005636	0.00124238	0.10927374	A_07_P027896	1027
pepE	+10.05	8.63	+3.33	6.96	0.1	10.29	0.1	0.00000137	0.00008682	0.00249746	0.14726592	A_07_P008748	1021
pepN	+8.81	9.39	+3.14	7.82	0.1	10.96	0.3	0.00001423	0.00031323	0.00334669	0.16826923	A_07_P013734	2280
pepT	+7.74	9.56	+2.95	8.09	0.1	11.04	0.0	0.00000290	0.00012407	0.00413808	0.18616286	A_07_P006587	1127
perM	-3.44	9.18	-1.76	10.07	0.1	8.29	0.0	0.00006440	0.00088107	0.01225229	0.33842105	A_07_P028120	2_3009
pfkB	+5.58	9.50	+2.58	8.26	0.1	10.74	0.1	0.00001253	0.00009212	0.00807673	0.24885540	A_07_P041560	c_2123
pfkB	+6.05	9.61	+2.60	8.31	0.1	10.90	0.1	0.00000546	0.00015512	0.00492214	0.18188683	A_07_P018613	b2723
pfkA	-3.37	12.82	-1.75	13.69	0.0	11.94	0.1	0.00006673	0.00060725	0.01191169	0.34615000	A_07_P004958	b0962
pflB	+14.86	11.26	+3.89	9.32	0.1	13.15	0.0	0.00000072	0.00006152	0.00000000	0.10025129	A_07_P028661	b0903
pgaD	-3.93	9.23	-1.97	10.22	0.0	8.24	0.5	0.00094607	0.00262698	0.00765871	0.27630588	A_07_P001332	b3021
pgi	-2.07	8.75	-1.05	8.22	0.3	9.27	0.1	0.00730844	0.00867313	0.06854691	0.60050748	A_07_P000767	b4025
pgk	+6.76	12.84	+2.25	11.71	0.1	13.96	0.0	0.00001305	0.00029749	0.01418895	0.29185065	A_07_P011776	b2926
pgl	-6.60	9.23	-2.59	7.94	0.0	10.52	0.3	0.00002566	0.00046019	0.00520838	0.24122685	A_07_P029038	b0767
pheS	+4.05	11.27	+2.02	10.26	0.0	12.28	0.0	0.00002141	0.00041080	0.01456668	0.33565517	A_07_P018621	b1714
pheT	+2.97	10.30	+1.57	9.51	0.1	11.08	0.0	0.00001716	0.00132575	0.02733994	0.42908084	A_07_P018619	b1713
phoH	+2.25	8.45	+1.17	7.87	0.1	9.04	0.1	0.00072301	0.00505692	0.04679510	0.54952074	A_07_P037761	c_5106
phoI	-3.83	10.91	-1.94	11.88	0.1	9.94	0.2	0.00004109	0.00086212	0.28979452	0.28979452	A_07_P013231	b4099
phoJ	-3.57	9.71	-1.84	10.63	0.3	8.80	0.1	0.00103004	0.00221785	0.01604296	0.42160604	A_07_P000402	c_5105
phoJ	+2.25	7.45	+1.17	6.86	0.2	8.04	0.2	0.00115285	0.00271138	0.04092299	0.55208571	A_07_P013230	b4098
phoK	-2.13	7.59	-1.09	7.14	0.2	8.23	0.3	0.00468870	0.02863144	0.05796025	0.58868887	A_07_P013229	b4097
phoA	-2.83	8.53	-1.50	9.28	0.2	7.78	0.0	0.00025676	0.00239370	0.02281010	0.45027091	A_07_P021029	b0383
phoB	-2.70	11.57	-2.96	10.26	0.1	10.09	0.0	0.00000250	0.00011564	0.00004953	0.08056452	A_07_P013103	c_0508
phoB	-8.01	11.26	-3.00	12.76	0.0	9.76	0.0	0.00000180	0.00009954	0.00056021	0.07603448	A_07_P021109	b0399
phoB	-7.32	11.48	-2.87	12.92	0.0	10.05	0.0	0.00000375	0.00014266	0.00079713	0.08388228	A_07_P043823	2069
phoR	-3.32	8.21	-1.73	9.08	0.1	7.35	0.1	0.00003512	0.00100543	0.01385480	0.35410714	A_07_P021115	b0400
phoU	+2.70	8.87	+1.43	8.16	0.2	9.59	0.2	0.00003094	0.00618686	0.04413364	0.46975524	A_07_P020542	b3724
pinD	-2.17	10.81	-1.12	11.37	0.4	10.26	0.0	0.00908503	0.03645116	0.05482797	0.62154730	A_07_P041818	c_4093
pirA	-3.34	8.33	-1.74	9.20	0.1	7.46	0.0	0.00007988	0.00100604	0.01349017	0.34834426	A_07_P014850	b1224
pmbA	+3.32	8.90	+1.73	8.04	0.2	9.77	0.2	0.00032446	0.00282692	0.02256034	0.39913881	A_07_P003729	b4235
pnuA	-6.21	8.74	-2.63	7.42	0.2	10.06	0.4	0.00013885	0.00152444	0.00480458	0.23545055	A_07_P026648	b1602
pnuB	+2.21	9.58	+1.14	9.01	0.2	10.15	0.1	0.00126513	0.00773824	0.05038564	0.55851304	A_07_P026644	b1602
pnuB	-2.32	9.25	-1.21	8.65	0.2	9.86	0.1	0.00068976	0.00487650	0.04568106	0.52973398	A_07_P026645	2207
poiA	+6.60	9.02	+2.72	7.66	0.2	10.38	0.0	0.00000738	0.00021133	0.00580158	0.22009639	A_07_P019099	b3863
poiB	+4.49	8.99	+2.17	7.91	0.4	10.08	0.0	0.00016068	0.00370704	0.01424126	0.30152207	A_07_P012560	2508
poiB	-4.67	10.55	-2.22	11.66	0.0	9.44	0.2	0.00003483	0.00054774	0.00402058	0.20962265	A_07_P019889	b0960
polC	-2.82	10.60	-1.49	10.87	0.4	9.85	0.2	0.00024660	0.00230877	0.02461374	0.45902961	A_07_P000583	b1126
polC	-5.77	11.51	-2.53	12.77	0.0	10.24	0.3	0.00003123	0.00053304	0.00195884	0.14616114	A_07_P000671	b1124
porD	+2.09	12.54	+1.06	12.01	0.0	13.07	0.1	0.00142163	0.00842385	0.05362283	0.58989711	A_07_P012611	2176 2
porD	+2.21	12.41	+1.15	11.85	0.1	12.99	0.1	0.00117147	0.00785152	0.05102452	0.55942201	A_07_P018919	b1123
porE	+3.17	8.00	+1.67	7.17	0.2	8.84	0.1	0.00202169	0.00201497	0.02466010	0.41568522	A_07_P009978	b0692
ppc	+4.01	9.13	+2.01	8.13	0.1	10.13	0.1	0.00003460	0.00014313	0.01560349	0.33082137	A_07_P018952	b3956
ppdA	+2.71	8.00	+1.44	7.28	0.2	8.72	0.1	0.00005457	0.00413428	0.03293890	0.46468638	A_07_P043261	2414 3
ppdA	+2.76	8.24	+1.46	7.50	0.1	8.97	0.1	0.00001826	0.00231227	0.01688312	0.45883912	A_07_P012800	c_3420
ppdA	+2.11	8.32	+1.24	8.76	0.0	8.75	0.2	0.00317231	0.01582536	0.05799154	0.58777132	A_07_P006115	b2826
ppiB	-3.58	7.97	-1.84	8.88	0.3	7.05	0.2	0.00005045	0.00209520	0.01027221	0.37227227	A_07_P022119	b2734
ppiB	+2.36	12.80	+1.24	12.18	0.1	13.42	0.1	0.00065556	0.00471498	0.04396627	0.51943694	A_07_P016413	b0525
ppiC	+2.66	8.22	+1.04	7.76	0.1	8.74	0.1	0.00160402	0.00399174	0.04773111	0.59705240	A_07_P027519	b3775
ppk	+2.96	9.74	+1.57	8.92	0.2	10.52	0.1	0.00028870	0.00260187	0.02802973	0.43435039	A_07_P013561	b2501
ppn	-6.20	13.75	-2.63	12.44	0.0	15.07	0.2	0.00002148	0.00023182	0.00466949	0.22149652	A_07_P018562	b3702
ppsA	-2.32	10.08	-1.21	10.69	0.1	9.47	0.0	0.00074065	0.00515964	0.04707571	0.57543478	A_07_P007006	b1211
prfB	-1.50	13.96	-1.32	14.62	0.0	13.29	0.0	0.00005821	0.00456855	0.00486209	0.51847469	A_07_P006421	b2891
prfB	-2.85	14.32	-1.51	15.07	0.0	13.56	0.2	0.00023409	0.00227709	0.02339876	0.44118563	A_07_P022852	c_5423
prfB	-6.37	10.40	-2.23	12.01	0.0	8.78	0.1	0.00000176	0.00006825	0.00028281	0.05488095	A_07_P008853	c_0382
prfB	-9.50	10.65	-3.25	12.28	0.2	9.03	0.1	0.00000297	0.00012541	0.00027058	0.05282405	A_07_P007894	b0236
prfB	-6.44	9.05	-3.24	10.67	0.1	7.43	0.0	0.00000128	0.00008261	0.00003600	0.05300000	A_07_P062922	EC0263
prfB	-6.60	9.31	-2.73	10.67	0.0	7.95	0.3	0.00002154	0.00061173	0.00116870	0.11084337	A_07_P014892	2097
prfA	-3.06	9.96	-1.61	10.76	0.2	9.15	0.3	0.00080002	0.00550019	0.01804243	0.38700272	A_07_P019449	c_4888
prfC	+2.22	8.78	+1.46	8.20	0.0	9.35	0.1	0.00064203	0.00464101	0.04994347	0.55766647	A_07_P027826	b3498
prfC	+2.35	9.38	+1.24	8.76	0.0	10.00	0.1	0.00042967	0.00350504	0.04392276	0.51993985	A_07_P041321	c_4297
prmC	-2.18	9.89	-1.12	10.45	0.2	9.33	0.0	0.00087570	0.00591975	0.05736657	0.61655605	A_07_P027012	b3212
prmC	+2.02	9.25	+1.01	8.74	0.0	9.75	0.0	0.00142238	0.00762763	0.06182259	0.60548849	A_07_P021045	b0386
prsA	-6.86	10.06	-2.78	11.45	0.1	8.67	0.2	0.00006036	0.00019314	0.00150214	0.10092114	A_07_P013312	b4111
prsV	-2.08	8.97	-1.06	9.50	0.0	8.45	0.0	0.00105283	0.00677115	0.06602253	0.65128814	A_07_P030555	c_3230
prsV	-2.82	8.57	-1.50	9.32	0.4	7.83	0.4	0.02301832	0.01113223	0.02375523	0.44416982	A_07_P018819	b3677
prsW	-2.46	8.60	-1.30	9.26	0.0	7.95	0.1	0.00466058	0.00368276	0.03911966	0.53556522	A_07_P001861	b2678
prsX	+3.29	8.35	+1.73	7.49	0.0	9.21	0.1	0.00161174	0.00505224	0.04988266	0.59205240	A_07_P002866	b3679
prsX	+5.23	9.01	+2.34	7.68	0.0	10.35	0.0	0.00005120	0.00074921	0.00092018	0.26875458	A_07_P030557	c_3232
prsB	-3.40	10.13	-1.76	11.01	0.1	9.25	0.2	0.00021278	0.00200373	0.01082431	0.34510924	A_07_P008344	b0130
prsB	-3.41	10.99	-1.77	11.87	0.3	10.10	0.3	0.00063087	0.00459623	0.01236691	0.33631488	A_07_P033011	c_0450
prsF	-2.10	8.84	-1.07	9.37	0.2	8.31	0.2	0.00146678	0.01374172	0.04232967	0.54562681	A_07_P042746	EC4544
prsF	-2.03	8.94	-1.02	9.45	0.1	8.43	0.0	0.00138860	0.00828407	0.07329055	0.66785560	A_07_P051681	2980
prsB	-6.59	10.15	-3.10	11.75	0.1	8.60	0.1	0.00000234	0.00011598	0.00004588	0.06758056	A_07_P014506	b1305
psbC	-15.95	10.57	-4.00	12.57	0.0	8.58	0.1	0.00000054	0.00005412	0.00003176	0.01767514	A_07_P014514	b1306
psgA	+5.59	11.49	+2.48	10.25	0.1	12.73	0.1	0.00001199	0.00009964	0.00802337	0.24946427	A_07_P014522	b1308
psgC	+2.87	11.25	+1.52	10.49	0.1	12.01	0.5	0.00403115	0.01905578	0.03942365	0.44765421	A_07_P014532	b1308
psiA	-2.02	9.84	-1.01	10.35	0.3	9.34	0.0	0.00969087	0.02965092	0.07248873	0.67024075	A_07_P048618	2568
psiA	+2.92	9.30	+1.55	8.52	0.1	10.07	0.0	0.00161942	0.02828125	0.04787711	0.54287711	A_07_P018829	b2585
psiC	-10.29	10.25	-1.63	11.06	0.1	9.44	0.2	0.00017086	0.00178857	0.01737129	0.38656510	A_07_P005555	b3726
psiC	-4.40	10.20	-2.14	11.27	0.1	9.13	0.1	0.00002210	0.00061925	0.00489139	0.22798024	A_07_P005556	b3727
psiS	-2.52	9.95	-1.34	10.52	0.1	9.18	0.1	0.00036762	0.00311361	0.03491870	0.51140665	A_07_P005561	b3728
pta	+13.72	10.84	+4.78	8.56	0.1	12.73	0.2	0.00000504	0.00027096	0.00012996	0.05422552	c_2840	b2297
pta	+9.77	9.65	+3.29	8.01	0.3	11.30	0.2	0.00001276	0.00029390	0.00276042	0.15236890	A_07_P013771	b2297
ptb	-1.73	10.94	-1.60	9.99	0.1	11.88	0.0	0.00003536	0.00057410	0.01802147	0.35333748	A_07_P008671	b1004
ptrB	-6.17	8.36	-2.06	9.39	0.1	7.33	0.2	0.00000854	0.00062303	0.00626016	0.25888766	A_07_P015904	b1845
ptrB	-10.69	9.81	-3.42	11.52	0.0	8.10	0.0	0.00000355	0.00027600	0.00010384	0.03764555	A_07_P015122	c_2256
ptrB	-19.35	10.01	-4.27	12.14	0.2	7.87	0.0	0.00000072	0.00006192	0.00002223	0.01458333	A_07_P052572	22896
ptsI	+2.24	11.54	+1.16	10.96	0.0	12.13	0.2	0.00010528	0.00064555	0.00469390	0.55145403	A_07_P013132	b2415
ptsI	+8.99	13.15	+3.17	11.57	0.1	14.74	0.1	0.00000216	0.00010631	0.00318852	0.16677741	A_07_P013136	b2416
ptsI	+7.73	13.57	+2.95	12.10	0.1	15.04	0.1	0.00000137	0.00012665	0.00241601	0.18616046	A_07_P013136	b2416
ptsI	+7.73	12.67	+2.95	11.19	0.1	14.14	0.4	0.00004114	0.00063933	0.00423272	0.18824859	A_07_P013136	b2416
ptsI	+7.79	13.65	+2.96	12.17	0.1	15.13	0.1	0.00000282	0.00012327	0.00246154	0.18327176	A_07_P013136	b2416
ptsI	+7.34	13.60	+2.88	12.16	0.1	15.03	0.1	0.00000483	0.00014704	0.00452426	0.19251351	A_07_P013136	b2416
ptsN	-2.28	11.39	-1.50	11.84	0.1	12.03	0.2	0.00002119	0.00087307	0.00482302	0.47068392	A_07_P012498	b3204
purA	-2.28	10.57	-1.19	10.16	0.1	11.97	0.5	0.00079948	0.01853055	0.04846498	0.58630321	A_07_P021601	b4177
purB	+2.14	11.12	+1.09	10.57	0.0	11.67	0.1	0.00112278	0.00708782	0.05442581	0.57087275	A_07_P006806	b1131
purC	+19.20	10.29	+4.26	8.16	0.1	12.42	0.0	0.00000608	0.00004858	0.00027482	0.02142604	A_07_P013843	b2476
purD	+19.98	10.12	+4.32	7.96	0.1	12.28	0.2	0.00000092	0.00006439	0.00199415	0.07180690	A_07_P008690	b4005
purE	-3.19	9.32	-1.67	8.49	0.3	10.16	0.3	0.01011264	0.00704458	0.02839356	0.41091603	A_07_P028401	b0523
purF	+3.20	8.66	+1.68	7.82	0.1	9.50	0.2	0.00005526	0.00364940	0.02399517	0.41063043	A_07_P013849	b2312
purF	+5.71	9.58	+2.51	8.72	0.1	10.44	0.1	0.00000620	0.00018976	0.00788354	0.24782421	A_07_P026252	c_2856
purF	+3.49	8.87	+1.80	7.97	0.2	9.77	0.3	0.00005850	0.00047195	0.01249024	0.37321176	A_07_P042612	23574
purH	-1.72	8.76	-1.67	9.63	0.1	10.60	0.2	0.00000110	0.00007956	0.00152639	0.11837438	A_07_P017562	b2049
purH	+34.86	10.25	+5.12	7.69	0.0	12.81	0.1	0.00000069	0.00003427	0.00008003	0.02377358	A_07_P037651	c_4964
purH	+13.13	8.87	+2.73	7.02	0.1	10.73	0.0	0.00000068	0.00006127	0.00145516	0.11537057	A_07_P047711	2083
purH	+13.21	8.97	+2.72	7.31	0.1	10.84	0.2	0.00000104	0.00007542	0.00143039	0.11548718	A_07_P008693	b4006
purH	+2.96	9.10	+1.57	8.32	0.1	9.88	0.4	0.00007984	0.00483817	0.02880051	0.43432212	A_07_P028397	b0522
purL	+7.18	9.03	+2.84	7.61	0.3	10.45	0.5	0.00015490	0.00166013	0.00506161	0.20752604	A_07_P019686	b2557
purM	-22.95	11.32	-4.52	9.66	0.0	13.00	0.1	0.00000014	0.00003340	0.00003155	0.02527727	A_07_P013551	b2499
purN	+12.22	10.54	+3.61	8.73	0.1	12.35	0.0	0.00000094	0.00007037	0.00166349	0.12069124	A_07_P013559	b2500
purS	-6.13	11.19	-2.02	9.68	0.1	12.70	0.0	0.00000203	0.00015441	0.00048146	0.18000000	A_07_P000133	c_1018
purT	+15.08	9.45	+3.91	7.49	0.0	11.41	0.0	0.00000036	0.00004756	0.00010483	0.09820087	A_07_P015921	b3849
pulA	+19.98	10.82	+3.26	9.17	0.2	12.43	0.1	0.00001521	0.00285993	0.00153138	0.05124138	A_07_P041092	c_1151
pulB	-51.09	10.40	-5.67	7.57	0.2	13.24	0.2	0.00000016	0.00003548	0.00000000	0.01008000	A_07_P000104	b0014
pulP	+8.47	10.12	+3.08	8.58	0.5	11.66	0.2	0.00007186	0.00095259	0.00355882	0.17346749	A_07_P001306	b1015
pykA	+8.51	10.68	+3.09	9.34	0.0	12.02	0.0	0.00000207	0.00005025	0.00000000	0.11726385	A_07_P013946	b1854
pyrB	+17.76	10.13	+4.15	8.06	0.1	12.21	0.1	0.00000145	0.00009005	0.00070449	0.07861248	A_07_P003778	b4245
pyrC	+4.97	8.80	+2.31	7.65	0.0	9.96	0.1	0.00001586	0.00013838	0.00239551	0.29797438	A_07_P015513	b1802
pyrD	+4.76	9.56	+2.25	8.43	0.1	10.69	0.1	0.00001553	0.00013216	0.01145960	0.29186175	A_07_P005175	b0945
pyrF	+2.62	9.84	+1.39	9.14	0.1	10.53	0.1	0.00003386	0.00258732	0.01153036	0.47725522	A_07_P014388	b1281
pyrG	+6.13	11.38	+2.05	10.36	0.1	12.40	0.2	0.00006227	0.00086079	0.01498676	0.33042017	A_07_P002348	b2790
pyrH	-2.60	12.44	-1.38	13.10	0.0	11.75	0.2	0.00001155	0.00365777	0.01158024	0.49770771	A_07_P018814	b0173
pyrI	+11.22	9.43	+3.49	7.68	0.1	11.17	0.1	0.00000093	0.00007006	0.00201791	0.13182573	A_07_P001774	b4244
qor	-6.46	9.33	-2.08	7.79	0.1	10.87	0.1	0.00002127	0.00168651	0.00165435	0.17181230	A_07_P008897	b1831
quuD	-2.43	8.79	-1.26	9.43	0.2	8.15	0.1	0.00149856	0.00878057	0.04019690	0.54276158	A_07_P020616	b1559
rabA	+6.75	14.18	+5.12	11.42	0.1	16.94	0.0	0.00000006	0.00003344	0.00002239	0.01458968	A_07_P018989	b2597
rarA	+2.12	10.63	+1.08	9.89	0.1	10.97	0.2	0.00175516	0.00998282	0.05689977	0.58436399	A_07_P004906	b0892
rarD	-2.32	9.16	-1.21	9.77	0.1	8.55	0.1	0.00060996	0.00447691	0.03483263	0.57542024	A_07_P000663	b3819
rawA	-2.15	9.07	-1.10	9.62	0.0	8.52	0.5	0.01262704	0.04743502	0.05965361	0.62885410	A_07_P005654	b3746
rbaA	+3.64	9.08	+1.86	8.15	0.1	10.02	0.2	0.00001512	0.00343810	0.01809563	0.36051109	A_07_P000787	b4886
rbfA	-4.80	12.61	-2.26	13.74	0.0	11.48	0.4	0.00010938	0.00127906	0.00382368	0.20476190	A_07_P000559	b3167
rbn	-6.17	9.62	-2.63	8.31	0.1	10.94	0.1	0.00002116	0.00032333	0.00186847	0.23168008	A_07_P000563	c_4633
rbsB	+6.26	14.62	+2.65	13.29	0.1	15.94	0.3	0.00003582	0.00057956	0.00627957	0.22931507	A_07_P005677	b3751
rbsC	+11.14	10.49	+3.48	8.75	0.0	12.23	0.0	0.00000076	0.00006301	0.00206940	0.13127213	A_07_P005671	b3750
rbsK	+2.62	10.58	+1.39	9.88	0.0	11.27	0.1	0.00005431	0.00237897	0.01193659	0.47772621	A_07_P005685	b3752
rbsR	+5.25	10.19	+1.17	9.60	0.0	10.77	0.2	0.00103043	0.00941651	0.04948488	0.55411807	A_07_P005686	b3753
rcsA	-3.63	7.93	-1.86	8.86	0.7	7.00	0.0	0.00404822	0.02008683	0.03312179	0.32463828	A_07_P002939	b2206
rcsB	+2.29	10.30	+1.19	9.70	0.0	10.90	0.1	0.00059194	0.00438119	0.04803223	0.53473875	A_07_P002365	c_2760
rcsD	+4.54	9.66	+2.18	8.57	0.2	10.75	0.4	0.00005666	0.00303329	0.01975551	0.37208870	A_07_P008870	b2216
rcsF	+2.19	11.18	+1.13	10.61	0.1	11.75	0.1	0.00113462	0.00713681	0.05244674	0.56438141	A_07_P041460	c_0237
rdgC	-12.66	10.00	-4.41	9.29	0.3	10.71	0.1	0.00095780	0.00622157	0.01218352	0.47727728	A_07_P021080	b0193
rdsA	+3.92	10.71	+1.97	9.73	0.1	11.70	0.1	0.00003202	0.00053978	0.01662030	0.34521108	A_07_P019079	b1859
recA	-4.14	14.52	-2.05	15.55	0.0	13.50	0.1	0.00000194	0.00006651	0.00004750	0.03450000	A_07_P013691	b2699
recF	-2.30	11.26	-1.68	12.10	0.0	10.42	0.1	0.00008709	0.00108651	0.01178951	0.37325826	A_07_P005612	b3700
recJ	-3.14	9.08	-1.65	9.90	0.0	8.25	0.1	0.00010876	0.00127349	0.01239711	0.37975591	A_07_P006645	2420
recJ	-2.71	8.32	-1.44	9.04	0.1	7.60	0.2	0.00047814	0.00378674	0.02692284	0.47853814	A_07_P006426	b2892
recJ	-4.63	11.05	-2.23	12.16	0.1	9.95	0.0	0.00001288	0.00024693	0.00005495	0.02808106	A_07_P042711	2068
recR	+6.91	11.71	+2.79	10.32	0.1	13.10	0.1	0.00000900	0.00022748	0.00515180	0.20797436	A_07_P021466	b0472
recX	-7.85	10.95	-2.97	12.44	0.0	9.46	0.3	0.00001323	0.00029669	0.00008385	0.07272273	A_07_P026405	EC0555
recX	-8.17	11.18	-3.03	12.69	0.0	9.66	0.4	0.00002400	0.00044341	0.00049606	0.07036336	A_07_P001938	b2698
recX	-3.05	10.76	-1.61	11.56	0.1	9.96	0.2	0.00007261	0.00126565	0.01811851	0.39286192	A_07_P001939	2601
rep	-2.91	8.92	+1.54	8.15	0.1	9.69	0.0	0.00007976	0.00150019	0.00726054	0.27281623	A_07_P020646	b3561
rfaH	-3.71	9.27	-1.89	10.22	0.1	8.31	0.1	0.00046174	0.00268445	0.01077279	0.31073279	A_07_P019819	b3842
rfaJ	-10.33	12.34	-3.37	14.03	0.0	10.66	0.1	0.00000124	0.00003113	0.00496774	0.19398025	A_07_P019805	c_4453
rfaP	-3.65	12.12	-1.41	12.89	0.0	11.42	0.2	0.00055602	0.00302353	0.00498032	0.18788268	A_07_P019808	c_4454
rfaP	-3.14	12.37	-1.65	13.20	0.2	11.55	0.1	0.00024154	0.00228676	0.01664444	0.37793366	A_07_P019808	c_4454
rfaP	-4.27	11.75	-2.09	12.80	0.1	10.70	0.1	0.00007282	0.00057424	0.00509743	0.21573174	A_07_P019808	c_4454
rfaP	-3.01	12.43	-1.59	13.22	0.0	11.63	0.2	0.00015835	0.00168912	0.01942899	0.39881356	A_07_P019808	c_4454
rfaP	-2.73	12.30	-1.45	13.02	0.0	11.57	0.2	0.00037146	0.00313916	0.01945599	0.37190000	A_07_P019808	c_4454
rfbA	+2.91	8.46	+1.54	7.69	0.1	9.23	0.1	0.00019216	0.00194432	0.02889919	0.43953307	A_07_P005832	b3791
rfbC	-2.66	8.02	-1.41	7.52	0.1	8.51	0.1	0.00019512	0.01725854	0.04112741	0.57993552	A_07_P005835	b3790
rfbD	-2.15	7.82	-1.11	7.27	0.1	8.38	0.1	0.00094599	0.00260698	0.05327777	0.56923957	A_07_P005811	b3787
rfbG	-2.22	7.46	-1.15	6.89	0.0	8.04	0.0	0.00063644	0.00461448	0.04962513	0.57284005	A_07_P005829	b3789
rfbM	+2.95	7.87	+1.56	7.09	0.1	8.65	0.1	0.00011158	0.00146726	0.02770135	0.43398831	A_07_P005

sbcB	+2.55	10.41	+1.35	9.74	0.0	0.00025176	0.00235792	0.0139800	0.0	0.00025176	0.00235792	0.48601660	A_007_P03291	cmr/Exodeoxyribonuclease I [c_2539]
sbmA	-2.59	9.34	-1.37	10.03	0.1	0.0	0.00019134	0.00366018	0.0123663	0	0.00019134	0.53363007	A_007_P02899	bb377	cmr/sensitivity to microcin B17, possibly envelop protein [bb0377]
sbp	-6.51	10.95	-2.70	12.30	0.0	0.0	0.00000612	0.00018856	0.00125127	0	0.00000612	0.11588235	A_007_P03964	bb917	cmr/periplasmic sulfate-binding protein [bb0917]
sdaA	-2.44	10.49	-1.29	9.85	0.1	0.0	0.00037511	0.00016336	0.04077236	0	0.00037511	0.49993769	A_007_P01761	b1814	cmr/L-serine deaminase [b1814]
sdcC	-2.56	11.48	-1.35	10.80	0.1	0.0	0.00044088	0.00016882	0.03725238	0	0.00044088	0.68620053	A_007_P02426	bb796	cmr/probable serine transporter [bb796]
sdhA	+8.76	11.58	+3.13	10.01	0.1	0.0	0.00001344	0.00030273	0.00336336	0	0.00001344	0.16879981	A_007_P03135	b0723	cmr/succinate dehydrogenase, flavoprotein subunit [b0723]
sdhA	+11.54	10.17	+3.53	8.40	0.2	0.0	0.00000195	0.00019612	0.00136513	0	0.00000195	0.12925345	A_007_P01706	28877	cmr/succinate dehydrogenase, flavoprotein subunit [28877]
sdhA	+10.66	10.27	+3.41	8.57	0.0	0.0	0.0	0.00000245	0.00011451	0.0220274	0	0.00000245	0.13615543	A_007_P06310	EC45748
sdhB	+7.05	11.73	+2.82	10.32	0.1	0.0	0.0	0.00000616	0.00018932	0.00550380	0	0.00000616	0.20925729	A_007_P03139	b0724
sdhC	+69.31	12.62	+5.62	9.81	0.1	0.0	0.0	0.00000006	0.00003344	0.00002414	0	0.00000006	0.01151515	A_007_P03122	b0721
sdhD	+27.43	12.30	+4.78	9.91	0.1	0.0	0.0	0.00000010	0.00003344	0.0018483	0	0.00000010	0.03730769	A_007_P03122	b0722
sdiA	-19.49	10.26	-1.80	11.16	0.1	0.0	0.0	0.0	0.00012925	0.00144554	0.0114367	0	0.33160221	A_007_P01493	b3916
sdsA	-4.40	8.24	-2.14	9.31	0.1	0.0	0.0	0.0	0.00003408	0.00056193	0.00497332	0	0.22961877	A_007_P03869	cmr/Regulatory protein sdsR [c_2182]
secA	+2.96	9.07	+1.57	8.29	0.0	0.0	0.0	0.0	0.00014092	0.00154399	0.02752541	0	0.43206381	A_007_P00261	b0068
secB	+7.92	11.92	+2.99	10.03	0.1	0.0	0.0	0.0	0.00003376	0.00014394	0.00394754	0	0.18919634	A_007_P01888	b3269
secE	-6.07	13.62	-2.03	14.63	0.0	0.0	0.0	0.0	0.00004149	0.00063960	0.00637386	0	0.25730769	A_007_P08570	b3981
secG	-2.04	11.90	-1.03	12.41	0.1	0.0	0.0	0.0	0.00016455	0.00060474	0.04028417	0	0.63792712	A_007_P00590	b3175
secY	+2.65	15.08	+1.41	14.38	0.1	0.0	0.0	0.0	0.00055617	0.00419969	0.03466685	0	0.47309627	A_007_P02927	b3300
selA	-2.13	10.08	+1.09	9.53	0.1	0.0	0.0	0.0	0.00014144	0.00658842	0.05478532	0	0.57311628	A_007_P03895	b3591
selB	+2.17	10.79	+1.18	9.60	0.0	0.0	0.0	0.0	0.00062336	0.00453203	0.04817137	0	0.54653308	A_007_P03899	b3593
selA	-2.17	9.95	-1.12	9.39	0.2	0.0	0.0	0.0	0.00187148	0.01063078	0.05433431	0	0.57907078	A_007_P03895	b3591
selB	+2.20	7.33	+1.14	6.76	0.3	0.0	0.0	0.0	0.00240044	0.01272050	0.05265180	0	0.56586476	A_007_P03899	b3593
selD	+6.77	10.28	+2.25	9.15	0.0	0.0	0.0	0.0	0.00005033	0.00074401	0.01097243	0	0.28648625	A_007_P03866	b1764
serS	+7.75	9.66	+2.96	7.59	0.0	0.0	0.0	0.0	0.0000555	0.00017942	0.00407773	0	0.10573832	A_007_P04011	b0893
sfaB	+9.45	8.83	+3.24	7.21	0.1	0.0	0.0	0.0	0.0000133	0.00008557	0.00288522	0	0.15501718	A_007_P04081	c_1218
sfaC	+4.55	8.03	+2.18	6.94	0.1	0.0	0.0	0.0	0.00001188	0.00019176	0.01242279	0	0.30902308	A_007_P04082	c_1217
sfaD2	+7.77	9.29	+2.96	7.81	0.0	0.0	0.0	0.0	0.0000251	0.00011582	0.00410063	0	0.18519886	A_007_P04093	c_1240
sfuA	+3.13	10.69	+1.34	10.02	0.0	0.0	0.0	0.0	0.01092416	0.04217507	0.04076347	0	0.50021824	A_007_P03869	c_2179
sfuA	+2.32	10.23	+1.21	9.63	0.1	0.0	0.0	0.0	0.00363713	0.00461617	0.04550114	0	0.52907681	A_007_P02692	b0146
sgbH	+4.60	7.95	+2.20	6.85	0.1	0.0	0.0	0.0	0.00001680	0.00037681	0.01496965	0	0.29596369	A_007_P01850	b3561
sgbU	+3.22	7.90	+1.69	7.06	0.2	0.0	8.75	0.0	0.0001563	0.00132585	0.02352325	0	0.40922652	A_007_P03678	c_4405
sgcR	-2.74	8.35	-1.45	9.08	0.5	0.0	7.63	0.0	0.00510676	0.02317529	0.02417952	0	0.4667369	A_007_P04028	b4300
sgcX	+3.10	7.56	+1.63	6.74	0.0	0.0	8.38	0.0	0.0001769	0.00278650	0.02585587	0	0.42415016	A_007_P04054	b4305
sia	-2.55	9.27	-1.35	9.95	0.1	0.0	8.59	0.0	0.00044227	0.00158664	0.03918676	0	0.52715244	A_007_P03876	c_1600
siiC	-2.13	8.45	-1.09	9.00	0.1	0.0	7.91	0.0	0.00112854	0.00715163	0.06162221	0	0.63135036	A_007_P03873	c_1599
siiC	+6.75	8.28	2.25	9.41	0.2	0.0	7.16	0.0	0.00025740	0.00236648	0.04481024	0	0.21032573	A_007_P03873	c_1598
skp	+6.65	12.57	+2.73	11.20	0.0	0.0	13.93	0.0	0.0003063	0.00268778	0.00603784	0	0.22579572	A_007_P00847	b0178
slyA	+2.74	15.43	+1.45	9.70	0.5	0.0	11.15	0.0	0.00007118	0.01507177	0.47407841	0	0.47007881	A_007_P05860	2033
slt	+2.71	8.23	+1.44	7.51	0.3	0.0	8.95	0.0	0.01128598	0.07839911	0.03307040	0	0.46997364	A_007_P03645	b4392
slt	+2.68	8.00	+1.43	7.29	0.2	0.0	8.72	0.0	0.00021532	0.00138025	0.03338605	0	0.46852877	A_007_P03645	b4392
slt	+2.43	8.41	+1.28	7.77	0.0	0.0	9.05	0.0	0.00061285	0.00340132	0.04121380	0	0.50417249	A_007_P03645	b4392
slt	+2.57	8.56	+1.36	7.48	0.1	0.0	8.84	0.0	0.00032951	0.00285827	0.03671240	0	0.48348201	A_007_P03645	b4392
slt	+2.31	8.11	+1.21	7.51	0.1	0.0	8.72	0.0	0.00056547	0.00413833	0.04509428	0	0.52959916	A_007_P03645	25994
slt	+2.49	8.39	+1.32	7.73	0.1	0.0	9.05	0.0	0.00092988	0.00618506	0.03925211	0	0.49480509	A_007_P03645	b4392
slyB	-2.43	12.89	-1.28	15.53	0.0	0.0	12.25	0.4	0.01338813	0.01624870	0.06462047	0	0.54386054	A_007_P03652	c_2033
smg	+5.86	9.58	+2.55	8.30	0.1	0.0	10.85	0.0	0.0001204	0.00028605	0.00373106	0	0.24481122	A_007_P03260	c_4045
smg	+3.65	9.10	+1.87	8.17	0.2	0.0	10.03	0.0	0.0001905	0.00152559	0.01898009	0	0.36060606	A_007_P02853	b3284
smg	+2.71	11.06	+1.44	10.34	0.3	0.0	11.78	0.0	0.00067649	0.00482179	0.03396885	0	0.46727778	A_007_P04582	26655
smpA	-4.72	12.14	-2.24	13.26	0.1	0.0	11.02	0.0	0.00001400	0.00003664	0.00379764	0	0.20476027	A_007_P03965	b2617
smpB	-3.53	12.19	-1.82	13.10	0.0	0.0	11.29	0.0	0.0000223	0.00086079	0.01162279	0	0.33285993	A_007_P03980	b2620
sodA	-3.18	9.86	-1.13	9.30	0.0	0.0	10.42	0.0	0.00070107	0.00491783	0.05130374	0	0.56226006	A_007_P04167	c_4859
sodB	+2.08	7.80	+1.06	7.27	0.1	0.0	8.33	0.0	0.00435251	0.02039497	0.05036766	0	0.59547543	A_007_P04703	25453
sodA	+2.10	8.40	+1.07	7.87	0.0	0.0	8.94	0.0	0.00473968	0.02186104	0.04605272	0	0.56011104	A_007_P04167	b3908
sodB	+7.71	12.71	+2.95	11.24	0.1	0.0	14.19	0.2	0.00004760	0.00435211	0.18928177	0	A_007_P03842	b3656
sodB	-4.22	12.84	-2.08	11.80	0.0	0.0	13.88	0.5	0.00001466	0.00386851	0.01884169	0	0.31676471	A_007_P04233	c_2050
sodC	+2.12	9.21	+1.09	8.67	0.2	0.0	9.75	0.0	0.02269425	0.01360305	0.05709413	0	0.58369481	A_007_P02863	b3646
sofA	-2.07	7.82	-1.05	7.29	0.1	0.0	8.34	0.1	0.00015618	0.00650678	0.03941712	0	0.53432227	A_007_P03509	b3359
soeA	+2.31	7.68	-1.45	9.41	0.1	0.0	7.96	0.0	0.00057656	0.00430688	0.02817010	0	0.47519906	A_007_P00859	b4063
speA	-2.24	9.32	+1.16	8.74	0.1	0.0	9.90	0.0	0.00169291	0.00862004	0.04930651	0	0.55138078	A_007_P02963	c_3524
speA	+2.15	9.76	+1.10	9.21	0.0	0.0	10.32	0.2	0.00155427	0.00813575	0.05377985	0	0.56902554	A_007_P01837	b2938
speB	+3.36	9.58	+2.55	8.30	0.1	0.0	8.90	0.0	0.0003836	0.00023566	0.00492785	0	0.56273393	A_007_P01801	b2937
speD	+3.82	10.55	+1.93	9.58	0.1	0.0	10.03	0.2	0.00009275	0.00113501	0.01716019	0	0.34605455	A_007_P00565	b0120
speF	+13.25	9.41	+3.73	7.55	0.4	0.0	11.28	0.4	0.0002971	0.00051171	0.00137767	0	0.11476190	A_007_P00981	b0693
speG	-3.21	10.69	-1.69	11.54	0.1	0.0	11.02	0.0	0.00012661	0.00144828	0.01485057	0	0.37315385	A_007_P02654	b3184
spr	+2.40	12.36	+1.26	11.51	0.1	0.0	12.98	0.1	0.00006133	0.00086079	0.01162279	0	0.33285993	A_007_P01980	b2620
srlA	-2.32	7.67	-1.22	7.56	0.0	0.0	8.28	0.3	0.00270107	0.00491783	0.05130374	0	0.56226006	A_007_P04167	c_4859
srlA	+2.39	8.24	+1.25	7.61	0.2	0.0	8.86	0.2	0.00132802	0.00862315	0.04308284	0	0.51760722	A_007_P04162	c_3256
srlA_1	+2.13	7.85	+1.09	6.80	0.0	0.0	7.93	0.0	0.00078331	0.00539155	0.04245623	0	0.57061456	A_007_P04096	24005
srlB	+3.73	7.53	+1.90	6.58	0.2	0.0	8.48	0.2	0.00010047	0.00193470	0.01737565	0	0.35167506	A_007_P03966	b2704
srlE	-2.72	7.35	-1.44	6.63	0.1	0.0	7.07	0.3	0.00080609	0.00513202	0.03345294	0	0.46817376	A_007_P03955	c_2357
srlE	+2.74	7.55	+1.45	6.83	0.0	0.0	7.28	0.2	0.00056391	0.00423782	0.03272739	0	0.46296699	A_007_P03964	b2703
srlE_1	+2.20	8.48	+1.14	8.11	0.0	0.0	8.94	0.0	0.00164875	0.00948819	0.05221701	0	0.56302029	A_007_P03964	24007
srmB	+3.84	8.92	+1.94	7.95	0.1	0.0	9.89	0.2	0.00015814	0.00168799	0.01700457	0	0.34633894	A_007_P04926	23859
srmB	+7.72	9.35	+1.90	8.40	0.0	0.0	10.29	0.1	0.00003648	0.00058676	0.01824759	0	0.36822317	A_007_P02317	c_2100
ssb	-3.45	12.98	-1.79	13.87	0.0	0.0	12.09	0.1	0.00006916	0.00092982	0.01190930	0	0.33542039	A_007_P00840	b4059
sseB	+12.79	14.55	+3.68	11.75	0.0	0.0	16.07	0.1	0.00000117	0.00008616	0.00152419	0	0.11881188	A_007_P05138	23460
sseA	+11.60	11.78	+3.54	10.01	0.1	0.0	13.55	0.1	0.00000172	0.00009748	0.00188770	0	0.12978166	A_007_P03661	b2521
sspA	-5.07	13.46	-2.34	14.63	0.0	0.0	13.29	0.0	0.00001284	0.00029436	0.00292008	0	0.18031157	A_007_P03516	b3229
sspB	-6.30	13.85	-2.66	15.17	0.0	0.0	12.52	0.0	0.00000748	0.00016012	0.00136369	0	0.12410405	A_007_P02612	b3228
ssrT	-2.18	8.32	-1.25	7.70	0.1	0.0	8.95	0.1	0.00022984	0.00464719	0.04306148	0	0.51312726	A_007_P00073	b3089
stpA	-3.35	10.61	-1.23	10.22	0.0	0.0	9.99	0.2	0.00080283	0.00551710	0.04242971	0	0.56306386	A_007_P03199	b3069
suaA	+116.82	10.82	+6.87	7.39	0.0	0.0	14.25	0.5	0.0000048	0.00005238	0.00000000	0	0.00000000	A_007_P01049	b0726
suaB	-86.25	12.52	-6.48	9.32	0.0	0.0	10.98	0.1	0.0000008	0.00003344	0.00000181	0	0.00461538	A_007_P01051	b0727
suaC	-94.51	11.60	-6.56	9.32	0.0	0.0	14.88	0.0	0.0000002	0.00003344	0.0000254	0	0.00400000	A_007_P01059	b0728
suaD	-54.91	10.83	-5.78	7.94	0.0	0.0	13.72	0.3	0.0000007	0.00004211	0.00003842	0	0.00207474	A_007_P01065	b0729
sugE	-5.05	11.54	-2.34	12.75	0.1	0.0	10.37	0.0	0.0001387	0.00010876	0.00303290	0	0.18365385	A_007_P03585	c_5236
sugE	-3.14	9.59	-1.61	10.42	0.1	0.0	8.77	0.0	0.00008255	0.00104207	0.01703760	0	0.37831568	A_007_P04823	25755
sugE	-3.49	10.37	-1.80	11.27	0.2	0.0	9.47	0.0	0.00015938	0.00169545	0.01169545	0	0.31221569	A_007_P03653	b4148
sugE	-12.07	8.98	-3.59	10.77	0.1	0.0	7.18	0.1	0.0000076	0.00006289	0.00007749	0	0.02375410	A_007_P03472	b4148
suiA	+3.70	15.26	+1.89	14.31	0.0	0.0	16.20	0.0	0.0000479	0.00056765	0.01844322	0	0.35497555	A_007_P00240	b0958
syrM	-2.52	11.37	-1.12	12.03	0.0	0.0	10.75	0.0	0.00046148	0.02584570	0.03405546	0	0.51832271	A_007_P01762	b4347
tdcA	-4.90	9.14	-2.29	10.29	0.0	0.0	7.99	0.3	0.00004192	0.00064831	0.00345084	0	0.19403571	A_007_P03700	b2559
tdcA	+2.51	8.22	+1.13	7.55	0.3	0.0	8.88	0.1	0.00122245	0.00968705	0.08968766	0	0.49524564	A_007_P01377	b2464
tdcB	+2.90	9.97	+1.54	9.20	0.1	0.0	10.74	0.0	0.00016970	0.00178003	0.02883399	0	0.44028155	A_007_P03731	b0008
tdcC	+2.63	10.97	+1.40	10.27	0.1	0.0	11.67	0.2	0.00006508	0.00047365	0.01543703	0	0.47771556	A_007_P03732	b0009
tdcE	-3.79	13.45	-1.92	14.41	0.0	0.0	12.49	0.4	0.00069558	0.00387598	0.00955170	0	0.30581545	A_007_P01899	b3838
tesA	-3.01	8.38	-1.59	9.14	0.0	0.0	7.54	0.0	0.00046636	0.00466377	0.01852359	0	0.39369267	A_007_P03367	c_0472
tdcA	+13.69	10.35	+3.77	8.46	0.2	0.0	12.24	0.1	0.0000122	0.00008163	0.00133575	0	0.11306452	A_007_P00316	b3118
tdcB	+17.79	9.20	+4.15	7.04	0.2	0.0	11.27	0.4	0.00000024	0.00008039	0.00008233	0	0.07782714	A_007_P00312	b3117
tdcC	+6.79	10.10	+2.72	7.24	0.2	0.0	12.96	0.3	0.00004211	0.00008233	0.00008233	0	0.01088333	A_007_P00305	b3116
tdcD	+18.75	8.38	+4.23	6.27	0.1	0.0	10.50	0.4	0.0000267	0.00012042	0.00009822	0	0.07246154	A_007_P00305	b3115
tdcD	+97.02	10.53	+6.60	7.23	0.0	0.0	10.50	0.4	0.0000254	0.00003344	0.00002254	0	0.00214889	A_007_P03899	24667
tdcE	+10.28	10.03	+3.36	8.35	0.0	0.0	11.71	0.4	0.0000002	0.00003344	0.00002476	0	0.00244444	A_007_P03476	c_3872
tdcE	+10.64	9.84	+3.41	8.14	0.0	0.0	11.55	0.2	0.0000033	0.00013159	0.00422481	0	0.13676510	A_007_P04899	b2614
tdcF	+8.18	10.13	+3.03	8.62	0.2	0.0	11.65	0.1	0.0000601	0.00018702	0.00380145	0	0.17861672	A_007_P00294	b3113
tdh	+14.97	10.64	+3.90	8.69	0.0	0.0	12.59	0.0	0.0000007	0.00004793	0.00004768	0	0.09696429	A_007_P01924	b3616
tdhA	+2.21	9.08	+1.15	8.51	0.1	0.0	9.65	0.2	0.01160162	0.00833983	0.05111598	0	0.55880806	A_007_P00242	b3430
tfaR	-4.31	9.19	-2.11	10.25	0.0	0.0	8.14	0.0	0.00031664	0.00034782	0.01347743	0	0.23917614	A_007_P01481	b1373
tgt	+9.84	10.68	+3.30	9.03	0.0	0.0	12.33	0.1	0.0000158	0.00009392	0.00218814	0	0.14880866	A_007_P02144	b0406
thiD	-7.21	9.79	-2.85	11.22	0.0	0.0	8.37	0.0	0.00007017	0.00021522	0.00079617	0	0.08791367	A_007_P02728	b2103
thiG	-2.14	6.84	-1.02	7.32	0.2	0.0	7.39	0.0	0.01164229	0.00946767	0.05488222	0	0.57361142	A_007_P00618	b3991
thiG	-2.52	8.06	-1.32	7.60	0.0	0.0	8.72	0.3	0.00150588	0.00674135	0.03825114	0	0.49398382	A_007_P00618	b3991
thiK	+2.57	10.93	+1.36	10.25	0.0	0.0	11.61	0.2	0.00045066	0.00362743	0.03688770	0	0.48517962	A_007_P01731	b1106
thiM	-3.37	9.36	-1.75	10.24	0.4	0.0	8.49	0.4	0.00131686	0.01631987	0.04916197	0	0.54963146	A_007_P03184	23268
thiM	-4.80	9.05	-2.26	10.18	0.0	0.0	7.92	0.3	0.00005453	0.00078934	0.03036489	0	0.20034767	A_007_P03284	b2104
thrA	+2.88	7.94	+1.53	7.18	0.1	0.0	8.70	0.0	0.00027954	0.00255874	0.02564840	0	0.44347056	A_007_P03704	b0002
thrB	+3.50	8.18	+1.81	7.27	0.2	0.0	9.08	0.2	0.00024535	0.00231443	0.02023565	0	0.37437133	A_007_P03710	b0003
thrC	+3.50	9.91	+1.81	8.65	0.0	0.0	10.45	0.0	0.00004254	0.00063463	0.02303156	0	0.37308456	A_007_P03606	c_0005
thyA	+4.26	9.41	+1.70	8.54	0.1	0.0	10.26	0.0	0.00036507	0.00186771	0.02238776	0	0.40264480	A_007_P00619	b3917
tiS	-2.40	8.78	-1.26	9.41	0.0	0.0	8.14	0.0	0.00111097	0.00704150	0.04262111	0	0.55701245	A_007_P00899	b0188
tktA	+7.09	11.63	+2.83	10.22	0.0	0.0	13.04	0.0	0.00012787	0.00143388	0.00524217	0	0.20988734	A_007_P00012	b2935
tktA	+3.18	8.86	+1.67	8.03	0.6	0.0	9.70	0.1	0.00508733	0.02630882	0.02497667	0	0.41882854	A_007_P04596	24279
tktA	+5.45	8.56	+2.45	7.34	0.0	0.0	9.78	0.1	0.00005752	0.00083364	0.00379759	0	0.25171154	A_007_P01823	b2935
tldD	+2.24	9.36	+1.17	8.78	0.4	0.0	9.95	0.0	0.00425300	0.02001174	0.05079141	0	0.55842179	A_007_P04184	c_3999
tnaA	-108.28	10.02	-6.76	9.64	0.0	0.0	13.39	0.2	0.0000007	0.00003344	0.00000000	0	0.00000000	A_007_P05646	cmr/tryptophanase [EC4645]
tnaA	+53.25	11.43	+5.73	8.56	0.1	0.0	14.30	0.1	0.0000006	0.00003344	0.00000842	0	0.00966667	A_007_P00561	b3708
tnaB	+112.63	10.34	+6.82	6.93	0.1	0.0	13.75	0.1	0.0000002	0.00003344	0.00000000	0	0.00000000	A_007_P04991	25203
tnaB	+6.82	8.66	+2.27	7.52	0.3	0.0	9.79	0.0	0.00011523	0.00132359	0.01687716	0	0.28494176	A_007_P04909	c_4632
tnaB	+2.79	7.76	+1.48	7.02	0.3	0.0	8.50	0.0	0.00187237	0.00539155	0.01918154	0	0.49164895	A_007_P03653	b4159
tnaB	+5.76	10.90	+2.53	9.64	0.2	0.0	12.18	0.0	0.00001282	0.00022422	0.00766197	0	0.24703262	A_007_P02216	b0740
tnaC	+2.25	10.20	+1.17	9.61	0.0	0.0	10.78	0.4	0.00760108	0.02225545	0.05050704	0	0.55832254	A_007_P03838	b3835
tolQ	-2.05	11.18	-1.04	11.70	0.1	0.0	10.66	0.3	0.00791185	0.03032437	0.06326702	0	0.65814122	A_007_P03005	b0737
tolQ	-2.08	7.89	-1.06	8.42	0.0	0.0	7.37	0.0	0.00000365	0.00003344	0.00000000	0	0.00000000	A_007_P03006	cmr/part of trimethylamine-N-oxide oxidoreductase [EC1153]
torS	-2.56	12.53	-1.36	13.20	0.1	0.0	11.85	0.0	0.0000671	0.00027199	0.01432673	0	0.51129612	A_007_P00197	b0993
tpiA	+4.95	13.11	+2.31	11.95	0.0	0.0	14.26	0.0	0.0000993	0.00015049	0.00040303	0	0.08022184	A_007_P03975	b3919
tpx	+9.35	11.22	+3.22	9.60	0.0	0.0	12.83	0.1	0.0000146	0.00009605	0.00287983	0	0.15527397	A_007_P04605	b3324
trmA	+3.43	8.47	+1.78	7.58	0.1	0.0	9.36	0.2	0.00010552	0.00187435	0.02169325	0	0.38267172	A_007_P03751	b4240
trmB	-3.60	11.44	-1.85	12.36	0.1	0.0	10.53	0.3	0.0002360	0.00227378	0.01050585	0	0.32348249	A_007_P03760	b4241
trmA	-3.11	9.11	-1.63	9.93	0.1	0.0	8.30	0.1	0.00014388	0.00156332	0.01758448	0	0.38558496	A_007_P04777	25526
trmH	-2.75	10.42	-1.46	11.15	0.1	0.0	9.68	0.1	0.00019329	0.00195328	0.01603329	0	0.46839729	A_007_P01768	b3651
trmJ	+6.02	12.75	+2.59	11.46	0.0	0.0	14.05	0.1	0.0000800	0.00022294	0.00696329	0	0.23812609	A_007_P01943	b2960
trmJ	-10.10	13.37	-3.34	15.04	0.0	0.0	11.70	0.4	0.0000195	0.00038447	0.00109627	0	0.04546118	A_007_P03564	b3532
trpB	+36.35	10.01	+4.72	7.65	0.1	0.0	12.37	0.2	0.0000034	0.00004570	0.00021659	0	0.04011765	A_007_P01491	b2261
trpB	+32.52	9.82	+4.52	8.31	0.0	0.0	13.34	0.0	0.0000007	0.00003370	0.00002234	0	0.02738814	A_007_P03978	c_1726
trpB	+22.36	10.17	+4.48	7.93	0.1	0.0	12.41	0.1	0.0000023	0.00004002	0.00036522	0	0.05476190	A_007_P04133	23550
trpC	+21.35	10.42	+4.55	8.15	0.1	0.0	12.70	0.2	0.0000028	0.00004221	0.00032524	0	0.05035256	A_007_P01496	b2262
trpD	+12.09	9.88	+3.60	8.08	0.3	0.0	11.67	0.1	0.0000479	0.00016636	0.00179748	0	0.12235294	A_007_P03884	c_1729
trpE	+38.40	9.45	+5.32	6.93	0.1	0.0	11.70	0.1	0.0000018	0.00003156	0.00002751	0	0.03720000	A_007_P01504	b2263
trpE	+8.12	8.58	+2.67	7.33	0.3	0.0	10.09	0.3	0.0000576	0.00074664	0.00387649	0	0.18002950	A_007_P03886	c_1730
trpR	+6.54	9.32	+2.71	7.96	0.0	0.0	10.67	0.1	0.0000533	0.00027677	0.00188466	0	0.12347412	A_007_P01764	b4393
trxA	-5.89	14.05	-2.56	15.33	0.0	0.0	12.77	0.1	0.0000560	0.00017942	0.00176131	0	0.

ybbz	-2.29	10.67	-1.19	11.26	0.0	10.07	0.0	0.00050030	0.00390441	0.04882211	0.58303030	A_07_P031124	c_0609	cmr|Hypothetical protein ybbz [c_0609]
ybbT	-13.97	8.72	-11.99	7.72	0.3	9.71	0.2	0.00050328	0.00162391	0.01930306	0.33948229	A_07_P031234	c_0620	cmr|Dihydroglycolate hydrolase [c_0620]
ybbW	-13.08	8.45	-11.62	7.64	0.2	9.26	0.1	0.00051567	0.00201521	0.02586255	0.42416583	A_07_P016343	b0511	cmr|putative transport protein [b0511]
ybcJ	-2.17	9.72	-1.12	10.28	0.1	9.16	0.5	0.01307121	0.04880085	0.05890434	0.62365510	A_07_P016429	b0528	cmr|Hypothetical protein [b0528]
ybcM	-3.25	11.69	-1.70	12.54	0.0	10.84	0.0	0.00050594	0.00083813	0.01458375	0.36642746	A_07_P016496	b0546	cmr|putative AMC-type regulatory protein [b0546]
ybcO	+6.80	11.96	+2.26	10.83	0.0	13.08	0.1	0.00001273	0.00029390	0.01100229	0.28631405	A_07_P016514	b0549	cmr|Hypothetical protein [b0549]
ybcU	-2.02	7.84	-1.02	7.33	0.1	8.35	0.1	0.01544852	0.03853489	0.06389896	0.60581626	A_07_P018504	c_1564	cmr|Bacr protein homology from lambdoid prophage DLP12 [c_1564]
ybcW	-2.15	10.90	-1.10	11.46	0.1	10.35	0.2	0.00252223	0.01324992	0.05985328	0.62863909	A_07_P016559	b0559	cmr|Hypothetical protein [b0559]
ybdD	+5.68	8.78	+2.51	7.52	0.0	10.03	0.1	0.00008807	0.00022450	0.00775561	0.24670707	A_07_P031917	ABE-0285351	asap|conserved protein [b4512]
ybdJ	-2.00	8.77	-1.00	9.27	0.0	8.27	0.0	0.01039598	0.03691253	0.07452051	0.67532818	A_07_P016663	b0580	cmr|Hypothetical protein [b0580]
ybdM	-2.47	7.99	-1.30	8.64	0.1	7.34	0.2	0.00641296	0.02482738	0.06194794	0.52840212	A_07_P016675	b0601	cmr|Hypothetical protein [b0601]
ybdN	-5.89	10.59	-2.56	11.87	0.0	9.31	0.1	0.00000617	0.00001840	0.00176512	0.13825871	A_07_P016768	b0602	cmr|Hypothetical protein [b0602]
ybeA	-4.00	12.22	-2.00	13.22	0.0	11.22	0.1	0.00003810	0.00060130	0.00466414	0.26728386	A_07_P016797	b0636	cmr|Hypothetical protein [b0636]
ybeB	-4.04	13.24	-2.01	14.24	0.0	12.23	0.1	0.00002500	0.00045582	0.00680450	0.26451852	A_07_P016752	b0637	cmr|Hypothetical protein [b0637]
ybeJ	+2.94	11.92	+1.56	11.14	0.0	12.70	0.0	0.00011607	0.00118504	0.02783654	0.41930279	A_07_P016835	b0655	cmr|putative periplasmic binding transport protein [b0655]
ybeL	+2.55	11.05	+1.35	10.38	0.3	11.73	0.2	0.00175638	0.00998282	0.03793128	0.48720440	A_07_P009784	b0643	cmr|putative alpha helical protein [b0643]
ybeT	+9.99	10.52	+2.60	9.52	0.0	11.52	0.1	0.00003563	0.00057774	0.01930203	0.33974656	A_07_P009856	b0659	cmr|Hypothetical protein [b0659]
ybeZ	+3.07	10.51	+1.62	9.71	0.0	11.32	0.1	0.00100030	0.00120402	0.02570376	0.42419287	A_07_P009865	b0660	cmr|putative ATP-binding protein in pho regulon [b0660]
ybfA	-7.31	11.14	-2.87	12.58	0.1	9.71	0.2	0.00000598	0.00018440	0.00078252	0.08880000	A_07_P016854	b0699	cmr|Hypothetical protein [b0699]
ybfE	-3.31	11.64	-1.73	12.50	0.1	10.77	0.0	0.00006699	0.00060852	0.01404599	0.35667742	A_07_P009941	b0685	cmr|Hypothetical protein [b0685]
ybfL	-2.80	10.53	-1.48	11.27	0.4	9.79	0.0	0.00193026	0.01857532	0.03477037	0.45452214	A_07_P010041	b0705	cmr|putative receptor protein [b0705]
ybgA	-6.50	9.45	-2.70	10.80	0.1	8.10	0.1	0.00000633	0.00019153	0.00124174	0.11568047	A_07_P033376	c_0786	cmr|Hypothetical protein ybgA [c_0786]
ybgC	-3.12	11.08	-1.08	11.62	0.1	10.53	0.0	0.01006541	0.03683382	0.06237511	0.63893299	A_07_P010098	b0736	cmr|Hypothetical protein [b0736]
ybgE	+8.14	9.53	+3.19	7.54	0.0	11.52	0.0	0.00000172	0.00009748	0.00806529	0.16268647	A_07_P010104	b0735	cmr|Hypothetical protein [b0735]
ybgD	+2.34	7.54	+1.23	6.93	0.1	8.15	0.3	0.01090200	0.01058953	0.04547320	0.52916265	A_07_P010097	b0716	cmr|Hypothetical protein [b0716]
ybgG	+2.05	7.46	+1.03	6.94	0.1	7.98	0.1	0.02102628	0.01149938	0.05468107	0.59573883	A_07_P010264	b0753	cmr|putative homeobox protein [b0753]
ybhA	+2.02	9.86	+1.01	9.35	0.1	10.37	0.2	0.03190959	0.01587525	0.06325512	0.61330472	A_07_P046367	2B936	cmr|putative phosphatase [2B936]
ybhC	+2.57	7.98	+1.36	7.30	0.0	8.66	0.3	0.00992192	0.00614247	0.03738115	0.48619601	A_07_P013991	2D843	cmr|putative pectinesterase [2D843]
ybhC	+2.14	8.53	+1.10	7.98	0.1	9.08	0.2	0.02269787	0.01271122	0.05198577	0.57913272	A_07_P004315	b0772	cmr|putative pectinesterase [b0772]
ybhI	-3.80	9.90	-1.92	10.86	0.2	8.93	0.3	0.00146984	0.00161942	0.04860981	0.30230599	A_07_P010342	b0770	cmr|putative membrane pump protein [b0770]
ybhM	-3.09	9.50	-1.63	10.32	0.0	8.69	0.2	0.00023482	0.00224565	0.01802464	0.38748870	A_07_P004392	b0788	cmr|Hypothetical protein [b0788]
ybhQ	+2.20	10.34	+1.14	9.78	0.1	10.91	0.1	0.00080609	0.00644673	0.05130369	0.55977824	A_07_P004406	b0791	cmr|Hypothetical protein [b0791]
ybiB	+4.09	12.14	+2.03	11.12	0.1	13.15	0.2	0.00004516	0.00068369	0.01522104	0.33329624	A_07_P004455	b0800	cmr|putative enzyme [b0800]
ybiB	+3.99	10.35	+1.99	9.35	0.1	11.34	0.1	0.00003284	0.00045466	0.01136179	0.33917679	A_07_P004483	2J021	cmr|putative enzyme [2J021]
ybiB	+5.17	11.40	+2.37	10.21	0.1	12.58	0.1	0.00001668	0.00003485	0.00944487	0.26841155	A_07_P041584	c_0884	cmr|Hypothetical protein ybiB [c_0884]
ybiC	+5.09	9.04	+2.35	7.86	0.1	10.21	0.1	0.00003519	0.00022468	0.00959738	0.27308885	A_07_P042097	c_0885	cmr|Hypothetical oxidoreductase ybiC [c_0885]
ybiC	+2.05	9.01	+1.04	8.49	0.0	9.53	0.1	0.01048168	0.00869341	0.06263686	0.59824086	A_07_P004457	b0801	cmr|putative dehydrogenase [b0801]
ybiH	-2.15	7.58	-1.23	6.96	0.2	8.20	0.3	0.04079665	0.02012601	0.08409556	0.52650049	A_07_P004632	b0796	cmr|putative transcriptional regulator [b0796]
ybiJ	-4.61	9.85	-2.20	10.95	0.2	8.75	0.0	0.00003067	0.00052425	0.00417692	0.21135048	A_07_P004663	b0802	cmr|Hypothetical protein [b0802]
ybiO	-4.49	9.52	-2.17	10.60	0.1	8.44	0.2	0.00005617	0.00078813	0.00467634	0.22630094	A_07_P004691	b0808	cmr|putative transport protein [b0808]
ybiR	-2.56	9.86	-1.36	10.54	0.1	9.18	0.2	0.00005858	0.00434342	0.03363154	0.55658654	A_07_P004542	b0818	cmr|Hypothetical protein [b0818]
ybiS	-3.18	10.93	-1.73	11.66	0.0	9.56	0.1	0.00121353	0.01608898	0.03703428	0.47704547	A_07_P004547	b0819	cmr|Hypothetical protein [b0819]
ybiS	-3.32	12.09	-1.73	12.96	0.1	11.23	0.1	0.00008685	0.00108440	0.01376515	0.35245928	A_07_P042114	c_0905	cmr|Protein ybiS precursor [c_0905]
ybiT	-13.54	10.35	-3.76	12.23	0.1	8.47	0.0	0.00000051	0.00005264	0.00004700	0.02176471	A_07_P004555	b0820	cmr|putative ATP-binding component of a transport system [b0820]
ybjC	-43.08	10.68	-5.43	13.40	0.0	7.97	0.1	0.00000007	0.00003344	0.00000004	0.00250000	A_07_P004640	b0841	cmr|Hypothetical protein [b0841]
ybjJ	-12.66	10.04	-3.66	11.87	0.1	8.21	0.2	0.00002022	0.00015505	0.00005780	0.02275000	A_07_P004688	b0847	cmr|putative transport protein [b0847]
ybjM	-3.48	9.18	-1.80	10.08	0.1	8.28	0.1	0.00007198	0.00095259	0.01162793	0.33468007	A_07_P004692	b0849	cmr|Hypothetical protein [b0849]
ybjN	+3.04	10.43	+1.61	9.63	0.1	11.24	0.3	0.00066740	0.00372408	0.02615804	0.42689162	A_07_P004718	b0853	cmr|putative sensory transduction regulator [b0853]
ybjP	+2.30	9.13	+1.20	8.52	0.1	9.73	0.2	0.01107546	0.00681316	0.04648842	0.51431686	A_07_P012022	2J005	cmr|putative enzyme [2J005]
ybjT	+2.53	7.76	+1.34	7.09	0.0	8.43	0.2	0.00620209	0.00453656	0.03388045	0.48844390	A_07_P004800	b0869	cmr|putative dTDP-glucose enzyme [b0869]
ybjX	-5.14	10.65	-2.36	11.83	0.0	9.47	0.2	0.00002142	0.00041880	0.00280742	0.17539683	A_07_P004839	b0877	cmr|putative enzyme [b0877]
ybjX	-6.09	12.32	-2.61	13.62	0.0	11.02	0.1	0.00000580	0.00018220	0.00154789	0.12826316	A_07_P042136	c_1012	cmr|Hypothetical protein ybjX [c_1012]
ycaD	-2.28	9.13	-1.19	8.82	0.4	9.44	0.1	0.01003015	0.00664600	0.04975546	0.58146138	A_07_P031821	c_1337	cmr|Hypothetical protein ycaD [c_1337]
ycaO	+2.05	8.90	+1.03	8.38	0.1	9.42	0.1	0.00155606	0.00814256	0.06340045	0.59823678	A_07_P051726	2J251	cmr|Hypothetical protein [2J251]
ycaO	+2.76	9.16	+1.47	8.43	0.0	9.90	0.2	0.00028602	0.00260187	0.01027774	0.45611009	A_07_P004973	b0905	cmr|Hypothetical protein [b0905]
ycbF	-3.43	11.57	-1.78	12.46	0.1	10.68	0.3	0.00029387	0.00264683	0.01242505	0.33668515	A_07_P005167	b0944	cmr|putative chaperone [b0944]
ycbG	+4.43	9.46	+2.15	8.38	0.0	10.54	0.1	0.00001640	0.00034470	0.00130608	0.30776615	A_07_P005176	b0956	cmr|putative dehydrogenase [b0956]
ycbJ	+4.14	9.42	+2.05	8.39	0.0	10.44	0.1	0.00002684	0.00047665	0.01493458	0.32977560	A_07_P005042	b0919	cmr|Hypothetical protein [b0919]
ycbQ	-2.38	9.01	-1.25	9.64	0.4	8.39	0.0	0.00182968	0.02257690	0.04437365	0.54969603	A_07_P005137	b0938	cmr|putative fimbrial-like protein [b0938]
ycci	+3.52	9.60	+1.82	8.69	0.3	10.50	0.1	0.00026536	0.00245180	0.01983041	0.36947929	A_07_P001246	b1003	cmr|Hypothetical protein [b1003]
ycci	-11.91	12.93	-1.97	13.91	0.1	11.94	0.2	0.00001918	0.00734712	0.07437512	0.27615566	A_07_P005289	b0968	cmr|Hypothetical protein [b0968]
ycdT	-2.40	11.28	-1.24	11.91	0.1	10.65	0.1	0.00058366	0.00434242	0.04698895	0.54506223	A_07_P041100	c_1164	cmr|Hypothetical protein ycdT [c_1164]
ycdT	-7.95	10.59	-2.99	12.08	0.0	9.09	0.1	0.00000211	0.00010505	0.00058054	0.07746763	A_07_P001352	b1025	cmr|Hypothetical protein [b1025]
ycdZ	-5.86	9.63	-2.55	10.91	0.1	8.36	0.5	0.00019172	0.00184108	0.00867215	0.20319191	A_07_P001391	b1036	cmr|Hypothetical protein [b1036]
ycek	-2.09	10.04	-1.07	10.57	0.1	9.50	0.1	0.01113600	0.07014267	0.06479989	0.64818702	A_07_P001482	b1055	cmr|Hypothetical protein [b1055]
ycef	-2.54	7.80	-1.34	7.13	0.0	8.47	0.1	0.00037198	0.00314193	0.03763783	0.48691044	A_07_P001639	b1087	cmr|Hypothetical protein [b1087]
ycfH	+3.88	8.70	+1.96	7.72	0.2	9.68	0.1	0.00005108	0.00074921	0.01677782	0.34484334	A_07_P040780	c_1334	cmr|Hypothetical protein ycefH [c_1334]
ycehI	+2.86	8.56	+1.52	7.60	0.1	9.52	0.2	0.00010210	0.00261524	0.02988554	0.44387736	A_07_P001540	b1067	cmr|Hypothetical protein [b1067]
ycem	+2.15	8.09	+1.10	7.54	0.2	8.64	0.2	0.02288038	0.01266107	0.05325534	0.57135714	A_07_P052072	2J704	cmr|Hypothetical protein [2J704]
yceM	-2.09	10.19	-1.07	9.66	0.0	10.72	0.0	0.00095527	0.00625521	0.05475813	0.58307080	A_07_P001544	b1068	cmr|putative viulence factor [b1068]
yceQ	-2.00	8.80	-1.00	9.30	0.1	8.30	0.0	0.00460831	0.02138323	0.07464518	0.67541379	A_07_P001627	b1085	cmr|Hypothetical protein [b1085]
ycfJ	-7.12	9.73	-2.83	11.16	0.1	8.29	0.0	0.00002098	0.00012344	0.00092007	0.09720000	A_07_P001753	b1110	cmr|Hypothetical protein [b1110]
ycfL	-4.14	9.66	-2.05	8.63	0.3	10.68	0.0	0.00511862	0.00707230	0.04469972	0.32713881	A_07_P001721	b1104	cmr|Hypothetical protein [b1104]
ycfP	-12.90	13.78	-4.56	13.01	0.1	14.54	0.3	0.00072774	0.00514889	0.02817221	0.44396584	A_07_P001743	b1108	cmr|Hypothetical protein [b1108]
ycfQ	-8.22	10.92	-3.04	12.44	0.1	9.40	0.2	0.00000475	0.00016425	0.00045668	0.06788019	A_07_P001759	b1111	cmr|Hypothetical protein [b1111]
ycfZ	-2.10	7.58	-1.07	8.12	0.1	7.05	0.1	0.00146454	0.00853400	0.06484710	0.64565722	A_07_P001786	b1117	cmr|homology of virulence factor [b1121]
ygaK	+4.81	10.51	+2.05	9.38	0.0	11.64	0.1	0.00001306	0.00029749	0.01117959	0.28758804	A_07_P008843	b1178	cmr|Hypothetical protein [b1178]
ygaM	+2.76	9.26	+1.47	8.53	0.1	9.99	0.1	0.00029898	0.00267603	0.01025571	0.45936883	A_07_P008851	b1180	cmr|putative isomerase [b1180]
ygbF	+2.12	7.42	+1.08	6.88	0.1	7.96	0.3	0.00303999	0.01530590	0.05447294	0.58302295	A_07_P008861	b1202	cmr|putative adhesion and penetration protein [b1202]
ygaE	+6.19	9.46	+2.63	8.14	0.2	10.77	0.1	0.00001697	0.00003267	0.00664761	0.23309577	A_07_P042226	c_1607	cmr|Hypothetical protein ygaE [c_1607]
ychA	+4.47	10.21	+1.80	9.31	0.2	11.12	0.1	0.00011745	0.00133755	0.02849616	0.37908061	A_07_P009924	b1214	cmr|Hypothetical protein [b1214]
ychM	+2.54	10.61	+1.35	9.94	0.0	11.29	0.0	0.00024754	0.00233088	0.01736648	0.48670520	A_07_P009978	b1265	cmr|Hypothetical protein [b1265]
ychM	-3.22	8.88	-1.69	9.72	0.0	8.04	0.1	0.00010949	0.00123820	0.01556602	0.37290804	A_07_P009976	c_1664	cmr|Putative sulfate transporter ychM [c_1664]
ychM	-2.99	8.80	-1.58	9.59	0.2	8.01	0.1	0.00039998	0.00319315	0.01941188	0.39898172	A_07_P050776	2J977	cmr|Hypothetical protein [2J977]
ychM	-2.48	8.76	-1.31	9.42	0.4	8.10	0.2	0.00336153	0.01650778	0.03734327	0.52575134	A_07_P008881	b1266	cmr|Hypothetical protein [b1266]
ychN	+3.40	9.34	+1.77	8.45	0.3	10.22	0.2	0.00047753	0.00378609	0.02159362	0.38809361	A_07_P007047	b1219	cmr|Hypothetical protein [b1219]
ychN	+2.64	9.00	+1.40	8.39	0.2	9.61	0.2	0.00241341	0.01382168	0.03583779	0.47697284	A_07_P007062	2J094	cmr|Hypothetical protein [2J094]
ychO	-2.60	8.26	-1.38	8.94	0.2	7.57	0.3	0.02862884	0.01461735	0.03858510	0.49475523	A_07_P007051	b1220	cmr|putative factor [b1220]
ycIC	-4.30	12.58	-2.10	13.64	0.2	11.53	0.2	0.00009081	0.00111789	0.00562764	0.24417627	A_07_P031880	b1259	cmr|Hypothetical protein [b1259]
ycIH	+2.53	11.49	+1.34	10.82	0.1	12.16	0.1	0.00066603	0.00371502	0.03798802	0.48717427	A_07_P041123	c_1751	cmr|Protein ycIH [c_1751]
ycII	+2.74	11.69	+1.45	10.96	0.0	12.41	0.1	0.00018207	0.00187162	0.02352185	0.45959927	A_07_P007101	b1282	cmr|Hypothetical protein [b1282]
ycII	+15.42	10.25	+3.95	8.27	0.1	12.22	0.2	0.00000105	0.00007542	0.00096481	0.09493750	A_07_P007091	b1251	cmr|Hypothetical protein [b1251]
ycII	+15.10	10.55	+3.92	8.59	0.1	12.51	0.1	0.00000045	0.00005132	0.00048493	0.09760432	A_07_P050796	2J029	cmr|Hypothetical protein [2J029]
ycIK	+2.87	10.99	+1.52	10.23	0.1	11.75	0.2	0.00031156	0.00275265	0.02976911	0.44153220	A_07_P014337	b1271	cmr|putative oxidoreductase [b1271]
ycIM	-4.37	11.05	-2.13	12.12	0.1	9.99	0.1	0.00062163	0.00454461	0.00354412	0.23881020	A_07_P014381	b1280	cmr|putative heat shock protein [b1280]
ycIN	+2.22	10.30	+1.15	9.73	0.0	10.88	0.0	0.00062683	0.00457316	0.04986789	0.55721789	A_07_P014346	b1273	cmr|Hypothetical protein [b1273]
ycIO	-2.27	8.91	-1.18	9.50	0.1	8.32	0.1	0.00054188	0.00413348	0.05037386	0.58645683	A_07_P044117	2J543	cmr|Hypothetical protein [2J543]
ycIO	-3.18	10.68	-1.65	11.51	0.0	9.85	0.2	0.00017562	0.00182148	0.01672955	0.37749957	A_07_P008891	c_1732	cmr|Protein ycIO [c_1732]
ycIO	-2.81	9.62	-1.49	10.38	0.0	8.86	0.2	0.00018284	0.00247207	0.02457926	0.45135525	A_07_P014319	b1267	cmr|Hypothetical protein [b1267]
ycIW	-2.65	12.25	-1.41	12.95	0.3	11.54	0.3	0.00343679	0.00963339	0.03004426	0.49596251	A_07_P014418	b1287	cmr|putative oxidoreductase [b1287]
ycJD	-3.59	9.23	-1.85	10.15	0.1	8.30	0.1	0.00007642	0.00069942	0.01043128	0.32265226	A_07_P014428	b1289	cmr|Hypothetical protein [b1289]
ycJF	-2.87	7.82	-1.52	7.06	0.3	8.58	0.1	0.00113876	0.00715430	0.04460241	0.49422847	A_07_P014427	c_1794	cmr|Hypothetical protein ycJF [c_1794]
ycjF	-2.49	11.70	-1.32	12.36	0.0	11.04	0.1	0.00064854	0.00471013	0.03697282	0.52136101	A_07_P048661	2J658	cmr|putative IC 2.1 enzymes [2J658]
ycjC	-2.31	7.76	-1.21	8.36	0.3	7.16	0.2	0.02284543	0.01454495	0.04420391	0.52246479	A_07_P014713	b1347	cmr|Hypothetical protein [b1347]
ycjE	-2.38	8.98	-1.25	9.61	0.2	8.35	0.2	0.01010982	0.00701703	0.04329224	0.55861928	A_07_P010386	ABE-0285047	asap|Rec prophage; conserved protein [b4526]
ycjG	-2.38	9.76	-1.25	10.39	0.1	9.14	0.0	0.00050655	0.00442484	0.04197012	0.55839738	A_07_P014803	2J414	cmr|Unknown protein encoded within prophage CP-933B [2J414]
ycjV	-3.37	9.68	-1.75	10.56	0.1	8.81	0.3	0.00239247	0.01329141	0.03598432	0.34588430	A_07_P014777	b1360	cmr|putative DNA protection protein [b1360]
ydbH	+2.09	7.92	+1.07	7.39	0.1	8.45	0.0	0.01055061	0.00676135	0.05700680	0.51484865	A_07_P014885	b1381	cmr|Hypothetical protein [b1381]
ydbK	-3.07	10.59	-1.62	9.79	0.1	11.40	0.1	0.00009527	0.00115468	0.02588651	0.42435667	A_07_P010609	ABE-0285050	asap|predicted protein [b4529]
ydbK	+4.86	8.92	+2.28	7.78	0.1	10.06	0.1	0.00003377	0.00016206	0.00872564	0.28335582	A_07_P014866	b1378	cmr|putative oxidoreductase, Fe-S subunit [b1378]
ydcB	+15.38	9.49	+3.94	7.52	0.0	11.47	0.1	0.00000045	0.00005132	0.00096227	0.09528302	A_07_P008222	b1426	cmr|putative oxidoreductase [b1426]
ydcI	-2.12	8.65	-1.08	9.20	0.1	8.11	0.0	0.00089445	0.00602286	0.06250572	0.63943470	A_07_P008234	b1422	cmr|Hypothetical protein regulator LYSR-type [b1422]
ydcM	-2.06	9.15	-1.04	9.67	0.1	8.63	0.4	0.00808694	0.03323866	0.06848893	0.65712630	A_07_P009252	b1432	cmr|putative viulence protein [b1432]
ydcY	+4.11	11.98	+2.04	10.96	0.0	13.00	0.0	0.00002003	0.00019347	0.01458179	0.32988566	A_07_P009321	b1446	cmr|Hypothetical protein [b1446]
ydeA	-2.23	7.58	-1.15	8.15	0.3	7.02	0.3	0.02271935	0.01369726	0.05305233	0.59918938	A_07_P009570	b1496	cmr|putative ATP-binding component of a transport system [b1496]
ydeB	-2.58	7.45	-1.37	8.14	0.4	6.76	0.1	0.00315532	0.01354469	0.03165894	0.49771318	A_07_P048054	2J213	cmr|Hypothetical protein [2J213]
ydeH	+2.00	8.71	+1.00	8.20	0.1	9.21	0.1	0.00175621	0.00998282	0.06377668	0.61452428	A_07_P034960	c_1909	cmr|Hypothetical protein ydeH [c_1909]
ydeK	+4.98	8.38	+2.32	9.53	0.0	7.22	0.0	0.00003181	0.00061529	0.00320621	0.19902072	A_07_P009296	b1528	cmr|putative resistance / regulatory protein [b1528]
ydeN	-2.60	8.59	-1.38	7.80	0.2	9.38	0.2	0.00069035	0.00388423	0.03501527	0.47919492	A_07_P009302	b1498	cmr|putative sulfatase [b1498]
ydeT	-2.20	9.34	-1.14	9.91	0.1	8.77	0.0	0.00030750	0.00621733	0.05130869	0.60808659	A_07_P009612	b1505	cmr|putative outer membrane protein [b1505]
ydeU	-2.02	9.08	-1.02	9.59	0.1	8.57	0.1	0.02154052	0.01328788	0.07355399	0.66996481	A_07_P010527	c_2894	cmr|Hypothetical protein ydeU [c_2894]
ydfG	-2.90	8.46	-1.54	7.69	0.0	9.23	0.1	0.00112277	0.00199716	0.02850927	0.43918787	A_07_P020342	b1539	cmr|putative oxidoreductase [b1539]
ydfH	-3.02	9.15	-1.05	9.66	0.1	8.64	0.1	0.02482526	0.01303865	0.07385115	0.66919487	A_07_P034945	2J157	cmr|Hypothetical protein [2J157]
ydfM	-7.98	8.71	-3.00	10.21	0.1	7.21	0.0	0.00000255	0.00011704	0.00058117	0.07698076	A_07_P031275	c_0649	cmr|Tail fiber assembly protein homolog from lambdoid [c_0649]
ydfZ	-12.77	11.37	-4.47	10.63	0.1	12.10	0.2	0.00042646	0.00349184	0.02102747	0.45956545	A_07_P020351	b1541	cmr|Hypothetical protein [b1541]
ydgA	-2.02	9.19	-1.01	8.69	0.1	9.70	0.2	0.02281610	0.01221501	0.06154599	0.60497910	A_07_P044604	2J617	cmr|Hypothetical protein [2J617]
ydgB	-2.48	9.49	-1.31	8.83	0.1	10.15	0.0	0.00015176	0.00277757	0.03924969	0.49482819	A_07_P035103	c_2006	cmr|Hypothetical protein ydgB [c_2006]
ydgH	+3.80	9.76	+1.93	8.78	0.2	10.73	0.1	0.00008859	0.00109740	0.01722815	0.34863753	A_07_P020654	b1604	cmr|Hypothetical protein [b1604]
ydgJ	-19.99	8.78	-6.00	11.78	0.1	5.78	0.1	0.00000035	0.00007114	0.00018605	0.03899244	A_07_P035111	c_2016	cmr|Hypothetical oxidoreductase ydgJ [c_2016]
ydgJ	+2.72	7.94	+1.45	7.22	0.0	8.67	0.1	0.00023139	0.00221327	0.03247331	0.46142599	A_07_P020751	b1624	cmr|Hypothetical protein [b1624]
ydgK	-3.43	9.14	-1.76	10.03	0.1	8.25	0.1	0.00007081	0.00084222	0.01245158	0.33604255	A_07_P020765	b1626	cmr|Hypothetical protein [b1626]
ydhF	+2.36	9.44	+1.24	8.82	0.1	10.06	0.1	0.00008886	0.00649153	0.04452045	0.52260202	A_07_P020869	b1647	cmr|Hypothetical protein [b1647]
ydhI	-3.61	8.22	-1.85	8.94	0.1	7.29	0.0	0.00008179	0.00102609	0.01820996	0.32468858	A_07_P020928	b1643	cmr|Hypothetical protein [b1643]
ydhJ	-2.17	7.68	-1.12	8.24	0.2	7.12	0.2	0.02366642	0.01773944	0.05786204	0.61887228	A_07_P020852	b1644	cmr|putative membrane protein [b1644]
ydhJ	-2.24	7.67	-1.17	8.16	0.2	7.09	0.1	0.00011760	0.00092212	0.01482244	0.33134058	A_07_P020853	b1644	cmr|putative membrane protein [b1644]
ydhJ	-2.71	7.96	-1.44	8.68	0.1	7.24	0.2	0.00031727	0.00278587	0.02760304	0.47542670	A_07_P020852	b1644	cmr|putative membrane protein [b1644]
ydhJ	-2.42	7.81	-1.27	8.45	0.1	7.18	0.1	0.00043055	0.00358687	0.04408828	0.54758471	A_07_P020852	b1644	cmr|putative membrane protein [b1644]
ydhP	-2.70	7.80	-1.43	8.51	0.3	7.08	0.3	0.02300054	0.01105143	0.02766578	0.47346565	A_07_P018348	b1657	cmr|putative transport protein [b1657]
ydhR	+2.30	8.94	+1.20	8.34	0.1	9.54	0.1	0.00027697	0.00539515	0.04489215	0.53497826	A_07_P031887	b1667	cmr|Hypothetical protein [b1667]
ydhS	-3

yfgM	+3.83	10.95	+1.94	9.98	0.0	1.0	0.1	0.00002806	0.00049142	0.01723123	0.34820268	A_07_P02363	b2513	cmr|orf, hypothetical protein b2513|
yfhB	-6.26	9.98	-2.65	11.30	0.1	8.65	0.1	0.00008621	0.00018975	0.00145352	0.13497308	A_07_P01973	b2560	cmr|orf, hypothetical protein b2560|
yfiC	-2.24	8.47	+1.16	7.88	0.2	9.05	0.1	0.00138910	0.00828407	0.05696035	0.15726407	A_07_P019777	b2575	cmr|putative enzyme|b2575|
yfiD	+6.31	11.53	+2.66	10.21	0.0	1.1	0.1	12.86	0.4	0.00008899	0.00110064	0.00656949	0.23295045	A_07_P019799	b2579	cmr|putative formate acetyltransferase|b2579|
yfiF	+7.42	13.01	+2.89	9.56	0.0	1.1	0.1	12.45	0.1	0.00000375	0.00014386	0.00445549	0.19002740	A_07_P019806	b2581	cmr|orf, hypothetical protein b2581|
yfiH	-2.18	9.36	-1.12	9.92	0.1	8.80	0.1	0.00091408	0.00631098	0.05708079	0.61956613	A_07_P019847	b2593	cmr|orf, hypothetical protein b2593|
yfiQ	-7.07	9.58	-2.82	8.17	0.0	11.00	0.2	0.00030629	0.00015341	0.00502858	0.20889182	A_07_P019821	b2584	cmr|putative formyltetrahydrofolate synthetase|b2584|
yfiZ	-2.26	11.72	-1.17	12.30	0.1	11.13	0.3	0.00415273	0.01962000	0.05173272	0.59236909	A_07_P019968	b2618	cmr|orf, hypothetical protein b2618|
yfjH	-2.09	8.01	-1.06	8.54	0.4	7.47	0.0	0.00821125	0.01827376	0.06390073	0.64581410	A_07_P019987	b2623	cmr|putative histone|b2623|
yfjI	-2.02	10.34	-1.02	10.84	0.1	9.83	0.0	0.01055536	0.00904937	0.07264545	0.67002343	A_07_P019999	b2625	cmr|orf, hypothetical protein b2625|
yfjJ	-2.06	7.34	-1.04	7.86	0.4	6.82	0.0	0.01281814	0.04513879	0.08409722	0.85159269	A_07_P020026	b2626	cmr|orf, hypothetical protein b2626|
yjaA	-3.26	9.19	-1.77	10.21	0.1	8.34	0.0	0.00007274	0.00005677	0.01468051	0.36398425	A_07_P020601	c_3263	cmr|Hypothetical sigma-54-dependent transcriptional regulator|c_3263|
yjaD	+6.49	10.22	+2.70	8.88	0.0	11.57	0.2	0.00003228	0.00021944	0.00601194	0.22545884	A_07_P020346	b2700	cmr|orf, hypothetical protein b2700|
yjaP	-2.33	11.27	-1.22	11.88	0.5	10.66	0.1	0.09200548	0.03680429	0.04548209	0.56876092	A_07_P020192	b2668	cmr|orf, hypothetical protein b2668|
yjaT	-2.49	8.48	-1.31	9.14	0.0	7.82	0.0	0.00038325	0.00023164	0.02796303	0.52892020	A_07_P020216	c_3207	cmr|Hypothetical protein gcvT| c_3207|
yjaV	+2.92	8.65	+1.55	8.07	0.2	9.43	0.1	0.00206887	0.00267603	0.02887957	0.43972921	A_07_P020189	b2667	cmr|orf, hypothetical protein b2667|
yjaW	-7.61	11.51	-2.93	12.97	0.1	10.04	0.4	0.00004361	0.00068917	0.00466914	0.08047244	A_07_P020325	b2670	cmr|orf, hypothetical protein b2670|
yjaZ	-2.01	10.00	-1.01	10.50	0.2	9.49	0.1	0.00322064	0.01598039	0.07158916	0.66773563	A_07_P001881	b2682	cmr|orf, hypothetical protein b2682|
yjdD	-2.54	8.73	-1.34	9.40	0.0	8.06	0.1	0.00008731	0.00324526	0.03437535	0.51256819	A_07_P003701	c_3116	cmr|Hypothetical protein gcdC| c_3116|
yjdJ	+3.88	8.85	+1.96	7.87	0.1	9.83	0.2	0.00307611	0.00098704	0.01683562	0.34558018	A_07_P003675	c_3297	cmr|Hypothetical oxidoreductase gldA| c_3297|
yjdJ	+2.26	7.91	+1.18	7.32	0.1	8.49	0.0	0.00005819	0.00048400	0.04795754	0.54457023	A_07_P002127	b2736	cmr|putative dehydrogenase|b2736|
yjdK	+2.94	8.32	+1.56	7.54	0.2	9.09	0.2	0.00029429	0.00264913	0.02855371	0.43901367	A_07_P002131	b2737	cmr|orf, hypothetical protein b2737|
yjDL	-2.78	11.79	-1.48	12.53	0.1	11.06	0.2	0.00344394	0.00358698	0.02589621	0.46330582	A_07_P002137	b2738	cmr|putative epimerase/aldolase|b2738|
yjdM	+2.43	7.70	+1.28	7.06	0.4	8.34	0.1	0.00410088	0.01945349	0.04306306	0.51338636	A_07_P002141	b2739	cmr|orf, hypothetical protein b2739|
yjeC	-4.35	9.33	-2.12	10.39	0.1	8.27	0.2	0.00003412	0.00054193	0.00526613	0.23756647	A_07_P032628	c_3342	cmr|Hypothetical protein gcvT| c_3342|
yjeN	-2.12	9.27	-1.08	9.81	0.0	8.72	0.2	0.00179238	0.01009969	0.04150597	0.72022728	A_07_P002728	b2766	cmr|orf, hypothetical protein b2766|
yjeP	-2.07	10.29	-1.05	10.82	0.0	9.77	0.1	0.00150605	0.00882312	0.06657647	0.65185323	A_07_P002288	b2768	cmr|putative anti-terminator regulatory protein|b2768|
yjeR	-2.08	10.62	-1.06	11.15	0.1	10.09	0.1	0.00184658	0.01004442	0.06506827	0.64958771	A_07_P002320	b2770	cmr|putative transport protein|b2770|
yjeT	+2.12	8.02	+1.08	7.48	0.0	8.56	0.1	0.00096158	0.00634234	0.05556657	0.57707124	A_07_P002636	c_3352	cmr|Glucarate dehydratase related protein| c_3352|
yjgBM	+4.70	9.97	+2.23	8.65	0.1	11.09	0.0	0.00016575	0.00034847	0.01166413	0.29092683	A_07_P002424	b2795	cmr|orf, hypothetical protein b2795|
yjgEL	-2.94	10.72	-1.56	11.50	0.1	9.94	0.1	0.00014340	0.00156135	0.02110074	0.41787421	A_07_P002656	c_3383	cmr|Hypothetical protein gpdL| c_3383|
yjgEQ	-3.56	8.19	-1.36	8.87	0.1	7.52	0.1	0.00032985	0.00285964	0.03334159	0.55571291	A_07_P002641	b2812	cmr|putative transport protein|b2812|
yjgHM	-2.91	11.13	-1.54	11.90	0.2	10.36	0.2	0.00063174	0.00459849	0.02146087	0.42126676	A_07_P002657	b2855	cmr|putative 2-component transcriptional regulator|b2855|
yjgHR	-13.39	9.90	-3.74	11.77	0.0	8.03	0.1	0.00000503	0.00005021	0.00005272	0.02245243	A_07_P002665	b2861	cmr|putative lipoprotein|b2861|
yjgT	+3.04	8.06	+1.61	7.86	0.1	8.86	0.1	0.00012380	0.00139736	0.02628693	0.42622887	A_07_P002831	c_3445	cmr|Xanthine dehydrogenase, FAD binding subunit| c_3445|
yjfA	-3.30	9.36	-1.72	10.23	0.1	8.50	0.0	0.00006018	0.00084075	0.01455323	0.35657600	A_07_P002925	b2912	cmr|putative ligase|b2912|
yjfB	-2.41	13.56	-1.27	14.20	0.0	12.93	0.2	0.01007334	0.00686939	0.04178733	0.54909774	A_07_P006514	b2909	cmr|orf, hypothetical protein b2909|
yjfI	-2.04	7.10	-1.03	7.61	0.1	6.58	0.2	0.00019760	0.01188963	0.04933432	0.63775436	A_07_P006568	b2921	cmr|putative transcriptional regulator LYSR-type|b2921|
yjfJ	-2.18	9.42	-1.13	9.98	0.2	8.85	0.1	0.00178976	0.01012870	0.05716336	0.61642466	A_07_P006352	b2877	cmr|orf, hypothetical protein b2877|
yjfN	-3.06	11.23	-1.61	12.08	0.0	10.42	0.4	0.01129506	0.00787670	0.01888236	0.39573667	A_07_P006446	b2896	cmr|orf, hypothetical protein b2896|
yjfZ	-2.33	11.82	-1.22	11.21	0.1	12.42	0.0	0.00047815	0.00378674	0.04510607	0.52642698	A_07_P006456	b2898	cmr|orf, hypothetical protein b2898|
yjgB	-3.92	8.75	-1.55	10.00	0.0	8.98	0.1	0.00015984	0.00169918	0.02179306	0.42411619	A_07_P002921	c_3512	cmr|Hypothetical protein gpgB| c_3512|
yjgEL	+4.58	13.13	+2.19	12.10	0.0	14.22	0.0	0.00031609	0.00003993	0.01218941	0.29892523	A_07_P001938	b2959	cmr|orf, hypothetical protein b2959|
yjgP	-2.44	8.36	-1.29	8.90	0.1	7.61	0.1	0.00056879	0.00402231	0.03945430	0.53876843	A_07_P001806	b2932	cmr|orf, hypothetical protein b2932|
yjgX	-3.14	10.78	-1.65	9.96	0.1	11.61	0.0	0.00007686	0.00095965	0.02434616	0.41220302	A_07_P001954	b2962	cmr|orf, hypothetical protein b2962|
yjgW	-7.68	13.23	-2.94	12.70	0.0	9.76	0.1	0.00002296	0.00012541	0.00068534	0.08112782	A_07_P002180	b3009	cmr|orf, hypothetical protein b3009|
yjhU	+3.15	8.38	+1.65	7.65	0.1	9.10	0.1	0.00090045	0.00111579	0.02430088	0.41452027	A_07_P012078	b2989	cmr|orf, hypothetical protein b2989|
yjhU	+5.16	9.34	+2.37	7.96	0.1	10.33	0.1	0.00000952	0.00024416	0.00940485	0.26872958	A_07_P041281	c_3726	cmr|Hypothetical GST-like protein yghU| c_3726|
yjhZ	+4.59	9.86	+2.30	8.76	0.1	10.96	0.2	0.00002761	0.00068179	0.00235754	0.29746914	A_07_P012136	b3001	cmr|putative reductase|b3001|
yjiC	+3.23	8.66	+1.69	7.79	0.3	9.48	0.3	0.00386372	0.00585633	0.02392616	0.41124654	A_07_P012323	b3038	cmr|putative synthetase/amidase|b3038|
yjiE	-3.16	11.60	-1.66	12.43	0.0	10.77	0.2	0.00012346	0.00196525	0.01645178	0.37290627	A_07_P006003	b3054	cmr|orf, hypothetical protein b3054|
yjiF	-3.39	12.66	-1.76	13.54	0.0	11.78	0.2	0.00008984	0.00110941	0.01246166	0.33703448	A_07_P041286	c_3802	cmr|Hypothetical protein gpF| c_3802|
yjjN	+10.89	10.45	+4.44	8.72	0.1	12.17	0.2	0.00000242	0.00001169	0.00158488	0.06115227	A_07_P012178	b3029	cmr|orf, hypothetical protein b3029|
yjjP	-3.43	9.97	-1.78	10.86	0.0	9.08	0.1	0.00005246	0.00074042	0.01127734	0.33810051	A_07_P006891	c_3810	cmr|Hypothetical transcriptional regulator gpP| c_3810|
yjjW	-3.31	12.33	-1.73	13.19	0.0	11.47	0.3	0.00005182	0.00030256	0.01436039	0.36001592	A_07_P000906	b3074	cmr|putative tRNA synthetase|b3074|
yjjP	-5.77	9.20	-2.53	10.47	0.1	7.94	0.2	0.00001234	0.00028962	0.00191629	0.14504808	A_07_P000914	b3085	cmr|Hypothetical protein| b3085|
yjjP	-11.27	10.59	-3.49	12.34	0.0	8.84	0.3	0.00000329	0.00001224	0.00300304	0.03590909	A_07_P000904	c_3841	cmr|Hypothetical protein gpP| c_3841|
yjjQ	-3.67	8.06	-1.80	8.96	0.0	7.17	0.0	0.00004560	0.00008835	0.01186801	0.33607914	A_07_P041292	c_3844	cmr|Hypothetical protein gpQ| c_3844|
yjjQ	-2.89	8.20	-1.53	8.97	0.1	7.44	0.2	0.00134452	0.00713681	0.02182722	0.42483951	A_07_P000910	b3086	cmr|orf, hypothetical protein b3086|
yjjR	+5.69	9.31	+2.51	8.06	0.1	10.57	0.1	0.00000779	0.00021851	0.00777312	0.24623742	A_07_P000665	b3087	cmr|orf, hypothetical protein b3087|
yjjRV	+3.27	9.30	+1.71	8.44	0.1	10.16	0.1	0.00010188	0.00015332	0.02280410	0.40257559	A_07_P004047	c_3847	cmr|Hypothetical symporter| gpJ| c_3847|
yjraC	+2.23	9.36	+1.16	8.78	0.2	9.94	0.1	0.00166154	0.00813889	0.05092239	0.55797346	A_07_P004086	c_3893	cmr|D-galactarate dehydratase| c_3893|
yjraG	+4.21	9.45	+2.07	8.41	0.2	10.48	0.2	0.00007297	0.00095734	0.01442518	0.32444286	A_07_P004896	28480	cmr|putative hydrolase|28480|
yjraJ	+2.85	9.82	+1.54	9.06	0.1	10.58	0.1	0.00019419	0.00149894	0.02843479	0.44592760	A_07_P004054	b3105	cmr|putative transcriptional regulator LYSR-type|b3105|
yjraK	+7.05	11.56	+2.82	10.15	0.1	12.98	0.1	0.00000375	0.00014386	0.00445549	0.19002740	A_07_P004064	b3107	cmr|putative synthetase/amidase|b3108|
yjraL	-2.56	13.50	-1.38	14.18	0.0	12.81	0.1	0.00002482	0.00282608	0.02268723	0.50553045	A_07_P000572	b3170	cmr|orf, hypothetical protein b3170|
yjraZ	+2.64	8.07	+1.40	7.37	0.1	8.77	0.1	0.00019574	0.00198408	0.03458779	0.47311034	A_07_P000878	b3153	cmr|orf, hypothetical protein b3153|
yjtBU	+2.02	10.72	+1.01	10.22	0.2	11.22	0.3	0.00291855	0.01485119	0.06362741	0.61344152	A_07_P000511	b3158	cmr|putative collagenase|b3158|
yjtMW	-2.30	8.41	-1.14	7.85	0.4	8.98	0.1	0.00268049	0.02827779	0.05248349	0.56441257	A_07_P004111	c_3913	cmr|Hypothetical protein gpM| c_3913|
yjtbY	+2.06	11.28	+1.04	10.76	0.1	11.80	0.1	0.01177987	0.01008723	0.06052464	0.59968534	A_07_P000614	b3180	cmr|orf, hypothetical protein b3180|
yjtcB	+5.72	12.66	+2.52	11.60	0.0	13.72	0.0	0.00008564	0.00022344	0.00472066	0.24601172	A_07_P012640	b3233	cmr|orf, hypothetical protein b3233|
yjtcH	+2.03	7.75	+1.02	7.24	0.1	8.26	0.1	0.01144884	0.00813689	0.06117569	0.60272215	A_07_P012577	b3221	cmr|orf, hypothetical protein b3221|
yjtcH	-5.77	8.32	-2.53	7.66	0.0	8.99	0.0	0.00000705	0.00020411	0.00748031	0.14288609	A_07_P004165	c_3975	cmr|Hypothetical protein gHcH| c_3975|
yjtcH	+3.63	8.24	+1.86	7.31	0.3	9.17	0.1	0.00018148	0.00184421	0.01858831	0.35645554	A_07_P045957	24579	cmr|orf, hypothetical protein| 24579|
yjtcI	-3.82	7.99	-1.93	8.92	0.1	6.95	0.2	0.00018320	0.00187642	0.01731136	0.34746631	A_07_P053815	24580	cmr|putative NAGC-like transcriptional regulator| 24580|
yjtcJ	-6.45	8.72	-2.69	7.38	0.2	10.06	0.1	0.00001090	0.00026728	0.00634710	0.12559441	A_07_P041791	c_3977	cmr|Hypothetical protein gHcJ| c_3977|
yjtcJ	-7.53	8.68	-2.91	7.23	0.1	10.13	0.2	0.00000586	0.00018329	0.00430639	0.08926413	A_07_P041304	c_3977	cmr|Hypothetical protein gHcJ| c_3977|
yjtcK	-2.32	9.62	-1.21	10.22	0.0	9.01	0.0	0.00047031	0.00374156	0.04714876	0.57546411	A_07_P034168	c_3980	cmr|Hypothetical transcriptional regulator| chvI| c_3980|
yjtcX	-3.19	7.57	-1.67	8.41	0.1	6.74	0.0	0.00010051	0.00120434	0.01384858	0.37489295	A_07_P035544	c_3997	cmr|Hypothetical protein gHcX| c_3997|
yjtcX	-3.84	8.30	-1.94	9.27	0.0	7.33	0.2	0.00008636	0.00018170	0.00759645	0.23784410	A_07_P048607	24601	cmr|Hypothetical protein| 24601|
yjtdE	+1.07	9.30	+1.42	8.49	0.2	10.11	0.1	0.00029213	0.00263163	0.02765197	0.42476440	A_07_P012715	b3248	cmr|orf, hypothetical protein b3248|
yjtdH	-10.26	10.25	-4.44	8.51	0.1	11.99	0.3	0.00000551	0.00017942	0.00208858	0.13376018	A_07_P014191	c_4009	cmr|Protein yjtdH| c_4009|
yjtdH	+6.04	8.75	+2.60	7.45	0.2	10.05	0.2	0.00302027	0.00019679	0.00690106	0.23826754	A_07_P012736	b3253	cmr|putative dehydrogenase| b3253|
yjtdZ	+3.05	8.20	+1.61	7.39	0.1	9.00	0.1	0.00014231	0.00155599	0.02421824	0.42642562	A_07_P012823	b3271	cmr|putative ATP-binding component of a transport system| b3271|
yjtef	-3.82	8.08	-1.93	9.04	0.1	7.11	0.0	0.00003602	0.00058156	0.00831143	0.29676471	A_07_P034126	c_4096	cmr|Probable general secretion pathway protein D precursor| c_4096|
yjtefM	-2.63	8.11	-1.39	8.81	0.1	7.41	0.4	0.02216679	0.01253730	0.03210282	0.44349162	A_07_P017750	b3344	cmr|orf, hypothetical protein b3344|
yjtehN	-3.00	9.35	-1.58	9.84	0.1	8.86	0.3	0.00063041	0.00459501	0.02014799	0.40824968	A_07_P052135	24703	cmr|orf, hypothetical protein| 24703|
yjtehT	-2.67	10.41	-1.42	11.12	0.3	9.70	0.1	0.00116683	0.00754146	0.02880556	0.48079031	A_07_P017533	b3345	cmr|orf, hypothetical protein b3345|
yjtehO	-2.54	10.40	-1.35	11.08	0.0	9.73	0.3	0.00051564	0.00387371	0.01548082	0.51532288	A_07_P017560	b3346	cmr|orf, hypothetical protein b3346|
yjtes5	-2.36	11.16	-1.24	11.78	0.1	10.54	0.1	0.00066605	0.00073344	0.04400221	0.56228896	A_07_P017766	b3352	cmr|putative ATP-binding component of a transport system| b3352|
yjtfC	-5.14	8.31	-2.36	9.49	0.1	7.13	0.2	0.00001588	0.00031838	0.00277691	0.17418327	A_07_P048329	c_4139	cmr|Hypothetical protein gfvC| c_4139|
yjtfL	-2.06	7.66	-1.04	8.18	0.0	7.14	0.2	0.00176446	0.01001419	0.04604370	0.65541812	A_07_P017874	b3369	cmr|orf, hypothetical protein b3369|
yjtfS	-3.18	10.78	-1.67	11.61	0.0	9.94	0.2	0.00019381	0.00195589	0.01635861	0.37653509	A_07_P017907	b3376	cmr|orf, hypothetical protein b3376|
yjtfS	-2.61	8.36	-1.39	8.95	0.2	7.57	0.3	0.00186914	0.01046583	0.03882047	0.49447543	A_07_P034275	c_4146	cmr|Hypothetical protein gfvS| c_4146|
yjtfU	-2.67	8.83	-1.42	9.54	0.2	8.13	0.1	0.00055148	0.00417027	0.02929300	0.48149919	A_07_P017919	b3378	cmr|orf, hypothetical protein b3378|
yjtfZ	-2.35	8.25	-1.23	7.63	0.1	8.86	0.0	0.00060105	0.00103378	0.04439877	0.52166418	A_07_P017944	b3383	cmr|orf, hypothetical protein b3383|
yjtgF	-2.54	10.18	-1.34	9.50	0.0	10.85	0.0	0.00025771	0.00239798	0.03757812	0.48693827	A_07_P018065	b3407	cmr|orf, hypothetical protein b3407|
yjtgH	-2.05	7.72	-1.03	7.21	0.0	8.24	0.3	0.00147936	0.00632734	0.01779942	0.36602774	A_07_P041831	c_4190	cmr|Hypothetical protein gfvH| c_4190|
yjtgM	-2.17	11.71	-1.24	11.09	0.0	12.34	0.2	0.00078806	0.00562276	0.04240885	0.51735693	A_07_P041315	c_4196	cmr|Hypothetical protein gfvM| c_4196|
yjtmA	+2.17	8.68	+1.12	8.12	0.1	9.23	0.1	0.00114041	0.00715494	0.05328235	0.56881436	A_07_P018259	b3448	cmr|orf, hypothetical protein b3448|
yjtnU	-2.56	11.06	-1.56	11.88	0.5	10.28	0.1	0.00361266	0.01756570	0.06205425	0.41126437	A_07_P018368	b3484	cmr|putative receptor| b3484|
yjtq3	-2.63	8.03	-1.40	7.33	0.2	8.72	0.1	0.00052981	0.00404719	0.03531992	0.47746781	A_07_P007361	b3485	cmr|putative transporter| b3485|
yjtsM	-2.33	7.64	-1.22	7.03	0.2	8.25	0.0	0.00114669	0.00718839	0.04396608	0.52940015	A_07_P007271	b3467	cmr|putative receptor| b3467|
yjtsM	-2.60	8.01	-1.38	7.32	0.0	8.70	0.0	0.00021526	0.00211288	0.03549289	0.47719898	A_07_P007271	b3467	cmr|putative receptor| b3467|
yjtsM	-2.05	8.20	-1.03	7.68	0.2	8.72	0.0	0.00216176	0.01174434	0.06089050	0.60179515	A_07_P007271	b3467	cmr|putative receptor| b3467|
yjtsS	-2.43	8.26	-1.28	8.90	0.1	7.62	0.3	0.01187110	0.01047078	0.04102229	0.54475949	A_07_P007303	b3473	cmr|putative transport| b3473|
yjtsU	-2.64	10.36	-1.40	11.06	0.1	9.66	0.3	0.00115052	0.00722808	0.03103944	0.49431912	A_07_P041853	c_4208	cmr|4-phosphopantothenoyl-L-cysteine synthetase ycsP| c_4208|
yjtsW	-2.19	8.97	-1.13	8.40	0.0	9.54	0.1	0.00087296	0.00591391	0.05115917	0.55895212	A_07_P018221	b3439	cmr|orf, hypothetical protein b3439|
yjtsX	-2.42	9.49	-1.28	8.86	0.0	10.13	0.0	0.00168648	0.01088886	0.03190041	0.50501235	A_07_P018230	b3440	cmr|putative regulator| b3440|
yjtsZ	-2.67	14.44	-1.42	14.86	0.0	13.99	0.0	0.00486859	0.00467558	0.02001486	0.48304700	A_07_P007675	b3508	cmr|putative transport ATPase| b3508|
yjtsI	-2.13	11.22	-1.34	10.55	0.0	11.88	0.2	0.00035135	0.00405508	0.03822663	0.48773475	A_07_P007574	b3487	cmr|putative membrane protein| b3487|
yjtsN	-3.78	10.80	-1.92	11.76	0.1	9.84	0.1	0.00004550	0.00068746	0.00882277	0.30230435	A_07_P007396	b3492	cmr|orf, hypothetical protein b3492|
yjtsP	-14.24	10.31	-1.69	9.46	0.0	11.15	0.0	0.00002620	0.00084499	0.01207722	0.40603679	A_07_P007419	b3496	cmr|putative transport protein| b3496|
yjtsQ	-2.24	8.06	-1.16	8.65	0.1	7.47	0.1	0.00242425	0.00615538	0.05194995	0.59182344	A_07_P007422	b3497	cmr|orf, hypothetical protein b3497|
yjtsR	-5.29	12.37	-2.40	13.57	0.1	11.17	0.4	0.00009479	0.00026791	0.00242576	0.17153527	A_07_P007519	b3499	cmr|orf, hypothetical protein b3499|
yjtsW	-2.32	8.78	-1.21	9.39	0.0	8.17	0.3	0.00267158	0.01381689	0.04559007	0.56875594	A_07_P039549	c_4326	cmr|Hypothetical transcriptional regulator yhiW| c_4326|
yjtU	-2.98	9.15	-1.57	9.73	0.0	8.56	0.1	0.00124357	0.00849499	0.04112204	0.49149426	A_07_P018268	24841	cmr|orf, hypothetical protein| 24841|
yjtU	-2.75	9.92	-1.46	10.45	0.0	9.19	0.1	0.00022055	0.00214748	0.02689969	0.47179600	A_07_P039556	c_4339	cmr|Protein yhjU precursor| c_4339|
yjtQ	-1.69	8.59	-2.51	9.85	0.1	7.34	0.2	0.00082601	0.00266542	0.00201410	0.14680556	A_07_P007604	b3534	cmr|orf, hypothetical protein b3534|
yjtqR	-2.32	8.77	-1.21	9.38	0.0	8.17	0.0	0.00154545	0.00813575	0.04107729	0.56835322	A_07_P007606	b3535	cmr|orf, hypothetical protein b3535|
yjtsC	-3.20	9.97	-1.68	10.80	0.1	9.13	0.4	0.00105621	0.00679733	0.01623984	0.37710914	A_07_P007676	b3550	cmr|orf, hypothetical protein b3550|
yjtsC	-3.51	9.37	-1.33	10.03	0.1	8.70	0.0	0.00043904	0.00316045	0.01607722	0.51573137	A_07_P018272	c_4348	cmr|Hypothetical acetyltransferase gacC| c_4348|
yjtsF	-2.16	10.20	-1.11	9.65	0.0	10.76	0.1	0.00007766	0.00642954	0.05331110	0.56903729	A_07_P007698	b3554	cmr|orf, hypothetical protein b3554|
yjtsK	-3.97	8.68	-1.99	7.69	0.0	9.68	0.2	0.00026448	0.00067660	0.01417696	0.34232527	A_07_P007803	b3575	cmr|putative dehydrogenase| b3575|
yjtsL	-12.50	7.72	-1.07	7.19	0.2	8.26	0.1	0.00257134	0.01364214	0.05624275	0.58344241	A_07_P039647	c_4397	cmr|Hypothetical protein gfvL| c_4397|
yjtsMN	-3.22	7.26	-1.69	6.41	0.0	8.10	0.1	0.00007204	0.00005356	0.00241306	0.60921111	A_07_P039665	c_4400	cmr|Hypothetical protein gfvMN| c_4400|
yjtsR	-2.35	10.04	-1.24	10.66	0.0	9.42	0.3	0.00168978	0.00967148	0.04155589	0.56876000	A_07_P018913	b3594	cmr|orf, hypothetical protein| b3594|
yjtsF	-4.39	8.56	-2.13	7.49	0.0	9.63	0.1	0.00002407	0.00038627	0.01138061	0.32423163	A_07_P018805	b3592	cmr|orf, hypothetical protein b3592|
yjtU	-2.10	9.38	-1.07	8.85	0.0	9.91	0.0	0.00000188	0.00065770	0.05435417	0.58237848	A_07_P018974	b3606	cmr|orf, hypothetical protein b3606|
yjtT	-2.18	9.55	-1.13	8.98	0.1	10.11	0.1	0.00102065	0.00642100	0.05238604	0.56439465	A_07_P018559	asap|predicted protein| b4554|	
yicL	-2.59	8.46	-1.37	7.75	0.4	9.13	0.3	0.02134008	0.01328788	0.03769309	0.48682527	A_07_P041337	c_4582	cmr|Hypothetical transport protein yicL| c_4582|
yicL	-2.54	8.72	-1.34	8.06	0.2	9.38	0.1	0.00001118	0.00242251	0.04842521	0.48682562	A_07_P042211	c_4586	cmr|putative permease transporter| 25146|
yicL	+2.26	8.46	+1.18	7.87	0.0	9.05	0.1	0.00055518	0.00419421	0.04797829	0.54424570	A_07_P017240	b3660	cmr|putative permease transporter| b3660|
yidC	-2.12	12.75	-1.08	12.28	0.1	13.21	0.1	0.00276964	0.00363445	0.06436286	0.63153340	A_07_P007451	b3705	c

ynaK	-5.94	8.79	-2.57	10.08	0.3	7.50	0.2	0.00030212	0.00054058	0.00165667	0.13166667	A_07_P014801	b1365	cmr|rorf, hypothetical protein |b1365|
ynbE	-2.90	7.87	+1.54	7.10	0.0	8.64	0.1	0.00031928	0.00191511	0.02856787	0.43078024	A_07_P014809	c_1829	cmr|Hypothetical protein ybdZ |c_1829|
ynbE	-3.13	8.55	-1.65	9.37	0.7	7.73	0.2	0.00873328	0.03525507	0.06169172	0.37696084	A_07_P048215	2327	cmr|rorf, hypothetical protein |2327|
ynci	-2.05	8.62	-1.03	9.13	0.1	8.10	0.0	0.00136874	0.00839926	0.06690493	0.65895572	A_07_P009272	b1436	cmr|rorf, hypothetical protein |b1436|
ynerl	-4.68	9.89	-2.23	11.00	0.1	8.78	0.4	0.00031745	0.00278588	0.00410354	0.21575949	A_07_P020270	b1524	cmr|putative glutaminase |b1524|
ynei	-3.23	9.25	-1.69	10.09	0.0	8.40	0.4	0.00070128	0.00493783	0.01763178	0.37128019	A_07_P035026	c_1948	cmr|Aldehyde-dehydrogenase like protein ynei |c_1948|
ynei	-2.16	11.39	-1.11	11.94	0.0	10.83	0.1	0.00093152	0.00618762	0.05808053	0.62346801	A_07_P020279	b1526	cmr|putative transcriptional regulator LYSR-type |b1526|
ynfB	-5.24	13.95	-2.39	15.14	0.0	12.75	0.0	0.00000770	0.00021737	0.00266959	0.17016194	A_07_P020550	b1583	cmr|rorf, hypothetical protein |b1583|
ynfE	-5.41	8.10	-2.44	8.88	0.3	9.31	0.2	0.00007463	0.00097312	0.00875205	0.25992653	A_07_P020568	b1587	cmr|putative oxidoreductase, major subunit |b1587|
ynfE	-7.04	8.66	-2.82	7.25	0.0	10.07	0.1	0.00000139	0.00013496	0.00056606	0.20716883	A_07_P042931	c_1977	cmr|Putative dimethyl sulfoxide reductase chain ynfE precursor |c_1977|
ynfF	-13.70	9.48	-4.99	8.54	0.3	10.42	0.1	0.00016648	0.00185614	0.01825775	0.35111268	A_07_P020575	b1588	cmr|putative oxidoreductase, major subunit |b1588|
ynfG	-11.05	9.05	-3.47	7.30	0.3	10.79	0.0	0.00000387	0.00009141	0.00240840	0.13163265	A_07_P020576	b1589	cmr|putative oxidoreductase, Fe-S subunit |b1589|
ynfH	-2.17	8.75	-1.12	8.19	0.2	9.31	0.1	0.00168433	0.01088886	0.05466564	0.56936455	A_07_P020582	b1593	cmr|putative DMSO reductase anchor subunit |b1593|
ynfL	-2.61	10.97	-1.39	11.67	0.2	10.28	0.1	0.00368132	0.00840060	0.03175522	0.49847458	A_07_P020609	b1595	cmr|putative transcriptional regulator LYSR-type |b1595|
ynfM	-4.13	11.47	-2.05	12.49	0.4	10.45	0.3	0.00046089	0.00516408	0.00468509	0.26379446	A_07_P020616	b1596	cmr|putative transport protein |b1596|
ynIA	-9.58	9.05	-3.26	7.42	0.0	10.68	0.1	0.00000135	0.00008589	0.00270599	0.15391608	A_07_P018674	b1725	cmr|rorf, hypothetical protein |b1725|
ynJA	-4.25	8.48	-1.17	7.90	0.1	9.06	0.1	0.00094706	0.00624493	0.04924223	0.55238661	A_07_P018811	b1753	cmr|rorf, hypothetical protein |b1753|
ynjB	-3.69	8.05	+1.88	7.10	0.0	8.99	0.1	0.00003509	0.00057133	0.01692927	0.35137805	A_07_P018816	b1754	cmr|rorf, hypothetical protein |b1754|
ynjE	-6.17	9.42	-2.63	8.11	0.4	10.73	0.1	0.00005533	0.00078934	0.00664380	0.21348214	A_07_P018817	b1757	cmr|putative thiosulfate sulfur transferase |b1757|
ynjH	-8.04	9.53	+3.01	8.03	0.0	11.04	0.0	0.00000168	0.00009954	0.00390117	0.18064706	A_07_P015736	b1809	cmr|rorf, hypothetical protein |b1809|
ynlB	-2.69	8.75	-1.43	8.04	0.1	9.46	0.1	0.00021968	0.00314334	0.03109431	0.46775801	A_07_P015953	b1843	cmr|rorf, hypothetical protein |b1843|
ynhF	-2.08	9.86	-1.05	10.39	0.0	9.33	0.1	0.00113773	0.00715066	0.06670795	0.64953383	A_07_P003448	b2137	cmr|putative oxidoreductase |b2137|
ynHG	-5.70	9.88	-2.51	11.14	0.0	8.62	0.1	0.00000778	0.00021851	0.00280581	0.14688372	A_07_P042601	c_2991	cmr|Hypothetical protein ypFG precursor |c_2991|
ynfG	-3.32	9.65	-1.73	10.51	0.1	8.78	0.1	0.00007107	0.00094588	0.00184615	0.35364228	A_07_P020581	b2466	cmr|rorf, hypothetical protein |b2466|
ynfE	-5.40	12.61	-2.43	13.82	0.0	11.39	0.3	0.00005361	0.00077607	0.00252858	0.16940426	A_07_P019639	b2547	cmr|putative ATP-binding component of a transport system |b2547|
ynfF	-2.01	8.03	-1.09	8.53	0.2	7.53	0.1	0.00432552	0.02029232	0.07446304	0.67577918	A_07_P019645	b2548	cmr|putative LACI-type transcriptional regulator |b2548|
ynaA	-3.84	9.82	-1.94	10.79	0.1	8.85	0.2	0.00007240	0.00095580	0.00832444	0.29718821	A_07_P001920	b2689	cmr|rorf, hypothetical protein |b2689|
ynaB	-7.67	11.18	-2.94	12.44	0.0	9.71	0.0	0.00000231	0.00011009	0.00027962	0.08167939	A_07_P030582	c_2247	cmr|Hypothetical protein ypaB |c_2247|
ynaF	-4.93	11.00	-2.30	12.15	0.0	9.84	0.2	0.00003681	0.00059023	0.00330158	0.19251852	A_07_P001923	b2690	cmr|putative phosphatase |b2690|
ynaA	-4.38	9.75	-2.13	8.68	0.1	10.81	0.0	0.00001302	0.00003041	0.01138605	0.31101007	A_07_P002396	b2790	cmr|rorf, hypothetical protein |b2790|
ynaP	-2.49	8.58	-1.22	9.24	0.2	7.92	0.0	0.00060986	0.00467491	0.03609485	0.52488602	A_07_P006342	b2875	cmr|putative synthase |b2875|
ynaC	-2.81	8.62	-1.49	9.37	0.2	7.88	0.3	0.00132760	0.00882315	0.02499682	0.45456769	A_07_P006347	b2876	cmr|rorf, hypothetical protein |b2876|
ynfA	-2.64	9.63	-1.40	8.93	0.1	10.33	0.1	0.00028109	0.00256847	0.03491512	0.47512768	A_07_P006461	b2899	cmr|putative oxidoreductase |b2899|
ynfB	-2.15	7.64	-1.23	7.03	0.1	8.26	0.0	0.00438310	0.00157125	0.02429291	0.12173034	A_07_P006468	b2938	cmr|putative ATP-binding component |b2938|
ynfB	+2.53	7.62	-1.34	6.95	0.1	8.29	0.0	0.00037361	0.00315126	0.03790523	0.48795536	A_07_P006548	b2238	cmr|rorf, hypothetical protein |b2238|
ynfB	-1.68	10.14	-1.42	9.43	0.1	10.86	0.0	0.00022144	0.00206317	0.01035932	0.46843338	A_07_P006568	b2900	cmr|rorf, hypothetical protein |b2900|
ynfB	+2.54	10.45	+1.34	9.78	0.1	11.12	0.1	0.00032480	0.00282698	0.03754993	0.48677924	A_07_P032874	c_3481	cmr|Hypothetical protein ypFB |c_3481|
ynfS	-2.81	12.58	-1.50	13.33	0.2	11.83	0.1	0.00002507	0.00016126	0.00149135	0.14873672	A_07_P006593	b2915	cmr|rorf, hypothetical protein |b2915|
yngE	-3.20	10.60	-1.68	9.76	0.1	11.43	0.2	0.00016307	0.00172651	0.02288275	0.41138950	A_07_P013885	b2948	cmr|rorf, hypothetical protein |b2948|
ynfH	-2.81	8.99	-1.49	9.74	0.0	8.25	0.0	0.00013718	0.00154157	0.02494411	0.45559165	A_07_P012144	b3002	cmr|rorf, hypothetical protein |b3002|
ynfH	+3.58	10.55	+1.84	9.63	0.2	11.47	0.2	0.00013502	0.00149807	0.01954522	0.36720764	A_07_P012186	b3011	cmr|putative oxidoreductase |b3011|
ynjK	-2.07	7.56	-1.05	8.06	0.1	7.03	0.2	0.00388188	0.01854264	0.06594446	0.64890071	A_07_P016874	c_3799	cmr|Hypothetical protein ypJK |c_3799|
ynjA	-8.36	11.31	-3.06	12.84	0.0	9.78	0.1	0.00000204	0.00010341	0.00462371	0.09674476	A_07_P000202	b3095	cmr|rorf, hypothetical protein |b3095|
ynjA	-8.51	10.95	-3.25	12.57	0.0	9.32	0.1	0.00000176	0.00009825	0.00204771	0.05200000	A_07_P041768	c_3853	cmr|Hypothetical protein ypJA |c_3853|
ynjB	-3.12	10.57	-1.64	11.39	0.1	9.74	0.1	0.00019576	0.00196808	0.01896669	0.37948645	A_07_P000208	b3096	cmr|rorf, hypothetical protein |b3096|
ynjC	+2.75	10.35	+1.46	9.62	0.1	11.08	0.6	0.00037661	0.00315126	0.03399391	0.47037852	A_07_P000212	b3097	cmr|rorf, hypothetical protein |b3097|
ynjF	+3.19	11.25	+1.67	10.42	0.1	12.09	0.1	0.00011083	0.00129056	0.02422574	0.41233514	A_07_P000873	b3271	cmr|rorf, hypothetical protein |b3271|
ynxP	+4.35	10.29	+2.12	9.23	0.0	11.35	0.1	0.00002506	0.00045582	0.01343412	0.31381306	A_07_P000475	b3150	cmr|putative periplasmic protein |b3150|
ynfxA	+2.12	10.14	+1.21	9.53	0.1	10.74	0.2	0.00105497	0.00675214	0.04403582	0.51022375	A_07_P012426	b3160	cmr|rorf, hypothetical protein |b3160|
ynfB	+2.05	8.65	+1.04	8.13	0.2	9.16	0.0	0.00242470	0.01303067	0.06900147	0.60147870	A_07_P035537	c_3950	cmr|Hypothetical protein ypfB |c_3950|
ynfJD	-2.75	11.07	-1.46	11.80	0.0	10.34	0.2	0.00032624	0.00283779	0.02836290	0.47916667	A_07_P012441	b3193	cmr|rorf, hypothetical protein |b3193|
ynfbE	-6.02	10.95	-2.01	11.95	0.1	9.94	0.0	0.00007013	0.00093648	0.00676606	0.26356839	A_07_P012449	b3194	cmr|rorf, hypothetical protein |b3194|
ynfxF	-2.85	10.97	-1.51	11.73	0.2	10.20	0.1	0.00028212	0.00257640	0.02386760	0.47236010	A_07_P012451	b3195	cmr|putative ATP-binding component of a transport system |b3195|
ynfbE	+2.22	12.38	+1.15	11.81	0.0	12.96	0.2	0.00110334	0.00802484	0.05828325	0.55804742	A_07_P012474	b3199	cmr|rorf, hypothetical protein |b3199|
ynfbL	-11.73	9.55	-3.89	8.61	0.3	10.50	0.1	0.00002428	0.00020171	0.01793761	0.35257179	A_07_P012510	26570	cmr|rorf, hypothetical protein |26570|
ynfbL	-13.87	10.22	-1.95	9.25	0.0	11.20	0.1	0.00002925	0.00050543	0.01602962	0.34615584	A_07_P012512	b3207	cmr|rorf, hypothetical protein |b3207|
ynfxN	-2.29	8.70	-1.29	8.10	0.2	9.29	0.2	0.00206648	0.01466316	0.04869139	0.54720749	A_07_P000501	c_4040	cmr|Protein ynfx |c_4040|
ynfxN	-2.94	8.91	+1.16	8.32	0.3	9.49	0.0	0.00392623	0.01872602	0.05047193	0.55802669	A_07_P000249	c_4040	cmr|Protein ynfx |c_4040|
ynfxN	-2.00	8.70	+1.00	8.20	0.1	9.20	0.2	0.00225365	0.01770167	0.06556593	0.62751976	A_07_P000249	c_4040	cmr|Protein ynfx |c_4040|
ynfD	-2.45	9.03	-1.29	8.38	0.0	9.68	0.2	0.00084821	0.00577854	0.04068153	0.50165588	A_07_P012850	b3283	cmr|putative DNA topoisomerase |b3283|
ynfQ	+2.13	7.97	+1.09	7.42	0.1	8.51	0.1	0.00132608	0.00819026	0.05431663	0.57087783	A_07_P004394	c_4165	cmr|Hypothetical protein ynfQ |c_4165|
ynfT	-3.86	9.61	-1.95	10.59	0.0	8.64	0.0	0.00002804	0.00069142	0.00794164	0.28742529	A_07_P004400	c_4169	cmr|Putative membrane protein ypn homolog |c_4169|
ynfF	-2.75	9.03	-1.46	9.76	0.0	8.30	0.3	0.00075474	0.00524629	0.02600387	0.46518729	A_07_P018019	b3398	cmr|putative dehydrogenase |b3398|
ynfH	-2.94	10.46	-1.56	11.27	0.2	9.70	0.2	0.00028399	0.00208898	0.02130907	0.41988736	A_07_P018611	b4212	cmr|rorf, hypothetical protein |b4212|
ynfI	-2.68	10.23	-1.42	10.94	0.0	9.51	0.0	0.00022308	0.00162406	0.02850356	0.47791267	A_07_P015591	c_5311	cmr|rorf, hypothetical protein |c_5311|
ynfJ	+2.07	8.55	+1.05	8.03	0.4	9.08	0.1	0.00864795	0.03563425	0.06250581	0.66577757	A_07_P015596	c_5315	cmr|Hypothetical protein ynfJ |c_5315|
ynfL	-2.12	9.05	-1.08	9.59	0.1	8.50	0.1	0.00109334	0.00695496	0.06216845	0.63805737	A_07_P003641	b4218	cmr|putative transport protein |b4218|
ynfQ	+6.65	9.69	+2.73	8.32	0.1	11.05	0.1	0.00000862	0.00023008	0.00570275	0.21875912	A_07_P037048	c_5325	cmr|ABC transporter Periplasmic binding protein ynfQ precursor |c_5325|
ynfQ	+2.23	8.18	+1.16	7.57	0.0	8.73	0.1	0.00088123	0.00644763	0.06948469	0.55379977	A_07_P003689	b4227	cmr|putative LACI-type transcriptional regulator |b4227|
20024	-2.28	8.23	-1.19	8.83	0.3	7.64	0.0	0.02236368	0.01258499	0.04972561	0.59154974	A_07_P018284	20024	cmr|putative type-1 fimbrial protein |20024|
20056	-2.61	12.05	-1.27	12.69	0.1	11.41	0.1	0.00040851	0.00107771	0.04609931	0.54394737	A_07_P049148	20056	cmr|putative antisoem of gyrase inhibiting toxin-antitoxin system |20056|
20202	-2.54	11.07	-1.51	11.73	0.2	10.39	0.1	0.00028212	0.00257640	0.01498304	0.51197151	A_07_P049248	20202	cmr|rorf, unknown function |20202|
20255	-2.22	9.78	-1.15	10.36	0.3	9.21	0.1	0.00024937	0.00199969	0.05366171	0.60260342	A_07_P049311	20255	cmr|rorf, unknown function |20255|
20259	-2.01	9.48	-1.01	9.98	0.1	8.97	0.0	0.00169218	0.00667732	0.07331410	0.67480834	A_07_P049313	20259	cmr|rorf, unknown function |20259|
20268	-2.09	10.26	-1.07	10.80	0.0	9.73	0.0	0.00100347	0.00654457	0.06438803	0.64833333	A_07_P049319	20268	cmr|rorf, unknown function |20268|
20269	-3.79	12.60	-1.56	13.56	0.0	11.64	0.3	0.00012837	0.00143849	0.04678811	0.30408791	A_07_P049395	20269	cmr|putative cl repressor protein for prophage CP-933N |20269|
20310	-2.50	7.91	-1.04	7.09	0.1	8.14	0.2	0.00287248	0.05349959	0.15913856	A_07_P049398	20310	cmr|putative cII antiterminator protein for prophage CP-933H |20310|
20311	-5.59	13.22	-2.48	11.97	0.0	14.46	0.4	0.00007141	0.00064797	0.00822218	0.25087097	A_07_P049403	20311	cmr|putative O-replication protein for prophage CP-933H |20311|
20325	-3.25	11.11	-1.70	11.96	0.0	10.26	0.5	0.00157397	0.00914077	0.01152139	0.37167951	A_07_P049462	20325	cmr|unknown protein encoded in prophage CP-933I |20325|
20332	-2.37	8.21	-1.24	9.83	0.1	8.59	0.1	0.00038632	0.00404342	0.04401232	0.55198703	A_07_P049492	20332	cmr|putative activator encoded in prophage CP-933I |20332|
20370	+3.72	8.51	+1.89	7.56	0.2	9.46	0.2	0.00013958	0.00153034	0.01790206	0.35275344	A_07_P049596	20370	cmr|rorf, unknown function |20370|
20374	+2.39	7.56	+1.26	6.93	0.0	8.19	0.2	0.00084085	0.00573833	0.04285442	0.51268997	A_07_P049615	20374	cmr|rorf, unknown function |20374|
20377	-2.03	7.83	-1.02	7.32	0.1	8.34	0.2	0.00243818	0.01287715	0.06310150	0.60949080	A_07_P049620	20377	cmr|putative dehydrogenase |20377|
20393	-2.45	9.42	-1.29	9.84	0.4	7.77	0.1	0.00176644	0.01002075	0.03807755	0.52809524	A_07_P049660	20393	cmr|rorf, unknown function |20393|
20397	-2.14	10.08	-1.10	10.62	0.0	9.53	0.3	0.00741341	0.03101693	0.05947599	0.62670707	A_07_P049675	20397	cmr|rorf, unknown function |20397|
20476	-3.10	12.25	-1.63	13.07	0.3	11.43	0.2	0.00063848	0.00462381	0.01786531	0.38636364	A_07_P049504	20476	cmr|rorf, unknown function |20476|
20491	-2.19	10.47	-1.13	11.03	0.1	9.91	0.1	0.00267438	0.01381663	0.05665206	0.61551414	A_07_P049917	20491	cmr|rorf, unknown function |20491|
20666	+2.58	7.50	+1.36	6.81	0.0	8.18	0.2	0.00057658	0.00420688	0.03688318	0.48451342	A_07_P049951	20666	cmr|rorf, unknown function |20666|
20949	+11.72	10.84	+3.55	9.07	0.3	12.62	0.2	0.00000645	0.00015912	0.00177551	0.12538117	A_07_P049386	20949	cmr|unknown protein encoded by prophage CP-933K |20949|
20950	+35.48	9.98	+4.67	7.65	0.1	12.32	0.2	0.00000026	0.00004211	0.00022802	0.04174419	A_07_P049393	20950	cmr|unknown protein encoded by prophage CP-933K |20950|
20951	+4.97	13.10	+2.31	11.94	0.1	14.26	0.3	0.00007774	0.00028138	0.00280155	0.28005197	A_07_P049394	20951	cmr|putative exonuclease encoded by prophage CP-933K |20951|
20952	+1.94	12.52	+1.98	11.53	0.1	13.51	0.3	0.00023106	0.00221327	0.01566184	0.33798082	A_07_P049403	20952	cmr|putative Bet recombination protein of prophage CP-933K |20952|
20960	-16.27	10.09	+4.72	7.71	0.1	12.45	0.1	0.00000016	0.00003548	0.00020108	0.03975000	A_07_P049405	20960	cmr|putative lysozyme protein 9 of prophage CP-933K |20960|
20964	-3.26	8.67	-1.18	9.26	0.0	8.08	0.1	0.00068334	0.00484533	0.05022203	0.58643227	A_07_P049446	20964	cmr|putative DNA packaging protein of prophage CP-933K |20964|
20965	-2.52	9.76	-1.33	10.43	0.1	9.09	0.4	0.00239166	0.01286874	0.02869477	0.51796545	A_07_P049451	20965	cmr|putative head-tail connector protein of prophage CP-933K |20965|
20966	-2.48	8.26	-1.31	8.92	0.1	7.61	0.0	0.00032291	0.00281814	0.03723831	0.52134050	A_07_P049460	20966	cmr|unknown protein encoded by prophage CP-933K |20966|
20966	-2.72	8.23	-1.44	8.96	0.0	7.51	0.1	0.00002425	0.00028874	0.01788674	0.47328004	A_07_P049460	20966	cmr|unknown protein encoded by prophage CP-933K |20966|
20966	-3.49	8.08	-1.80	8.98	0.0	7.18	0.1	0.00005420	0.00078198	0.01152122	0.33258881	A_07_P049460	20966	cmr|unknown protein encoded by prophage CP-933K |20966|
20966	-3.63	8.07	-1.87	8.77	0.0	7.32	0.1	0.00002337	0.00019530	0.03888577	0.49635145	A_07_P049460	20966	cmr|unknown protein encoded by prophage CP-933K |20966|
20966	-3.13	9.24	-1.65	9.56	0.1	8.92	0.1	0.00011757	0.00131575	0.01705125	0.37926450	A_07_P049460	20966	cmr|unknown protein encoded by prophage CP-933K |20966|
20971	+2.34	7.36	+1.23	6.75	0.0	7.97	0.1	0.00058390	0.00434242	0.04436286	0.52121639	A_07_P049483	20971	cmr|putative tail component of prophage CP-933K |20971|
20974	-2.57	7.36	-1.36	10.40	0.3	9.05	0.2	0.00387913	0.01052231	0.02422777	0.50122772	A_07_P049487	20974	cmr|putative tail component of prophage CP-933K |20974|
20977	+3.45	9.24	+1.79	8.35	0.3	10.13	0.2	0.00006546	0.00069774	0.00310564	0.38010564	A_07_P049512	20977	cmr|putative tail component of prophage CP-933K |20977|
20979	-2.61	8.48	-1.38	7.79	0.0	9.17	0.0	0.00030908	0.00206175	0.02424019	0.47670940	A_07_P049522	20979	cmr|putative tail component of prophage CP-933K |20979|
21046	+2.91	7.51	+1.54	6.74	0.0	8.28	0.0	0.00012056	0.00136756	0.02835559	0.43891176	A_07_P049587	21046	cmr|rorf, unknown function |21046|
21058	-2.04	7.80	-1.03	7.81	0.0	7.79	0.1	0.00122849	0.00757192	0.04907417	0.65669148	A_07_P049618	21058	cmr|putative tail component |21058|
21098	-2.42	11.40	-1.27	12.04	0.1	10.76	0.2	0.00141911	0.00841525	0.04660557	0.54189125	A_07_P046651	21098	cmr|rorf, unknown function |21098|
21099	+2.30	9.02	+1.20	8.42	0.1	9.62	0.2	0.00091737	0.00631969	0.04678986	0.53405955	A_07_P046659	21099	cmr|rorf, hypothetical protein |21099|
21102	+3.05	7.78	+1.61	6.98	0.1	8.59	0.3	0.00058025	0.00422758	0.02385294	0.42649897	A_07_P046662	21102	cmr|putative nucleotide di-P sugar epimerase or dehydratase |21102|
21121	+5.26	9.06	+2.96	7.86	0.3	10.26	0.1	0.00003832	0.00006814	0.00126347	0.26835793	A_07_P046679	21121	cmr|rorf, unknown function |21121|
21124	+2.62	7.50	+1.39	6.40	0.1	7.79	0.2	0.00047277	0.00375737	0.03538427	0.47736932	A_07_P046689	21124	cmr|putative phage regulatory protein |21124|
21125	-2.48	10.90	-1.31	11.55	0.5	10.24	0.1	0.00601185	0.02646168	0.03705893	0.52177552	A_07_P046692	21125	cmr|rorf, unknown function |21125|
21139	-3.05	13.36	-1.61	14.17	0.3	12.56	0.5	0.00470015	0.02045695	0.01988692	0.39593377	A_07_P046708	21139	cmr|putative helicase |21139|
21131	-2.22	9.21	-1.15	9.78	0.0	8.64	0.1	0.00066527	0.00476326	0.03697294	0.60523504	A_07_P046719	21131	cmr|unknown protein encoded in tRNA-Ile |21131|
21133	+2.04	9.29	+1.03	8.77	0.1	9.80	0.1	0.00188874	0.01057812	0.06410959	0.60341423	A_07_P046726	21133	cmr|partial putative transposase |21133|
21134	-2.09	8.02	-1.06	8.55	0.0	7.49	0.0	0.00061033	0.00448348	0.06330544	0.64874735	A_07_P046735	21134	cmr|unknown in tRNA-Gly |21134|
21139	-4.04	9.46	-2.02	10.47	0.9	8.45	0.1	0.00813311	0.03338923	0.00766110	0.26852657	A_07_P046753	21139	cmr|putative dehydrogenase |21139|
21150	-3.08	8.44	-1.06	8.97	0.1	7.91	0.0	0.00150874	0.00953187	0.06433384	0.65192343	A_07_P046801	21150	cmr|unknown in 6 |21150|
21160	-3.49	9.65	-1.80	10.55	0.1	8.75	0.1	0.00013645	0.00115331	0.01122304	0.31973193	A_07_P046840	21160	cmr|unknown in tRNA-Ile |21160|
21161	-2.54	8.84	-1.35	9.51	0.0	8.16	0.0	0.00025453	0.00237968	0.03485519	0.53124248	A_07_P046841	21161	cmr|unknown in tRNA-Ile |21161|
21169	-3.78	9.53	-1.92	10.29	0.1	8.77	0.0	0.00019638	0.00186037	0.03105948	0.48508837	A_07_P046867	21169	cmr|unknown in 6 |21169|
21203	-2.21	10.65	-1.15	11.23	0.2	10.08	0.1	0.00148797	0.00872499	0.05410882	0.60107219	A_07_P050909	21203	cmr|unknown |21203|
21210	-2.49	7.66	-1.12	8.22	0.1	7.00	0.3	0.00126510	0.00773824	0.03438899	0.57375956	A_07_P050942	21210	cmr|putative histone |21210|
21212	-1.69	11.99	-2.51	13.24	0.0	10.73	0.1	0.00000701	0.00020362	0.00196900	0.14622642	A_07_P050946	21212	cmr|unknown |21212|
21213	-3.42	9.78	-1.78	10.67	0.0	8.89	0.0	0.00004845	0.00072132	0.01324936	0.33685764	A_07_P050951	21213	cmr|unknown |21213|
21217	-2.24	8.30	-1.17	8.88	0.0	7.71	0.2	0.00145542	0.00854925	0.05181657	0.59188811	A_07_P050973	21217	cmr|putative DNA repair protein, RADC family |21217|
21335	-2.10	10.95	-1.07	11.49	0.1	10.42	0.3	0.00869714	0.02904994	0.04488837	0.64832487	A_07_P054076	21335	cmr|unknown protein encoded by cryptic prophage CP-933M |21335|
21340	-4.67	9.47	-2.22	10.58	0.4	8.36	0.3	0.00046682	0.00362203	0.00415968	0.21194175	A_07_P051002	21340	cmr|unknown protein encoded by cryptic prophage CP-933M |21340|
21352	-3.57	9.17	-1.84	10.09	0.4	8.26	0.5	0.01337777	0.01642840	0.01056585	0.12316832	A_07_P051141	21352	cmr|putative endolysin of cryptic prophage CP-933M |21352|
21364	-5.80	10.70	-2.53	11.97	1.1	9.44	0.1	0.00560614	0.02495386	0.00158155	0.12835052	A_07_P051194	21364	cmr|putative DNA primase/helicase protein of cryptic prophage CP-933M |21364|
21373	-2.04	10.87	-1.56	11.65	0.1	10.09	0.1	0.00016687	0.00175732	0.02135671	0.41977528	A_07_P051220	21373	cmr|unknown protein encoded by cryptic prophage CP-933M |21373|
21428	+20.30	9.42	+4.34	7.24	0.1	11.59	0.2	0.00000065	0.00005973	0.00047574	0.06139344	A_07_P048529	21428	cmr|unknown protein encoded by bacteriophage BP-933W |21428|
21433	+35.48	11.26	+5.15	8.69	0.2	13.84	0.2	0.00000054	0.00004611	0.00038969	0.02611111

24340	-3.21	11.79	-1.68	12.63	0.0	10.95	0.0	0.00006838	0.00092248	0.01558117	0.37224583	A_07_P045803	24340	cmr\unknown protein encoded by ISEc8 [24340]
24343	+2.58	10.15	+1.37	9.46	0.2	10.83	0.1	0.00005269	0.00401015	0.03670986	0.44905360	A_07_P045808	24343	cmr\orf, hypothetical protein [24343]
24385	-3.34	8.18	-1.74	9.05	0.0	7.31	0.0	0.00005674	0.00080476	0.01362933	0.35006894	A_07_P045844	24385	cmr\putative ATP-binding protein of ABC transporter family [24385]
24400	-3.53	13.02	-1.92	13.93	0.1	12.11	0.4	0.00047714	0.00078609	0.01081428	0.32492366	A_07_P045859	24400	cmr\orf Unknown function [24400]
24400	-3.08	13.64	-1.62	14.45	0.0	12.83	0.0	0.00008055	0.00102432	0.01836756	0.38862772	A_07_P045859	24400	cmr\orf Unknown function [24400]
24400	-4.17	13.17	-2.06	14.20	0.0	12.14	0.3	0.00010444	0.00123820	0.00630907	0.25666667	A_07_P045859	24400	cmr\orf Unknown function [24400]
24400	-6.44	13.86	-2.69	15.21	1.0	12.52	0.1	0.00355656	0.01732505	0.00130907	0.12052632	A_07_P045859	24400	cmr\orf Unknown function [24400]
24400	-2.71	13.60	-1.44	14.32	0.0	12.88	0.1	0.00021894	0.00227925	0.02762703	0.47486716	A_07_P045859	24400	cmr\orf Unknown function [24400]
24487	+3.87	7.66	+1.95	6.68	0.0	8.63	0.1	0.00002864	0.00049816	0.01674162	0.34545216	A_07_P045901	24487	cmr\putative phosphotransferase system enzyme subunit [24487]
24488	+3.72	8.65	+1.89	7.70	0.1	9.60	0.0	0.00005049	0.00074433	0.01811770	0.35341584	A_07_P045910	24488	cmr\putative phosphotransferase system enzyme subunit [24488]
24501	-35.26	11.75	-5.14	14.32	0.0	9.18	0.1	0.00000007	0.00003344	0.00000254	0.00444444	A_07_P045934	24501	cmr\orf hypothetical protein [24501]
24801	+2.66	8.47	+1.41	7.76	0.2	9.18	0.1	0.00034514	0.00296290	0.03429116	0.47068875	A_07_P046078	24801	cmr\putative ATP-dependent DNA helicase [24801]
24803	+2.13	7.75	+1.22	7.14	0.1	8.36	0.1	0.00084463	0.00575614	0.04516139	0.52847345	A_07_P046088	24803	cmr\putative ATP-dependent DNA helicase [24803]
24850	-2.09	8.46	-1.06	8.99	0.0	7.93	0.2	0.00218812	0.01185470	0.06586128	0.65133166	A_07_P046137	24850	cmr\putative O-methyltransferase [24850]
24854	-3.16	10.21	-1.66	11.08	0.0	9.38	0.1	0.00007843	0.00100395	0.01650025	0.37758721	A_07_P046157	24854	cmr\putative acyl carrier protein [24854]
24862	+2.44	7.47	+1.29	6.83	0.0	8.12	0.2	0.00309315	0.00695496	0.04123793	0.50407609	A_07_P046200	24862	cmr\orf Unknown function [24862]
24863	+2.88	7.63	+1.52	6.87	0.1	8.39	0.1	0.00014223	0.00155099	0.02931204	0.44071154	A_07_P046205	24863	cmr\putative 3-oxoacyl- [24863]
24864	+2.11	7.67	+1.07	7.13	0.2	8.20	0.2	0.00453425	0.02107684	0.05999682	0.59670878	A_07_P046210	24864	cmr\orf Unknown function [24864]
24875	+2.40	7.69	+1.26	7.06	0.2	8.32	0.2	0.00342894	0.00845252	0.04308832	0.51326778	A_07_P046212	24875	cmr\putative phosphotransferase system enzyme subunit [24875]
24878	-2.43	8.96	-1.28	9.60	0.1	8.32	0.4	0.00560315	0.02422876	0.04057565	0.54362553	A_07_P046246	24878	cmr\putative xylulose kinase [24878]
24883	-2.09	10.55	-1.07	11.08	0.1	10.01	0.1	0.00118900	0.00778206	0.06471100	0.64851050	A_07_P046368	24883	cmr\orf Unknown function [24883]
24950	-3.69	9.99	-1.88	10.93	0.2	9.04	0.1	0.00011941	0.00135835	0.00952236	0.31298539	A_07_P046440	24950	cmr\orf Unknown function [24950]
24999	-2.89	7.94	-1.53	8.70	0.1	7.17	0.2	0.00040274	0.00334608	0.02222831	0.43171393	A_07_P046484	24999	cmr\orf Unknown function [24999]
25088	+2.40	7.46	+1.27	6.83	0.0	8.09	0.1	0.00052427	0.00401856	0.04216908	0.51075000	A_07_P046618	25088	cmr\unknown protein encoded by rSH11 within prophage [25088]
25200	-2.29	7.76	-1.20	8.36	0.1	7.16	0.1	0.00054456	0.00412987	0.04872793	0.58263478	A_07_P046909	25200	cmr\orf Unknown function [25200]
25522	-3.39	11.68	-1.76	12.56	0.1	10.80	0.0	0.00006094	0.00084745	0.01288808	0.34391525	A_07_P047170	25522	cmr\putative hippuricase [25522]
25523	-3.62	11.79	-1.86	12.72	0.1	10.86	0.4	0.00080460	0.00552445	0.01083714	0.32499048	A_07_P047173	25523	cmr\putative citrate permease [25523]
25618	-2.04	7.57	-1.03	8.09	0.1	7.06	0.3	0.00574300	0.02546982	0.06933943	0.65803496	A_07_P047247	25618	cmr\D-glucitol-6-phosphate dehydrogenase [25618]
25852	-12.11	13.85	-5.01	16.35	0.0	11.35	0.1	0.00000010	0.00003427	0.00000381	0.00461538	A_07_P047387	25852	cmr\orf Unknown function [25852]
25886	-2.07	10.59	-1.05	11.11	0.0	10.06	0.3	0.00466284	0.02168535	0.06763402	0.65307096	A_07_P047426	25886	cmr\orf Unknown function [25886]
25899	-2.29	8.36	-1.19	8.96	0.0	7.76	0.3	0.00253450	0.01328788	0.04945694	0.58457207	A_07_P047482	25899	cmr\putative ATP-dependent helicase [25899]
25940	+3.60	8.15	+1.85	7.23	0.0	9.08	0.1	0.00004144	0.00064284	0.01918128	0.36384337	A_07_P047549	25940	cmr\orf Unknown function [25940]
25987	+4.08	8.96	+2.03	7.95	0.0	9.98	0.2	0.00004437	0.00067775	0.01127058	0.33391667	A_07_P050868	25987	cmr\orf Unknown function [25987]
25988	+5.97	8.93	+2.58	7.64	0.0	10.22	0.2	0.00001056	0.00026108	0.00708206	0.24134199	A_07_P050871	25988	cmr\putative lipoate-protein ligase A [25988]
25988	+5.63	8.42	+2.49	7.18	0.2	9.67	0.3	0.00009252	0.00113352	0.00805132	0.24952756	A_07_P050871	25988	cmr\putative lipoate-protein ligase A [25988]
25988	+5.07	8.73	+2.34	7.55	0.1	9.90	0.0	0.00000921	0.00023970	0.00984629	0.27388693	A_07_P050871	25988	cmr\putative lipoate-protein ligase A [25988]
25988	+6.33	8.91	+2.66	7.58	0.1	10.24	0.1	0.00000657	0.00019615	0.00630490	0.22613426	A_07_P050871	25988	cmr\putative lipoate-protein ligase A [25988]
25988	+5.64	8.93	+2.50	7.68	0.1	10.18	0.2	0.00001436	0.00031409	0.00709636	0.24890438	A_07_P050871	25988	cmr\putative lipoate-protein ligase A [25988]
26024	+2.00	7.97	+1.00	7.47	0.0	8.47	0.1	0.00139180	0.00829394	0.06283600	0.60767199	A_07_P044177	26024	cmr\unknown protein encoded by cryptic prophage CP-933P [26024]
26030	+2.94	8.05	+1.56	7.27	0.3	8.82	0.5	0.00534362	0.02401652	0.02959794	0.44107774	A_07_P044196	26030	cmr\putative tail component of cryptic prophage CP-933P [26030]
26036	-2.25	10.55	-1.17	11.13	0.0	9.97	0.1	0.00077752	0.00537131	0.05127731	0.59186950	A_07_P044215	26036	cmr\putative tail assembly protein of cryptic prophage [26036]
26054	-2.49	9.88	-1.32	10.54	0.1	9.22	0.2	0.00080088	0.00600171	0.03742950	0.52588243	A_07_P044256	26054	cmr\conserved hypothetical Y3\5 family protein encoded by [26054]
26060	-3.77	8.11	-1.92	9.06	0.4	7.15	0.7	0.00776836	0.03221944	0.00816629	0.29287016	A_07_P044262	26060	cmr\putative Q-antiterminator encoded by prophage CP-933P [26060]
zntA	+2.12	9.12	+1.08	8.58	0.0	9.66	0.3	0.00529656	0.02388003	0.05484838	0.58275885	A_07_P034561	c_4262	cmr\lead, cadmium, zinc and mercury transporting ATPase [c_4262]
znuC	-2.20	9.23	-1.14	9.80	0.0	8.66	0.1	0.00076322	0.00529343	0.05494347	0.60831927	A_07_P015968	b1858	cmr\putative ATP-binding component of a transport system [b1858]
zwf	+2.80	9.48	+1.49	8.74	0.0	10.22	0.1	0.00014565	0.00157814	0.03066184	0.44906047	A_07_P015938	b1852	cmr\glucose-6-phosphate dehydrogenase [b1852]

C. coli ATCC 25922 amaR SB31 pBK-Qnr51 (SC+20 wells)	Significant differential expression (equal to or greater than two-fold, P value <0.05)

Gene Name (ProbeID)	Fold Change	logSignal (A)	logRatio (M)	logControl	StdErr (logControl)	logExpérriment	StdErr (logExpérriment)	pval (limma)	FDR (limma)	pval (RankProd)	FDR (RankProd)	Oligo	Systematic Name	Description
aseA	-28.43	9.42	-4.83	11.83	0.1	7.00	0.2	0.00000145	0.00015308	0.00005588	0.00000000	A_07_P012680	b2241	cmr/putative membrane protein [b2241]
aseB	-5.17	8.00	-2.37	9.18	0.1	6.81	0.0	0.00003208	0.00062191	0.0582017	0.24711550	A_07_P012673	b2240	cmr/conf. hypothetical protein [b2240]
aseR	-3.84	8.17	-1.94	9.15	0.0	7.20	0.0	0.00006848	0.00096742	0.0137201	0.17179002	A_07_P010572	b2242	cmr/conf. hypothetical protein [b2242]
ABE-0012311	-2.22	9.42	-1.15	8.84	0.1	9.99	0.1	0.00136760	0.00847608	0.0544601	0.59012281	A_07_P012617	ABE-0012311	aap/acetolactate synthase II, large subunit, C-ter fragment (pseudogene) [b3768]
ABE-0285070	-4.14	8.75	-2.05	9.77	0.2	7.72	0.2	0.00047217	0.00387253	0.0136560	0.34413538	A_07_P010568	ABE-0285070	aap/predicted protein, C-ter fragment (pseudogene) [b4549]
ABE-0285081	-12.68	11.96	-3.66	13.79	0.0	10.13	0.1	0.00000254	0.00018134	0.0002726	0.05181822	A_07_P010669	ABE-0285081	aap/IS21 phage-like element; predicted transposase fragment (pseudogene) [b4562]
ABE-0285085	-6.33	8.34	-2.12	9.40	0.1	7.29	0.2	0.00016210	0.00182033	0.0966717	0.31124764	A_07_P010678	ABE-0285085	aap/ISL transposase InsAB', C-ter fragment (pseudogene) [b4564]
ABH-0247653	-24.83	11.62	-4.63	13.94	0.0	9.30	0.1	0.00000881	0.00012560	0.0000366	0.01827506	A_07_P048654	ABH-0247653	aap/predicted protein []
ABH-0285233	-3.29	8.79	-1.72	9.65	0.1	7.93	0.2	0.00033964	0.00305558	0.0267022	0.45008827	A_07_P048532	ABH-0285233	aap/non-LEE-encoded type III secreted effector []
ABH-0081722	-12.84	10.32	-4.55	9.56	0.0	5.77	0.2	0.00028106	0.00266247	0.0159912	0.67940778	A_07_P015523	ABH-0081722	aap/predicted protein [b5436]
ABH-0081747	-3.55	12.76	-1.83	13.67	0.0	11.85	0.1	0.00034560	0.00167812	0.0180470	0.40933718	A_07_P015421	ABH-0081747	aap/toxic membrane protein []
ABH-0081753	-6.31	8.66	-2.66	9.66	0.1	7.13	0.2	0.00006319	0.00084231	0.0314824	0.18656604	A_07_P014363	ABH-0081753	aap/predicted ferredoxin []
ABH-0081753	-8.65	11.17	-3.11	9.51	0.1	12.73	0.1	0.00003707	0.00028168	0.0845264	0.20931507	A_07_P041110	ABH-0081753	aap/predicted protein []
ACA-0244198	-2.28	8.70	-1.19	9.29	0.0	8.10	0.3	0.00464091	0.02238620	0.0631966	0.60948603	A_07_P058943	ACA-0244198	aap/Type II secretion pathway related protein []
ACA-0264202	-5.02	9.73	-2.33	10.89	0.0	8.57	0.0	0.00002518	0.00056604	0.0661858	0.25225389	A_07_P062880	ACA-0264202	aap/predicted protein []
ACA-0264210	-5.68	11.08	-2.51	12.33	0.1	9.82	1.0	0.00748294	0.03372207	0.0478563	0.23681154	A_07_P059088	ACA-0264210	aap/predicted protein []
ACA-0264225	-2.37	10.03	-1.25	10.65	0.1	9.41	0.4	0.00050417	0.00721628	0.0481682	0.22928909	A_07_P059044	ACA-0264225	aap/predicted protein []
ACA-0264238	-3.01	8.69	-1.59	9.49	0.2	7.89	0.1	0.00039158	0.00336992	0.0294324	0.48722397	A_07_P059459	ACA-0264238	aap/predicted protein []
ACA-0285117	-2.99	11.83	-1.58	12.62	0.1	10.04	0.3	0.00196833	0.01350693	0.0008796	0.49220648	A_07_P062819	ACA-0285117	aap/toxic polypeptide, small []
acoA	-3.00	9.51	-1.58	10.31	0.1	8.72	0.1	0.00022771	0.00232347	0.0296258	0.48746611	A_07_P002882	b0185	cmr/acetylCoA carboxylase, carboxyltransferase component, alpha subunit [b0185]
acoB	-8.27	11.24	-4.05	9.72	0.1	12.77	0.0	0.00000739	0.00008887	0.0003360	0.26532062	A_07_P012725	b3255	cmr/acetylCoA carboxylase, BCCP subunit; carrier of biotin [b3255]
acoC	+2.78	10.75	+1.48	10.02	0.1	11.49	0.1	0.00016631	0.00352830	0.0374392	0.48745850	A_07_P012747	b3256	cmr/acetylCoA carboxylase, biotin carboxylase subunit [b3256]
acoD	-3.23	11.74	-1.69	12.59	0.1	10.90	0.1	0.00015174	0.00173176	0.0238768	0.41775883	A_07_P012792	b3265	cmr/transcarboxylase protein affecting septum formation and cell membrane permeability [b3265]
acoE	+12.24	9.62	+3.61	7.82	0.0	11.43	0.1	0.00000260	0.00018134	0.0024870	0.14424242	A_07_P008720	b4015	cmr/isocitrate lyase [b4015]
acoK	-14.50	9.55	-4.82	7.64	0.3	11.46	0.2	0.00003139	0.00048729	0.0178504	0.12480000	A_07_P037462	c_4972	cmr/isocitrate lyase [c_4972]
acoR	+48.72	10.03	+5.61	7.23	0.0	12.84	0.3	0.00000102	0.00012946	0.0001259	0.02924242	A_07_P008715	b4014	cmr/malate synthase A [b4014]
acoX	+101.26	12.18	+6.66	8.65	0.0	15.51	0.0	0.00000009	0.00003569	0.0000168	0.01458039	A_07_P012795	b0118	cmr/pyruvate dehydrogenase [b0114]
acoY	+27.25	12.58	+4.77	10.20	0.1	14.97	0.1	0.00000087	0.00012765	0.0003681	0.05970588	A_07_P002536	b0115	cmr/pyruvate dehydrogenase [b0115]
acsA	+4.81	12.78	+2.27	11.64	0.1	13.91	0.0	0.00003360	0.00064348	0.0116080	0.03121170	A_07_P011766	b2296	cmr/acetate kinase [b2296]
acnA	+5.37	9.51	+2.42	8.29	0.1	10.72	0.1	0.00002454	0.00051591	0.0125829	0.29669162	A_07_P014361	b1276	cmr/aconitate hydrase 1 [b1276]
acnB	+10.46	10.52	+3.39	8.82	0.0	12.21	0.3	0.00000145	0.00015192	0.0032281	0.16826047	A_07_P012521	b0118	cmr/aconitate hydrase B [b0118]
acpD	+3.67	8.69	+1.88	7.76	0.1	9.63	0.1	0.00011421	0.00142293	0.0231293	0.39948018	A_07_P052470	z2315	cmr/acyl carrier protein phosphodiesterase [z2315]
acpD	+3.80	9.35	+1.93	8.39	0.2	10.31	0.0	0.00011316	0.00157532	0.0219763	0.38652605	A_07_P063175	ECs2014	cmr/acyl carrier protein phosphodiesterase [ECs2014]
acpS	+3.70	8.63	+1.89	7.68	0.1	9.57	0.1	0.00016121	0.00181157	0.0292873	0.39888998	A_07_P019720	b2563	cmr/CoA-apo- [b2563]
acpS	+5.14	8.83	+2.36	7.65	0.0	10.01	0.1	0.00008631	0.00085813	0.0135896	0.31004567	A_07_P053485	ECs3429	cmr/CoA-apo- [ECs3429]
acpS	-2.92	8.61	+1.55	7.83	0.1	9.38	0.0	0.00030417	0.00282365	0.0445316	0.47195313	A_07_P042915	z3864	cmr/CoA-apo- [z3864]
acrB	+2.84	10.58	+1.50	9.83	0.0	11.33	0.1	0.00031422	0.00289985	0.0364133	0.48213625	A_07_P021417	b0462	cmr/acridine efflux pump [b0462]
acrE	-3.74	9.18	-1.90	10.13	0.0	8.22	0.8	0.01203158	0.04790218	0.0193527	0.39090984	A_07_P012792	b3265	cmr/transcarboxylase protein affecting septum formation and cell membrane permeability [b3265]
aes	+34.42	9.22	+4.61	6.91	0.1	11.52	0.5	0.00002864	0.00058160	0.0055100	0.07021210	A_07_P012329	z5668	cmr/acetyl-CoA synthetase [z5668]
acs	+27.07	9.39	+4.53	7.13	0.2	11.66	0.0	0.00000229	0.00017963	0.0007609	0.07198413	A_07_P008986	b4069	cmr/acetyl-CoA synthetase [b4069]
acsP	+5.68	8.35	+2.51	7.10	0.2	9.60	0.1	0.00009422	0.00125289	0.0113192	0.28215781	A_07_P063694	ECs5049	cmr/putative transport protein [ECs5049]
acsP	+6.39	8.19	+2.68	6.85	0.1	9.53	0.4	0.00013191	0.00209393	0.0873951	0.20603887	A_07_P052321	z5666	cmr/putative transport protein [z5666]
actP	+6.17	8.75	+2.67	7.42	0.1	10.09	0.1	0.00020650	0.00214550	0.0088926	0.26091248	A_07_P008980	b4067	cmr/putative transport protein [b4067]
ade	+6.06	8.81	+2.60	7.52	0.0	10.11	0.0	0.00003159	0.00038685	0.0010036	0.27232624	A_07_P027301	b3665	cmr/probable adenine deaminase [b3665]
adhE	+2.88	8.39	+1.53	7.62	0.1	9.15	0.1	0.00030803	0.00285605	0.0352757	0.47631791	A_07_P007343	b1241	cmr/CoA-linked acetaldehyde dehydrogenase and iron-dependent alcohol dehydrogenase; pyruvate-formate-lyase deactivase [b1241]
adk	-2.15	10.18	-1.10	10.73	0.2	9.63	0.1	0.00232607	0.01305870	0.0739182	0.67192224	A_07_P021477	b0474	cmr/adenylate kinase activity; phenotypic effects on glycerol-3-phosphate acyltransferase activity [b0474]
ade	-22.63	10.52	-4.50	12.77	0.1	8.27	0.0	0.00000146	0.00012946	0.0000747	0.01735294	A_07_P021486	b0476	cmr/putative lipase [b0476]
aspA	+4.54	7.89	+2.18	6.80	0.0	8.99	0.1	0.00000214	0.00017123	0.0143074	0.34192092	A_07_P011484	b4139	cmr/PTS system, cytoplasmic, N-acetylgalactosamine-specific IIB component 1 [b4138]
agaS	+26.86	9.21	+4.75	6.84	0.1	11.59	0.0	0.00000083	0.00012615	0.0004176	0.06219048	A_07_P034110	c_3893	cmr/Putative tagatose-6-phosphate ketose/aldose isomerase [c_3893]
agaS	+16.44	9.03	+4.04	7.03	0.1	10.61	0.1	0.00000205	0.00017536	0.0013843	0.10842245	A_07_P008404	b4136	cmr/putative tagatose-6-phosphate ketose/aldose isomerase [b4136]
agaY	+23.46	8.77	+4.55	6.50	0.1	11.05	0.3	0.00000497	0.00024091	0.0005691	0.07168000	A_07_P000390	b3133	cmr/PTS system, cytoplasmic, N-acetylgalactosamine-specific IIB component 2 [b3133]
agaYR	+18.45	9.62	+4.23	7.52	0.3	10.64	0.1	0.00000564	0.00005427	0.0008913	0.08607362	A_07_P000391	b3134	cmr/PTS system N-acetylgalactosamine-specific IIC component 2 [b3134]
agp	+7.20	10.37	+2.85	8.95	0.3	11.80	0.2	0.00008200	0.00113151	0.0070363	0.23837259	A_07_P033695	c_1137	cmr/Glucose-1-phosphatase precursor [c_1137]
agp	+8.65	10.36	+3.11	8.71	0.1	11.82	0.1	0.00003442	0.00038421	0.0040834	0.23102602	A_07_P001341	b1002	cmr/periplasmic glucose-1-phosphatase [b1002]
ahpC	+5.87	16.01	+2.55	14.73	0.1	17.28	0.0	0.00000169	0.00042417	0.0227290	0.27776605	A_07_P016791	b0605	cmr/alkyl hydroperoxide reductase, C22 subunit; detoxification of hydroperoxides [b0605]
aldB	-3.46	9.14	-1.79	10.03	0.3	8.24	0.5	0.00447612	0.02174390	0.0203607	0.42951153	A_07_P011655	b4187	cmr/putative acyl coenzyme A dehydrogenase [b4187]
aldA	-8.29	8.99	-4.05	7.46	0.1	10.51	0.1	0.00000712	0.00008183	0.0053649	0.27197994	A_07_P009166	b1415	cmr/aldehyde dehydrogenase, NAD-linked [b1415]
aldB	+6.06	9.64	+2.60	8.42	0.1	10.69	0.1	0.00003896	0.00068231	0.0196951	0.27153709	A_07_P016349	b0512	cmr/putative hydrolase [b0512]
aldD	+19.36	9.13	+4.27	6.99	0.0	11.26	0.1	0.00000168	0.00015927	0.0008496	0.07198779	A_07_P016372	b0517	cmr/putative malate dehydrogenase [b0517]
alr	-3.45	9.79	-1.79	10.68	0.0	8.90	0.2	0.00019952	0.00210254	0.0190342	0.49187658	A_07_P008909	b4053	cmr/alanine racemase 1 [b4053]
alsB	-20.23	9.87	+4.34	7.70	0.1	12.04	0.1	0.00000169	0.00015859	0.0007869	0.38242727	A_07_P011177	b4088	cmr/putative LACI-type transcriptional regulator [b4088]
alsC	+2.63	9.81	+1.40	9.12	0.0	10.51	0.1	0.00443307	0.02363143	0.0420156	0.51032265	A_07_P011170	b4086	cmr/putative transport system permease protein [b4086]
alsE	+3.16	10.23	+1.66	9.40	0.1	11.06	0.1	0.00018961	0.00209942	0.0002414	0.44177570	A_07_P011164	b4085	cmr/putative epimerase [b4085]
alsK	+4.10	9.82	+2.03	8.80	0.2	10.84	0.0	0.00009398	0.00125073	0.0196347	0.37624088	A_07_P011158	b4084	cmr/putative NAGC-like transcriptional regulator [b4084]
amiA	-8.11	11.97	-3.19	13.56	0.0	10.37	0.1	0.00011020	0.00140200	0.0009136	0.33055944	A_07_P042594	c_2969	cmr/Probable N-acetylmuramoyl-L-alanine amidase amiA precursor [c_2969]
amiA	-6.59	12.17	-2.79	13.53	0.0	10.81	0.1	0.00001410	0.00003025	0.0027266	0.17679012	A_07_P052353	z3700	cmr/N-acetylmuramoyl-L-alanine amidase I [z3700]
amiA	-7.11	11.56	-2.83	12.97	0.0	10.15	0.2	0.00003753	0.00004603	0.0021835	0.15049664	A_07_P052334	z3435	cmr/N-acetylmuramoyl-L-alanine amidase I [z3435]
amiB	-2.77	10.59	-1.47	11.33	0.1	9.86	0.2	0.00061426	0.00472975	0.0371361	0.52573942	A_07_P011563	b4169	cmr/N-acetylmuramoyl-L-alanine amidase II; a murein hydrolase [b4169]
amn	-36.81	10.50	-4.79	7.73	0.4	12.67	0.0	0.00000008	0.00004309	0.0004209	0.06342024	A_07_P011527	b3582	cmr/AMP nucleosidase [b3582]
ampD	+6.25	12.68	+2.64	11.36	0.1	14.01	0.2	0.00003143	0.00061555	0.0094782	0.26775583	A_07_P041423	c_0129	cmr/AmpD protein [c_0129]
ampD	+7.35	11.41	+2.88	9.97	0.0	13.07	0.1	0.00000807	0.00028787	0.0068361	0.23638528	A_07_P002511	b0110	cmr/regulates ampC [b0110]
ampE	+2.43	9.26	+1.28	8.62	0.0	9.90	0.1	0.00094388	0.00659868	0.0479287	0.54516669	A_07_P002518	b0111	cmr/regulates ampC [b0111]
amyA	-3.81	8.93	-1.93	9.89	0.2	7.96	0.1	0.00034507	0.00325845	0.0449568	0.38036667	A_07_P014999	b1927	cmr/cytoplasmic alpha-amylase [b1927]
anmK	+2.70	10.46	+1.43	9.74	0.1	11.18	0.1	0.00054740	0.00432645	0.0349674	0.46782329	A_07_P052526	Z2654	cmr/conf. hypothetical protein [Z2654]
anmK	+2.69	10.30	+1.43	9.59	0.1	11.02	0.1	0.00055187	0.00435323	0.0399682	0.49937551	A_07_P062211	ECs2348	cmr/hypothetical protein [ECs2348]
anmK	+2.24	8.62	+1.16	8.04	0.2	9.20	0.2	0.00467702	0.02250445	0.0578139	0.59602243	A_07_P062239	ECs2479	cmr/cytoplasmic 1-x-anpanhydrase [ECs2479]
anmR	+54.77	13.11	+5.78	10.22	0.1	15.99	0.0	0.00000210	0.00008010	0.0001053	0.02859649	A_07_P011926	b2957	cmr/periplasmic 1-x-anpanhydrase [b2957]
anoP	-3.26	8.22	-1.18	8.81	0.0	7.64	0.1	0.00015899	0.00772199	0.0657905	0.45579887	A_07_P009360	b2453	cmr/1,x-aspartate permease [b2453]
apbA	+2.78	9.57	+1.47	8.84	0.1	10.31	0.0	0.00033222	0.00302296	0.0375860	0.48767148	A_07_P011138	c_0536	cmr/2-dehydropantoate 2-reductase [c_0536]
apbA	+5.76	9.93	+2.52	7.67	0.2	10.20	0.2	0.00049753	0.00077641	0.0110261	0.28835541	A_07_P008918	b4055	cmr/diaminosuccinate hydrogenase [b4055]
apbA	+5.95	10.89	+2.57	9.60	0.1	12.17	0.4	0.00023056	0.00234535	0.0010805	0.27418803	A_07_P042001	c_5045	cmr/Class B acid phosphatase precursor [c_5045]
aspZ	-2.26	7.66	-1.18	8.25	0.1	7.08	0.0	0.00107926	0.00725023	0.0640772	0.82705071	A_07_P004830	b0875	cmr/transmembrane sensor kinase, aspartate-2 [b0875]
araA	+7.23	8.68	+2.85	7.26	0.1	9.01	0.0	0.00003697	0.00062202	0.0070696	0.23854701	A_07_P010999	b0062	cmr/L-arabinose isomerase [b0062]
araB	+3.82	8.26	+1.93	7.29	0.1	8.62	0.1	0.00016672	0.00140023	0.0218124	0.39018038	A_07_P011001	b0063	cmr/L-ribulokinase [b0063]
araC	+2.74	11.23	+1.46	10.50	0.0	11.96	0.0	0.00029169	0.00271188	0.0365028	0.49472358	A_07_P011010	b0064	cmr/transcriptional regulator for ara operon [b0064]
araF	-2.14	8.84	+2.42	7.63	0.1	10.05	0.1	0.00004266	0.00073197	0.0123615	0.29168871	A_07_P011021	b1801	cmr/L-arabinose-binding periplasmic protein [b1801]
arcA	-2.95	12.69	-1.56	13.47	0.0	11.91	0.1	0.00035019	0.00312194	0.0310681	0.49112000	A_07_P017689	b4401	cmr/negative response regulator of genes in aerobic pathways, [b4401]
arcB	+5.10	12.76	+2.35	11.58	0.1	13.93	0.1	0.00002061	0.00475301	0.0130452	0.35281711	A_07_P012528	b3210	cmr/aerobic respiration sensor response protein; histidine protein kinase/phosphatase, sensor for arcA [b3210]
argE	+4.65	8.91	+2.22	7.80	0.2	10.02	0.0	0.00007249	0.00010660	0.0157488	0.33750681	A_07_P039521	c_4916	cmr/Acetylornithine deacetylase [c_4916]
argG	+3.25	7.84	+1.70	6.99	0.2	8.69	0.5	0.00437060	0.02133709	0.0261839	0.43637634	A_07_P008486	b3957	cmr/acetylornithine deacetylase [b3957]
argG	+2.53	8.09	+1.34	7.42	0.2	8.76	0.1	0.00120584	0.00795007	0.0469870	0.52123874	A_07_P000576	b3172	cmr/argininosuccinate synthetase [b3172]
argG	-2.24	8.62	-1.17	8.84	0.1	8.21	0.0	0.00103875	0.00710949	0.0648821	0.59273072	A_07_P041781	c_3929	cmr/Argininosuccinate synthetase [c_3929]
argD	-3.26	7.66	-1.18	8.45	0.0	7.24	0.1	0.01237825	0.03022293	0.0614928	0.61288604	A_07_P011564	b3923	cmr/conf. hypothetical protein [b3923]
argR	-3.89	11.10	-1.96	12.08	0.0	10.12	0.1	0.00008715	0.00098530	0.0328279	0.36435040	A_07_P012656	b2237	cmr/repressor of arg regulon; cer-mediated site-specific recombination [b2237]
argS	-6.25	11.63	-2.64	12.95	0.0	10.30	0.2	0.00009169	0.00055166	0.0021710	0.38609037	A_07_P012665	b1876	cmr/arginine tRNA synthetase [b1876]
arsC	+2.91	8.56	+1.54	7.79	0.1	9.33	0.3	0.00099733	0.00884967	0.0349017	0.47319363	A_07_P001665	b2255	cmr/putative transferase [b2255]
arsC	-6.29	10.23	+2.65	8.91	0.2	11.56	0.0	0.00003783	0.00057043	0.0047691	0.26791033	A_07_P001663	b2254	cmr/putative sugar transferase [b2254]
arsT	+5.69	8.93	+2.51	7.67	0.2	10.18	0.2	0.00007767	0.00109371	0.0111280	0.28219355	A_07_P001072	b2257	cmr/conf. hypothetical protein [b2257]
arsA	+3.67	9.18	+1.79	8.28	0.1	10.08	0.0	0.00010145	0.00144613	0.0254863	0.41149945	A_07_P011815	c_3264	cmr/3-phosphoshikimate 1-carboxylphenylransferase [c_3264]
aroG	+2.66	8.12	+1.45	7.42	0.2	8.83	0.0	0.00067143	0.00259975	0.0407631	0.50301961	A_07_P010251	b0754	cmr/3-deoxy-D-arabinoheptulosonate-7-phosphate synthase [b0754]
aroK	-3.08	11.58	-1.62	12.39	0.0	10.77	0.1	0.00038233	0.00267123	0.0277490	0.40211021	A_07_P017076	b1390	cmr/shikimate kinase I [b1390]
aroM	-2.57	7.88	-1.36	8.56	0.0	7.20	0.1	0.00044066	0.00368021	0.0464627	0.57488208	A_07_P031086	c_0498	cmr/AroM protein [c_0498]
aroM	-2.57	7.88	-1.36	8.56	0.0	7.20	0.1	0.00102216	0.00710241	0.0714240	0.57582205	A_07_P008486	z0486	cmr/conf. hypothetical protein [z0486]
arrD	+5.00	9.12	+2.32	7.96	0.1	10.28	0.1	0.00000626	0.00008800	0.0145079	0.31964132	A_07_P016536	b0555	cmr/bacteriophage lambda lysozyme homolog [b0555]
artI	+7.39	9.19	+2.89	7.75	0.1	10.63	0.1	0.00003127	0.00004601	0.0027884	0.23419426	A_07_P004766	b0863	cmr/arginine 3rd transport system periplasmic binding protein [b0863]
artP	+7.96	9.36	+2.99	7.87	0.2	10.86	0.2	0.00003528	0.00056109	0.0056192	0.22238554	A_07_P004773	b0864	cmr/ATP-binding component of 3rd arginine transport system [b0864]
artQ	-2.61	8.29	+1.38	7.59	0.2	8.98	0.3	0.00376022	0.01885287	0.0415882	0.51796828	A_07_P011780	c_0965	cmr/Arginine transport system permease protein and p_0965
asd	+1.91	10.23	+1.28	8.59	0.1	11.87	0.0	0.00000465	0.00032240	0.0038160	0.18385321	A_07_P018394	b3433	cmr/aspartate-semialdehyde dehydrogenase [b3433]
asnA	-13.95	10.75	-3.80	12.65	0.0	8.85	0.0	0.00003150	0.00003748	0.0002196	0.00000000	A_07_P005641	b3744	cmr/asparagine synthetase A [b3744]
asnS	-2.68	10.21	-1.31	10.86	0.0	9.55	0.0	0.00052202	0.00417189	0.0512248	0.60178216	A_07_P005086	b0930	cmr/asparagine tRNA synthetase [b0930]
aspA	+10.66	15.86	+3.45	14.15	0.0	17.56	0.1	0.00000345	0.00002618	0.0000318	0.01426	A_07_P011426	b4139	cmr/aspartate ammonia-lyase [b4139]
aspC	+9.55	11.21	+3.26	9.58	0.2	10.36	0.5	0.01236687	0.00812060	0.0184547	0.36312500	A_07_P052047	Z1275	cmr/aspartate aminotransferase [Z1275]
aspC	-6.32	10.40	-2.66	11.73	0.0	9.07	0.1	0.00003132	0.00038273	0.0031962	0.38679104	A_07_P009616	b0928	cmr/aspartate aminotransferase [b0928]
astA	+8.45	9.05	+3.08	7.51	0.0	10.58	0.2	0.00001051	0.00004033	0.0013021	0.21367725	A_07_P014783	b1747	cmr/conf. hypothetical protein [b1747]
astC	-2.20	7.54	+1.14	6.58	0.1	7.71	0.1	0.01361116	0.03825255	0.0568369	0.59142424	A_07_P011768	b3748	cmr/arginosuccinate deacetylase [b3748]
astD	+3.06	7.63	+1.61	6.82	0.0	8.44	0.0	0.00017523	0.00159062	0.0318509	0.45267695	A_07_P014776	b1746	cmr/putative aldehyde dehydrogenase [b1746]
ATC	+7.52	9.13	+2.91	7.67	0.1	10.58	0.0	0.00000146	0.00012844	0.0000158	0.23098876	A_07_P009884	b2220	cmr/response regulator of dcu, anaerobic decarboxylase antisyme [b2220]
atoS	+7.61	9.95	+2.93	7.88	0.1	11.41	0.1	0.00000846	0.00030484	0.0061606	0.23807339	A_07_P000883	b2219	cmr/sensor protein AtoS for response regulator AtoC [b2219]
atpA	-6.44	15.52	-2.69	14.18	0.0	16.86	0.0	0.00003154	0.00037048	0.0090908	0.26214418	A_07_P005391	b3734	cmr/membrane-bound ATP synthase, F1 sector, alpha-subunit [b3734]
atpC	+2.57	13.11	+1.36	12.43	0.1	13.79	0.2	0.00086260	0.00615350	0.0415803	0.51397882	A_07_P005580	b3731	cmr/membrane-bound ATP synthase, F1 sector, epsilon-subunit [b3731]
atpD	+5.52	11.67	+2.46	10.44	0.0	12.90	0.1	0.00002855	0.00057424	0.0119373	0.29073895	A_07_P005582	b3732	cmr/membrane-bound ATP synthase, F0 sector, subunit c [b3732]
atpE	+4.92	12.70	+2.30	11.58	0.0	13.85	0.1	0.00003865	0.00068020	0.0146031	0.32246659	A_07_P005607	b3737	cmr/membrane-bound ATP synthase, F0 sector, subunit c [b3737]
atpG	+4.63	12.21	+2.15	11.14	0.0	13.29	0.1	0.00002244	0.00028364	0.0170329	0.34892748	A_07_P005587	b3733	cmr/membrane-bound ATP synthase, F1 sector, gamma-chain [b3733]
atpH	+8.48	13.14	+3.08	11.60	0.1	14.68	0.3	0.00003615	0.00056813	0.0513690	0.21307292	A_07_P005596	b3735	cmr/membrane-bound ATP synthase, F1 sector, delta-subunit [b3735]
atpI	-2.02	13.37	-1.01	13.87	0.0	12.86	0.0	0.00176130	0.01059474	0.0819767	0.72271646	A_07_P005664	b3739	cmr/membrane-bound ATP synthase, F0 sector, dicyclohexylamine-binding protein, affects expression of atpB [b3739]
azoR	+3.23	9.03	+1.69	8.19	0.2	9.88	0.1	0.00040756	0.00340705	0.0291919	0.44760496	A_07_P009153	b0412	cmr/acyl carrier protein phosphodiesterase [b0412]
b0157	-12.79	14.68	-3.68	16.51	0.0	12.84	0.1	0.00000373	0.00003748	0.0003314	0.05417524	A_07_P007992	b0157	cmr/putative transposase [b0157]
b0322	-6.29	9.10	-2.65	10.43	0.1	7.77	0.1	0.00002747	0.00056718	0.0332451	0.18699634	A_07_P008305	b0322	cmr/conf. hypothetical protein [b0322]
b0559	-2.75	8.46	-1.45	9.18	0.1	7.74	0.1	0.00138511	0.00883234	0.0488542	0.53516614	A_07_P010924	b0559	cmr/putative transferase [b0559]
b0559	-2.09	7.85	-1.06	8.38	0.1	7.32	0.1	0.00259398	0.01420014	0.0118394	0.69452217	A_07_P010289	b0559	cmr/putative transferase [b0559]
b0574	-8.06	8.09	-3.01	9.60	0.1	6.59	0.1	0.00003344	0.00038460	0.0194835	0.12751051	A_07_P020983	b0574	cmr/putative flagellin structural protein [b0574]
b0595	-2.02	7.88	+1.02	6.87	0.1	7.89	0.1	0.00276950	0.01

c_0965	-2.15	8.02	-1.10	8.57	0.1	7.47	0.2	0.00335318	0.01737166	0.07310976	0.66882045	A_07_P033690	c_0965	cmr	Phage baseplate assembly protein [c_0965]
c_1020	-3.09	8.72	-2.35	9.60	0.1	7.55	0.1	0.0000312	0.00061325	0.06611153	0.25052292	A_07_P033805	c_1020	cmr	Hypothetical protein [c_1020]
c_1094	-2.58	10.65	-1.37	11.33	0.3	8.96	0.1	0.01578674	0.01608540	0.04521556	0.57117230	A_07_P033878	c_1094	cmr	Hypothetical protein [c_1094]
c_1109	-2.45	7.36	-1.29	8.01	0.2	6.72	0.1	0.00136602	0.00873191	0.05187691	0.68096938	A_07_P033900	c_1109	cmr	Hypothetical protein [c_1109]
c_1138	-4.44	9.83	-2.15	8.56	0.3	10.71	0.1	0.00336663	0.00323752	0.01659007	0.34765304	A_07_P033937	c_1138	cmr	Hypothetical protein [c_1138]
c_1165	-4.05	10.54	-2.02	11.55	0.1	9.53	0.3	0.00033452	0.00302754	0.01215109	0.34617060	A_07_P033966	c_1165	cmr	Putative F4-family integrase [c_1165]
c_1166	-14.00	9.49	-8.31	7.99	0.2	11.79	0.1	0.00005552	0.00052298	0.00188135	0.13052214	A_07_P033974	c_1166	cmr	Conserved hypothetical protein [c_1166]
c_1172	-3.92	8.18	-1.97	9.17	0.1	7.20	0.2	0.00026658	0.00256661	0.01358159	0.36934097	A_07_P034010	c_1172	cmr	Hypothetical protein [c_1172]
c_1173	-7.27	11.03	-2.86	12.46	0.1	9.59	0.4	0.00014505	0.00167512	0.01364516	0.15014563	A_07_P034004	c_1173	cmr	Hypothetical protein [c_1173]
c_1174	-2.55	10.03	-1.35	10.70	0.2	9.35	0.3	0.00350400	0.01798140	0.04948830	0.57231804	A_07_P034026	c_1174	cmr	Hypothetical protein [c_1174]
c_1176	-2.12	9.66	-1.08	10.50	0.1	9.41	0.2	0.00266431	0.01448443	0.07819397	0.68272828	A_07_P034026	c_1176	cmr	Hypothetical protein [c_1176]
c_1175	+6.89	8.26	+2.79	8.57	0.1	9.66	0.3	0.00008006	0.00111049	0.00770198	0.24797546	A_07_P034022	c_1175	cmr	Putative aminotransferase [c_1175]
c_1187	-5.89	7.64	-2.56	6.36	0.4	8.92	0.0	0.00016727	0.00187302	0.01046050	0.27769462	A_07_P034261	c_1187	cmr	2-oxoacyl-[c_1187]
c_1189	+5.20	8.29	+2.38	7.10	0.0	9.48	0.0	0.00002203	0.00050626	0.01328869	0.30561584	A_07_P034271	c_1189	cmr	Putative 3-oxoacyl- [c_1189]
c_1190	+8.69	8.57	+3.12	7.01	0.0	10.13	0.0	0.00003852	0.00030648	0.00481898	0.20843407	A_07_P034280	c_1190	cmr	Conserved hypothetical protein [c_1190]
c_1191	+2.05	7.23	+1.06	6.71	0.1	7.74	0.2	0.00475415	0.02276887	0.06378887	0.64174721	A_07_P034284	c_1191	cmr	Conserved hypothetical protein [c_1191]
c_1192	+4.34	8.63	+2.12	7.57	0.1	9.68	0.0	0.00006550	0.00075592	0.01775152	0.35278130	A_07_P034286	c_1192	cmr	Conserved hypothetical protein [c_1192]
c_1193	+7.00	9.36	+2.81	7.96	0.1	10.76	0.2	0.00003170	0.00061914	0.00749174	0.26624217	A_07_P034293	c_1193	cmr	Hypothetical protein [c_1193]
c_1194	+4.78	7.97	+2.26	6.84	0.0	9.10	0.1	0.00003914	0.00068369	0.01511433	0.33050800	A_07_P034296	c_1194	cmr	Putative enzyme [c_1194]
c_1200	+2.01	10.26	+1.00	9.75	0.0	10.76	0.1	0.00245447	0.01356706	0.06988313	0.66080480	A_07_P034321	c_1200	cmr	Putative acyl carrier protein [c_1200]
c_1205	-2.17	9.21	-1.12	9.77	0.0	8.65	0.1	0.00115753	0.00775881	0.07166552	0.67156340	A_07_P034348	c_1205	cmr	Hypothetical protein [c_1205]
c_1209	-2.23	9.65	-1.16	10.23	0.2	9.07	0.4	0.01197511	0.04785138	0.06433117	0.64841869	A_07_P034366	c_1209	cmr	Hypothetical protein [c_1209]
c_1210	-3.76	8.04	-1.67	8.79	0.1	7.31	0.3	0.00180614	0.01078199	0.03774454	0.52916296	A_07_P034372	c_1210	cmr	Hypothetical protein [c_1210]
c_1215	-3.68	12.79	-1.88	13.67	0.0	11.79	0.1	0.00008572	0.00110948	0.01570759	0.28291601	A_07_P034390	c_1215	cmr	Entry exclusion protein 2 [c_1215]
c_1219	-2.58	8.19	-1.37	8.88	0.0	7.51	0.5	0.00761766	0.03332381	0.04539317	0.57127898	A_07_P034407	c_1219	cmr	Putative Transposase [c_1219]
c_1220	-2.07	9.22	-1.05	9.74	0.2	8.69	0.2	0.00875090	0.03796027	0.08548979	0.71267829	A_07_P034413	c_1220	cmr	Phosphe-2-dehydro-3-deoxyheptonate aldolase, Trp-sensitive [c_1220]
c_1225	-2.71	10.02	-1.44	10.73	0.1	9.30	0.3	0.00175968	0.01059037	0.03802022	0.53562017	A_07_P034430	c_1225	cmr	Transposase IncE for insertion sequence ISAs8/B/C/D/E/F/N/R [c_1225]
c_1235	-12.55	8.68	-3.65	10.51	0.0	6.86	0.0	0.00003232	0.00017963	0.00013276	0.05439108	A_07_P034469	c_1235	cmr	Conserved hypothetical protein [c_1235]
c_1236	-7.97	8.79	-2.99	10.29	0.0	7.29	0.1	0.00003828	0.00030193	0.00149644	0.12874317	A_07_P034474	c_1236	cmr	Conserved hypothetical protein [c_1236]
c_1240	-7.11	10.49	-2.83	9.07	0.1	11.90	0.1	0.00003320	0.00041877	0.00731995	0.24409664	A_07_P034521	c_1240	cmr	Hypothetical protein [c_1240]
c_1253	-3.62	9.79	-1.86	10.72	0.1	8.86	0.1	0.00012043	0.00147672	0.01668321	0.39703480	A_07_P034560	c_1253	cmr	ATP binding cassette [c_1253]
c_1257	-10.51	11.11	-4.36	11.29	0.1	8.93	0.1	0.00003127	0.00014546	0.00069572	0.02000300	A_07_P034573	c_1257	cmr	Putative conserved protein [c_1257]
c_1258	-2.36	7.73	-1.24	8.35	0.4	7.11	0.0	0.00566401	0.02623543	0.05457965	0.61680958	A_07_P034577	c_1258	cmr	Hypothetical protein [c_1258]
c_1259	-2.13	10.01	-1.09	10.55	0.2	9.46	0.3	0.01075793	0.04409664	0.07868481	0.68452640	A_07_P034585	c_1259	cmr	Hypothetical protein [c_1259]
c_1261	-2.01	9.53	-1.00	10.03	0.0	9.03	0.2	0.00365562	0.01863115	0.09113979	0.72454040	A_07_P034595	c_1261	cmr	Hypothetical protein [c_1261]
c_1268	-2.05	8.46	-1.03	8.98	0.0	7.94	0.1	0.00224821	0.01312861	0.06428862	0.70775667	A_07_P034616	c_1268	cmr	Hypothetical protein [c_1268]
c_1272	-3.75	8.18	-1.91	9.13	0.1	7.22	0.1	0.00031683	0.00160881	0.01488758	0.38614948	A_07_P034636	c_1272	cmr	Hypothetical protein yeeP [c_1272]
c_1273	-7.59	11.90	-2.92	10.43	0.1	13.36	0.2	0.00002542	0.00056498	0.00644881	0.23032676	A_07_P034643	c_1273	cmr	Antigen 43 precursor [c_1273]
c_1278	-2.62	9.47	-1.07	9.70	0.0	8.46	0.3	0.00379027	0.01910752	0.05272991	0.60420670	A_07_P034661	c_1278	cmr	Hypothetical protein yeeP [c_1278]
c_1284	-4.43	11.18	-2.15	12.26	0.2	10.11	0.6	0.00290038	0.01564459	0.08669372	0.31069388	A_07_P034687	c_1284	cmr	Hypothetical protein yeeP [c_1284]
c_1286	-9.03	9.86	-3.18	11.45	0.0	8.27	0.0	0.00001133	0.00035103	0.01005818	0.10412500	A_07_P034696	c_1286	cmr	Hypothetical protein [c_1286]
c_1294	-3.68	7.74	-1.80	8.64	0.0	6.84	0.1	0.00160534	0.00167760	0.03093032	0.43984722	A_07_P034732	c_1294	cmr	Hypothetical protein [c_1294]
c_1323	+2.74	8.01	+1.45	7.29	0.1	8.74	0.0	0.00032449	0.00266322	0.00438928	0.49605924	A_07_P034769	c_1323	cmr	Cytochrome b561 homolog 2 [c_1323]
c_1406	-3.49	8.26	-1.80	9.16	0.1	7.36	0.4	0.00175340	0.01054472	0.03837607	0.41337143	A_07_P034862	c_1406	cmr	Hypothetical protein [c_1406]
c_1413	-4.06	9.67	-2.02	10.68	0.2	8.66	0.1	0.00037714	0.01693940	0.01835023	0.36278439	A_07_P034889	c_1413	cmr	Unknown protein encoded within prophage [c_1413]
c_1417	-2.57	10.14	-1.16	10.82	0.1	9.46	0.3	0.02239329	0.01368814	0.04700320	0.57606202	A_07_P034899	c_1417	cmr	Unknown protein encoded within prophage [c_1417]
c_1419	-3.68	9.78	-1.88	10.72	0.3	8.84	0.1	0.00047650	0.00372058	0.01584013	0.39146113	A_07_P034893	c_1419	cmr	Unknown protein encoded within prophage [c_1419]
c_1414	-2.99	8.83	-1.58	9.63	0.2	8.04	0.6	0.00991262	0.04113502	0.03014176	0.49062500	A_07_P034893	c_1414	cmr	Hypothetical protein [c_1414]
c_1414	-2.45	8.97	-1.30	9.62	0.1	8.33	0.1	0.00016490	0.00486152	0.01318205	0.18172177	A_07_P034893	c_1414	cmr	Hypothetical protein [c_1414]
c_1414	-2.01	9.02	-1.01	9.52	0.0	8.52	0.2	0.00515178	0.02431532	0.01942721	0.72551915	A_07_P034893	c_1414	cmr	Hypothetical protein [c_1414]
c_1414	-2.24	8.80	-1.16	9.38	0.0	8.22	0.1	0.00118692	0.00785490	0.04678100	0.66473455	A_07_P034893	c_1414	cmr	Hypothetical protein [c_1414]
c_1421	-11.90	9.55	-3.57	11.34	0.1	7.76	0.0	0.00000334	0.00001859	0.00040550	0.06213592	A_07_P034925	c_1421	cmr	Hypothetical protein [c_1421]
c_1436	-2.91	8.73	-1.54	9.50	0.2	7.96	0.3	0.00130710	0.01662261	0.03119982	0.49179170	A_07_P034220	c_1436	cmr	Probable lysozyme from lambdoid prophage Qin [c_1436]
c_1448	+11.89	10.84	+3.57	9.05	0.1	12.63	0.2	0.00008537	0.00024927	0.02248809	0.14354015	A_07_P034321	c_1448	cmr	Putative capsid assembly protein of prophage [c_1448]
c_1453	+6.09	10.94	+2.61	9.64	0.1	12.25	0.2	0.00008416	0.00078282	0.00397722	0.27033163	A_07_P034818	c_1453	cmr	Putative head-tail joining protein of prophage [c_1453]
c_1459	+2.00	8.32	+1.00	7.82	0.3	8.82	0.1	0.01115716	0.04526940	0.07630780	0.68069109	A_07_P034838	c_1459	cmr	Putative tail component of prophage [c_1459]
c_1461	-2.09	8.22	-1.06	7.69	0.2	8.76	0.0	0.00275176	0.01478968	0.06394881	0.62281584	A_07_P034846	c_1461	cmr	Putative tail fiber component M of prophage [c_1461]
c_1487	-2.38	10.35	-1.25	10.98	0.1	9.72	0.3	0.00297776	0.01582777	0.05558181	0.61360059	A_07_P038235	c_1487	cmr	Hypothetical protein [c_1487]
c_1496	-3.34	9.26	-1.74	10.13	0.5	8.39	0.3	0.00534692	0.02497852	0.02018893	0.43428699	A_07_P038279	c_1496	cmr	Unknown protein encoded by prophage [c_1496]
c_1499	+2.00	8.47	+1.00	7.97	0.0	8.97	0.3	0.00520615	0.02456795	0.07251207	0.67194232	A_07_P038295	c_1499	cmr	Putative capsid protein of prophage [c_1499]
c_1501	+2.63	8.87	+1.39	8.37	0.0	9.56	0.1	0.00045664	0.00376599	0.04177391	0.59861562	A_07_P038305	c_1501	cmr	Hypothetical protein [c_1501]
c_1506	-3.10	8.02	-1.63	8.83	0.0	7.20	0.3	0.00125088	0.00691212	0.02758892	0.48103883	A_07_P038330	c_1506	cmr	Unknown protein encoded by prophage [c_1506]
c_1514	-5.32	11.55	-2.41	12.75	0.0	10.34	0.1	0.00002420	0.00052203	0.00514101	0.23125714	A_07_P038334	c_1514	cmr	Hypothetical protein [c_1514]
c_1522	+12.23	9.47	+4.60	7.66	0.4	11.27	0.2	0.00002302	0.00082314	0.00216038	0.14382239	A_07_P038354	c_1522	cmr	Hypothetical protein [c_1522]
c_1523	+6.52	10.62	+2.73	9.26	0.1	11.99	0.2	0.00003677	0.00060214	0.00840467	0.25593810	A_07_P038459	c_1523	cmr	Unknown protein encoded by bacteriophage [c_1523]
c_1524	-5.43	9.34	-2.44	8.12	0.0	10.56	0.6	0.00136265	0.00872024	0.01314486	0.28594627	A_07_P038365	c_1524	cmr	Hypothetical protein [c_1524]
c_1525	+12.04	11.23	+3.59	9.44	0.0	13.03	0.2	0.00000470	0.00032240	0.00246888	0.14449814	A_07_P038369	c_1525	cmr	Hypothetical protein [c_1525]
c_1526	+9.60	9.39	+3.26	7.76	0.1	11.02	0.0	0.00005644	0.00027934	0.00386179	0.18424242	A_07_P038374	c_1526	cmr	Hypothetical protein [c_1526]
c_1527	+5.41	8.86	+2.44	7.65	0.3	10.08	0.1	0.00021694	0.00223672	0.01210048	0.29219325	A_07_P038377	c_1527	cmr	Hypothetical protein [c_1527]
c_1528	+6.19	9.20	+2.09	7.65	0.3	10.74	0.3	0.00008505	0.00116565	0.00509654	0.21397313	A_07_P038381	c_1528	cmr	Hypothetical protein [c_1528]
c_1530	-2.98	9.55	-1.57	10.33	0.0	8.76	0.5	0.00376543	0.01904978	0.02869013	0.48417197	A_07_P038389	c_1530	cmr	Hypothetical protein [c_1530]
c_1531	+11.98	9.85	+3.58	7.98	0.0	11.72	0.1	0.00004644	0.00028417	0.00438939	0.13422031	A_07_P038395	c_1531	cmr	Hypothetical protein [c_1531]
c_1536	-1.01	12.18	-1.59	12.98	0.1	11.38	0.2	0.00055291	0.00435904	0.02944741	0.48699580	A_07_P038406	c_1536	cmr	Putative recombination protein ilet of prophage [c_1536]
c_1538	-12.71	11.30	-4.44	10.67	0.0	12.11	0.1	0.00039818	0.00340501	0.00166428	0.49911859	A_07_P038419	c_1538	cmr	Hypothetical protein [c_1538]
c_1542	-66.74	13.12	-5.55	15.89	0.0	10.35	0.1	0.00000027	0.00000047	0.00000191	0.00375000	A_07_P038431	c_1542	cmr	Lambda anti-restriction protein [c_1542]
c_1544	-2.06	8.49	-1.04	9.01	0.0	7.97	0.3	0.00275176	0.01478968	0.06394881	0.62281584	A_07_P038443	c_1544	cmr	Putative tail fiber component M of prophage [c_1544]
c_1546	-4.07	13.02	-2.03	13.42	0.0	11.39	0.3	0.00023714	0.00238260	0.01175940	0.34998110	A_07_P038451	c_1546	cmr	Repressor protein [c_1546]
c_1547	-2.74	11.08	-1.45	11.83	0.1	10.36	0.2	0.00372865	0.00545616	0.03766813	0.52993576	A_07_P038456	c_1547	cmr	Hypothetical protein [c_1547]
c_1548	-2.75	10.57	-1.46	11.30	0.2	9.84	0.0	0.00056572	0.00496004	0.03846830	0.53427184	A_07_P038465	c_1548	cmr	Putative Regulatory protein CII of bacteriophage [c_1548]
c_1551	-3.23	12.85	-2.39	14.05	0.0	11.66	0.2	0.00005928	0.00090081	0.00568213	0.24568245	A_07_P038478	c_1551	cmr	Putative exclusion protein rer of prophage [c_1551]
c_1554	+6.58	9.29	+2.73	7.93	0.2	10.65	0.2	0.00002259	0.00051403	0.00846329	0.26608966	A_07_P038485	c_1554	cmr	Unknown protein encoded within prophage [c_1554]
c_1555	+3.64	8.28	+1.86	7.35	0.1	9.21	0.6	0.00542090	0.02536304	0.02456967	0.40482263	A_07_P038490	c_1555	cmr	Putative DNA N-6-adenine-methyltransferase of bacteriophage [c_1555]
c_1556	+4.65	9.22	+2.07	7.28	0.1	10.17	0.1	0.00016491	0.00400501	0.01406604	0.12300077	A_07_P038493	c_1556	cmr	Hypothetical protein [c_1556]
c_1565	+5.92	12.80	+2.57	11.51	0.2	14.08	0.0	0.00006106	0.00009144	0.01045986	0.27723906	A_07_P038514	c_1565	cmr	Partial tonB-like membrane protein encoded within prophage [c_1565]
c_1567	+2.96	9.64	+1.56	8.86	0.1	10.42	0.1	0.00036981	0.00258239	0.01838106	0.46790167	A_07_P038518	c_1567	cmr	Hypothetical protein [c_1567]
c_1570	+3.09	11.03	+1.63	10.21	0.4	11.84	0.0	0.00239982	0.01133149	0.01165523	0.45266122	A_07_P038512	c_1570	cmr	Putative DNA packaging protein of prophage [c_1570]
c_1572	+4.79	9.23	+2.26	8.10	0.0	10.36	0.1	0.00005122	0.00088157	0.01583194	0.31717155	A_07_P038528	c_1572	cmr	Putative capsid protein of prophage [c_1572]
c_1573	+25.59	10.19	+6.68	7.86	0.1	12.53	0.3	0.00003363	0.00026691	0.00047256	0.06584071	A_07_P038541	c_1573	cmr	Putative capsid assembly protein of prophage [c_1573]
c_1574	+13.26	10.19	+3.73	8.32	0.1	12.05	0.2	0.00005578	0.00025782	0.00201791	0.11292087	A_07_P038551	c_1574	cmr	Putative capsid protein of prophage [c_1574]
c_1575	+11.58	9.11	+3.53	7.34	0.2	10.87	0.1	0.00000730	0.00028727	0.00268229	0.15028470	A_07_P038556	c_1575	cmr	Putative capsid protein of prophage [c_1575]
c_1576	+8.83	9.22	+4.14	7.65	0.1	10.79	0.2	0.00003621	0.00045227	0.00422527	0.20318807	A_07_P038564	c_1576	cmr	Hypothetical protein [c_1576]
c_1577	+10.65	8.74	+3.41	7.03	0.1	10.44	0.0	0.00003460	0.00032328	0.00320694	0.16663366	A_07_P038569	c_1577	cmr	Putative head-tail joining protein of prophage [c_1577]
c_1579	+4.53	10.64	+2.18	9.55	0.1	11.73	0.8	0.00600228	0.02752681	0.01682674	0.32703903	A_07_P038580	c_1579	cmr	Putative tail component of prophage [c_1579]
c_1580	+24.47	9.33	+4.61	7.03	0.0	11.64	0.2	0.00000181	0.00016633	0.00050051	0.06851274	A_07_P038581	c_1580	cmr	Tail protein [c_1580]
c_1583	+7.22	9.32	+2.85	7.89	0.0	10.75	0.2	0.00000316	0.00057634	0.00700681	0.23993246	A_07_P038584	c_1583	cmr	Putative tail component of prophage [c_1583]
c_1585	+2.85	9.65	+1.51	8.89	0.2	10.40	0.2	0.00117138	0.00778480	0.03629953	0.48093513	A_07_P038605	c_1585	cmr	Putative tail component of prophage [c_1585]
c_1591	+3.06	9.52	+1.61	8.72	0.0	10.32	0.0	0.00121892	0.00802385	0.01822677	0.47869819	A_07_P038627	c_1591	cmr	Hypothetical protein [c_1591]
c_1593	+2.70	7.89	+1.43	7.17	0.2	8.60	0.1	0.00070403	0.00525566	0.03933117	0.49777331	A_07_P038645	c_1593	cmr	Hypothetical protein [c_1593]
c_1596	+2.44	9.06	+1.28	8.70	0.0	9.42	0.2	0.01004283	0.00721961	0.02136697	0.60356115	A_07_P038656	c_1596	cmr	Hypothetical protein [c_1596]
c_1605	+2.27	11.93	+1.18	12.52	0.1	11.34	0.1	0.01404321	0.00890456	0.04478859	0.65051520	A_07_P038687	c_1605	cmr	Putative tail component of prophage [c_1605]
c_1611	-2.70	8.22	-1.44	8.93	0.1	7.50	0.5	0.00986607	0.04101699	0.04278220	0.54479881	A_07_P038708	c_1611	cmr	Hypothetical protein [c_1611]
c_1640	-2.55	12.17	-1.35	12.85	0.1	11.50	0.3	0.00245007	0.01365867	0.04756606	0.59873261	A_07_P038726	c_1640	cmr	Putative Na (+_1640
c_1657	+7.68	8.66	+2.94	7.19	0.1	10.13	0.2	0.00002191	0.00084911	0.00622269	0.22783721	A_07_P038777	c_1657	cmr	Protein yogD [c_1657]
c_1660	-3.13	9.56	-1.64	10.38	0.0	8.74	0.1	0.00018403	0.00199406	0.01223122	0.47329296	A_07_P038788	c_1660	cmr	Hypothetical protein [c_1660]
c_1714	-8.09	10.75	-3.02	12.25	0.1	9.24	0.0	0.00000804	0.00029787	0.00143610	0.12631285	A_07_P038863	c_1714	cmr	Hypothetical protein [c_1714]
c_1752	-2.19	7.90	-1.13	8.47	0.0	7.34	0.1	0.00181297	0.01081697	0.07126919	0.68479559	A_07_P038919	c_1752	cmr	Hypothetical protein [c_1752]
c_1755	+2.57	9.09	+1.36	8.41	0.0	9.77	0.2	0.00077220	0.00564414	0.04302973	0.51283876	A_07_P038912	c_1755	cmr	Conserved hypothetical protein [c_1755]
c_1800	-5.46	9.31	-2.45	8.09	0.1	10.54	0.0	0.00002239	0.00051096	0.01214663	0.26246404	A_07_P047601	c_1800	cmr	Conserved hypothetical protein [c_1800]
c_1812	-3.02	9.58	-1.60	10.38	0.2	8.78	0.0	0.00113219	0.00759093	0.02815611	0.48167573	A_07_P047985	c_1812	cmr	Hypothetical protein [c_1812]
c_1825	+5.16	10.46	+2.43	9.25	0.3	11.67	0.1	0.00016609	0.00145453	0.01243663	0.29571512	A_07_P048801	c_1825	cmr	Hypothetical protein [c_1825]
c_1862	+2.32	7.63	+1.21	7.02	0.1	8.24	0.2	0.00279918	0.01607013	0.05195876	0.56478849	A_07_P042298	c_1862	cmr	Hypothetical protein [c_1862]
c_1889	-2.03	8.26	-1.02	8.77	0.1	7.74	0.2	0.00492419	0.02012275	0.08614266	0.75385226	A_07_P042839	c_1889	cmr	Hypothetical protein [c_1889]
c_1935	-3.60	8.72	-1.85	9.65	0.2	7.80	0.1	0.00024641	0.00240404	0.01743521	0.40427099	A_07_P043887	c_1935	cmr	Chaperone protein fimC precursor [c_1935]
c_1956	-3.65	11.00	-1.87	11.94	0.2	10.07	0.2	0.00004119	0.00460227	0.01602960	0.39248884	A_07_P045043	c_1956	cmr	Putative outer membrane protein yeeC precursor [c_1956]
c_1989	-6.56	10.87	-2.71	12.23	0.1	9.51	0.2	0.00000123	0.00060413	0.00284172	0.17549098	A_07_P050078	c_1989	cmr	Putative acid shock protein [c_1989]
c_1994	+3.13	9.44	+1.65	8.62	0.1	10.26	0.1	0.00018037	0.00195682	0.00357882	0.44536000	A_07_P050084	c_1994	cmr	NAD [c_1994]
c_2032	+2.41	10.55	+1.27	9.92	0.0	11.19	0.1	0.00091344	0.00646629	0.04634232	0.54741565	A_07_P051530	c_2032	cmr	Hypothetical protein ybfM [c_2032]
c_2146	+1.35	8.10	+1.30	8.25	0.1	9.95	0.1	0.00017967	0.00195827	0.02862360	0.43892334	A_07_P042367	c_2146	cmr	Succinylglutamic semialdehyde dehydrogenase [c_2146]
c_2148	+5.05	8.40	+2.34	7.24	0.4	9.57	0.0	0.00049455	0.00364142	0.01340705	0.30814599	A_07_P042398	c_2148	cmr	Succinylornithine transaminase [c_2148]
c_2155	+9.37	9.89	+3.23	8.28	0.2	11.51	0.0	0.00003272	0.00037366	0.00421494	0.19179391	A_07_P042371	c_2155	cmr	Protein yrqB [c_2155]
c_2158	+6.86	9.73	+2.78	8.34	0.0	11.12	0.1	0.00013117	0.00034997	0.00792692	0.24854582	A_07_P042171	c_2158	cmr	Putative thiosulfate sulfurtransferase yrqB precursor [c_2158]
c_2225	-2.20	7.59	-1.13	8.16	0.2	7.02	0.1	0.00138551	0.01948807	0.09915015	0.65822249	A_07_P053300	c_2225	cmr	Hypothetical protein [c_2225]
c_2255	-18.72	9.92	-4.84	12.35	0.0	7.50	0.0	0.00000047	0.00009262	0.00011068	0.01138664	A_07_P053318	c_2255	cmr	Hypothetical protein [c_2255]
c_2348	+55.15	10.34	+5.79	7.45	0.4	13.23	0.1	0.00000348	0.00032221	0.00010163	0.02962963	A_07_P053389	c_2348	cmr	Outer membrane porin protein nmpC precursor [c_2348]
c_2393	+3.50	8.20	+1.81	7.30	0.0	9.10	0.2	0.00043122	0.00360802	0.02520490	0.41147150	A_07_P053420	c_2393	cmr	Hypothetical protein [c_2393]
c_2405	+2.59	8.13	+1.37	7.44	0.1	8.81	0.0	0.00074688	0.00388371	0.04237071	0.51036043	A_07_P053475	c_2405	cmr	Hypothetical protein [c_2405]
c_2406	+2.87	8.89	+1.52	8.13	0.0	9.65	0.2	0.00055159	0.00411787	0.03179322	0.47801189	A_07_P053476	c_2406	cmr	Hypothetical protein [c_2406]
c_2412	-2.58	9.43	-1.37	10.12	0.4	8.75	0.1	0.00481865	0.02006011	0.04496380	0.57120648	A_07_P053509	c_2412	cmr	Hypothetical protein [c_2412]
c_2418	-2.32	9.21	-1.22	9.82	0.3	8.60	0.2	0.00541862	0.02135948	0.06039888	0.61484653	A_07_P053511	c_2418	cmr	Prophage P4 integrase [c_2418]
c_2438	-3.34	8.06	-1.74	8.93	0.1	7.19	0.0	0.00104725	0.01069348	0.01238891	0.44064389	A_07_P053423	c_2438	cmr	Hypothetical protein [c_2438]
c_2450	+5.76	12.50	+2.53	11.24	0.0	13.77	0.1	0.00001824	0.00004319	0.01016126	0.28047725	A_07_P053448	c_2450	cmr	Hypothetical protein [c_2450]
c_2451	+14.98	11.70	+3.91	9.75	0.0	13.65	0.1	0.00000175	0.00016311	0.00161141	0.12131534	A_07_P053451	c_2451	cmr	Putative thioesterase [c_2451]
c_2452	+3.60	10.50	+1.58	9.60	0.0	11.20	0.0	0.00009054	0.00058846	0.00419195	0.32788272	A_07_P053458	c_2452	cmr	Hypothetical protein [c_2452]
c_2453	+4.60	8.77	+2.20	7.67	0.1	9.87	0.1	0.00008211	0.00092690	0.01617886	0.33917643	A_07_P053461	c_2453	cmr	Putative polyketide synthase [c_2453]
c_2454	+14.68	9.51	+3.88	7.57	0.0	11.45

c_3655	+9.86	11.91	+3.30	10.26	0.1	13.56	0.1	0.00000621	0.00026588	0.00369538	0.18124611	A_07_P036451	c_3655	cmr	Antigen 43 precursor [c_3655]
c_3656	+2.13	7.87	+1.09	7.33	0.1	8.42	0.2	0.00048264	0.02060378	0.06413237	0.63343789	A_07_P036463	c_3656	cmr	Hypothetical protein [c_3656]
c_3658	-35.95	14.03	-5.17	16.62	0.0	11.45	0.0	0.00000035	0.00009317	0.00000572	0.00750000	A_07_P036466	c_3658	cmr	Hypothetical protein [c_3658]
c_3659	-49.34	9.69	-5.62	12.50	0.0	6.88	0.2	0.00000040	0.00009146	0.00000591	0.00500000	A_07_P036474	c_3659	cmr	Unknown protein encoded by GlcK [c_3659]
c_3660	-48.03	9.74	-5.59	12.53	0.0	6.95	0.1	0.00000027	0.00009047	0.00000327	0.00400000	A_07_P036480	c_3660	cmr	Unknown protein encoded by GlcK [c_3660]
c_3662	-2.37	11.71	-1.24	12.13	0.1	11.09	0.1	0.00389006	0.00626937	0.03808816	0.62319956	A_07_P036488	c_3662	cmr	Unknown protein encoded by GlcK [c_3662]
c_3663	-4.87	8.67	-2.28	9.82	0.1	7.53	0.2	0.00037089	0.00169306	0.00487919	0.07977556	A_07_P036493	c_3663	cmr	Hypothetical protein [c_3663]
c_3665	+2.26	11.30	+1.18	10.72	0.0	11.89	0.1	0.00123504	0.00811203	0.05436992	0.57951515	A_07_P036501	c_3665	cmr	Hypothetical protein [c_3665]
c_3666	-2.28	8.08	-1.19	8.68	0.0	7.49	0.1	0.00104263	0.00712961	0.06123056	0.61288320	A_07_P036509	c_3666	cmr	Hypothetical protein pilE [c_3666]
c_3668	-2.61	8.97	-1.39	9.66	0.1	8.27	0.2	0.00136309	0.00872024	0.04452236	0.50988018	A_07_P036519	c_3668	cmr	Hypothetical protein pilE [c_3668]
c_3670	-4.73	8.85	-2.24	9.97	0.0	7.72	0.2	0.00006553	0.00067634	0.00714700	0.28425837	A_07_P036528	c_3670	cmr	Hypothetical protein [c_3670]
c_3672	-3.03	9.12	-1.60	9.92	0.1	8.32	0.4	0.02048863	0.01184927	0.02919661	0.48483232	A_07_P036541	c_3672	cmr	Hypothetical protein [c_3672]
c_3675	2.76	9.63	-1.47	10.36	0.0	8.89	0.2	0.00068017	0.00512982	0.03792492	0.53074667	A_07_P036560	c_3675	cmr	Hypothetical protein [c_3675]
c_3678	-2.10	8.72	-1.07	9.26	0.1	8.19	0.2	0.04848374	0.02028854	0.07766641	0.67894503	A_07_P036567	c_3678	cmr	Conserved hypothetical protein [c_3678]
c_3681	-10.84	11.97	-3.44	13.68	0.0	10.25	0.1	0.00025343	0.00055367	0.00035669	0.07972566	A_07_P036583	c_3681	cmr	Hypothetical protein [c_3681]
c_3682	-9.50	11.96	-3.25	12.78	0.0	9.54	0.2	0.00001168	0.00035700	0.00087970	0.00822695	A_07_P036586	c_3682	cmr	Hypothetical protein [c_3682]
c_3683	-34.22	12.32	-5.10	14.86	0.0	9.77	0.0	0.00000039	0.00009117	0.00000635	0.00660667	A_07_P036593	c_3683	cmr	Hypothetical protein [c_3683]
c_3686	+16.66	10.71	+6.06	8.68	0.1	12.74	0.1	0.00000274	0.00018406	0.00126524	0.10539683	A_07_P036604	c_3686	cmr	Hypothetical protein yrbI [c_3686]
c_3689	+16.21	10.05	+4.02	8.04	0.1	12.05	0.1	0.00000108	0.00017252	0.00113040	0.10958115	A_07_P036613	c_3689	cmr	3-deoxy-manno-octulosonate cytidylyltransferase [c_3689]
c_3693	+7.73	9.61	+2.95	8.14	0.2	11.09	0.2	0.00005910	0.00088898	0.06613758	0.72577103	A_07_P036636	c_3693	cmr	Hypothetical protein [c_3693]
c_3693	+9.97	10.32	+3.32	8.66	0.1	11.98	0.1	0.00001779	0.00045523	0.00373666	0.38270186	A_07_P036636	c_3693	cmr	Hypothetical protein [c_3693]
c_3693	+7.13	9.84	+2.83	8.42	0.0	11.25	0.5	0.00032740	0.00298128	0.00760047	0.23854077	A_07_P036636	c_3693	cmr	Hypothetical protein [c_3693]
c_3694	+10.44	10.10	+3.38	8.41	0.1	11.79	0.2	0.00008846	0.00308484	0.03330221	0.16770968	A_07_P036636	c_3693	cmr	Hypothetical protein [c_3693]
c_3694	+10.46	10.13	+3.39	8.44	0.1	11.83	0.1	0.00000741	0.00028894	0.00192005	0.16827622	A_07_P036636	c_3693	cmr	Hypothetical protein [c_3693]
c_3694	+6.33	11.98	+2.66	10.64	0.0	13.31	0.1	0.00001670	0.00042422	0.00938865	0.26867031	A_07_P036641	c_3694	cmr	Hypothetical protein [c_3694]
c_3695	+7.63	10.41	+2.93	8.95	0.1	11.88	0.1	0.00002595	0.00055173	0.00423412	0.22772622	A_07_P036649	c_3695	cmr	Hypothetical protein [c_3695]
c_3696	+2.46	13.22	+1.30	12.57	0.1	13.87	0.2	0.00189270	0.01116147	0.04656059	0.53782008	A_07_P036652	c_3696	cmr	Putative glycerol-3-phosphate cytidyltransferase [c_3696]
c_3751	+2.12	8.03	+0.09	7.49	0.2	8.57	0.2	0.00612378	0.03262178	0.06446956	0.63650800	A_07_P036708	c_3751	cmr	Hypothetical oxidoreductase yrbI [c_3751]
c_3771	-2.25	9.35	-1.17	9.94	0.1	8.77	0.1	0.00153200	0.00948854	0.06463377	0.65585991	A_07_P036801	c_3771	cmr	Putative iron compound-binding protein of ABC transporter [c_3771]
c_3774	-2.08	7.98	-1.06	8.51	0.0	7.45	0.2	0.00147554	0.00926022	0.08115178	0.69673646	A_07_P036822	c_3774	cmr	Ferric enterobactin transport ATP-binding protein fepC [c_3774]
c_3819	-8.69	14.74	-3.12	16.30	0.0	13.18	0.1	0.00000629	0.00002673	0.00116235	0.10958084	A_07_P036906	c_3819	cmr	Putative conserved protein [c_3819]
c_3873	+124.02	11.50	+8.34	7.33	0.1	15.67	0.5	0.00000088	0.00012806	0.00000594	0.00125200	A_07_P036983	c_3873	cmr	Putative conserved protein [c_3873]
c_3890	+9.08	9.50	+3.18	7.90	0.7	11.09	0.1	0.00078566	0.00579910	0.04435531	0.19424929	A_07_P036996	c_3890	cmr	PTS system, N-acetylglucosamine-specific IID component [c_3890]
c_3891	+7.92	8.92	+2.99	7.43	0.3	10.41	0.1	0.00005266	0.00058872	0.02235427	0.22245627	A_07_P036997	c_3891	cmr	Putative phosphotransferase system enzyme subunit [c_3891]
c_3928	+3.54	7.81	+1.82	6.90	0.0	8.73	0.0	0.00009181	0.00122709	0.02478214	0.40941238	A_07_P037039	c_3928	cmr	Hypothetical protein [c_3928]
c_3976	+5.82	8.24	+2.54	6.97	0.1	9.51	0.2	0.00000425	0.00004354	0.00107236	0.12715774	A_07_P041300	c_3976	cmr	Hypothetical protein [c_3976]
c_4010	+2.45	9.37	+1.29	8.73	0.1	10.02	0.1	0.00029505	0.00652407	0.04700965	0.54023358	A_07_P037196	c_4010	cmr	Hypothetical protein [c_4010]
c_4014	-6.97	8.82	-2.80	10.22	0.1	7.42	0.2	0.00000540	0.00006265	0.00127579	0.15784141	A_07_P037204	c_4014	cmr	Hypothetical protein [c_4014]
c_4015	-2.24	8.52	-1.17	9.11	0.1	7.94	0.2	0.00188868	0.01115353	0.06329713	0.69327039	A_07_P037205	c_4015	cmr	Ribose transport system permease protein rbsC [c_4015]
c_4016	-5.16	8.70	-2.37	9.88	0.0	7.51	0.1	0.00002589	0.00055176	0.00570585	0.24127237	A_07_P037206	c_4016	cmr	Ribose transport ATP-binding protein rbsA [c_4016]
c_4020	+2.11	8.71	+1.08	8.17	0.1	9.25	0.2	0.00204066	0.01182053	0.06303290	0.62690661	A_07_P037213	c_4020	cmr	Hypothetical protein [c_4020]
c_4021	+3.28	8.60	+1.71	7.51	0.3	9.46	0.0	0.00069330	0.00479325	0.02863614	0.43841640	A_07_P037217	c_4021	cmr	Hypothetical protein [c_4021]
c_4021	+3.14	8.54	+1.65	7.72	0.0	9.37	0.2	0.00304380	0.01391064	0.03063515	0.44576710	A_07_P037217	c_4021	cmr	Hypothetical protein [c_4021]
c_4021	+3.18	8.71	+1.67	7.88	0.1	9.55	0.0	0.00016769	0.00187507	0.02943534	0.43927014	A_07_P037217	c_4021	cmr	Hypothetical protein [c_4021]
c_4021	+2.03	8.30	+1.02	7.79	0.1	8.81	0.1	0.00340795	0.01796239	0.06813229	0.61363186	A_07_P037217	c_4021	cmr	Hypothetical protein [c_4021]
c_4053	-2.94	11.10	-1.55	11.88	0.0	10.32	0.3	0.00083611	0.00806511	0.03088895	0.49281818	A_07_P041813	c_4053	cmr	Zn [c_4053]
c_4064	-5.59	8.63	-1.37	9.31	0.0	7.94	0.1	0.00048021	0.00391124	0.04570185	0.57241846	A_07_P041279	c_4064	cmr	Hypothetical protein [c_4064]
c_4074	-7.69	7.30	-1.43	8.02	0.1	6.59	0.3	0.00041062	0.00349068	0.04137858	0.55358899	A_07_P041295	c_4074	cmr	Hypothetical protein [c_4074]
c_4088	-2.24	8.82	-1.16	9.40	0.0	8.24	0.2	0.00249183	0.01582246	0.06791575	0.63873862	A_07_P041418	c_4088	cmr	Hypothetical protein [c_4088]
c_4206	-2.24	7.89	-1.16	8.48	0.3	7.31	0.1	0.00478331	0.02026799	0.08004433	0.65963133	A_07_P041455	c_4206	cmr	Hypothetical protein [c_4206]
c_4222	+0.07	10.80	+1.62	9.99	0.1	11.61	0.0	0.00022971	0.00234082	0.01597414	0.41306022	A_07_P041505	c_4222	cmr	Putative DNA processing protein [c_4222]
c_4223	+7.09	9.33	+2.83	7.91	0.0	10.74	0.0	0.00000925	0.00032221	0.00742060	0.24692662	A_07_P041506	c_4223	cmr	Putative conserved protein [c_4223]
c_4276	+2.02	10.50	+1.01	9.98	0.1	11.02	0.2	0.00510058	0.02066455	0.07016617	0.68209774	A_07_P041580	c_4276	cmr	Putative regulator [c_4276]
c_4277	+3.52	8.18	+1.82	7.02	0.3	9.09	0.2	0.00110803	0.00746025	0.02546176	0.41241770	A_07_P041581	c_4277	cmr	Putative phosphotransferase system enzyme subunit [c_4277]
c_4278	+4.52	8.97	+2.18	7.88	0.3	10.06	0.4	0.00116921	0.00768985	0.01615742	0.34280600	A_07_P041582	c_4278	cmr	Putative phosphotransferase system enzyme subunit [c_4278]
c_4279	+3.08	8.00	+1.62	7.18	0.1	8.81	0.1	0.00030374	0.00382296	0.03143293	0.45153285	A_07_P041593	c_4279	cmr	PTS system, galactitol-specific IIC component [c_4279]
c_4284	-2.20	10.66	-1.14	11.23	0.1	10.09	0.3	0.00054423	0.00661871	0.07108676	0.66192639	A_07_P041612	c_4284	cmr	Putative aldolase [c_4284]
c_4303	-2.14	7.65	-1.09	8.19	0.2	7.10	0.0	0.00033135	0.01597377	0.07452744	0.67123858	A_07_P041649	c_4303	cmr	Putative conserved protein [c_4303]
c_4352	-2.91	7.66	-1.54	8.43	0.0	6.89	0.1	0.00033631	0.00303844	0.03227261	0.49619141	A_07_P041574	c_4352	cmr	Hypothetical protein [c_4352]
c_4360	-4.69	9.08	-2.17	10.16	0.1	8.00	0.0	0.00004388	0.00076045	0.00879827	0.30178649	A_07_P041932	c_4360	cmr	Hypothetical protein [c_4360]
c_4376	-2.01	8.95	-1.01	9.45	0.3	8.44	0.1	0.00732095	0.03161655	0.08059134	0.72299952	A_07_P041629	c_4374	cmr	Hypothetical protein [c_4376]
c_4391	-3.02	8.34	-1.02	8.85	0.0	7.83	0.1	0.00159240	0.01132675	0.08455429	0.75075130	A_07_P039642	c_4391	cmr	Hypothetical protein [c_4391]
c_4422	-2.96	12.20	-1.57	12.98	0.2	11.41	0.2	0.00006652	0.00076548	0.03138338	0.49211437	A_07_P039723	c_4422	cmr	Hypothetical protein [c_4422]
c_4424	-2.22	8.77	-1.15	8.35	0.2	7.20	0.3	0.01042101	0.04260485	0.06777734	0.69001925	A_07_P039724	c_4424	cmr	Putative adhesin [c_4424]
c_4437	+2.58	7.44	+1.37	6.76	0.0	8.13	0.1	0.00054708	0.00426007	0.04215668	0.51179604	A_07_P039756	c_4437	cmr	Hypothetical protein [c_4437]
c_4437	+2.60	7.42	+1.36	6.68	0.1	8.25	0.0	0.00076119	0.00558185	0.04848735	0.56025927	A_07_P039756	c_4437	cmr	Hypothetical protein [c_4437]
c_4437	+2.10	7.52	+1.07	6.98	0.1	8.06	0.0	0.00195507	0.00958321	0.06248095	0.62650051	A_07_P039756	c_4437	cmr	Hypothetical protein [c_4437]
c_4437	+2.29	7.55	+1.20	6.95	0.1	8.15	0.2	0.00196152	0.01487958	0.05446202	0.57976863	A_07_P039756	c_4437	cmr	Hypothetical protein [c_4437]
c_4481	-2.18	10.33	-1.12	10.89	0.1	9.77	0.2	0.00303082	0.01595014	0.07071392	0.66387597	A_07_P039839	c_4481	cmr	Conserved hypothetical protein [c_4481]
c_4485	+4.76	8.57	+2.25	7.44	0.0	9.69	0.2	0.00011089	0.00139667	0.01518610	0.33149858	A_07_P039858	c_4485	cmr	Putative PTS enzyme IV [c_4485]
c_4486	+3.76	7.60	+1.91	6.65	0.2	8.56	0.0	0.00032755	0.00238308	0.02263592	0.39513829	A_07_P039865	c_4486	cmr	PTS system, fructose-like 2-IIB component 1 [c_4486]
c_4486	+4.30	7.73	+2.00	6.68	0.1	8.78	0.1	0.00066495	0.00466187	0.03830481	0.56022905	A_07_P039865	c_4486	cmr	PTS system, fructose-like 2-IIB component 1 [c_4486]
c_4486	+4.28	7.67	+2.10	6.63	0.0	8.72	0.2	0.00011061	0.00139657	0.01838934	0.36473033	A_07_P039865	c_4486	cmr	PTS system, fructose-like 2-IIB component 1 [c_4486]
c_4486	+2.91	7.50	+1.54	6.73	0.2	8.27	0.3	0.00149702	0.00932888	0.03479611	0.47349179	A_07_P039865	c_4486	cmr	PTS system, fructose-like 2-IIB component 1 [c_4486]
c_4486	+2.79	7.83	+1.48	7.09	0.2	8.57	0.3	0.00235328	0.01698829	0.03844449	0.49403796	A_07_P039865	c_4486	cmr	PTS system, fructose-like 2-IIB component 1 [c_4486]
c_4487	+5.47	8.38	+2.45	7.16	0.1	9.61	0.2	0.00074045	0.00476945	0.03120220	0.39181585	A_07_P039870	c_4487	cmr	Putative phosphotransferase system [c_4487]
c_4488	+3.12	7.63	+1.64	6.81	0.0	8.45	0.0	0.00016572	0.00185829	0.03044144	0.44591984	A_07_P039873	c_4488	cmr	Putative transcriptional Antiterminator [c_4488]
c_4493	-3.69	8.09	-1.88	9.03	0.1	7.15	0.2	0.00008725	0.00118419	0.01577744	0.35303774	A_07_P039886	c_4493	cmr	Hypothetical protein [c_4493]
c_4522	-2.59	7.80	-1.37	8.49	0.3	7.12	0.2	0.00138246	0.01748880	0.04438896	0.56859121	A_07_P040004	c_4522	cmr	Hypothetical protein [c_4522]
c_4523	-3.39	8.48	-1.76	9.36	0.2	7.60	0.3	0.00146720	0.00938111	0.03114329	0.43015567	A_07_P040008	c_4523	cmr	Conserved hypothetical protein [c_4523]
c_4529	+2.18	7.49	+1.12	6.93	0.1	8.05	0.2	0.00244828	0.01165537	0.06075649	0.61752244	A_07_P040039	c_4529	cmr	Hypothetical protein [c_4529]
c_4541	-2.18	9.04	-1.13	9.60	0.0	8.48	0.2	0.00207090	0.01195411	0.07115727	0.68326128	A_07_P040098	c_4541	cmr	Putative maturase-related protein [c_4541]
c_4580	-3.82	8.94	-1.93	9.91	0.2	7.98	0.2	0.00132233	0.00295389	0.01444329	0.37891486	A_07_P040163	c_4580	cmr	Hypothetical protein [c_4580]
c_4605	-3.04	8.13	-1.60	8.93	0.3	7.33	0.5	0.00798713	0.03428845	0.02914190	0.48448786	A_07_P040004	c_4605	cmr	Hypothetical protein [c_4605]
c_4630	-4.48	8.93	-2.16	10.01	0.0	7.85	0.1	0.00004148	0.00070349	0.00879466	0.30297593	A_07_P041601	c_4630	cmr	Probable tRNA modification GTPase trmE [c_4630]
c_4688	+3.80	8.23	+1.93	7.27	0.6	9.20	0.2	0.00418159	0.02061078	0.02243267	0.39505593	A_07_P039063	c_4688	cmr	Hypothetical protein [c_4688]
c_4748	-3.27	9.70	-1.71	10.56	0.0	8.85	0.1	0.00018956	0.00203942	0.02256615	0.45025349	A_07_P039154	c_4748	cmr	Hypothetical protein ipb [c_4748]
c_4758	+3.01	8.46	+1.59	7.66	0.3	9.26	0.1	0.00114632	0.00765015	0.02923882	0.46330008	A_07_P039181	c_4758	cmr	PTS system, glucose-specific IIBC component [c_4758]
c_4770	-2.17	7.88	-1.12	7.33	0.0	8.44	0.2	0.00242694	0.01138291	0.06151580	0.61331140	A_07_P039202	c_4770	cmr	Hypothetical protein [c_4770]
c_4775	+2.03	7.26	+1.02	6.75	0.2	7.77	0.1	0.00367911	0.01868515	0.06743458	0.68895477	A_07_P039252	c_4775	cmr	Hypothetical protein [c_4775]
c_4776	+7.70	9.21	+2.94	7.34	0.3	10.68	0.0	0.00016412	0.00064147	0.00613059	0.22657277	A_07_P039258	c_4776	cmr	Putative conserved protein [c_4776]
c_4777	+9.12	8.54	+3.19	6.94	0.0	10.13	0.0	0.00004695	0.00023989	0.00434345	0.19386164	A_07_P039263	c_4777	cmr	Putative conserved protein [c_4777]
c_4778	+4.72	8.47	+2.10	7.43	0.1	9.52	0.1	0.00006633	0.00098696	0.01783826	0.35912298	A_07_P039269	c_4778	cmr	Putative conserved protein [c_4778]
c_4779	+4.04	8.52	+2.01	7.51	0.1	9.52	0.1	0.00009560	0.00126806	0.02080702	0.37781751	A_07_P039274	c_4779	cmr	Putative transcriptional regulator [c_4779]
c_4811	-2.94	8.22	-1.56	9.00	0.1	7.44	0.1	0.00027443	0.00261782	0.01139609	0.49148080	A_07_P039321	c_4811	cmr	Hypothetical protein [c_4811]
c_4836	+5.92	11.36	+2.57	10.64	0.0	12.64	0.1	0.00001839	0.00044550	0.00153417	0.27734114	A_07_P039365	c_4836	cmr	Putative lipase [c_4836]
c_4837	-49.80	11.92	-5.64	14.74	0.0	9.10	0.2	0.00000039	0.00009117	0.00000127	0.00500000	A_07_P039369	c_4837	cmr	Hypothetical protein [c_4837]
c_4838	-2.67	12.65	-1.42	13.35	0.1	11.94	0.1	0.00049828	0.00407230	0.04113694	0.55261092	A_07_P039373	c_4838	cmr	Hypothetical protein [c_4838]
c_4839	-34.97	11.23	-4.64	13.51	0.1	8.91	0.1	0.00000094	0.00012946	0.00000231	0.00153714	A_07_P039376	c_4839	cmr	Hypothetical protein [c_4839]
c_4848	-2.52	8.50	-1.69	9.34	0.4	7.65	0.4	0.00536244	0.02155512	0.02261649	0.44988636	A_07_P039409	c_4848	cmr	Putative conserved protein [c_4848]
c_4924	-2.43	8.06	-1.28	8.70	0.0	7.42	0.0	0.00034909	0.00435542	0.05439242	0.60864961	A_07_P039536	c_4924	cmr	Putative hippuricase [c_4924]
c_4925	-2.59	8.36	-1.37	9.05	0.1	7.68	0.2	0.00145758	0.01391378	0.04753935	0.57175258	A_07_P039541	c_4925	cmr	Putative cytrate permease [c_4925]
c_4928	-5.61	8.63	-2.49	9.67	0.1	7.19	0.3	0.00031227	0.00157046	0.04852617	0.23518896	A_07_P037396	c_4928	cmr	tRNA [c_4928]
c_4978	+2.70	7.45	+1.43	6.73	0.2	8.17	0.0	0.00088159	0.00682535	0.03919379	0.49428824	A_07_P037478	c_4978	cmr	Hypothetical protein [c_4978]
c_5008	+2.16	7.32	+1.11	6.76	0.0	7.87	0.2	0.00208399	0.01200525	0.06028331	0.61416181	A_07_P037543	c_5008	cmr	Hypothetical protein [c_5008]
c_5019	-6.99	8.56	-2.80	9.96	0.0	7.16	0.5	0.00046055	0.00368021	0.02117778	0.34693171	A_07_P037601	c_5019	cmr|Hypothetical protein [gb|_5019]
c_5029	-2.47	7.68	-1.31	8.33	0.0	7.03	0.1	0.00068321	0.00519948	0.05199251	0.60100587	A_07_P037590	c_5029	cmr	Putative transporter [c_5029]
c_5035	+3.10	8.28	+1.63	7.47	0.1	9.10	0.0	0.00028355	0.00247476	0.03112249	0.45091996	A_07_P037619	c_5035	cmr	Putative 2-nuclopiridoxin dehydrogenase [c_5035]
c_5058	-3.19	8.78	-1.68	9.62	0.2	7.95	0.2	0.00080787	0.00581178	0.02449632	0.46022673	A_07_P037663	c_5058	cmr	Putative transcriptional regulator [c_5058]
c_5061	-3.74	8.72	-1.90	9.68	0.7	7.77	0.3	0.00735621	0.02488867	0.01468444	0.38610512	A_07_P037671	c_5061	cmr	Hypothetical protein [c_5061]
c_5061	-3.07	8.55	-1.62	9.36	0.2	7.74	0.1	0.00037196	0.00324276	0.02734121	0.47862091	A_07_P037671	c_5061	cmr	Hypothetical protein [c_5061]
c_5062	+17.95	9.60	+4.16	7.52	0.1	11.68	0.1	0.00000213	0.00002613	0.00102246	0.09468571	A_07_P037679	c_5062	cmr	Putative synthetase [c_5062]
c_5081	+2.54	7.61	+1.35	6.94	0.1	8.28	0.0	0.00067113	0.00507975	0.04102087	0.52207802	A_07_P037721	c_5081	cmr	Putative conserved protein [c_5081]
c_5088	-2.89	7.48	-1.53	8.24	0.0	6.71	0.1	0.00029959	0.00278936	0.03131641	0.50260116	A_07_P037731	c_5088	cmr	Hypothetical protein [c_5088]
c_5153	-4.88	9.62	-2.29	10.77	0.0	8.47	0.0	0.00000682	0.00007631	0.00689660	0.26942928	A_07_P037845	c_5153	cmr	Hypothetical protein [c_5153]
c_5154	-3.26	9.04	-1.70	9.89	0.1	8.19	0.1	0.00055159	0.00413787	0.02368847	0.45163770	A_07_P037850	c_5154	cmr	Hypothetical protein [c_5154]
c_5158	-2.01	8.35	-1.01	8.85	0.0	7.85	0.1	0.00207830	0.01196415	0.08985520	0.72157262	A_07_P037866	c_5158	cmr	Hypothetical protein [c_5158]
c_5166	-3.10	9.70	-1.63	10.52	0.0	8.88	0.1	0.00039518	0.00207030	0.02837371	0.47918801	A_07_P037902	c_5166	cmr	Partial Transposase [c_5166]
c_5211	-2.13	8.22	-1.09	9.78	0.0	8.69	0.2	0.00205546	0.01560328	0.07978002	0.68428849	A_07_P038078	c_5211	cmr	Hypothetical protein [c_5211]
c_5286	+2.69	8.27	+1.43	7.56	0.5	8.99	0.1	0.01939246	0.04662152	0.04137767	0.50696968	A_07_P038980	c_5286	cmr	Hypothetical protein [c_5286]
c_5295	-6.20	10.50	-2.63	11.82	0.0	9.19	0.2	0.00020770	0.00056928	0.01819748	0.39450909	A_07_P039064	c_5295	cmr	Hypothetical protein [c_5295]
c_5296	-12.85	12.38	-3.68	14.12	0.0	10.44	0.1	0.00000274	0.00018406	0.00029726	0.05218627	A_07_P037000	c_5296	cmr	Hypothetical protein [c_5296]
c_5297	-2.00	9.37	-1.00	9.87	0.0	8.88	0.1	0.00559984	0.02379351	0.06235102	0.57729094	A_07_P037001	c_5297	cmr	Hypothetical protein [c_5297]
c_5303	-2.02	8.39	-1.02	8.90	0.0	7.88	0.2	0.00738204	0.02150080	0.08534807	0.71113933	A_07_P037031	c_5303	cmr	Putative oxacyl reductase [c_5303]
c_5321	-2.32	9.13	-1.21	9.73	0.1	8.52	0.1	0.00181752	0.01083984	0.06533190	0.62231025	A_07_P037062	c_5321	cmr	Putative conserved protein [c_5321]
c_5341	-138.61	11.38	-7.11	14.93	0.1	7.82	0.1	0.00000009	0.00007032	0.00000000	0.00000000	A_07_P042071	c_5341	cmr	Mg [c_5341]
c_5343	-40.46	9.66	-5.34	12.33	0.1	6.99	0.2	0.00000058	0.00010330	0.00000191	0.00300000	A_07_P037072	c_5343	cmr	Hypothetical protein [c_5343]
c_5349	+2.05	7.78	+1.03	7.26	0.0	8.29	0.2	0.00422334	0.02076184	0.06863130	0.65598063	A_07_P037091	c_5349	cmr	Carbamate kinase [c_5349]
c_5350	-2.65	7.34	-1.40	8.63	0.2	6.04	0.1	0.00098287	0.00418691	0.04147231	0.55694969	A_07_P037099	c_5350	cmr	Putative arginine deiminase [c_5350]
c_5356	-2.22	7.86	-1.15	8.41	0.1	7.28	0.2	0.00378822	0.01914050	0.06478617	0.65613583	A_07_P037109	c_5356	cmr	Hypothetical protein [c_5356]
c_5376	-2.85	10.45	-1.51	11.21	0.2	9.70	0.4	0.00260647	0.01157454	0.03809197	0.52289575	A_07_P037149	c_5376	cmr	Hypothetical protein [c_5376]
c_5416	+3.80	8.82	+1.92	7.86	0.2	9.78	0.1	0.00020051	0.00210910	0.02114748	0.39178652	A_07_P037232	c_5416	cmr	Hypothetical protein [c_5416]
c_5455	-2.41	8.40	-1.27	8.97	0.1	7.83	0.1	0.00100922	0.00852581	0.04684224	0.54664699	A_07_P037291	c_5455	cmr	Hypothetical protein [c_5455]
caiA	-8.49	11.86	-3.09	13.41	0.0	10.32	0.1	0.00000641	0.00027019	0.00119284	0.10982456	A_07_P038884	b0039	cmr	probable carnitine operon oxidoreductase [b0039]
caiC	-2.39	8.76	-1.76	7.87	0.1	9.64	0.1	0.00019839	0.00203646	0.03010662	0.43573144	A_07_P035675	c_0046	cmr	Probable crotonobetaine/carnitine-CoA

disF	-2.53	10.26	-1.34	10.93	0.0	9.59	0.2	0.00080911	0.00583808	0.04820567	0.57979374	A_07_P008863	b4044		cmr/DNA-damage-inducible protein F [b4044]
disG	-17.17	11.62	-2.84	10.20	0.1	13.04	0.1	0.00000466	0.00009588	0.00720793	0.24144681	A_07_P004448	b0799		cmr/probably ATP-dependent helicase [b0799]
disI	-15.45	12.97	-3.95	14.94	0.0	10.99	0.0	0.00000142	0.00015187	0.00130656	0.09909691	A_07_P015037	b1061		cmr/damage-inducible protein I [b1061]
dipZ	-2.74	8.40	-1.46	7.67	0.1	9.12	0.2	0.00080825	0.00518102	0.03870427	0.49552219	A_07_P011411	b4136		cmr/thiol:disulfide interchange protein; copper tolerance [b4136]
djlB	-3.58	11.86	-1.84	12.78	0.1	10.94	0.1	0.00013753	0.00163341	0.01716717	0.40041681	A_07_P009800	b0646		cmr/putative enzyme of polynucleotide modification [b0646]
dkgA	-4.23	9.03	-2.08	7.99	0.0	10.07	0.1	0.00005588	0.00086270	0.01844703	0.36349186	A_07_P012193	b3012		cmr/orf, hypothetical protein [b3012]
dkgB	-4.94	8.76	-2.30	9.91	0.1	7.61	0.4	0.00033107	0.00300506	0.06598807	0.26287734	A_07_P002965	b0307		cmr/putative oxidoreductase [b0307]
dld	+2.79	9.06	+1.48	8.32	0.1	9.80	0.3	0.02573995	0.04119995	0.03794398	0.49127667	A_07_P012211	c_2664		cmr/D-lactate dehydrogenase [c_2664]
dld	+15.51	8.70	+3.31	8.04	0.4	9.37	0.2	0.00540106	0.02545304	0.04629564	0.53637152	A_07_P045443	23382		cmr/D-lactate dehydrogenase, FAD protein, NAD(H) independent [23382]
dmsA	+10.26	10.49	+3.36	8.81	0.2	12.17	0.1	0.00001133	0.00035103	0.00341082	0.17156550	A_07_P031816	c_1031		cmr/Anaerobic dimethyl sulfoxide reductase chain A precursor [c_1031]
dmsA	+7.26	8.58	+2.86	7.15	0.1	10.01	0.2	0.00009453	0.00045147	0.00764649	0.20119123	A_07_P004916	b0884		cmr/putative dimethyl sulfoxide reductase subunit A [b0884]
dmsB	+8.09	8.99	+3.02	7.49	0.1	10.50	0.1	0.00000935	0.00032222	0.00550930	0.21943813	A_07_P004924	b0885		cmr/putative dimethyl sulfoxide reductase subunit B [b0885]
dmsC	+13.61	8.08	+3.87	7.15	0.1	9.02	0.1	0.00012741	0.00115883	0.02349149	0.40027056	A_07_P012033	21242		cmr/anaerobic dimethyl sulfoxide reductase subunit C [21242]
dmsC	+6.87	8.76	+2.78	7.37	0.0	10.15	0.1	0.00001288	0.00037639	0.00767729	0.24754491	A_07_P004926	b0886		cmr/anaerobic dimethyl sulfoxide reductase subunit C [b0886]
dmsD	-2.64	8.48	-1.40	7.78	0.1	9.18	0.2	0.00077318	0.00546424	0.04134809	0.51168221	A_07_P003292	b3191		cmr/putative oxidoreductase component [b3191]
dnaA	-6.30	13.48	-2.10	14.54	0.0	12.43	0.1	0.00004746	0.00077461	0.01004046	0.31628000	A_07_P005441	b3702		cmr/DNA biosynthesis; initiation of chromosome replication; can be transcription regulator [b3702]
dnaB	-2.28	9.25	-1.25	9.88	0.0	8.63	0.2	0.00004642	0.00492163	0.05807228	0.62261105	A_07_P008903	b4052		cmr/replicative DNA helicase; part of primosome [b4052]
dnaG	-11.91	11.12	-3.57	12.91	0.0	9.33	0.1	0.00000277	0.00018406	0.00040206	0.06267327	A_07_P000065	b3066		cmr/DNA biosynthesis; DNA primase [b3066]
dnaJ	+2.28	9.64	+1.39	9.05	0.1	10.24	0.0	0.01135886	0.03870376	0.05344618	0.57456023	A_07_P010763	b0015		cmr/chaperone with DnaK, heat shock protein [b0015]
dnaK	+3.93	11.67	+1.98	10.68	0.2	12.65	0.1	0.00016921	0.00170726	0.02057673	0.38112941	A_07_P010763	b0014		cmr/chaperone Hsp70; DNA biosynthesis; autoregulated heat shock proteins [b0014]
dnaN	-7.58	12.59	-2.92	14.05	0.0	11.13	0.2	0.00002431	0.00053302	0.01778320	0.27705326	A_07_P005456	b3701		cmr/DNA polymerase III, beta subunit [b3701]
dnaQ	+2.07	8.90	+1.05	8.37	0.0	9.42	0.1	0.00158816	0.01135628	0.06232929	0.62780057	A_07_P051886	20241		cmr/DNA polymerase III, epsilon subunit [20241]
dnaT	-2.88	12.95	-1.52	13.71	0.0	12.18	0.1	0.00034271	0.00307522	0.03131664	0.50286673	A_07_P017509	b4362		cmr/DNA biosynthesis; primosomal protein I [b4362]
dnaX	-6.22	11.07	-2.64	9.76	0.1	12.38	0.0	0.00001569	0.00041066	0.00962716	0.26820549	A_07_P021457	b0470		cmr/DNA polymerase III, tau and gamma subunits; DNA elongation factor III [b0470]
dpa	-3.44	9.73	-1.78	10.62	0.1	8.84	0.7	0.01076599	0.04205422	0.02003430	0.42914286	A_07_P009666	b0620		cmr/sequence similarity to Shigella regulator [b0620]
dpiB	-3.21	9.44	-1.68	10.28	0.1	8.60	0.1	0.00176741	0.01061184	0.02450711	0.45933333	A_07_P009663	b0619		cmr/putative sensor-type protein [b0619]
dppA	+3.18	8.22	+1.67	7.39	0.1	9.05	0.2	0.00028764	0.00270203	0.03030316	0.44198316	A_07_P007652	b3544		cmr/dipeptide transport protein [b3544]
dppD	+4.86	9.15	+2.38	8.01	0.1	10.29	0.1	0.00016856	0.00187949	0.01497679	0.32509073	A_07_P009583	c_4356		cmr/Dipeptide transport ATP-binding protein dppD [c_4356]
dppD	+3.94	8.46	+1.98	7.47	0.0	9.45	0.1	0.00006709	0.00098530	0.02056402	0.38134276	A_07_P007640	b3541		cmr/putative ATP-binding component of dipeptide transport system [b3541]
dps	+5.52	11.88	+2.47	10.64	0.1	13.11	0.3	0.00017552	0.00193274	0.01166249	0.28527316	A_07_P004515	b0812		cmr/global regulator, starvation conditions [b0812]
dsbA	+2.59	9.14	+1.37	8.45	0.1	9.83	0.0	0.00044896	0.00373401	0.04231199	0.51042743	A_07_P010981	b3860		cmr/protein disulfide isomerase I, essential for cytochrome c synthesis and formate-dependent reduction [b3860]
dsbB	-2.27	8.08	-1.18	8.67	0.1	7.49	0.2	0.00288715	0.01546525	0.06143942	0.61318730	A_07_P006878	b1185		cmr/revoxidizes DsbA protein following formation of disulfide bond in P-ring of flagella. [b1185]
dsbG	-2.03	9.52	-1.02	10.03	0.0	9.00	0.0	0.00133736	0.01746104	0.08569993	0.75280655	A_07_P016779	b0604		cmr/thiol:disulfide interchange protein [b0604]
dsdX	-7.50	8.40	-2.95	8.95	0.3	7.85	0.0	0.00705608	0.03243791	0.00653693	0.23164144	A_07_P011424	b1265		cmr/transport system permease [b1265]
dtd	+5.77	10.28	+2.53	9.51	0.2	10.94	0.2	0.00023278	0.00234931	0.03075583	0.27794069	A_07_P019212	b3887		cmr/orf, hypothetical protein [b3887]
duaA	-2.92	8.55	-1.55	9.33	0.1	7.78	0.1	0.00044086	0.00368221	0.01180564	0.49189349	A_07_P008884	b4949		cmr/orf, hypothetical protein [b4949]
duaC	-3.06	7.65	-1.61	8.46	0.1	6.84	0.0	0.00019204	0.00204031	0.02842822	0.48288817	A_07_P003464	b2140		cmr/putative regulator protein [b2140]
E1A_r60_a104	-2.00	9.82	-1.02	10.84	0.2	8.80	0.3	0.00035829	0.00366306	0.06084473	0.73545814	i_E1A_r60_a104	E1A_r60_a104		
E1A_r60_a104	-2.91	9.22	-1.54	9.69	0.1	8.15	0.0	0.00033277	0.00304280	0.03249492	0.49765137	i_E1A_r60_a104	E1A_r60_a104		
E1A_r60_a104	-2.23	9.99	-1.16	10.57	0.1	9.42	0.1	0.00117900	0.00781894	0.08844155	0.65855199	i_E1A_r60_a104	E1A_r60_a104		
E1A_r60_a107	-2.37	8.66	-1.24	9.28	0.1	8.04	0.1	0.00094086	0.00658934	0.05829922	0.62311821	i_E1A_r60_a107	E1A_r60_a107		
E1A_r60_a107	-3.33	9.03	-1.74	9.89	0.0	8.16	0.3	0.00429180	0.02109375	0.02808158	0.43419313	i_E1A_r60_a107	E1A_r60_a107		
E1A_r60_a107	-2.34	8.38	-1.23	9.00	0.1	7.77	0.2	0.00172656	0.01040894	0.06406611	0.63255331	i_E1A_r60_a107	E1A_r60_a107		
E1A_r60_a107	-2.63	8.58	-1.39	9.28	0.1	7.89	0.3	0.00330652	0.01719838	0.04302021	0.56546129	i_E1A_r60_a107	E1A_r60_a107		
E1A_r60_a107	-2.42	8.98	-1.28	9.62	0.3	8.35	0.3	0.00750608	0.03243791	0.05297673	0.60351195	i_E1A_r60_a107	E1A_r60_a107		
E1A_r60_a135	-3.75	8.99	-1.91	9.95	0.7	8.04	0.1	0.00728709	0.02181173	0.01508826	0.38799672	i_E1A_r60_a135	E1A_r60_a135		
E1A_r60_a135	-1.78	9.56	-1.48	10.30	0.1	8.82	0.0	0.00035144	0.00318846	0.03737969	0.52932294	i_E1A_r60_a135	E1A_r60_a135		
E1A_r60_a135	-3.58	8.98	-1.37	9.66	0.1	8.29	0.1	0.01898085	0.04452493	0.04425368	0.59322386	i_E1A_r60_a135	E1A_r60_a135		
E1A_r60_a20	-2.20	9.84	-1.14	10.41	0.1	9.27	0.3	0.00642110	0.02602104	0.06807546	0.65876616	i_E1A_r60_a20	E1A_r60_a20		
E1A_r60_a20	-2.85	10.12	-1.51	10.87	0.3	9.36	0.4	0.05345657	0.02540434	0.02386966	0.50048356	i_E1A_r60_a20	E1A_r60_a20		
E1A_r60_a20	-3.04	9.84	-1.60	10.64	0.1	9.04	0.1	0.00036417	0.00120148	0.02890976	0.48229008	i_E1A_r60_a20	E1A_r60_a20		
E1A_r60_a20	-2.65	9.71	-1.41	10.41	0.1	9.00	0.5	0.01126607	0.04562062	0.04270579	0.56315158	i_E1A_r60_a20	E1A_r60_a20		
E1A_r60_a20	-4.09	9.50	-2.03	10.52	0.1	8.48	0.6	0.00176679	0.01058187	0.02388016	0.34642087	i_E1A_r60_a20	E1A_r60_a20		
E1A_r60_a20	-2.51	9.86	-1.33	10.52	0.4	9.19	0.2	0.00789494	0.03412302	0.05038110	0.59194030	i_E1A_r60_a20	E1A_r60_a20		
E1A_r60_a20	-2.92	10.04	-1.55	10.82	0.3	9.27	0.6	0.01224556	0.04864060	0.05020262	0.69072239	i_E1A_r60_a20	E1A_r60_a20		
E1A_r60_a20	-4.09	9.58	-2.03	10.60	0.4	8.57	0.2	0.00127508	0.00830914	0.01189914	0.34628466	i_E1A_r60_a20	E1A_r60_a20		
E1A_r60_a20	-2.46	10.23	-1.30	10.88	0.0	9.58	0.4	0.00429159	0.02872515	0.05209893	0.68143463	i_E1A_r60_a20	E1A_r60_a20		
E1A_r60_a20	-2.51	9.84	-1.33	10.50	0.2	9.18	0.4	0.00143383	0.00903332	0.04917746	0.58478097	i_E1A_r60_a20	E1A_r60_a20		
E1A_r60_a22	-2.22	10.88	-1.15	11.46	0.1	10.31	0.1	0.00180706	0.01137786	0.06886561	0.67388517	i_E1A_r60_a22	E1A_r60_a22		
E1A_r60_a22	-2.31	10.64	-1.21	11.24	0.0	10.03	0.4	0.01015397	0.04198113	0.06175432	0.62712875	i_E1A_r60_a22	E1A_r60_a22		
E1A_r60_a22	-3.07	10.69	-1.62	11.50	0.4	9.88	0.1	0.00237125	0.01320152	0.02782417	0.48243595	i_E1A_r60_a22	E1A_r60_a22		
E1A_r60_a22	-3.31	10.56	-1.21	11.17	0.1	9.96	0.4	0.01138205	0.04507080	0.04224885	0.66052225	i_E1A_r60_a22	E1A_r60_a22		
E1A_r60_a22	-3.21	10.37	-1.68	11.21	0.1	9.53	0.3	0.00090297	0.00687483	0.02494538	0.46291928	i_E1A_r60_a22	E1A_r60_a22		
E1A_r60_a22	-2.65	10.63	-1.41	11.34	0.2	9.93	0.1	0.00097014	0.00676604	0.04291928	0.56323833	i_E1A_r60_a22	E1A_r60_a22		
E1A_r60_a22	-3.30	10.66	-1.20	11.26	0.0	10.06	0.3	0.00390835	0.01842681	0.02382824	0.44367571	i_E1A_r60_a22	E1A_r60_a22		
E1A_r60_a22	-3.50	10.37	-1.81	11.27	0.1	9.46	0.7	0.01219580	0.04848753	0.01938905	0.41894376	i_E1A_r60_a22	E1A_r60_a22		
E1A_r60_a22	-2.89	10.49	-1.52	11.26	0.2	9.73	0.2	0.00161975	0.00994979	0.03343931	0.50494757	i_E1A_r60_a22	E1A_r60_a22		
E1A_r60_a22	-2.15	10.79	-1.10	11.35	0.1	10.24	0.3	0.00845169	0.03628049	0.07928390	0.67467606	i_E1A_r60_a22	E1A_r60_a22		
E1A_r60_a22	-2.48	10.83	-1.31	11.49	0.1	10.18	0.1	0.00092439	0.00650293	0.05194741	0.60092579	i_E1A_r60_a22	E1A_r60_a22		
E1A_r60_a22	-2.14	10.69	-1.10	11.24	0.1	10.14	0.2	0.00128252	0.01542572	0.07738054	0.67556460	i_E1A_r60_a22	E1A_r60_a22		
E1A_r60_a22	-2.38	10.61	-1.25	11.24	0.2	9.99	0.2	0.00335547	0.01727782	0.05426664	0.62277665	i_E1A_r60_a22	E1A_r60_a22		
E1A_r60_a22	-3.57	10.27	-1.66	11.24	0.0	9.35	0.6	0.00535556	0.02513284	0.01717976	0.40078635	i_E1A_r60_a22	E1A_r60_a22		
E1A_r60_a22	-2.20	10.67	-1.14	11.24	0.2	10.10	0.1	0.00293347	0.01564519	0.07938877	0.66519957	i_E1A_r60_a22	E1A_r60_a22		
E1A_r60_a97	-2.63	8.17	-1.28	8.81	0.2	7.53	0.3	0.00708327	0.03155253	0.05418525	0.68816108	i_E1A_r60_a97	E1A_r60_a97		
E1A_r60_n11	-4.54	7.92	-2.18	9.01	0.2	6.83	0.1	0.00016601	0.00188177	0.00635584	0.29540909	i_E1A_r60_n11	E1A_r60_n11		
E1A_r60_n9	-2.12	7.41	-1.06	7.95	0.2	6.87	0.2	0.00606329	0.02602759	0.07277152	0.67861887	i_E1A_r60_n9	E1A_r60_n9		
eaeH	-3.02	12.09	-1.60	12.89	0.1	11.29	0.3	0.00078421	0.00571336	0.02836509	0.48278919	A_07_P008177	b2097		cmr/attaching and effacing protein, pathogenesis factor [b2097]
ebgR	-13.15	9.45	-1.65	8.62	0.1	10.27	0.0	0.00002717	0.00051374	0.00832403	0.44973222	A_07_P041769	c_3832		cmr/Escherichia coli sigma-70 factor, RpoD paralog [c_3832]
eco	+2.92	13.17	+1.55	12.39	0.1	13.94	0.0	0.00026490	0.00255703	0.03545854	0.47148180	A_07_P032326	c_2750		cmr/Escherichia coli precursor [c_2750]
EC0016	-3.31	12.57	-1.73	13.44	0.0	11.71	0.1	0.00020304	0.00212689	0.02339129	0.44797967	A_07_P054872	EC0016		cmr/Gef protein [EC0016]
EC0031	+2.61	10.06	+1.38	9.37	0.2	10.75	0.2	0.00069359	0.00796025	0.04496245	0.52069020	A_07_P062890	EC0031		cmr/putative FABE-type 3-(2-peptidyl-prolyl)-cis-trans isomerase [EC0031]
EC0037	+3.53	9.36	+1.82	8.45	0.3	10.27	0.2	0.00127284	0.00829795	0.02127248	0.41189641	A_07_P054876	EC0037		cmr/transcriptional regulator of cai operon [EC0037]
EC0052	-2.74	11.77	-1.45	12.50	0.0	11.05	0.1	0.00038477	0.00332667	0.03862127	0.53501052	A_07_P054912	EC0052		cmr/CcdA-like protein [EC0052]
EC0077	+2.16	9.24	+1.14	8.80	0.0	9.39	0.2	0.02295643	0.01574747	0.06137386	0.42179537	A_07_P054941	EC0077		cmr/3-isopropylmalate dehydrogenase [EC0077]
EC0092	-2.94	8.44	-1.56	9.21	0.1	7.66	0.3	0.00018921	0.00183930	0.04961538	0.49061538	A_07_P054952	EC0092		cmr/hypothetical protein [EC0092]
EC0192	-3.54	10.61	-1.82	11.52	0.1	9.70	0.3	0.00074672	0.00552202	0.01795574	0.40956585	A_07_P055013	EC0192		cmr/hypothetical protein [EC0192]
EC0230	-3.45	7.72	-1.79	8.61	0.2	6.82	0.0	0.00345821	0.01779265	0.01919011	0.41953103	A_07_P055608	EC0230		cmr/hypothetical protein [EC0230]
EC0237	-2.85	10.09	-1.51	10.85	0.3	9.34	0.1	0.01486612	0.00928472	0.03436166	0.50892756	A_07_P056629	EC0237		cmr/RNaG core protein with extension [EC0237]
EC0241	-2.76	10.67	-1.47	11.40	0.1	9.94	0.2	0.01003512	0.00712561	0.03846778	0.52308886	A_07_P055329	EC0241		cmr/rRNA 16S methyltransferase [EC0241]
EC0269	-2.47	8.71	-1.30	9.36	0.0	8.06	0.4	0.00440816	0.02149338	0.05020135	0.59115183	A_07_P062927	EC0269		cmr/gamma-glutamate kinase [EC0269]
EC0278	-6.30	11.30	-2.66	12.63	0.0	9.97	0.0	0.00002169	0.00037639	0.00306078	0.18112319	A_07_P053587	EC0278		cmr/replication protein [EC0278]
EC0280	-3.29	9.09	-1.72	9.95	0.3	8.23	0.1	0.00080689	0.00582945	0.02282139	0.45138191	A_07_P053597	EC0280		cmr/putative tail fiber protein [EC0280]
EC0290	-2.22	11.35	-1.15	11.93	0.1	10.78	0.2	0.00229564	0.01920154	0.09512518	0.82776212	A_07_P053647	EC0290		cmr/hypothetical protein [EC0290]
EC0296	-4.53	9.54	-2.18	10.63	0.2	8.45	0.6	0.00265024	0.01443903	0.00892040	0.30343413	A_07_P053677	EC0296		cmr/putative Dgc family transcription activator [EC0296]
EC0325	-2.30	8.33	-1.20	8.93	0.2	7.73	0.3	0.00659941	0.02970643	0.06135112	0.68389029	A_07_P053765	EC0325		cmr/hypothetical protein [EC0325]
EC0326	-2.55	8.04	-1.35	8.72	0.0	7.36	0.1	0.00057712	0.00450930	0.04785061	0.58040062	A_07_P053768	EC0326		cmr/hypothetical protein [EC0326]
EC0330	-2.57	8.90	-1.36	9.58	0.1	8.22	0.4	0.00625278	0.02882681	0.04378557	0.56442037	A_07_P053789	EC0330		cmr/hypothetical protein [EC0330]
EC0332	+3.66	8.51	+1.87	7.57	0.3	9.44	0.5	0.00416807	0.02057948	0.02388793	0.46266595	A_07_P053796	EC0332		cmr/hypothetical protein [EC0332]
EC0335	+3.17	7.75	+1.68	6.92	0.1	8.59	0.0	0.00016207	0.00180235	0.04948425	0.43916746	A_07_P053815	EC0335		cmr/putative outbreakstatus [EC0335]
EC0350	-2.10	10.32	-1.07	10.76	0.3	9.69	0.2	0.01462133	0.04300611	0.07619218	0.67916180	A_07_P053863	EC0350		cmr/putative adhesin [EC0350]
EC0357	+6.54	9.52	+2.18	8.43	0.0	10.61	0.0	0.00030477	0.00064621	0.01452417	0.36131570	A_07_P053871	EC0357		cmr/choline dehydrogenase [EC0357]
EC0376	+2.32	7.41	+1.21	6.80	0.3	8.02	0.2	0.00758878	0.03234422	0.05314977	0.57275154	A_07_P053957	EC0376		cmr/putative ATP-binding protein of abc transporter [EC0376]
EC0423	-5.81	9.63	-2.54	10.90	0.1	8.36	0.1	0.00002632	0.00005700	0.00403455	0.20894737	A_07_P053991	EC0423		cmr/5-aminolevulinate dehydratase [EC0423]
EC0440	-3.78	7.95	-1.47	8.68	0.2	7.21	0.2	0.00180874	0.00796582	0.04145262	0.52152649	A_07_P054001	EC0440		cmr/arginyl protein [EC0440]
EC0443	-2.23	10.35	-1.15	10.92	0.1	9.77	0.1	0.00185885	0.01101870	0.06813389	0.65890663	A_07_P054012	EC0443		cmr/hypothetical protein [EC0443]
EC0447	-2.64	8.42	-1.46	7.72	0.0	9.12	0.1	0.00086655	0.00560598	0.04110164	0.50552250	A_07_P054019	EC0447		cmr/ATP-dependent dsDNA exonuclease [EC0447]
EC0449	-7.02	11.61	-2.57	12.52	0.2	10.04	0.2	0.00001657	0.00042559	0.00226308	0.15765887	A_07_P054018	EC0449		cmr/positive response regulator for pho regulon PhoB [EC0449]
EC0477	-4.21	8.89	-2.07	9.92	0.0	7.85	0.1	0.00006145	0.00093973	0.01662427	0.32787109	A_07_P054057	EC0477		cmr/putative oxidoreductase [EC0477]
EC0483	+7.29	9.27	+2.87	7.83	0.2	10.70	0.4	0.00024695	0.00240098	0.00691311	0.23668870	A_07_P062971	EC0483		cmr/cytochrome o ubiquinol oxidase subunit IV [EC0483]
EC0541	-2.17	8.24	-1.24	7.62	0.3	8.86	0.1	0.00419600	0.02657168	0.06351004	0.55449405	A_07_P054682	EC0541		cmr/hypothetical protein [EC0541]
EC0549	-3.02	8.99	-1.59	9.71	0.1	8.19	0.4	0.00224603	0.01269157	0.07895027	0.48208562	A_07_P054128	EC0549		cmr/putative periplasmic binding transport protein [EC0549]
EC0551	-2.39	10.85	-1.26	11.48	0.1	10.22	0.0	0.00075855	0.00557260	0.06413777	0.67157862	A_07_P054138	EC0551		cmr/hypothetical protein [EC0551]
EC0573	+3.06	7.72	+1.61	6.92	0.0	8.53	0.1	0.00002068	0.00021689	0.01318544	0.45287783	A_07_P054166	EC0573		cmr/allanoinase [EC0573]
EC0679	-2.21	10.44	-1.15	11.01	0.0	9.87	0.1	0.00096215	0.00689689	0.07021617	0.68241662	A_07_P054223	EC0679		cmr/minor lipoprotein [EC0679]
EC0694	+4.51	11.61	+2.17	10.52	0.2	12.69	0.3	0.00027695	0.00262619	0.01658791	0.34272066	A_07_P056560	EC0694		cmr/putative periplasmic binding transport protein [EC0694]
EC0711	-2.84	10.06	-1.51	10.81	0.1	9.31	0.0	0.00041167	0.00346775	0.04784675	0.53008000	A_07_P056574	EC0711		cmr/putative carboxylase [EC0711]
EC0727	+3.24	11.45	+1.69	10.60	0.1	12.30	0.2	0.00045594	0.00377804	0.02887830	0.43847280	A_07_P063012	EC0727		cmr/putative carboxylase [EC0727]
EC0772	-3.32	10.39	-1.22	10.90	0.0	9.89	0.1	0.00006990	0.00062910	0.04173082	0.62730692	A_07_P056669	EC0772		cmr/inner membrane protein YceD [EC0772]
EC0778	-3.36	8.63	-1.75	9.50	0.0	7.75	0.1	0.00020884	0.00217593	0.02248910	0.44278942	A_07_P056671	EC0778		cmr/quinolinate synthetase A protein [EC0778]
EC0805	+7.84	9.12	+2.97	7.63	0.0	10.60	0.3	0.00005388	0.00084214	0.00588514	0.22276596	A_07_P056700	EC0805		cmr/hypothetical C4-type zinc finger protein TraR-family [EC0805]
EC0807	-2.45	8.50	-1.29	7.85	0.0	9.14	0.1	0.00036318	0.00259124	0.04792998	0.56072594	A_07_P056708	EC0807		cmr/hypothetical protein [EC0807]
EC0809	-3.86	10.82	-1.95	11.81	0.0	9.85	0.2	0.00024396	0.00242329	0.01432038	0.17928859	A_07_P056720	EC0809		cmr/exonuclease [EC0809]
EC0810	+9.46	9.05	+4.79	8.15	0.1	9.94	0.1	0.00031812	0.00145366	0.02549131	0.41590631	A_07_P056725	EC0810		cmr/NinE protein [EC0810]
EC0819	+7.03	9.39	+2.81	7.99	0.1	10.80	0.2	0.00004661	0.00074958	0.00755335	0.26621118	A_07_P056765	EC0819		cmr/endosyn [EC0819]
EC0820	+4.42	7.92	+2.14	6.85	0.1	8.99	0.2	0.00010702	0.00135068	0.01705295	0.34822269	A_07_P056768	EC0820		cmr/putative endopeptidase [EC0820]
EC0825	-2.93	8.63	-1.55	9.24	0.2	7.86	0.0	0.00038642	0.00333358	0.03162221	0.49195652	A_07_P056791	EC0825		cmr/putative terminase large subunit [EC0825]
EC0826	-2.03	7.61	-1.02	8.12	0.0	7.10	0.2	0.00365094	0.01862791	0.08649943	0.75413848	A_07_P056799	EC0826		cmr/hypothetical protein [EC0826]
EC0835	+2.02	7.12	+1.01	6.61	0.1	7.63	0.1	0.00323704	0.01626554	0.06929433	0.65878831	A_07_P056842	EC0835		cmr/putative minor tail protein [EC0835]
EC0837	-2.10	8.84	-1.07	8.30	0.1	9.37	0.2	0.00146425	0.01768161	0.06279915	0.62655675	A_07_P056851	EC0837		cmr/putative tail length tape-measure protein precursor [EC0837]
EC0840	+5.39	9.33	+2.43	8.11	0.2	10.55	0.2	0.00007588	0.00107529	0.01232588	0.29346512	A_07_P056866	EC0840		cmr/putative tail assembly protein [EC0840]
EC0842	-2.36	7.93	-1.18	7.35	0.2	8.52	0.3	0.00870085	0.03776556	0.05922266	0.69972006	A_07_P056875	EC0842		cmr/hypothetical protein [EC0842]
EC0878	+2.01	9.88	+1.01	9.38	0.0	10.39	0.1	0.00221648	0.01214470	0.06845226	0.65578342	A_07_P056893	EC0878		cmr/putative enzyme [EC0878]
EC0901	+2.40	7.26	+1.26	6.42	0.1	7.98	0.2	0.00015658	0.00071343	0.04834413	0.54757554	A_07_P057037	EC0901		cmr/hypothetical protein [EC0901]
EC0906	+4.65	11.10	+2.22	9.99	0.2	12.20	0.0	0.00008760	0.00118786	0.01592099	0.33645638	A_07_P056943	EC0906		cmr/hypothetical protein [EC0906]
EC0950	-3.38	11.14	-1.76	12.03	0.1	10.26	0.1	0.00022333	0.00224924	0.02003597	0.41456283	A_07_P056951	EC0950	

EC2478	-3.88	8.17	-1.95	9.15	0.1	7.19	0.1	0.00012193	0.00148828	0.13139166	0.13749017	A_07_P054936	ECs2478	cmr/putative transcriptase OrfB protein of insertion sequence 6629 [ECs2478]	
EC2481	-13.18	7.68	-11.13	7.12	0.4	8.24	0.0	0.00944444	0.03368288	0.18127877	0.62191649	A_07_P054964	ECs2481	cmr/putative kinase [ECs2481]	
EC2485	-2.85	9.29	-1.51	10.04	0.1	8.53	0.0	0.00191568	0.01126632	0.03124379	0.50329962	A_07_P054951	ECs2485	cmr/hypothetical protein [ECs2485]	
ECs2526	-6.51	8.68	-2.70	7.32	0.3	10.03	0.1	0.00308308	0.00909948	0.08867696	0.25971683	A_07_P054984	ECs2526	cmr/hypothetical protein [ECs2526]	
ECs2555	-6.40	10.52	-2.14	11.59	0.2	9.45	0.4	0.00086650	0.00521681	0.00918636	0.8707506	A_07_P052552	ECs2555	cmr/protease II [ECs2555]	
ECs2622	-2.21	7.56	-1.14	8.13	0.0	6.99	0.1	0.00145863	0.00956458	0.07091908	0.68345234	A_07_P055028	ECs2622	cmr/putative DNA-binding protein [ECs2622]	
ECs2646	-2.28	9.49	-1.19	10.08	0.2	8.89	0.3	0.00478221	0.02288484	0.06278011	0.44224172	A_07_P055345	ECs2646	cmr/putative tail protein [ECs2646]	
EC2718	-3.58	9.96	-1.82	10.87	0.1	9.06	0.5	0.00220803	0.01434165	0.03908537	0.41907950	A_07_P055157	EC2658	cmr/hypothetical protein [EC2658]	
EC2750	-2.90	8.04	-1.54	8.81	0.0	7.28	0.1	0.00031707	0.00295758	0.01248031	0.49792600	A_07_P053387	EC2750	cmr/hypothetical protein [EC2750]	
EC2720	-13.58	8.77	-11.84	7.85	0.0	9.69	0.0	0.00013439	0.00158606	0.02409078	0.40171095	A_07_P055249	EC2720	cmr/putative host specificity protein [EC2720]	
EC2720	-13.13	8.70	-11.60	7.88	0.1	9.52	0.1	0.00028665	0.00275624	0.02287039	0.44157209	A_07_P055249	EC2720	cmr/putative host specificity protein [EC2720]	
EC2714	-13.21	10.48	-11.68	9.64	0.1	11.32	0.0	0.00016679	0.00168943	0.02600025	0.42775647	A_07_P055282	EC2714	cmr/putative head completion protein [EC2714]	
EC2771	-2.65	8.10	-1.30	8.75	0.3	7.46	0.1	0.00430199	0.02107869	0.15145198	0.68138885	A_07_P055437	EC2771	cmr/hypothetical protein [EC2771]	
EC2782	-7.07	8.75	-2.82	10.16	0.1	9.34	0.0	0.00000112	0.00003947	0.00225864	0.15875000	A_07_P055462	EC2782	cmr/hypothetical protein [EC2782]	
EC2792	-5.63	8.81	-2.49	10.06	0.0	7.56	0.1	0.00003875	0.00015041	0.00475154	0.21728595	A_07_P055473	EC2792	cmr/hypothetical protein [EC2792]	
EC2793	-3.63	8.67	-1.86	9.60	0.1	7.74	0.4	0.00127615	0.00831269	0.01640652	0.39695955	A_07_P055479	EC2793	cmr/hypothetical protein [EC2793]	
EC2795	-7.81	10.62	-2.96	12.10	0.1	9.14	0.1	0.00000951	0.00032326	0.00163618	0.13162857	A_07_P055486	EC2795	cmr/putative transposase OrfB protein of insertion sequence 6629 [ECs2795]	
ECs2825	-13.29	9.15	-13.73	7.28	0.2	11.01	0.2	0.00003236	0.00038795	0.00203152	0.11278008	A_07_P062811	ECs2825	cmr/N- [ECs2825]	
ECs2827	-3.83	7.51	-1.50	6.76	0.1	8.26	0.1	0.00206207	0.01847881	0.04047881	0.48385028	A_07_P055553	ECs2827	cmr/phosphorbutyl-amp cyclohydrolase [ECs2827]	
ECs2828	-2.12	8.98	-1.09	9.52	0.1	8.44	0.1	0.00188092	0.01116606	0.07610854	0.67323975	A_07_P055560	ECs2828	cmr/regulator of length of O-antigen component of lipopolysaccharide chains [ECs2828]	
ECs2829	-4.15	8.71	-2.05	9.73	0.0	7.68	0.0	0.00035359	0.00096208	0.01342173	0.34408078	A_07_P055563	ECs2829	cmr/UDP-glucose 6-dehydrogenase [ECs2829]	
ECs2835	-2.12	10.28	-1.08	9.74	0.1	10.82	0.2	0.00318154	0.01686672	0.06376651	0.63148881	A_07_P055581	ECs2835	cmr/phosphomannomutase [ECs2835]	
ECs2845	-3.55	10.30	-1.83	11.22	0.0	9.39	0.1	0.00010089	0.00119807	0.01750889	0.40478708	A_07_P055631	ECs2845	cmr/putative glycosyl transferase [ECs2845]	
ECs2885	-3.06	7.46	-1.04	7.98	0.2	6.93	0.1	0.00484841	0.01777943	0.08469239	0.39053500	A_07_P055701	ECs2885	cmr/putative transport protein [ECs2885]	
ECs2905	-4.30	8.32	-2.10	9.38	0.1	7.27	0.1	0.00000660	0.00091356	0.00959598	0.31678788	A_07_P062818	ECs2905	cmr/hypothetical protein [ECs2905]	
ECs2907	-3.08	8.99	-1.05	9.52	0.2	8.46	0.2	0.00425601	0.02097684	0.08271723	0.70242718	A_07_P055723	ECs2907	cmr/hydroxyethylthiazole kinase [ECs2907]	
ECs2912	-2.05	9.97	-1.04	10.49	0.0	9.45	0.2	0.00427142	0.02096298	0.08618648	0.73141746	A_07_P055744	ECs2912	cmr/hypothetical protein [ECs2912]	
ECs2923	-2.42	7.92	-1.27	7.28	0.4	8.56	0.0	0.00916167	0.03859818	0.04992379	0.55391121	A_07_P055776	ECs2923	cmr/interrupted molybdate metabolism regulator [ECs2923]	
ECs2933	-2.74	9.38	-1.45	10.11	0.1	8.65	0.1	0.00038945	0.00335792	0.03853626	0.53474627	A_07_P055796	ECs2933	cmr/putative transposase OrfA protein of insertion sequence 6629 [ECs2933]	
ECs2976	-2.57	9.68	-1.36	10.36	0.1	9.00	0.1	0.00088620	0.00628768	0.04673926	0.57439500	A_07_P055924	ECs2976	cmr/hypothetical protein [ECs2976]	
EC2978	-3.99	8.14	-2.00	9.14	0.1	7.14	0.3	0.00026608	0.00256374	0.01287602	0.35816254	A_07_P052883	EC2978	cmr/hypothetical protein [EC2978]	
EC2981	-12.76	7.24	-11.46	6.50	0.2	7.97	0.3	0.00224592	0.01307955	0.03819323	0.49262319	A_07_P052891	EC2981	cmr/putative DNA methylase [EC2981]	
EC2983	-2.48	7.28	-1.31	7.93	0.4	6.63	0.0	0.00724452	0.03203869	0.05072282	0.59462398	A_07_P052902	EC2983	cmr/hypothetical protein [EC2983]	
EC2998	-5.63	11.72	-2.49	12.97	0.0	10.47	0.0	0.00003736	0.00040244	0.00441756	0.21599379	A_07_P053122	EC2998	cmr/Rd protein [EC2998]	
EC3001	-2.05	11.56	-1.03	12.08	0.1	11.05	0.0	0.00190070	0.01150082	0.08480501	0.70944008	A_07_P052993	EC3001	cmr/recombination protein bet [EC3001]	
EC3002	-3.63	10.13	-1.86	11.06	0.0	9.21	0.1	0.00011224	0.00145675	0.01685849	0.38718163	A_07_P053000	EC3002	cmr/exonuclease [EC3002]	
EC3003	-2.67	10.02	-1.42	9.31	0.1	10.72	0.1	0.00058709	0.00457583	0.04034934	0.50178515	A_07_P053004	EC3003	cmr/hypothetical protein [EC3003]	
EC3004	-2.47	8.38	-1.31	7.73	0.2	9.04	0.4	0.00830766	0.02375849	0.07377312	0.54424023	A_07_P053006	EC3004	cmr/hypothetical protein [EC3004]	
EC3005	-2.09	9.56	-1.06	9.03	0.3	10.09	0.2	0.01262762	0.04987975	0.07060754	0.66265939	A_07_P053011	EC3005	cmr/hypothetical protein [EC3005]	
EC3006	-13.61	7.69	-11.85	6.77	0.1	8.62	0.0	0.00013722	0.00144762	0.02378278	0.45153217	A_07_P053018	EC3006	cmr/putative C4-type zinc finger protein [EC3006]	
EC3020	-2.53	8.98	-1.34	8.31	0.5	9.65	0.0	0.00867517	0.03696495	0.04613186	0.53800000	A_07_P053058	EC3020	cmr/D-lactate dehydrogenase [EC3020]	
EC3029	-3.22	9.93	-1.68	10.78	0.6	9.09	0.3	0.00814068	0.03479944	0.04245805	0.45800984	A_07_P053079	EC3029	cmr/putative isomerase [EC3029]	
EC3042	-50.70	10.98	-5.46	8.15	0.1	13.81	0.8	0.00004993	0.00080150	0.00011879	0.02923875	A_07_P053100	EC3042	cmr/glucose-binding transport protein [EC3042]	
EC3098	-3.82	13.46	-1.93	12.50	0.1	14.43	0.1	0.00010699	0.00135089	0.02175622	0.38835601	A_07_P053126	EC3098	cmr/ecotin, a serine protease inhibitor [ECs3098]	
EC3104	-2.53	10.45	-1.34	9.78	0.0	11.12	0.0	0.00046115	0.00380984	0.04403613	0.52165411	A_07_P053132	EC3104	cmr/outer membrane protein c precursor [EC3104]	
EC3152	-2.16	8.74	-1.11	8.18	0.0	9.29	0.4	0.01001482	0.04153669	0.06143039	0.62167985	A_07_P053169	EC3152	cmr/2-oxoglutarate decarboxylase [ECs3152]	
EC3160	-11.98	8.56	-1.58	6.77	0.1	10.35	0.4	0.00003177	0.00003949	0.00232033	0.14378812	A_07_P062826	EC3160	cmr/NADH dehydrogenase I chain N [ECs3160]	
EC3163	-72.80	10.19	-6.19	7.10	0.1	13.29	0.1	0.00000015	0.00007760	0.00005716	0.02045955	A_07_P053173	EC3163	cmr/NADH dehydrogenase I chain K [ECs3163]	
EC3167	-55.13	11.95	-5.76	8.26	0.1	14.05	0.1	0.00000017	0.00010290	0.00008372	0.02883857	A_07_P053176	EC3167	cmr/NADH dehydrogenase I chain C [ECs3167]	
EC3169	-44.49	13.15	-5.48	10.41	0.2	15.89	0.1	0.00000103	0.00012946	0.00015180	0.03119444	A_07_P063350	EC3169	cmr/NADH dehydrogenase I chain E [ECs3169]	
EC3179	-4.16	10.20	-1.60	9.37	0.0	11.03	0.2	0.00027025	0.00258336	0.02983660	0.43691001	A_07_P053181	EC3179	cmr/hypothetical protein [EC3179]	
EC3190	-2.59	7.52	-1.37	6.83	0.0	8.20	0.2	0.00070288	0.00524958	0.04247967	0.51114988	A_07_P053195	EC3190	cmr/ATP-binding component of histidine transport [ECs3190]	
EC3196	-2.82	8.65	-1.49	7.60	0.0	9.70	0.4	0.00030145	0.00254717	0.03681313	0.48401808	A_07_P053197	EC3196	cmr/aminophosphorylhomoserine phosphate [ECs3196]	
EC3223	-2.98	8.47	-1.57	9.26	0.2	7.68	0.2	0.00093870	0.00657715	0.02966209	0.48747390	A_07_P053262	EC3223	cmr/hypothetical protein [ECs3223]	
EC3236	-2.63	8.95	-1.40	9.65	0.0	8.24	0.4	0.00957624	0.03869996	0.04128188	0.56423849	A_07_P053303	EC3236	cmr/putative replication protein [ECs3236]	
EC3275	-3.03	9.67	-1.60	10.47	0.1	8.87	0.1	0.00037351	0.00325790	0.02808526	0.48460213	A_07_P053371	EC3275	cmr/hypothetical protein [ECs3275]	
EC3286	-5.77	11.03	-2.53	12.30	0.1	9.77	0.1	0.00001542	0.00015642	0.00423590	0.21304600	A_07_P053396	EC3286	cmr/thiosulfate binding protein [ECs3286]	
EC3306	-7.88	11.50	-2.98	12.99	0.0	10.01	0.2	0.00001679	0.00042622	0.00158918	0.13031250	A_07_P053406	EC3306	cmr/N-acetylmuramoyl-l-alanine amidase [ECs3306]	
EC3311	-2.72	7.53	-1.49	8.81	0.0	6.25	0.1	0.00033744	0.00304380	0.03894518	0.49562652	A_07_P053415	EC3311	cmr/ethanolamine ammonia-lyase light chain [ECs3311]	
EC3382	-2.54	11.42	-1.35	12.10	0.1	10.75	0.1	0.00070691	0.00527472	0.04795287	0.57985407	A_07_P053440	EC3382	cmr/putative anaerobic dimethyl sulfoxide reductase chain C [ECs3382]	
EC3398	-13.22	12.95	-2.71	14.81	0.0	11.08	0.2	0.00008661	0.00027019	0.00328228	0.05309524	A_07_P053458	EC3398	cmr/putative ATP synthase beta subunit [ECs3398]	
EC3450	-13.62	9.66	-1.86	8.73	0.0	10.59	0.3	0.00074683	0.00550772	0.02430005	0.49418860	A_07_P053496	EC3450	cmr/hypothetical protein [EC3450]	
EC3484	-2.39	7.48	-1.26	8.11	0.2	6.85	0.0	0.00119913	0.00762488	0.05376276	0.61380620	A_07_P053513	EC3484	cmr/hypothetical protein [EC3484]	
EC3489	-3.15	11.61	-1.65	12.44	0.3	10.78	0.0	0.00010988	0.00072424	0.01576988	0.47175712	A_07_P053518	EC3489	cmr/hypothetical protein [EC3489]	
EC3492	-3.93	8.61	-1.97	9.60	0.0	7.62	0.2	0.00011296	0.00141151	0.01292792	0.35758377	A_07_P053476	EC3492	cmr/hypothetical protein [EC3492]	
EC3500	-2.35	10.90	-1.23	10.29	0.3	11.52	0.2	0.00640301	0.02919762	0.05411331	0.57952563	A_07_P053484	EC3500	cmr/hypothetical membrane protein [ECs3500]	
EC3535	-3.17	8.43	-1.67	7.59	0.0	9.26	0.4	0.00140195	0.00890369	0.03004510	0.44167134	A_07_P053585	EC3535	cmr/hypothetical protein [ECs3535]	
EC3559	-4.66	8.16	-2.22	7.05	0.0	9.27	0.1	0.00098667	0.00498663	0.01783570	0.31767663	A_07_P053616	EC3559	cmr/interrupted gluclo/cyrb/ceob-specific PTS system enzyme IIC component [ECs3559]	
EC3569	-2.68	7.96	-1.88	8.90	0.1	7.02	0.1	0.00100575	0.00135201	0.01578316	0.39253924	A_07_P053693	EC3569	cmr/electron transport protein HyaN [ECs3569]	
EC3585	-2.27	9.35	-1.18	8.75	0.1	9.94	0.2	0.02230035	0.01293914	0.05401740	0.57931125	A_07_P054003	EC3585	cmr/hydrogenase-maturation protein HypB [ECs3585]	
EC3586	-2.38	11.32	-1.25	10.69	0.1	11.94	0.2	0.00118893	0.00787482	0.04941274	0.55263822	A_07_P054010	EC3586	cmr/HypD protein [ECs3586]	
EC3627	-2.09	8.67	-1.06	8.81	0.2	8.53	0.2	0.00647556	0.02637378	0.08093814	0.69472968	A_07_P054088	EC3627	cmr/putative phosphotransferase [ECs3627]	
EC3663	-14.35	12.45	-3.84	10.53	0.0	14.37	0.1	0.00000211	0.00017779	0.00170732	0.12387097	A_07_P054139	EC3663	cmr/L-fucokinase [ECs3663]	
EC3670	-3.74	8.96	-1.90	9.91	0.1	8.01	0.4	0.00076634	0.00566068	0.01142128	0.38827662	A_07_P054162	EC3670	cmr/hypothetical protein [ECs3670]	
EC3683	-2.30	7.82	-1.20	7.22	0.4	8.42	0.1	0.00180169	0.01076563	0.05273776	0.57261247	A_07_P054166	EC3683	cmr/prolyl-tRNA synthetase [ECs3683]	
EC3718	-2.11	8.76	-1.08	9.30	0.1	8.22	0.2	0.00142212	0.01762441	0.07808941	0.68113024	A_07_P054198	EC3718	cmr/type III secretion protein EscU [ECs3718]	
EC3727	-2.09	8.18	-1.06	8.71	0.1	7.65	0.0	0.00152649	0.00945346	0.08180927	0.69428960	A_07_P054224	EC3727	cmr/type III secretion protein EscJ [ECs3727]	
EC3739	-3.11	8.30	-1.64	9.11	0.5	7.48	0.2	0.00616932	0.02812460	0.02438374	0.47432024	A_07_P054231	EC3739	cmr/type III secretion protein EscJ [ECs3739]	
EC3758	-2.34	8.97	-1.23	9.58	0.2	8.36	0.3	0.00474191	0.02271563	0.05454929	0.62368065	A_07_P054278	EC3758	cmr/putative oxidoreductase Fe-S subunit [ECs3758]	
EC3764	-3.04	9.37	-1.60	10.17	0.2	8.57	0.1	0.00084254	0.00369935	0.02938376	0.48219301	A_07_P054285	EC3764	cmr/sdhA exonuclease Rec2 [ECs3764]	
EC3771	-13.62	9.40	-1.86	8.47	0.2	10.33	0.0	0.00018778	0.00202082	0.02370681	0.49176534	A_07_P063449	EC3771	cmr/putative oxidoreductase [ECs3771]	
EC3774	-11.70	9.49	-1.55	7.71	0.1	11.26	0.1	0.00000467	0.00021240	0.00260513	0.14746604	A_07_P063454	EC3774	cmr/glycine decarboxylase [ECs3774]	
EC3778	-2.81	12.04	-1.46	11.29	0.1	12.78	0.0	0.00036769	0.00257334	0.01684547	0.48449247	A_07_P054295	EC3778	cmr/2-octaprenyl-6-methoxyphenol 4-monooxygenase [ECs3778]	
EC3800	-9.72	8.47	-3.28	6.83	0.1	10.11	0.2	0.00000453	0.00035511	0.00383384	0.18346505	A_07_P054318	EC3800	cmr/putative transporter [ECs3800]	
EC3801	-6.17	8.85	-2.63	7.53	0.1	10.16	0.2	0.00000576	0.00065463	0.00962527	0.26469823	A_07_P054323	EC3801	cmr/hypothetical lipoprotein [ECs3801]	
EC3802	-3.08	7.55	-1.62	6.74	0.0	8.36	0.0	0.00018691	0.00201440	0.03129446	0.45160403	A_07_P054330	EC3802	cmr/putative ABC transporter ATP-binding subunit [ECs3802]	
EC3812	-3.18	9.73	-1.13	10.29	0.1	9.16	0.0	0.00195085	0.00716524	0.07346001	0.68779274	A_07_P054353	EC3812	cmr/agmatinase [ECs3812]	
EC3813	-2.62	7.46	-1.86	8.39	0.4	6.54	0.0	0.00137345	0.00876513	0.01667238	0.39651057	A_07_P054349	EC3813	cmr/hypothetical lipoprotein [ECs3813]	
EC3844	-5.70	9.56	-2.51	10.82	0.0	8.31	0.0	0.00001648	0.00024217	0.00427877	0.21018809	A_07_P054361	EC3844	cmr/hypothetical protein [ECs3844]	
EC3845	-2.81	7.98	-1.49	7.23	0.4	8.72	0.1	0.00055999	0.00438729	0.07069316	0.48312941	A_07_P054367	EC3845	cmr/hypothetical protein [ECs3845]	
EC3846	-2.21	9.24	-1.21	9.84	0.1	8.64	0.1	0.00146683	0.00926568	0.06384909	0.64728912	A_07_P054371	EC3846	cmr/hypothetical protein [ECs3846]	
EC3851	-3.33	8.62	-1.74	9.49	0.5	7.76	0.3	0.00410179	0.02188532	0.02208524	0.44755322	A_07_P054397	EC3851	cmr/hypothetical protein [ECs3851]	
EC3853	-2.44	8.28	-1.29	8.93	0.0	7.64	0.0	0.00054544	0.00419323	0.03188211	0.60724409	A_07_P054407	EC3853	cmr/putative transposase [ECs3853]	
EC3860	-3.06	9.32	-1.61	10.13	0.3	8.51	0.6	0.01138253	0.04588144	0.03870300	0.48431155	A_07_P054442	EC3860	cmr/putative adherence factor [ECs3860]	
EC3869	-2.60	11.81	-1.38	12.59	0.1	11.12	0.1	0.00000294	0.00045648	0.00469189	0.57246668	A_07_P054468	EC3869	cmr/hypothetical protein [ECs3869]	
EC3870	-2.10	9.36	-1.07	9.89	0.3	8.82	0.2	0.01115507	0.04514123	0.08130018	0.69528888	A_07_P054475	EC3870	cmr/hypothetical protein [ECs3870]	
EC3878	-4.03	10.08	-2.05	9.07	0.2	11.08	0.1	0.00019042	0.00203528	0.01984552	0.25943357	A_07_P054483	EC3878	cmr/hypothetical protein [ECs3878]	
EC3879	-4.78	11.93	-2.26	10.80	0.0	13.06	0.2	0.00000702	0.00010790	0.01511179	0.33090403	A_07_P054488	EC3879	cmr/hydrogenase 2 maturation protease HybD [ECs3879]	
EC3913	-2.07	8.79	-1.05	9.31	0.3	8.26	0.1	0.00380671	0.01998027	0.08339316	0.70607775	A_07_P054506	EC3913	cmr/putative ferrichrome-binding protein [ECs3913]	
EC3916	-2.51	8.18	-1.34	8.85	0.1	7.51	0.4	0.04641863	0.02153773	0.04674916	0.57405616	A_07_P054524	EC3916	cmr/putative ABC-type iron-siderophore transport system ATP-binding protein [ECs3916]	
EC3930	-5.84	12.51	-2.55	13.78	0.1	11.24	0.0	0.00003899	0.00045450	0.00403011	0.20940594	A_07_P054534	EC3930	cmr/hypothetical protein [ECs3930]	
EC3972	-2.06	7.57	-1.06	7.65	0.0	8.09	0.1	0.00170720	0.01069332	0.04202837	0.63738668	A_07_P054583	EC3972	cmr/putative transcriptional regulator [ECs3972]	
EC3995	+073.10	11.70	-4.88	7.25	0.2	16.14	0.1	0.00000006	0.00000702	0.00000000	0.00000000	A_07_P054609	EC3995	cmr/putative kinase [ECs3995]	
EC4036	-1.86	9.08	-1.95	8.11	0.1	10.06	0.0	0.00007450	0.00131005	0.02123095	0.38553633	A_07_P054656	EC4036	cmr/putative hydrolase [ECs4036]	
EC4013	-5.02	8.00	-2.33	6.84	0.2	9.16	0.2	0.00010227	0.00102090	0.01403074	0.33681622	A_07_P054671	EC4013	cmr/N-acetylglucosamine-specific PTS system enzyme IID component [ECs4013]	
EC4014	-7.92	8.60	-2.99	7.60	0.1	10.09	0.1	0.00000265	0.00016131	0.00349011	0.22377960	A_07_P054680	EC4014	cmr/N-acetyl-galactosamine / galactosamine PTS system enzyme IIA component [ECs4014]	
EC4014	-4.79	8.89	-2.28	7.76	0.1	10.02	0.1	0.00000546	0.00007550	0.01514291	0.33664574	A_07_P054680	EC4014	cmr/N-acetyl-galactosamine / galactosamine PTS system enzyme IIB component [ECs4014]	
EC4014	-8.66	8.70	-3.12	7.15	0.3	10.26	0.0	0.00003329	0.00003141	0.00469366	0.21075881	A_07_P054680	EC4014	cmr/N-acetyl-galactosamine / galactosamine PTS system enzyme IIC component [ECs4014]	
EC4014	-5.40	8.98	-2.43	7.76	0.1	10.02	0.0	0.00002278	0.00051605	0.01245173	0.29611293	A_07_P054680	EC4014	cmr/N-acetyl-galactosamine / galactosamine PTS system enzyme IIA component [ECs4014]	
EC4014	-7.44	9.01	-2.90	7.55	0.1	10.45	0.1	0.00000045	0.00007611	0.00466187	0.23138130	A_07_P054680	EC4014	cmr/N-acetyl-galactosamine / galactosamine PTS system enzyme IIB component [ECs4014]	
EC4023	-12.17	11.79	-5.01	14.29	0.1	9.29	0.0	0.00000043	0.00000262	0.00000953	0.00789474	A_07_P054688	EC4023	cmr/truncated putative fimbrial protein [ECs4023]	
EC4093	-2.68	7.96	-1.31	8.62	0.2	7.31	0.0	0.00139163	0.00886375	0.01153201	0.65142228	A_07_P054691	EC4093	cmr/hypothetical protein [ECs4093]	
EC4052	-2.58	8.42	-1.37	7.74	0.1	9.10	0.0	0.00066985	0.00507658	0.02428693	0.51284074	A_07_P054701	EC4052	cmr/arginiosuccinate synthetase [ECs4052]	
EC4084	-3.38	7.95	-1.76	7.07	0.0	8.83	0.1	0.00206622	0.02675559	0.04216040	0.49124065	A_07_P054756	EC4084	cmr/hypothetical protein [ECs4084]	
EC4098	-13.24	8.00	-1.69	7.05	0.1	8.85	0.0	0.00014040	0.00162986	0.02873539	0.43831178	A_07_P054756	EC4098	cmr/N-acetylneuraminate lyase [ECs4098]	
EC4099	-2.56	9.58	-1.36	10.26	0.1	8.90	0.1	0.00075191	0.00553183	0.04647802	0.57188220	A_07_P054723	EC4099	cmr/putative transcriptional regulator [ECs4099]	
EC4115	-4.38	8.13	-2.13	9.20	0.1	7.07	0.1	0.00007719	0.00108795	0.00949949	0.30908826	A_07_P054857	EC4115	cmr/hypothetical protein [ECs4115]	
EC4150	-5.29	11.33	-2.40	10.13	0.1	12.53	0.1	0.00003385	0.00063751	0.01308877	0.30252585	A_07_P054737	EC4150	cmr/hypothetical protein [ECs4150]	
EC4196	-2.82	9.69	-1.50	10.44	0.2	8.94	0.2	0.01608604	0.03308584	0.06429954	0.52696627	A_07_P054525	EC4196	cmr/hypothetical protein [ECs4196]	
EC4237	-2.21	7.24	-1.14	6.67	0.1	7.81	0.1	0.00109286	0.00788759	0.05427541	0.58909574	A_07_P054765	EC4237	cmr/hypothetical protein [ECs4237]	
EC4253	-3.91	9.17	-1.54	9.94	0.1	8.40	0.4	0.00188200	0.01593190	0.03079426	0.49238821	A_07_P054783	EC4253	cmr/putative transcriptional regulator [ECs4253]	
EC4260	-13.40	9.11	-3.77	7.23	0.2	10.99	0.2	0.00000050	0.00034033	0.00190664	0.13384388	A_07_P054542	EC4260	cmr/positive regulator of mal regulon [ECs4260]	
EC4280	-3.95	11.17	-1.98	10.18	0.2	12.16	0.1	0.00032006	0.00183128	0.02076347	0.38239818	A_07_P054825	EC4280	cmr/putative DNA processing chain A [ECs4280]	
EC4281	+5.00	10.27	-2.32	9.11	0.0	11.43	0.1	0.00004579	0.00075800	0.01414126	0.10988506	A_07_P054828	EC4281	cmr/putative ATP-dependent DNA helicase [ECs4281]	
EC4282	-16.80	9.21	-4.77	7.83	0.1	10.59	0.0	0.00001329	0.00016418	0.00800313	0.24867950	A_07_P054831	EC4282	cmr/putative ATP-dependent DNA helicase [ECs4282]	
EC4330	-2.22	8.54	-1.15	9.11	0.2	7.96	0.2	0.02262625	0.01434015	0.08377779	0.65887271	A_07_P054920	EC4330	cmr/hypothetical membrane protein [ECs4330]	
EC4333	-3.63	7.55	-1.86	8.42	0.1	8.48	0.4	0.00091623	0.00642289	0.02395017	0.40231162	A_07_P054931	EC4333	cmr/hypothetical protein [ECs4333]	
EC4334	-7.55	9.42	-2.92	7.96	0.1	10.87	0.0	0.00001328	0.00038273	0.00651296	0.23142727	A_07_P054939	EC4334	cmr/hypothetical protein [ECs4334]	
EC4335	-5.45	8.61	-2.45	7.39	0.0	9.84	0.1	0.00001643	0.00015081	0.01216127	0.26241221	A_07_P054945	EC4335	cmr/hypothetical protein [ECs4335]	
EC4337	-7.93	8.45	-2.99	6.96	0.0	9.95	0.1	0.00001135	0.00015103	0.00594258	0.22329856	A_07_P054955	EC4337	cmr/hypothetical lipoprotein [ECs4337]	
EC4338	-6.89	8.44	-2.79	7.05	0.1	9.83	0.0	0.00001582	0.00017177	0.00786658	0.24813427	A_07_P054962	EC4338	cmr/putative 3-oxoacyl [ECs4338]	
EC4339	-8.36	8.04	-3.06	6.51	0.2	9.57	0.0

flgaB	+4.03	10.47	+2.01	9.46	0.0	11.47	0.1	0.00060022	0.00060997	0.01980310	0.37700121	A_07_P01829	b0928
flgBB	2.93	10.58	-1.55	10.82	0.0	8.27	0.1	0.00000344	0.00029176	0.02218846	0.49678031	A_07_P068442	b2895
flgK	2.22	9.42	-1.15	9.99	0.1	8.84	0.1	0.00018648	0.00786195	0.04882241	0.65788707	A_07_P016012	b1082
flgL	-2.85	8.43	-1.51	9.39	0.2	7.68	0.3	0.00199970	0.01159971	0.04948936	0.58984038	A_07_P001620	b1083
fliAO	+2.67	8.54	+1.42	7.83	0.0	9.25	0.1	0.00051873	0.00015407	0.00513054	0.02608811	A_07_P016140	b1922
fliA	-4.60	7.84	-2.20	8.94	0.1	6.74	0.2	0.00008025	0.00120512	0.00831551	0.29486486	A_07_P014973	b1922
fliE	-2.86	7.95	-1.52	8.71	0.3	7.19	0.1	0.00153235	0.00957690	0.03443082	0.30245688	A_07_P015189	b1927
fliI	-2.25	12.58	-1.27	13.13	0.3	11.99	0.1	0.00404343	0.02012275	0.06717861	0.65612590	A_07_P044091	23031
fliJ	-2.39	12.60	-1.26	13.23	0.4	11.98	0.1	0.00768753	0.03358281	0.05638935	0.61626123	A_07_P051201	EC2680
fliT	-2.38	8.94	-1.25	9.57	0.3	8.31	0.4	0.01156672	0.06646759	0.05480119	0.60976558	A_07_P014991	b1926
fliY	-4.39	13.08	-2.14	14.15	0.0	12.01	0.0	0.00059945	0.00068714	0.00144307	0.30879418	A_07_P041209	c_2315
fliY	-5.81	11.67	-2.54	12.93	0.1	10.40	0.4	0.00017660	0.00019847	0.00450578	0.20872549	A_07_P014964	b1920
fmt	-5.18	10.91	-2.43	9.70	0.5	12.13	0.0	0.00089734	0.00434668	0.01175269	0.28945701	A_07_P015380	b2000
fmt	-2.53	12.02	-1.34	12.69	0.0	11.35	0.1	0.00050019	0.00404054	0.04855246	0.58130308	A_07_P012874	b2888
fnr	-8.50	13.79	-3.09	15.33	0.0	12.25	0.1	0.00006440	0.00000000	0.01237330	0.11325581	A_07_P014647	b1334
FocA	+6.52	11.15	+2.70	9.80	0.1	12.50	0.1	0.00003286	0.00003639	0.00871761	0.25945180	A_07_P004969	b0904
FocA	+120.94	13.45	+6.92	9.99	0.0	16.91	0.1	0.00000011	0.00000532	0.00002370	0.00009991	A_07_P004986	c_1239
FocC	+15.24	10.13	+3.93	8.16	0.1	12.09	0.1	0.00000317	0.00019528	0.00153392	0.11955946	A_07_P040500	c_1241
FocD	+15.83	11.51	+3.98	8.52	0.3	14.50	0.1	0.00000758	0.00003974	0.00143039	0.11489756	A_07_P040505	c_1242
FocE	+19.76	11.05	+4.30	8.90	0.2	13.21	0.0	0.00000185	0.00016828	0.00808539	0.08453313	A_07_P040507	c_1243
FocG	+15.39	11.26	+3.96	9.31	0.3	13.20	0.2	0.00000910	0.01932130	0.00148628	0.17258756	A_07_P040512	c_1244
FocH	+14.79	10.76	+3.89	8.82	0.1	12.70	0.1	0.00000252	0.00018118	0.00163173	0.12350962	A_07_P040520	c_1245
FolB	3.97	9.82	-1.57	10.61	0.1	9.03	0.2	0.00061160	0.00671780	0.03083524	0.49186424	A_07_P000021	b0558
FolD	-2.14	11.30	-1.10	11.85	0.1	10.75	0.1	0.00159882	0.00938185	0.07616377	0.47314547	A_07_P013425	c_0645
FolD	-2.39	10.05	-1.26	10.68	0.1	9.42	0.4	0.02902842	0.03816958	0.05409454	0.61724697	A_07_P014422	b0529
FolD	-2.21	12.91	-1.15	13.48	0.0	12.33	0.2	0.02231614	0.01257572	0.07916006	0.66302521	A_07_P047965	20684
FolE	+3.18	12.06	+1.67	11.23	0.0	12.89	0.0	0.00014962	0.00170945	0.02958868	0.43907634	A_07_P003527	b2153
FolK	-2.24	8.45	-1.16	9.03	0.1	7.87	0.1	0.00129833	0.00842230	0.06845262	0.81793333	A_07_P000473	b0542
fpr	-2.94	9.32	-1.55	8.54	0.1	10.10	0.0	0.00037872	0.00328517	0.03421494	0.47046288	A_07_P019438	c_4876
fpr	+4.97	9.07	+2.31	7.91	0.1	10.22	0.1	0.00005659	0.00018455	0.01425110	0.32040257	A_07_P019396	b3924
frdA	+2.57	14.83	+1.36	14.14	0.0	15.51	0.0	0.00040351	0.00344325	0.04291540	0.51302661	A_07_P011501	b4154
frdB	+4.03	12.60	+2.01	11.59	0.1	13.60	0.1	0.00007887	0.00110461	0.01988328	0.37611718	A_07_P011487	b4153
frdC	+2.79	11.53	+1.48	10.79	0.2	12.27	0.0	0.00060780	0.00511569	0.03468738	0.48410342	A_07_P011491	b4152
frdD	+2.92	9.84	+1.55	9.06	0.2	10.61	0.1	0.00040459	0.00364142	0.04154459	0.47080487	A_07_P011497	b4151
frlD	+2.37	7.46	+1.25	6.84	0.1	8.09	0.0	0.00078349	0.00570374	0.04983072	0.55343684	A_07_P07800	b3374
frmR	+3.94	10.28	+1.98	9.29	0.1	11.27	0.1	0.00009061	0.00123866	0.00072536	0.38251324	A_07_P020911	b0357
frr	-4.46	12.99	-2.16	14.07	0.0	11.91	0.1	0.00004346	0.00073568	0.00915385	0.30536170	A_07_P059508	EC4574
frr	-3.77	13.69	-1.92	14.64	0.0	12.73	0.1	0.00003060	0.00144094	0.01426236	0.38042661	A_07_P004843	20183
frr	-3.33	13.51	-1.73	14.38	0.0	12.64	0.1	0.00012812	0.00154216	0.02164634	0.44498862	A_07_P035911	c_0208
frr	-4.71	12.93	-2.24	14.05	0.0	11.82	0.0	0.00006014	0.00068227	0.00771341	0.28641067	A_07_P002818	b0573
FruA	-2.64	8.91	-1.29	9.55	0.0	8.27	0.0	0.00055426	0.00436376	0.05424162	0.60824786	A_07_P000634	b2167
FruA	-2.24	9.14	-1.17	9.72	0.1	8.55	0.4	0.07978826	0.03439987	0.06480259	0.64820051	A_07_P042526	c_3702
FruR	+4.65	10.37	+2.22	9.26	0.1	11.48	0.0	0.00006175	0.00075157	0.01186192	0.33747297	A_07_P011076	b0080
FruR	+2.32	7.66	+1.21	7.05	0.3	8.26	0.1	0.00539726	0.02527498	0.05312055	0.57322138	A_07_P047079	25460
FruR	+2.02	7.37	+1.01	6.87	0.0	7.88	0.0	0.00183143	0.01068342	0.04347914	0.61367944	A_07_P047080	c_3703
fhaA	+0.99	14.08	8.05	0.0	12.14	0.0	0.00000120	0.00004031	0.00144047	0.10500000	A_07_P016193	b1905
fhaB	+2.91	9.88	+1.54	9.11	0.1	10.65	0.1	0.00003819	0.00245286	0.01478010	0.47372042	A_07_P016192	b1902
fhaC	-14.82	10.62	-3.89	12.57	0.0	8.68	0.2	0.00000337	0.00019956	0.00015307	0.00228070	A_07_P007255	b3463
fhaK	+3.38	10.54	+1.76	9.66	0.0	11.42	0.0	0.00000302	0.00014694	0.00176258	0.42092067	A_07_P004869	b0860
fhlA	-3.10	11.24	-1.72	12.10	0.1	10.38	0.3	0.00016877	0.00747554	0.02187627	0.44728870	A_07_P019442	b3933
fhlP	-2.15	9.15	-1.11	9.70	0.1	8.60	0.1	0.00134255	0.00862736	0.07491108	0.67317352	A_07_P012227	b3017
fhlW	+2.87	8.97	+1.52	8.21	0.1	9.73	0.1	0.00032427	0.00296307	0.03548875	0.47687447	A_07_P011122	b0089
fhuA	2.01	7.87	-1.01	8.37	0.1	7.38	0.1	0.00208312	0.01998882	0.08631005	0.72155066	A_07_P063559	EC4311
fhuA	-2.38	8.14	-1.25	8.71	0.1	7.52	0.0	0.00079350	0.00575440	0.05730628	0.61963346	A_07_P052174	24836
fhuA	-2.04	7.64	-1.03	8.16	0.1	7.13	0.1	0.00039783	0.01838386	0.08617015	0.71682227	A_07_P007366	b3462
fhuY	-8.48	12.69	-3.08	14.24	0.1	11.15	0.0	0.00000778	0.00029735	0.01162697	0.11502890	A_07_P007256	b3464
fhuZ	+2.96	13.53	+1.56	12.75	0.0	14.31	0.0	0.00000358	0.00038704	0.01837105	0.46778697	A_07_P002487	b0695
fucA	-10.52	11.68	-3.40	9.99	0.0	13.38	0.1	0.00000366	0.00000738	0.00322282	0.16690789	A_07_P005999	b2800
fucI	-2.24	11.00	-1.17	10.42	0.1	11.59	0.1	0.00140029	0.00860505	0.05369320	0.58837378	A_07_P006006	b2803
fucK	+6.53	9.85	+2.71	8.50	0.1	11.20	0.2	0.00003654	0.00065813	0.00879715	0.25994150	A_07_P006014	b2803
fucK	+14.64	12.66	+3.87	10.79	0.3	14.60	0.1	0.00003252	0.00007048	0.00168255	0.12263889	A_07_P043254	24120
fucO	+10.18	10.44	+3.35	8.77	0.0	12.11	0.7	0.00055462	0.00415846	0.00377541	0.38269231	A_07_P005991	b2799
fucR	+6.21	8.29	+2.07	7.26	0.1	9.33	0.1	0.00006676	0.00098312	0.01846291	0.36289638	A_07_P006024	b2805
fucU	+12.10	10.90	+3.60	10.30	0.1	11.50	0.0	0.00000360	0.00018316	0.00241171	0.14437262	A_07_P006028	b2804
fumA	+8.19	10.69	+4.19	8.50	0.1	10.38	0.3	0.00001887	0.00747554	0.02187627	0.44728870	A_07_P019442	b3933
fumC	+11.96	9.31	+3.75	7.46	0.0	11.21	0.1	0.00000225	0.00007963	0.00280013	0.13231092	A_07_P042302	c_2003
fumC	+19.97	9.48	+4.32	7.32	0.1	11.64	0.3	0.00000556	0.00025342	0.00079522	0.08517007	A_07_P020689	b1611
fur	3.81	12.22	1.93	13.18	0.0	11.25	0.2	0.00012518	0.00155183	0.01474607	0.38372027	A_07_P009983	b0683
gabT	+2.48	9.05	+1.31	8.40	0.2	9.71	0.2	0.00244725	0.01135589	0.04718369	0.58261182	A_07_P021692	b2662
gabT	-2.15	10.01	-1.11	9.46	0.1	10.57	0.2	0.00384654	0.01936243	0.06030336	0.61363165	A_07_P015326	b2662
gabR	+12.47	11.97	+3.64	10.15	0.1	13.79	0.1	0.00000373	0.00020748	0.02230341	0.14644882	A_07_P004240	b0757
gabM	+11.25	11.13	+3.49	9.38	0.1	12.87	0.1	0.00000342	0.00018237	0.00283600	0.15666207	A_07_P004241	b0756
gabP	-2.19	10.81	-1.13	11.37	0.1	10.24	0.1	0.00134997	0.00818958	0.07282012	0.66733411	A_07_P006169	b2837
gabS	-2.13	9.63	-1.65	8.80	0.2	10.45	0.2	0.00048126	0.00391173	0.03884794	0.44752212	A_07_P022345	c_2685
galS	+2.37	8.54	+1.25	7.92	0.0	9.17	0.1	0.00075424	0.00554378	0.04946229	0.55269695	A_07_P003519	b2151
galT	+3.38	10.60	+1.76	9.72	0.1	11.48	0.1	0.00000758	0.00034704	0.02710826	0.42291624	A_07_P004241	b0758
gapA	+20.28	10.88	+4.34	8.71	0.1	13.05	0.2	0.00000217	0.00017840	0.00074283	0.08398601	A_07_P015590	b1779
gapF	-2.06	7.90	-1.04	8.43	0.1	7.38	0.1	0.00189286	0.01136147	0.08378842	0.75640600	A_07_P000576	b3127
gcvH	+476.83	12.32	+8.90	7.88	0.0	16.77	0.0	0.00000002	0.00007032	0.00000000	0.00000000	A_07_P041711	c_3484
gcvH	+283.91	11.56	+8.15	7.49	0.2	15.64	0.1	0.00000007	0.00007032	0.00048255	0.12263889	A_07_P043254	24120
gcvH	+273.63	12.52	+8.33	8.57	0.3	16.46	0.2	0.00000024	0.00000947	0.00000935	0.00272727	A_07_P041275	c_3484
gcvP	+13.43	9.73	+3.75	7.86	0.1	11.60	0.0	0.00000234	0.00017963	0.00260432	0.13293388	A_07_P012879	c_3483
gcvP	+14.42	9.57	+3.85	7.65	0.1	11.49	0.0	0.00000369	0.00021124	0.00177210	0.12624434	A_07_P012779	24240
gcvP	+27.79	9.44	+4.80	7.04	0.0	11.84	0.0	0.00000052	0.00009944	0.00009132	0.06029126	A_07_P006481	b2903
gcvR	+6.17	9.09	+2.62	7.78	0.1	10.40	0.2	0.00004583	0.00075801	0.00936067	0.26278907	A_07_P013413	b2979
gcvT	+162.57	11.62	+7.34	7.95	0.0	15.29	0.0	0.00000029	0.00009047	0.00000762	0.00600000	A_07_P006491	b2905
gdhA	6.12	9.41	+2.46	8.08	0.1	10.74	0.0	0.00003306	0.00037797	0.00593151	0.26377737	A_07_P012646	b2731
gdhA	+5.34	9.86	+2.42	8.65	0.3	11.07	0.2	0.00023155	0.00234711	0.01231961	0.29412473	A_07_P018851	b1761
gef	-3.16	12.82	-1.66	13.65	0.0	11.99	0.1	0.00037151	0.00159371	0.02574886	0.46920159	A_07_P044842	20016
gef	-3.01	10.57	-1.59	11.36	0.1	9.77	0.0	0.00021578	0.00022917	0.02947345	0.48691501	A_07_P048478	20016
gfcA	-2.13	10.06	+1.09	9.52	0.1	10.61	0.2	0.00022035	0.01250268	0.06146453	0.62172237	A_07_P001576	b1033
gldB	-5.47	9.81	-2.45	11.04	0.1	8.58	0.0	0.00002346	0.00052393	0.04788510	0.62272189	A_07_P005423	b3740
gldB	+3.96	9.33	+1.98	8.33	0.1	10.32	0.1	0.00000221	0.00123129	0.02660658	0.38123884	A_07_P012916	b2976
gldB	+6.81	11.47	+2.77	10.09	0.1	12.85	0.2	0.00002597	0.00055176	0.00797828	0.24824111	A_07_P041726	c_3705
gltF	-12.21	9.38	+3.61	7.58	0.1	11.19	0.1	0.00000843	0.00023673	0.00182617	0.14414273	A_07_P012924	b2978
gltG	+72.20	10.10	+6.17	7.01	0.0	13.18	0.1	0.00000016	0.00007760	0.00005526	0.02022256	A_07_P012924	b2977
gltM	-20.87	12.93	+4.38	16.74	0.0	9.12	0.1	0.00000218	0.00017840	0.00374556	0.08216367	A_07_P019501	b3945
gltP	+17.00	11.50	+4.16	9.42	0.1	13.58	0.1	0.00000165	0.00015927	0.00107597	0.09625000	A_07_P018171	b3429
gltP	+9.42	10.32	+3.24	8.50	0.2	12.14	0.2	0.00003339	0.00038367	0.00413935	0.19116507	A_07_P018189	b3432
gltPC	+21.39	10.78	+4.41	8.57	0.1	12.98	0.0	0.00008109	0.00013374	0.00004429	0.07798615	A_07_P018179	b3430
gltP	+7.08	8.87	+2.82	7.46	0.3	10.28	0.1	0.00005891	0.00089791	0.00729357	0.24270956	A_07_P018166	b3428
gltS	+6.21	10.39	+2.28	8.79	0.0	12.00	0.0	0.00000472	0.00032340	0.00420732	0.18000000	A_07_P012366	b3049
gltX	-12.37	12.15	+4.56	9.87	0.1	14.43	0.2	0.00000215	0.00007840	0.00054751	0.07061574	A_07_P018432	b2431
glk	-2.74	8.13	-1.46	8.86	0.1	7.40	0.2	0.00000258	0.00005795	0.00882675	0.53010858	A_07_P014224	b2388
glmM	-2.04	10.84	+1.03	10.32	0.1	11.35	0.2	0.00131183	0.02509949	0.06702087	0.64348652	A_07_P000591	b3176
glmU	-2.31	11.75	-1.21	12.35	0.1	11.14	0.1	0.00014516	0.00080861	0.06126001	0.63443272	A_07_P005571	b3730
glmU	-3.13	12.63	-1.65	13.61	0.1	11.80	0.0	0.00017863	0.00016167	0.02641197	0.47361048	A_07_P052237	25228
glnA	-3.46	13.41	-1.79	14.30	0.0	12.51	0.1	0.00011433	0.00142293	0.01884941	0.42018802	A_07_P019502	b1870
glnB	+2.70	10.83	+1.43	10.12	0.1	11.55	0.0	0.00033814	0.00304380	0.03962081	0.49943155	A_07_P019668	b2553
glnD	+3.13	8.80	+1.82	7.89	0.1	9.71	0.1	0.00016341	0.00148449	0.01916391	0.40972917	A_07_P021761	b0167
glnE	-2.42	7.77	-1.28	8.41	0.2	7.14	0.2	0.00298235	0.01415162	0.05430894	0.60850940	A_07_P021363	b0450
glnG	-2.63	9.78	-1.40	10.48	0.2	9.08	0.1	0.00111173	0.00747564	0.04278867	0.56213133	A_07_P009919	b0880
glnS	+2.38	9.10	+1.25	8.47	0.2	9.74	0.2	0.00132396	0.00851580	0.04901232	0.54960826	A_07_P020890	b1651
glpB	-2.51	10.35	-1.33	11.02	0.1	9.69	0.1	0.00084041	0.00603072	0.04996605	0.58946777	A_07_P000998	b2342
glpE	-2.51	9.69	-1.33	10.36	0.0	9.03	0.0	0.00047351	0.00087577	0.05005843	0.58991013	A_07_P018513	b3425
glpF	-26.40	11.40	-4.72	8.05	0.1	12.77	0.1	0.00000071	0.00011547	0.00043382	0.06381178	A_07_P019412	b3927
glpK	+3.23	10.34	+1.69	9.40	0.1	11.09	0.0	0.00015179	0.00171170	0.02894118	0.43890917	A_07_P019409	b3926
glpQ1	-2.58	8.31	-1.37	7.63	0.2	8.99	0.3	0.00489773	0.03031244	0.04342515	0.57679888	A_07_P000892	b2239
glpT	+14.62	9.57	+3.87	7.63	0.1	11.50	0.0	0.00000287	0.00018535	0.01668884	0.12403943	A_07_P063326	EC3125
glpT	+11.50	9.63	+3.52	7.74	0.0	11.52	0.0	0.00000328	0.00019044	0.00247868	0.15116605	A_07_P012966	23498
glpT	+9.66	10.03	+3.27	8.39	0.2	11.67	0.1	0.00001193	0.00036114	0.00387830	0.18447130	A_07_P000990	b2240
glpX	-53.23	13.91	+5.79	11.04	0.1	16.78	0.0	0.00000033	0.00009117	0.00010861	0.02898005	A_07_P056596	EC4574
glsA	+15.90	11.19	+3.99	9.19	0.2	13.18	0.0	0.00000271	0.00018406	0.00137767	0.11238342	A_07_P010118	b0720
glsA	+61.57	14.45	+5.45	11.72	0.1	17.17	0.0	0.00000032	0.00009117	0.00010625	0.03243224	A_07_P046286	20873
gltB	-12.73	8.83	+1.65	8.11	0.1	9.56	0.0	0.00035091	0.00312664	0.03902185	0.49545161	A_07_P012545	b3213
gltB	-6.08	12.30	+2.60	10.89	0.1	13.50	0.1	0.00002286	0.00051443	0.00998920	0.27105517	A_07_P009841	b0651
gltJ	+5.76	9.78	+2.53	8.52	0.0	11.04	0.1	0.00001812	0.00044149	0.01115663	0.28239550	A_07_P008836	b0654
gltK	+11.86	9.35	+3.07	7.56	0.1	11.13	0.4	0.00001180	0.00024849	0.01842864	0.34428604	A_07_P008835	b0653
gltL	+15.19	9.93	+3.93	7.97	0.1	11.89	0.0	0.00000173	0.00016209	0.00115212	0.11930000	A_07_P008830	b0652
gltP	-2.83	8.57	+1.58	7.82	0.2	9.32	0.2	0.01468888	0.04931386	0.03676648	0.48936221	A_07_P018432	b2431
gltX	-2.74	12.56	-1.65	12.88	0.1	12.24	0.1	0.00034416	0.00382214	0.03867525	0.55056151	A_07_P014274	b2400
glyA	-4.24	9.26	-2.08	10.30	0.1	8.22	0.1	0.00089223	0.00616320	0.03015371	0.51846402	ME-G285077	ME-G285077
glyA	+4.27	11.28	+2.09	10.23	0.1	12.32	0.3	0.00023100	0.00246638	0.03181174	0.36447535	A_07_P019657	b2551
glyQ	-2.06	11.57	-1.04	12.09	0.0	11.05	0.1	0.00102662	0.00138132	0.06237900	0.70412660	A_07_P007728	b3560
gmhA	+3.97	9.39	+1.99	8.40	0.0	10.38	0.1	0.00005665	0.00096109	0.02043095	0.37939787	A_07_P053536	EC4249
gmhA	+3.03	9.19	+1.60	8.39	0.2	9.98	0.1	0.00006137	0.00072758	0.02349111	0.45932010	A_07_P043366	20280
gmhA	-7.08	11.73	-2.82	12.90	0.0	13.14	0.0	0.00000921	0.00003221	0.00749672	0.24532225	A_07_P030845	c_0372
gmk	-17.58	12.42	-4.14	14.48	0.0	10.35	0.0	0.00000246	0.00017989	0.00080638	0.02730000	A_07_P017381	b1649
gnaA	+2.74	11.11	+1.45	10.39	0.1	11.84	0.1	0.00009088	0.00470682	0.03879446	0.49530091	A_07_P000634	ME-G285038
gnaB	+19.99	10.23	+4.32	8.07	0.5	12.39	0.0	0.00003281	0.00062948	0.00808285	0.08483221	A_07_P020394	b1550
gntK	-2.41	9.33	-1.27	9.96	0.1	8.69	0.0	0.00082791	0.00595734	0.06425127	0.69337019	A_07_P019419	b3437
gntT	-2.00	7.35	-1.00	7.85	0.0	6.85	0.2	0.00366050	0.01862115	0.08867505	0.72224521	A_07_P018304	b3415
gntX	+2.06	11.50	+1.04	10.98	0.1	12.02	0.0	0.00231688	0.01908389	0.06587909	0.67193163	A_07_P041244	c_1791
gnrr	-5.73	10.61	-2.52	11.87	0.1	9.35	0.1	0.00003088	0.00009993	0.00425168	0.21126183	A_07_P018096	b3414
gnrr	-6.01	10.83	-2.59	12.12	0.1	9.54	0.2	0.00005150	0.00081576	0.00372523	0.20083911	A_07_P018096	b3414
gnrr	-5.61	10.73	-2.49	11.97	0.1	9.49	0.2	0.00006747	0.00098907	0.00458016	0.22051988	A_07_P018096	b3414
gnrr	-6.67	10.65	-2.74	12.02	0.1	9.28	0.2	0.00004627	0.00074659	0.00268895	0.17435845	A_07_P018096	b3414
gnrr	-5.48	10.76	-2.46	11.93	0.1	9.47	0.3	0.00013972	0.00164541	0.00945425	0.32491279	A_07_P018096	b3414
gnr	-3.21	11.07	-1.64	11.89	0.5	10.25	0.5	0.01258669	0.04976016	0.07231605	0.67885425	A_07_P007436	b3500
gph	+6.53	10.07	+2.71	8.72	0.1	11.42	0.1	0.00002251	0.00051378	0.00870046	0.25932410	A_07_P017954	b3385
gpmA	+3.24	7.85	+1.39	7.01	0.1	8.70	0.2	0.00008969	0.00318008	0.02612221	0.42791876	A_07_P004227	b0755
gpp	+3.01	9.46	+1.59	8.67	0.1	10.26	0.1	0.00028392	0.00267666	0.02364926	0.46018800	A_07_P005780	b3779
gpsA	-6.04	11.27	-2.59	9.87	0.1	12.67	0.1	0.00002108	0.00004176	0.00035335	0.27243600	A_07_P008683	b3608
grcA	-8.97	10.03	-3.17	11.62	0.1	8.45	0.2	0.00001756	0.00004403	0.01005673	0.10154677	A_07_P000616	b3181
grcA	-2.12	11.02	-1.15	11.59	0.1	10.44	0.1	0.00001786	0.00017842	0.08859756	0.65808380	A_07_P000615	b3456
grcL	+17.16	13.64	+4.10	11.54	0.0	15.69	0.0	0.00000131	0.00010463	0.00120363	0.10243243	A_07_P011446	b4143
grcS	+21.39	14.38	+4.41	12.17	0.1	16.59	0.0	0.00000100	0.00012946	0.00062707	0.07775194	A_07_P011443	b4142
grxA	-3.03	8.03	-1.60	8.83	0.1	7.23	0.1	0.00021600	0.00221369	0.02885607	0.48413902	A_07_P004906	b0849
grxB	+18.20	10.17	+4.08	8.08	0.2	12.28	0.1	0.00000269	0.00018806	0.00100864	0.09286550	A_07_P015121	b3164
grxD	-2.34	12.58	-1.23	13.19	0.1	11.97	0.0	0.00073992	0.00547084	0.06043003	0.61018027	A_07_P018331	b3164
grxHB	-4.35	10.15	-2.12	11.21	0.0	9.09	0.0	0.00000668	0.00070309	0.00968623	0.30993935	A_07_P001912	b2688
grxHB	+2.83	11.43	+1.50	10.68	0.1	12.18	0.1	0.00003184	0.00029049	0.00166141	0.48182010	A_07_P018176	b3947
gspA	+2.85	9.24	+1.53	8.49	0.2	10.00	0.0	0.00064372	0.00382438	0.03686422	0.47982264	A_07_P004599	b0829
gspD	-2.92	7.80	-1.55	8.57	0.0	7.01	0.2	0.00064654	0.00382719	0.03155170	0.49239313	A_07_P013055	b3325
gspL	-6.10	9.58	-2.04	10.60	0.1	8.56	0.1	0.00011136	0.00139929	0.01140589	0.34470250	A_07_P013091	b3333
gspM	-2.69	8.07	-1.31	8.72	0.1	7.41	0.1	0.00085569	0.00526157	0.05246117	0.59127571	A_07_P017939	b3334
gst	+11.30	10.41	+3.50	8.66	0.1	12.16	0.2	0.00000940	0.00003220	0.00288745	0.15784722	A_07_P020808	b1625
gtaB	-5.11	12.82	-2.35	13.99	0.0	11.64	0.0	0.00002412	0.00015498	0.00480005	0.24602882	A_07_P013586	b3208
gtaB	+2.03	11.91	+1.03	11.40	0.1	12.43	0.2	0.00370826	0.01881496	0.06758321	0.44998778	A_07_P011

intfC	-5.89	14.35	-2.56	15.63	0.0	1.0	0.00019976	0.00046811	0.00388974	0.20481605	A_07_P01836	b1718	cmr	protein chain initiation factor IF-3 [b1718]
insA	-3.68	9.03	-1.88	9.97	0.1	0.9	0.00046055	0.00396653	0.01578760	0.39205047	A_07_P008828	b0365	cmr	IS1 protein InsA [b0365]
insA	-3.70	10.29	-1.89	11.17	0.0	0.8	0.00047702	0.00389112	0.01505840	0.39124410	A_07_P003998	b4294	cmr	IS1 protein InsA [b4294]
insB	-3.71	9.25	-1.89	10.19	0.1	0.9	0.00202984	0.01404655	0.01504764	0.38647635	A_07_P005381	b0988	cmr	IS1 protein InsB [b0988]
insB	-3.65	9.51	-1.87	10.45	0.0	0.8	0.58	0.00408045	0.01417917	0.39463679	A_07_P010675	b0921	cmr	IS1 protein InsB [b0921]
insC	-2.19	9.57	-1.13	10.14	0.1	0.9	0.01	0.00730235	0.02322202	0.06888021	A_07_P013315	b1997	cmr	IS2 hypothetical protein [b1997]
insD	-3.29	12.15	-1.72	13.01	0.2	0.2	0.00045353	0.00379202	0.02717786	0.45046599	A_07_P009827	b0361	cmr	IS1 protein InsD [b0361]
insG	-24.20	10.64	-4.60	12.94	0.0	0.8	0.34	0.00000081	0.00012560	0.00003366	0.01766667	A_07_P002924	b4278	cmr	IS4 hypothetical protein [b4278]
insI	-2.00	9.00	-1.00	8.51	0.1	0.1	0.50	0.00122160	0.01682264	0.07002150	0.68137773	A_07_P007989	b0256	cmr	IS30 transposase [b0256]
insO	-2.41	7.77	-1.27	8.41	0.2	7.14	0.1	0.00145677	0.00911904	0.05609592	0.61678893	A_07_P050808	Z2036	cmr	putative integrase for prophage CP-933O [Z2036]
insV	-3.07	10.46	-1.62	11.21	0.1	0.9	0.50	0.00045353	0.00406682	0.02869074	0.48245633	A_07_P044913	Z2130	cmr	putative integrase for prophage CP-933U [Z2130]
intW	-2.20	9.87	-1.14	10.44	0.0	9.30	0.0	0.00108351	0.00708236	0.07126764	0.66460036	A_07_P051282	Z1424	cmr	integrase for bacteriophage BP-933W [Z1424]
intP	-5.69	11.57	-2.51	10.31	0.0	12.82	0.0	0.00003703	0.00130143	0.01147675	0.28509160	A_07_P021023	b0382	cmr	prf, hypothetical protein [b0382]
intQ	-2.17	9.35	-1.12	8.79	0.0	9.91	0.2	0.00236559	0.01319298	0.05991235	0.61250849	A_07_P040551	c_1252	cmr	Ferric enterochelin esterase [c_1252]
intR	-3.18	9.25	-1.67	10.09	0.1	8.42	0.3	0.00076215	0.00568413	0.02418489	0.45983213	A_07_P040551	c_1250	cmr	Siderophore receptor IroN [c_1250]
intX	-11.47	10.77	-3.52	12.53	0.1	9.01	0.3	0.00001571	0.00040346	0.00045605	0.06701080	A_07_P019544	b2528	cmr	putative regulator [b2528]
intX	-2.71	10.08	-2.95	11.55	0.1	8.60	0.3	0.00000910	0.00003222	0.00170541	0.13492462	A_07_P019560	b2531	cmr	prf, hypothetical protein [b2531]
intS	-5.30	11.53	-2.41	12.74	0.1	9.03	0.2	0.00005829	0.00089192	0.00538300	0.23940678	A_07_P019553	b2530	cmr	putative aminotransferase [b2530]
intU	-4.89	11.64	-2.29	12.78	0.0	10.49	0.1	0.00006736	0.00068580	0.00408580	0.26067662	A_07_P019547	b2529	cmr	prf, hypothetical protein [b2529]
intpU	-2.04	11.41	-1.03	11.93	0.0	10.90	0.1	0.00197928	0.01157712	0.08523776	0.71185048	A_07_P002826	b0174	cmr	prf, hypothetical protein [b0174]
iucA	-2.63	8.20	-1.40	7.50	0.0	8.90	0.2	0.00942244	0.00488910	0.06119325	0.07713896	A_07_P016221	c_3627	cmr	iucA protein [c_3627]
iucD	-2.90	10.18	-1.54	9.41	0.1	10.95	0.3	0.02140008	0.01222990	0.03549733	0.47645101	A_07_P036310	c_3624	cmr	iucD protein [c_3624]
iutA	-2.58	8.25	-1.37	8.93	0.0	7.56	0.2	0.00085411	0.00611791	0.05746949	0.57215985	A_07_P036302	c_3623	cmr	iutA protein [c_3623]
katG	+12.32	11.52	+3.62	9.31	0.1	0.0	0.1	0.00003087	0.00003100	0.00232604	0.14412451	A_07_P019488	b3942	cmr	catalase; hydroperoxidase HPI [b3942]
kbaY	+2.01	9.17	+1.00	8.67	0.1	9.67	0.1	0.02146029	0.01358911	0.06555139	0.65892290	A_07_P000407	b3137	cmr	tagatose-bisphosphate aldolase 2 [b3137]
kbaZ	+4.78	8.14	+2.26	7.01	0.1	9.27	0.0	0.00003950	0.00068714	0.01519563	0.33089903	A_07_P000381	b3132	cmr	putative tagatose 6-phosphate kinase 2 [b3132]
kdtI	+22.70	11.33	+4.50	9.07	0.1	13.58	0.5	0.00002333	0.00052262	0.00060658	0.07519685	A_07_P017030	b3617	cmr	2-amino-3-ketobutyrate CoA ligase [b3617]
kch	+3.10	8.82	+1.63	8.01	0.1	9.64	0.0	0.00027051	0.00258426	0.01318943	0.45139194	A_07_P007187	b1250	cmr	putative potassium channel protein [b1250]
kdgR	-2.43	9.66	-1.28	10.30	0.1	9.02	0.2	0.02178572	0.01239115	0.05137525	0.60360253	A_07_P015816	b1827	cmr	putative regulator [b1827]
kdpA	-2.73	8.67	-1.45	9.40	0.1	7.95	0.3	0.00184146	0.01056687	0.03932003	0.54127067	A_07_P010056	b0698	cmr	ATPase of high affinity potassium transport system, A chain [b0698]
kdpE	+3.56	10.13	+1.83	9.22	0.1	10.92	0.3	0.00000028	0.00465408	0.02460766	0.48846538	A_07_P033368	c_0779	cmr	KDP operon transcriptional Regulatory protein kdpE [c_0779]
kdpE	+3.04	8.78	+1.60	7.98	0.2	9.58	0.0	0.00039977	0.00341121	0.02129227	0.41797115	A_07_P000888	b0884	cmr	regulator of kdp operon [b0884]
kdsB	-2.12	9.48	-1.08	10.02	0.2	8.94	0.0	0.00332364	0.01806454	0.07565112	0.67468827	A_07_P042155	c_1659	cmr	3-deoxy-manno-octulosonate cytidylyltransferase [c_1659]
kdsC	-2.50	12.91	-1.32	13.57	0.0	12.25	0.0	0.00046025	0.00168215	0.05668101	0.59948968	A_07_P000868	b3198	cmr	prf, hypothetical protein [b3198]
kefB	-2.64	8.47	-1.40	9.17	0.0	7.77	0.1	0.00038644	0.00332667	0.04279408	0.56239566	A_07_P017779	b3350	cmr	K+/H+ efflux; NEM-activable K+/H+ antiporter [b3350]
kefG	-2.99	11.08	-1.58	11.87	0.1	10.29	0.0	0.00022682	0.00231589	0.00017213	0.49073347	A_07_P017784	b3351	cmr	putative NAD [b3351]
kpsC	+8.23	8.44	+3.04	6.92	0.0	9.96	0.2	0.00001547	0.00048806	0.05144970	0.21612091	A_07_P036425	c_3690	cmr	KpsC protein [c_3690]
kpsD	+5.71	11.58	+2.53	10.32	0.1	12.83	0.1	0.00000002	0.00018833	0.00007243	0.03161582	A_07_P036411	c_3688	cmr	KpsD protein [c_3688]
kpsE	+6.95	9.86	+2.80	8.46	0.1	11.26	0.2	0.00002352	0.00052457	0.00778963	0.24872668	A_07_P036406	c_3687	cmr	KpsE protein [c_3687]
kspA	-2.96	11.70	-1.57	12.48	0.0	10.91	0.3	0.01189842	0.00736719	0.03893019	0.49206284	A_07_P010944	b0351	cmr	5-adenosylmethionine-6-N,N-adenosyl [b0351]
L7002	-3.69	12.51	-1.88	13.45	0.4	11.57	0.0	0.00126397	0.00835326	0.01599559	0.39170654	A_07_P048661	AB-G24999	aap	unknown [L7002]
L7013	-3.75	8.78	-1.91	9.73	0.4	7.83	0.1	0.00088224	0.00580979	0.03103778	0.38760656	A_07_P048711	AB-G24027	aap	transposase (partial) [L7013]
L7045	-5.54	9.75	-2.47	10.98	0.1	8.51	0.2	0.00037808	0.00106068	0.00479435	0.22363663	A_07_P051850	AB-G24079	aap	hypothetical protein [L7045]
L7055	-2.76	10.99	-1.47	11.73	0.1	10.26	0.0	0.00030849	0.00285697	0.03793318	0.53039076	A_07_P048893	AB-G24096	aap	replication protein [L7055]
L7073	-2.16	10.23	-1.11	10.78	0.1	9.67	0.1	0.00193636	0.01136423	0.07496809	0.67220829	A_07_P048969	AB-G24142	aap	unknown [L7073]
L7079	-3.10	11.33	-1.63	12.15	0.0	10.52	0.2	0.00059778	0.00464073	0.02730979	0.47878889	A_07_P048996	AB-G24148	aap	unknown [L7079]
L7082	-5.41	9.25	-2.44	10.46	0.3	8.03	0.3	0.00034580	0.00309337	0.01460507	0.22153528	A_07_P049011	AB-G24151	aap	unknown [L7082]
lacA	+2.85	8.40	+1.53	7.65	0.1	9.16	0.2	0.00008098	0.00511060	0.03618324	0.48079258	A_07_P008405	b0342	cmr	thiogalactoside acetyltransferase [b0342]
lacA	+2.41	8.52	+1.27	7.88	0.1	9.15	0.2	0.02156891	0.01229864	0.04976637	0.51361582	A_07_P053984	EC4335	cmr	thiogalactoside acetyltransferase [EC4335]
lacI	+2.64	8.35	+1.40	7.65	0.1	9.05	0.0	0.00037134	0.00324276	0.04138783	0.53669518	A_07_P008419	b0345	cmr	transcriptional repressor of the lac operon [b0345]
lacY	+4.94	9.35	+1.98	8.36	0.5	10.34	0.2	0.02205680	0.01188584	0.02104802	0.38545167	A_07_P008437	b0343	cmr	galactoside permease [b0343]
lacZ	+23.17	9.32	+4.53	7.05	0.2	11.59	0.1	0.00008250	0.00018108	0.00056720	0.07201613	A_07_P010027	c_0459	cmr	beta-galactosidase [c_0459]
lacZ	+10.26	8.51	+3.36	6.83	0.3	10.19	0.1	0.00003658	0.00008164	0.00408006	0.17393615	A_07_P008419	b0344	cmr	beta-D-galactosidase [b0344]
lamB	+350.33	12.05	+8.45	7.82	0.1	16.28	0.0	0.00000003	0.00007032	0.00000000	0.00000000	A_07_P008822	b4036	cmr	phage lambda receptor protein; maltose high-affinity receptor [b4036]
lamB	+358.11	11.57	+8.48	7.33	0.0	15.81	0.1	0.00000003	0.00007032	0.00000000	0.00000000	A_07_P037158	c_5006	cmr	Maltoporin precursor [c_5006]
lar	-1.78	9.16	-1.68	9.90	0.1	8.42	0.3	0.00130634	0.00846030	0.03740847	0.52703893	A_07_P014757	b1348	cmr	restriction alleviation and modification enhancement [b1348]
larE	-2.63	9.25	-1.40	9.95	0.1	8.56	0.3	0.00225268	0.01389188	0.04245138	0.56195152	A_07_P052396	Z6006	cmr	prf, hypothetical protein [Z6006]
larJ	-2.36	11.14	-1.24	11.76	0.2	10.52	0.4	0.00921991	0.03878908	0.05684242	0.62512389	A_07_P037395	c_5490	cmr	Hypothetical tRNA/rRNA methyltransferase larJ [c_5490]
lbhA	-2.19	8.90	-1.13	8.34	0.1	9.47	0.2	0.00258959	0.02408491	0.06000000	0.61300804	A_07_P008478	b0380	cmr	fermentative D-lactate dehydrogenase, NAD-dependent [b1380]
lcdB	+3.32	9.67	+1.73	8.81	0.0	10.54	0.1	0.00015630	0.00177268	0.02737769	0.42394867	A_07_P035765	c_0090	cmr	3-isopropylmalate dehydrogenase [c_0090]
lcfA	-3.23	8.97	-2.21	10.17	0.1	7.37	0.2	0.00003994	0.00004703	0.00004703	0.10006711	A_07_P015885	b1798	cmr	prf, hypothetical protein [b1798]
lhr	-3.14	9.18	-1.65	10.01	0.3	8.36	0.0	0.00075887	0.00557260	0.02533221	0.46612729	A_07_P018310	b1813	cmr	member of ATP-dependent helicase superfamily II [b1813]
lgB	-2.88	8.07	-1.53	8.83	0.0	7.30	0.3	0.00104225	0.01126162	0.03203329	0.49154572	A_07_P017180	b3647	cmr	putative enzyme [b3647]
lgT	-2.38	10.57	-1.25	11.20	0.1	9.95	0.0	0.00082349	0.00592821	0.05732406	0.61943934	A_07_P018292	b1807	cmr	prf, hypothetical protein [b1807]
lipA	-2.29	12.86	-1.20	12.26	0.0	13.46	0.1	0.00034158	0.00344550	0.05364660	0.57301007	A_07_P009709	b0628	cmr	lipoate synthase, sulfur insertion? [b0628]
lipB	-25.34	11.59	-4.66	13.93	0.0	9.26	0.5	0.00002324	0.00052262	0.00002013	0.01237959	A_07_P009718	b0630	cmr	protein of lipoate biosynthesis [b0630]
livK	-3.83	8.20	-1.94	9.17	0.1	7.23	0.1	0.00008052	0.00111496	0.01396287	0.37508532	A_07_P034548	c_4248	cmr	Leucine-specific binding protein precursor [c_4248]
ldD	+6.83	8.94	+2.77	7.56	0.5	10.33	0.2	0.00037473	0.00325068	0.00768617	0.24836066	A_07_P018346	b1605	cmr	L-lactate dehydrogenase [b1605]
ldhP	+3.86	7.50	+1.95	6.52	0.1	8.47	0.0	0.00008677	0.00127819	0.02138148	0.38560137	A_07_P016959	b1603	cmr	L-lactate permease [b1603]
lexA	-7.68	8.81	-2.59	7.35	0.1	10.27	0.2	0.00002756	0.00056786	0.00627096	0.22801386	A_07_P016865	b4604	cmr	transcriptional regulator [b4604]
lipA	+4.41	9.87	+2.14	8.80	0.0	10.94	0.0	0.00004105	0.00070782	0.01727261	0.35134367	A_07_P004904	b0891	cmr	periplasmic protein effects the reduction of lipoproteins from inner membrane to outer [b0891]
lldD	+2.00	10.71	+1.00	10.21	0.1	11.21	0.1	0.00185122	0.01385122	0.07030869	0.66859570	A_07_P031164	c_0555	cmr	ATP-dependent protease La [c_0555]
lpcA	+6.39	10.88	+2.68	9.54	0.2	12.22	0.0	0.00001179	0.00015886	0.00690299	0.26316476	A_07_P007824	b0222	cmr	phosphoheptose isomerase [b0222]
lpp	+2.15	13.03	+1.10	12.47	0.1	13.58	0.0	0.00162713	0.00967389	0.05460908	0.61832943	A_07_P000348	b1677	cmr	murein lipoprotein [b1677]
lpxB	-2.33	11.30	-2.12	12.36	0.0	10.25	0.0	0.00004319	0.00073315	0.00983613	0.31348178	A_07_P002865	b0181	cmr	UDP-N-acetylglucosamine acetyltransferase; lipid A biosynthesis [b0181]
lpxC	-2.64	10.71	-1.03	11.22	0.1	10.19	0.1	0.00004778	0.01140271	0.08157602	0.71159577	A_07_P002870	b0182	cmr	tetracyclidinoline-14-2 lipid A biosynthesis, penultimate step [b0182]
lpxC	-6.57	14.40	-2.72	15.76	0.0	13.04	0.1	0.00005157	0.00084009	0.00273121	0.17592742	A_07_P002451	b0096	cmr	UDP-3-O-acyl N-acetylglucosamine deacetylase; lipid A biosynthesis [b0096]
lpxE	-6.49	9.81	-2.70	11.16	0.0	8.46	0.2	0.00003266	0.00062946	0.00379726	0.17407115	A_07_P005023	b0915	cmr	putative EC 1.2.1 enzyme [b0915]
lpxL	-4.88	11.47	-2.29	12.62	0.0	10.33	0.1	0.00006671	0.00076769	0.00604060	0.36926108	A_07_P001480	b1054	cmr	heat shock protein [b1054]
lpxP	-3.25	11.29	-1.70	12.14	0.0	10.44	0.1	0.00016468	0.00170909	0.01239215	0.45118519	A_07_P014174	b2378	cmr	putative heat shock protein [b2378]
lrhA	-5.43	11.68	-2.44	12.90	0.0	10.46	0.3	0.00009502	0.00136142	0.00490917	0.25319528	A_07_P013734	b2289	cmr	NADH dehydrogenase I transcriptional regulator, LysR family [b2289]
lrp	-13.49	9.80	-4.80	8.90	0.1	10.71	0.1	0.00017103	0.00190160	0.02150305	0.41257636	A_07_P004893	b0889	cmr	regulator for leucine [b0889]
lsaE	-5.66	9.51	-2.50	8.26	0.0	10.77	0.2	0.00003345	0.00061224	0.01133920	0.28267773	A_07_P004985	b0870	cmr	putative ecyhydrofuran [b0870]
lysS	-6.21	11.06	-2.63	12.38	0.1	9.74	0.2	0.00002566	0.00055176	0.00324060	0.18757353	A_07_P006416	b2890	cmr	lysine tRNA synthetase, constitutive; suppressor of Cole1 mutation in primer RNA [b2890]
lysU	-10.70	10.83	-4.30	9.41	0.2	12.24	0.4	0.00018011	0.00195627	0.00723831	0.24149468	A_07_P011381	b4129	cmr	lysine tRNA synthetase, inducible; heat shock protein [b4129]
lyx	-2.42	7.16	-1.27	6.52	0.0	7.80	0.1	0.00005857	0.00499931	0.04792111	0.54511728	A_07_P016844	b3580	cmr	L-xylulose kinase, cryptic [b3580]
lyxK	-8.35	8.41	-3.06	6.87	0.1	9.94	0.1	0.00003710	0.00238373	0.05207070	0.21292104	A_07_P017021	b3591	cmr	Cryptic L-xylulose kinase [c_4402]
mas	-8.02	9.42	-3.17	11.01	0.1	7.84	0.2	0.00001106	0.00049947	0.01100483	0.10407895	A_07_P021405	b0459	cmr	putative transferase [b0459]
masB	-3.05	8.69	-1.04	9.21	0.0	8.17	0.0	0.01622229	0.00995646	0.08492759	0.55971338	A_07_P004848	b0879	cmr	putative ATP-binding component of a transport system [b0879]
masA	-6.48	9.22	-2.70	7.87	0.1	10.57	0.1	0.00003086	0.00048725	0.00870764	0.26037714	A_07_P004886	b1479	cmr	NAD-linked malate dehydrogenase [b1479]
masB	-4.93	11.17	-2.30	10.02	0.1	12.32	0.2	0.00012744	0.00161341	0.01431129	0.32197143	A_07_P012701	b2463	cmr	putative multimodule enzyme [b2463]
matE	-72.51	11.94	-6.18	8.85	0.1	15.03	0.2	0.00000047	0.00000262	0.00000016	0.02108696	A_07_P008811	b4034	cmr	periplasmic maltose-binding protein; substrate recognition for transport and chemotaxis [b4034]
matF	-8.58	8.85	-3.10	7.30	0.0	10.40	0.3	0.00002820	0.00057601	0.00160064	0.21221624	A_07_P008865	b4033	cmr	part of maltose permease, periplasmic [b4033]
matG	-2.80	10.06	-1.48	9.32	0.1	10.81	0.0	0.00028054	0.00260935	0.03705899	0.48650124	A_07_P008801	b4032	cmr	part of maltose permease, inner membrane [b4032]
matK	-10.76	8.31	-4.43	6.59	0.0	10.02	0.1	0.00000053	0.00030546	0.04413104	0.14416604	A_07_P008816	b4031	cmr	ATP-binding component of transport system for maltose [b4031]
malM	+5.17	8.91	+2.37	7.72	0.1	10.09	0.2	0.00007951	0.00110776	0.01315739	0.30418502	A_07_P008827	b4037	cmr	periplasmic protein of mal regulon [b4037]
malP	-25.76	10.19	-4.68	7.85	0.1	12.53	0.1	0.00000121	0.00004501	0.00404514	0.06441444	A_07_P018111	b3417	cmr	maltodextrin phosphorylase [b3417]
malQ	+6.80	9.63	+2.77	8.25	0.1	11.01	0.4	0.00016915	0.00170726	0.00776154	0.24831084	A_07_P018108	b3416	cmr	4-alpha-glucanotransferase [b3416]
malT	+12.92	9.37	+4.24	7.25	0.0	11.49	0.0	0.00000101	0.00019946	0.00009320	0.08904762	A_07_P014438	c_4196	cmr	MalT Regulatory protein [c_4196]
malT	+10.52	8.87	+3.46	7.17	0.0	10.56	0.0	0.00008092	0.00021229	0.00010472	0.16645902	A_07_P018118	b4018	cmr	positive regulator of mal regulon [b4018]
malT	+11.43	9.20	+3.52	7.44	0.1	10.96	0.3	0.00002719	0.00056319	0.00275279	0.15149488	A_07_P012157	Z4774	cmr	positive regulator of mal regulon [Z4774]
malX	+3.68	9.75	+1.88	8.81	0.0	10.69	0.1	0.00013111	0.00145227	0.02210154	0.39869138	A_07_P020760	b3421	cmr	PTS system, maltose and glucose-specific II ABC [b3421]
malY	+2.60	9.17	+1.38	8.41	0.1	9.86	0.0	0.00002205	0.00475805	0.04179116	0.50846986	A_07_P024322	c_3014	cmr	MalY protein [c_3014]
manA	-2.59	8.89	-1.37	8.20	0.1	9.57	0.1	0.00074895	0.00510237	0.04279771	0.51183228	A_07_P020760	b1613	cmr	mannose-6-phosphate isomerase [b1613]
manA	-2.99	8.81	-1.58	8.02	0.1	9.60	0.1	0.00002383	0.00267294	0.03431178	0.46703638	A_07_P044397	Z2616	cmr	mannose-6-phosphate isomerase [Z2616]
manA	-2.61	8.81	-1.38	8.12	0.0	9.50	0.2	0.00042144	0.00158887	0.04292605	0.51019324	A_07_P009506	c_2005	cmr	Mannose-6-phosphate isomerase [c_2005]
manB	-2.88	12.70	-1.53	11.94	0.1	13.46	0.0	0.00035271	0.00314486	0.03250389	0.47619579	A_07_P019986	c_2557	cmr	Phosphomannomutase [c_2557]
manX	-19.40	10.41	-4.28	8.29	0.0	12.57	0.1	0.00000153	0.00018622	0.00682877	0.08651899	A_07_P011778	b1617	cmr	PTS enzyme IAB, mannose-specific [b1617]
manY	-6.28	9.81	-2.65	8.48	0.1	11.12	0.4	0.00001424	0.00039271	0.00948361	0.26758065	A_07_P015784	b1818	cmr	PTS enzyme IC, mannose-specific [b1818]
manZ	-6.89	9.84	-2.56	8.56	0.2	11.11	0.1	0.00006319	0.00066813	0.01814179	0.27709766	A_07_P015786	b1819	cmr	PTS enzyme ID, mannose-specific [b1819]
map	-2.16	8.96	-1.11	9.52	0.1	8.41	0.1	0.00210530	0.01288818	0.07298841	0.66775651	A_07_P002799	b0168	cmr	methionine aminopeptidase [b0168]
mcbB	-3.08	9.03	-1.25	8.41	0.4	9.65	0.2	0.01162025	0.04663502	0.06273556	0.27709366	A_07_P004642	c_1227	cmr	McbB protein [c_1227]
mchD	-2.77	11.56	-1.47	12.30	0.4	10.83	0.1	0.02266784	0.01469358	0.03719766	0.52618149	A_07_P040445	c_1230	cmr	Probable microcin H47 secretion ATP-binding protein [c_1230]
mchF	-2.37	10.53	-1.24	11.16	0.4	9.90	0.1	0.01853479	0.02569459	0.05492625	0.62211109	A_07_P040453	c_1231	cmr	Probable microcin H47 secretion ATP-binding protein [c_1232]
mdaB	+4.33	9.61	+2.11	8.55	0.2	10.66	0.1	0.00012614	0.00152533	0.01787919	0.35818599	A_07_P012273	b3028	cmr	modulator of drug activity B [b3028]
mdh	+19.83	12.39	+4.31	10.24	0.0	14.55	0.1	0.00000101	0.00012946	0.00079649	0.07972611	A_07_P012651	b1236	cmr	malate dehydrogenase [b1236]
mdlA	-2.17	7.92	-1.11	8.48	0.0	7.36	0.2	0.00265700	0.01445469	0.07236725	0.66824047	A_07_P021355	b0448	cmr	ATP-binding component of a transport system [b0448]
mdoG	-13.52	7.77	-3.80	7.37	0.0	8.43	0.0	0.00086013	0.00582981	0.00409661	0.13025430	A_07_P009213	b1424	cmr	putative glycosyltransferase [b1424]
mdtH	-3.03	9.49	-1.60	10.26	0.3	8.66	0.0	0.00005069	0.00468290	0.02669982	0.48491760	A_07_P001526	b1065	cmr	prf, hypothetical protein [b1065]
mdtI	+2.27	7.77	+1.18	7.18	0.1	8.36	0.2	0.00108889	0.01135633	0.05534116	0.58647887	A_07_P020626	b1599	cmr	possible chaperone [b1599]
mdtK	-4.42	10.94	-2.14	12.01	0.0	9.86	0.4	0.00015243	0.00420158	0.00695837	0.30697733	A_07_P018076	b1663	cmr	putative transport protein [b1663]
mdtL	-2.18	8.00	-1.12	8.56	0.3	7.44	0.1	0.00756691	0.03318881	0.07243775	0.68810779	A_07_P005475	b3710	cmr	putative transport protein [b3710]
melA	+4.77	9.20	+2.25	8.08	0.1	10.33	0.3	0.00230605	0.01408	0.01487043	0.32832022	A_07_P011333	b4119	cmr	alpha-galactosidase [b4119]
menB	+8.51	9.98	+3.09	8.43	0.1	11.52	0.1	0.00000913	0.00032069	0.00508535	0.21188172	A_07_P001100	b2362	cmr	dihydroxynaphtoic acid synthase [b2362]
menD	-2.59	8.72	-1.37	8.03	0.1	9.41	0.1	0.00077300	0.00564741	0.04230305	0.51183866	A_07_P001109	b2364	cmr	2-oxoglutarate decarboxylase, SHCHC synthase [b2364]
menD	+2.15	8.92	+1.13	8.37	0.2	9.48	0.2	0.00375176	0.01899281	0.06014482	0.41368762	A_07_P012389	c_2808	cmr	Menaquinone biosynthesis protein menD [c_2808]
metB	-2.58	8.90	-1.37	8.22	0.2	9.59	0.5	0.01288721	0.04819568	0.04695566	0.51275928	A_07_P019474	b1609	cmr	cystathionine gamma-synthase [b1609]
metH	+7.30	8.89	+2.87	7.46	0.3	10.33	0.0	0.00004711	0.00077097	0.00482693	0.23543005	A_07_P017969	EC4937	cmr	B12-dependent homocysteine-N5-methylhetrahydrofolate transmethylase [EC4937]
metH	+8.62	9.24	+3.11	7.69	0.0	10.80	0.1	0.00000714	0.00018181	0.00160750	0.20997283	A_07_P047319	b2463	cmr	B12-dependent homocysteine-N5-methylhetrahydrofolate transmethylase, repressor of metE and [Z5616]
metH	+4.20	8.24	+2.07	7.20	0.1	9.27	0.2	0.00179512	0.00195547	0.01904045	0.36936174	A_07_P008740	b4019	cmr	B12-dependent homocysteine-N5-methylhetrahydrofolate transmethylase, repressor of metE and metF [b4019]
metK	-5.49	9.67	-2.46	8.44	0.1	10.90	0.1	0.00000334	0.00004629	0.00270127	0.20239462	A_07_P037467	c_4876	cmr	S-methylmethionine synthetase, homozygote [c_4876]
metJ	-2.21	9.92	-1.14	10.50	0.0	9.34	0.0	0.00134745	0.00865120	0.06492279	0.66102826	A_07_P015559	c_4891	cmr	Met repressor [c_4891]
metN	-7.15	10.24	-2.84	11.66	0.1	8.83	0.1	0.00003215	0.00036408	0.00218639	0.15647009	A_07_P010955	b0199	cmr	ATP-binding component of a transporter [b0199]
metR	-2.68	9.82	-1.42	10.53	0.3	9.11	0.1	0.02670088	0.01450510	0.04392302	0.54503863	A_07_P039160	c_4750	cmr	Transcriptional activator protein metR [c_4750]
mfd	-2.14	7.25	-1.09	6.71	0.1	7.80	0.1	0.02214956	0.01236631	0.06193200	0.62738047	A_07_P017771	b1114	cmr	transcription-repair coupling factor; mutation frequency decline [b1114]
mfd	+3.71	8.10	+1.89	7.16	0.1	9.05	0.3	0.00074911	0.00551637	0.02316184

nusA4	+35.44	9.75	+5.15	7.18	0.2	12.32	0.1	0.00000104	0.00012946	0.00024073	0.04566265	A_07_P01174	b2277	cmr/NADH dehydrogenase I chain M [b2277]
nusA5	+14.38	8.64	+3.84	6.72	0.1	10.57	0.0	0.00000228	0.00017963	0.00179114	0.13648788	A_07_P01791	ZJ534	cmr/NADH dehydrogenase I chain N [ZJ534]
nusA6	+10.26	8.71	+3.36	7.03	0.2	10.39	0.0	0.00000867	0.00036865	0.00347180	0.17407643	A_07_P02539	c_2817	cmr/NADH dehydrogenase I chain O [c_2817]
nusA9	+8.39	8.73	+3.07	7.17	0.2	10.24	0.1	0.00002615	0.00055409	0.00513610	0.21374346	A_07_P01366	b2276	cmr/NADH dehydrogenase I chain N [b2276]
nusG	+6.83	10.38	+2.77	9.00	0.1	11.77	0.0	0.00003110	0.00034947	0.00764017	0.24803571	A_07_P01364	b2364	cmr/transport of nucleosides, permease protein [b2964]
nusA	-4.54	14.43	-2.18	15.52	0.1	13.34	0.1	0.00005076	0.00068800	0.00845020	0.29544444	A_07_P00566	b3169	cmr/transcription pausing; L factor [b3168]
nusB	-12.11	12.13	-3.60	13.93	0.0	10.33	0.1	0.00003007	0.00030966	0.00938776	0.29318776	A_07_P02194	b0416	cmr/transcription termination; L factor [b0416]
nusG	-2.51	8.92	-1.33	9.58	0.2	8.25	0.1	0.00139443	0.00887382	0.04917429	0.58148519	A_07_P00825	b3982	cmr/component in transcription antitermination [b3982]
nlpE	-5.67	9.47	-2.50	10.72	0.1	8.21	0.3	0.00009742	0.00128285	0.01438801	0.21423676	A_07_P01391	b3183	cmr/putative GTP-binding factor [b3183]
ompC	+3.93	9.77	+1.97	8.79	0.1	10.76	0.1	0.00010131	0.00131881	0.02083333	0.38117757	A_07_P02359	c_2758	cmr/Outer membrane protein C precursor [c_2758]
ompC	+3.37	8.93	+1.75	8.05	0.1	9.80	0.2	0.00027910	0.00266051	0.04369663	0.45228622	A_07_P00863	b2215	cmr/outer membrane protein 1b [b2215]
ompC	+2.39	10.40	+1.25	9.75	0.1	11.02	0.1	0.00124280	0.00814936	0.08497294	0.54993007	A_07_P04557	Z3473	cmr/outer membrane protein 1b [Z3473]
ompF	-7.59	10.25	-2.92	8.79	0.1	11.71	0.0	0.00003303	0.00034983	0.00644983	0.23025000	A_07_P00592	b0929	cmr/outer membrane protein 1a [b0929]
ompT	-7.54	9.10	-2.91	7.64	0.3	10.55	0.0	0.00006511	0.00096619	0.00645516	0.22991213	A_07_P01283	c_0652	cmr/Protease VII precursor [c_0652]
ompW	-66.95	10.48	-6.44	6.66	0.1	10.90	0.0	0.00000011	0.00007002	0.00000430	0.01500000	A_07_P01256	b3156	cmr/putative outer membrane protein [b3156]
ompW	+264.62	12.67	+8.05	8.65	0.0	16.70	0.0	0.00000003	0.00007032	0.00000254	0.00307692	A_07_P03872	c_1722	cmr/Outer membrane protein W precursor [c_1722]
ompX	-16.20	13.32	-4.00	15.32	0.0	10.21	0.1	0.00000155	0.00015822	0.00012513	0.07108681	A_07_P00424	b0814	cmr/outer membrane protein X [b0814]
ogpA	+315.13	12.27	+8.30	8.12	0.2	16.42	0.1	0.00000010	0.00007032	0.00000127	0.00200000	A_07_P07151	b1243	cmr/oligopeptide transport; periplasmic binding protein [b1243]
ogpA	+349.11	13.18	+8.45	8.95	0.0	17.40	0.1	0.00000003	0.00007032	0.00000064	0.00111111	A_07_P05267	Z2019	cmr/oligopeptide transport periplasmic binding protein [Z2019]
ogpB	+13.64	10.58	+3.77	8.70	0.0	12.47	0.1	0.00000257	0.00018134	0.00192708	0.12859302	A_07_P07157	b1244	cmr/oligopeptide transport permease protein [b1244]
ogpC	+15.22	9.18	+3.93	7.21	0.0	11.14	0.4	0.00003836	0.00045549	0.00514535	0.21985222	A_07_P07165	b1245	cmr/homolog of Salmonella ATP-binding protein of oligopeptide ABC transport system [b1245]
ogpD	+58.96	11.45	+5.88	8.51	0.2	14.39	0.2	0.00000085	0.00012742	0.00086638	0.02666667	A_07_P07166	b1246	cmr/homolog of Salmonella ATP-binding protein of oligopeptide ABC transport system [b1246]
ogpF	+35.53	9.84	+4.67	7.50	0.3	12.18	0.6	0.00007302	0.00109221	0.00505822	0.06811966	A_07_P07171	b1247	cmr/homolog of Salmonella ATP-binding protein of oligopeptide ABC transport system [b1247]
osmB	-4.36	9.16	-2.12	10.22	0.1	8.10	0.0	0.00005075	0.00068800	0.01396575	0.30963489	A_07_P01496	b1283	cmr/osmotically inducible lipoprotein [b1283]
osmE	+2.35	8.13	+1.23	7.52	0.1	8.75	0.1	0.00088007	0.00631227	0.05027185	0.55103506	A_07_P018764	b1739	cmr/activator of rtsA gene [b1739]
osmY	-2.40	8.73	+1.26	8.10	0.1	9.36	0.1	0.00135768	0.00869972	0.04835556	0.54771591	A_07_P01765	b4376	cmr/hyperosmotically inducible periplasmic protein [b4376]
pabA	-2.93	8.79	-1.55	9.56	0.0	8.01	0.3	0.00118261	0.00976826	0.03072853	0.49215666	A_07_P01829	b3360	cmr/p-aminobenzoate synthetase, component II [b3360]
pagB	+2.00	9.54	+1.00	9.04	0.1	10.04	0.2	0.00397609	0.01086019	0.07163882	0.66434086	A_07_P08756	b4023	cmr/f, hypothetical protein [b4023]
panB	-2.80	10.54	-1.49	11.28	0.0	9.79	0.1	0.00030925	0.00323332	0.03616262	0.51996347	A_07_P00243	b0134	cmr/3-methyl-2-oxobutanoate hydroxymethyltransferase [b0134]
panB	-3.69	12.47	-1.88	13.41	0.0	11.53	0.1	0.00012555	0.00150701	0.01540972	0.39166812	A_07_P01825	c_0165	cmr/3-methyl-2-oxobutanoate hydroxymethyltransferase [c_0165]
panC	-2.00	9.61	-1.00	10.11	0.1	9.11	0.1	0.02796659	0.01504766	0.09048717	0.72312671	A_07_P040200	z0144	cmr/pantothenate synthetase [Z0144]
panD	-2.07	11.15	-1.05	10.62	0.0	11.67	0.0	0.00152295	0.00945346	0.04419349	0.62547276	A_07_P00267	b0131	cmr/aspartate 1-decarboxylase [b0131]
panE	+2.00	8.89	+1.00	8.39	0.1	9.39	0.0	0.00232174	0.01690943	0.07015671	0.66093413	A_07_P021236	b0425	cmr/involved in thiamin biosynthesis, alternative pyrimidine biosynthesis [b0425]
papA	+32.06	9.74	+5.00	7.24	0.1	12.24	0.0	0.00000164	0.00015384	0.00238663	0.05010989	A_07_P03316	c_3592	cmr/Pap4 protein [c_3592]
papC	+11.21	9.71	+3.49	7.97	0.1	11.46	0.0	0.00000370	0.00020738	0.00288110	0.15804878	A_07_P033351	c_3590	cmr/PapC protein [c_3590]
papD_2	+7.64	10.12	+2.93	8.65	0.1	11.58	0.1	0.00001297	0.00037588	0.00627287	0.32755760	A_07_P03767	c_3185	cmr/PapD protein [c_3185]
papE	+10.00	10.37	+3.32	8.71	0.1	12.03	0.0	0.00000666	0.00027022	0.00361344	0.17833856	A_07_P033134	c_3585	cmr/PapE protein [c_3585]
papF	+3.25	8.80	+1.70	7.95	0.2	9.65	0.3	0.01035337	0.02726675	0.19291010	0.67216040	A_07_P033135	c_3584	cmr/PapF protein [c_3584]
papG	+2.59	10.14	+1.37	9.46	0.1	10.83	0.2	0.00115594	0.00941866	0.04260997	0.51228788	A_07_P033125	c_3583	cmr/PapG protein [c_3583]
papH	+9.24	11.23	+3.21	8.62	0.1	13.83	0.2	0.00004680	0.00078201	0.00424860	0.23213264	A_07_P033156	c_3591	cmr/PapH protein [c_3591]
papH_2	+12.26	9.43	+3.62	7.62	0.2	11.24	0.3	0.00001677	0.00042622	0.00240600	0.14458015	A_07_P037969	c_5187	cmr/PapH protein [c_5187]
papI_2	+7.17	8.51	+2.88	7.07	0.2	9.95	0.0	0.00002821	0.00057601	0.00672256	0.23419329	A_07_P037980	c_5189	cmr/Pap1 protein [c_5189]
papJ	+4.63	9.63	+2.21	8.52	0.0	10.74	0.1	0.00004566	0.00075648	0.00325579	0.33923716	A_07_P033147	c_3588	cmr/Pap2 protein [c_3588]
papK	+5.64	10.20	+2.50	8.86	0.2	11.45	0.4	0.00038548	0.00332912	0.01116489	0.28215088	A_07_P033137	c_3586	cmr/PapK protein [c_3586]
papX	+2.75	11.59	+1.46	10.86	0.1	12.32	0.2	0.00946640	0.05601052	0.10854851	0.49462918	A_07_P033116	c_3582	cmr/PapX protein [c_3582]
pck	+17.28	15.09	+4.11	13.03	0.1	17.14	0.2	0.00000321	0.00016528	0.00116425	0.10071429	A_07_P00491	b3403	cmr/phosphoenolpyruvate carboxykinase [b3403]
pcnB	-2.00	11.63	-1.00	12.13	0.1	11.13	0.2	0.03192070	0.01662717	0.28864139	0.72249472	A_07_P02041	b0143	cmr/poly [b0143]
pdhR	+2.27	11.87	+1.18	11.28	0.1	12.46	0.1	0.00096111	0.00668941	0.03598333	0.57908657	A_07_P002527	b0113	cmr/transcriptional regulator for pyruvate dehydrogenase complex [b0113]
pdxJ	+5.65	9.32	+2.50	8.08	0.0	10.57	0.1	0.00003650	0.00044610	0.01138275	0.28449022	A_07_P03721	b3264
pepA	+2.66	11.46	+1.41	11.78	0.0	11.13	0.1	0.00038527	0.00332912	0.04086763	0.50424765	A_07_P003848	b4260	cmr/aminopeptidase A/I [b4260]
pepB	+9.94	10.21	+3.33	8.56	0.0	11.87	0.2	0.00003800	0.00029787	0.00348066	0.18151125	A_07_P01874	b2523	cmr/putative peptidase [b2523]
pepD	+17.33	10.82	+4.12	8.76	0.1	12.88	0.0	0.00000168	0.00015927	0.00116997	0.10301574	A_07_P007896	b0237	cmr/aminacyl-histidine dipeptidase [b0237]
pepE	+3.22	7.81	+1.68	6.66	0.2	8.95	0.1	0.00370551	0.01658013	0.02878303	0.43825068	A_07_P007888	b4021	cmr/peptidase E, a dipeptidase where a mono-terminal residue is aspartate [b4021]
pepN	+16.66	9.85	+4.06	7.82	0.1	11.88	0.0	0.00000163	0.00015927	0.00124565	0.10470588	A_07_P01734	Z1280	cmr/aminopeptidase N [Z1280]
pepT	+1.71	9.03	+1.89	8.09	0.0	10.24	0.1	0.00002283	0.00031486	0.01161684	0.39940654	A_07_P006587	b1127	cmr/putative peptidase T [b1127]
perM	-3.62	9.14	-1.86	10.07	0.1	8.21	0.0	0.00011652	0.00164104	0.01478860	0.30772247	A_07_P030120	c_3009	cmr/Putative permease perM [c_3009]
pfkB	+6.02	9.56	+2.59	8.26	0.1	10.85	0.1	0.00000867	0.00036865	0.00139100	0.27133606	A_07_P041360	c_2121	cmr/6-phosphofructokinase isozyme 2 [c_2121]
pfkB	+5.32	9.51	+2.43	8.31	0.1	10.72	0.5	0.00055975	0.00487029	0.01226499	0.29346505	A_07_P018663	b1723	cmr/6-phosphofructokinase II; suppressor of pfkA [b1723]
pflA	-4.39	12.63	-2.13	13.69	0.0	11.56	0.0	0.00003889	0.00060231	0.00931728	0.30894654	A_07_P004958	b0902	cmr/pyruvate formate lyase activating enzyme 1 [b0902]
pflB	+15.10	11.27	+3.92	9.32	0.1	13.23	0.6	0.00000677	0.00127819	0.00152503	0.11045274	A_07_P004961	b0903	cmr/formate acetyltransferase 1 [b0903]
pflD	+21.22	9.16	+4.14	8.59	0.1	9.73	0.1	0.00132342	0.00946346	0.05688831	0.59152778	A_07_P008458	b3951	cmr/formate acetyltransferase 2 [b3951]
pgaD	-4.61	9.12	-2.25	10.22	0.0	8.01	0.0	0.00003242	0.00042637	0.00825965	0.29487528	A_07_P001332	b3321	cmr/f, hypothetical protein [b3321]
pgi	+3.25	9.07	+1.70	8.22	0.3	9.92	0.2	0.00156886	0.00964658	0.02898183	0.43874038	A_07_P008767	b4025	cmr/glucosephosphate isomerase [b4025]
pgk	+13.41	11.39	+3.38	11.71	0.1	11.10	0.0	0.00000185	0.00021001	0.00325905	0.16832797	A_07_P017976	b2926	cmr/phosphoglycerate kinase [b2926]
pgl	+7.94	9.43	+2.98	7.94	0.0	10.93	0.1	0.00003152	0.00035443	0.00594512	0.22267514	A_07_P004288	b3767	cmr/gluconolactonase [b3767]
phaP	-3.82	8.51	-1.50	9.26	0.1	7.76	0.1	0.00013093	0.00104106	0.03595147	0.53898843	A_07_P016642	b0576	cmr/phenylalanine-specific transport system [b0576]
pheS	+5.51	11.49	+2.46	10.26	0.0	12.72	0.2	0.00000471	0.00075050	0.01186039	0.29085670	A_07_P018621	b1714	cmr/phenylalanine tRNA synthetase, alpha-subunit [b1714]
pheT	+2.77	10.25	+1.47	9.51	0.1	10.98	0.0	0.00034603	0.00302714	0.03790904	0.49122634	A_07_P018619	b1713	cmr/phenylalanine tRNA synthetase, beta-subunit [b1713]
phnA	+2.34	8.48	+1.23	7.87	0.1	9.09	0.4	0.00607614	0.02778472	0.15135182	0.56345833	A_07_P037761	c_5106	cmr/PhnA protein [c_5106]
phnJ	-5.43	10.79	-2.18	11.88	0.1	9.70	0.6	0.01609563	0.01029914	0.08819229	0.30309190	A_07_P011231	b4099	cmr/phosphonate metabolism [b4099]
phnI	-2.85	9.88	-1.51	10.63	0.3	9.12	0.0	0.01189660	0.01116073	0.03409892	0.50285651	A_07_P041400	c_5105	cmr/PhnI protein [c_5105]
phnI	+2.12	7.41	+0.88	6.86	0.2	7.95	0.2	0.04806566	0.02806227	0.26117688	0.62473516	A_07_P011230	b4098	cmr/phosphonate metabolism [b4098]
phnK	+2.38	7.77	+1.25	7.87	0.1	9.09	0.4	0.02369916	0.01270569	0.05026312	0.55138899	A_07_P011223	b4097	cmr/ATP-binding component of phosphonate transport [b4097]
phnL	-4.40	8.68	-2.14	9.75	0.4	7.61	0.1	0.00054782	0.00432759	0.08898835	0.38401288	A_07_P041390	c_5103	cmr/Phosphonates transport ATP-binding protein phnL [c_5103]
phnO	-9.63	11.42	-3.27	13.06	0.1	9.79	0.2	0.00001036	0.00031836	0.00058510	0.09650000	A_07_P031103	c_0508	cmr/Phosphate regulon transcriptional Regulatory protein phoB [c_0508]
phoB	-6.04	11.17	-2.58	13.75	0.1	8.59	0.2	0.00003850	0.00083836	0.01010255	0.16473688	A_07_P021309	b0399	cmr/positive response regulator for pho regulon, sensor is PhoR [b0399]
phoB	-7.84	11.43	-2.97	9.32	0.0	9.95	0.2	0.00001543	0.00040762	0.01164761	0.13167513	A_07_P042823	z0467	cmr/positive response regulator for pho regulon, sensor [Z0467]
phoB	-3.26	8.23	-1.70	8.08	0.1	8.38	0.1	0.00220051	0.00226614	0.02343127	0.45288604	A_07_P021115	b0400	cmr/positive and negative sensor protein for pho regulon [b0400]
pinR	-2.48	8.55	-1.31	9.20	0.1	7.89	0.1	0.00093847	0.00657715	0.05274441	0.59443612	A_07_P014850	b1374	cmr/putative transposon resolvase [b1374]
pitA	-2.59	9.92	-1.27	10.61	0.1	9.24	0.1	0.00054476	0.00401420	0.04329931	0.57164595	A_07_P007401	b4893	cmr/low-affinity phosphate transport [b4893]
pitB	-2.34	8.23	-1.22	8.84	0.1	7.61	0.2	0.00230557	0.01177507	0.06975165	0.63051609	A_07_P012666	b2987	cmr/low-affinity phosphate transport [b2987]
plsB	-2.52	10.33	-1.33	10.99	0.1	9.66	0.3	0.00207602	0.01194615	0.04800551	0.57953988	A_07_P041964	c_4747	cmr/Lysophospholipase L2 [c_4747]
plsB8	-2.25	10.01	-1.17	10.59	0.1	9.42	0.0	0.00104629	0.00647076	0.06777121	0.60852580	A_07_P046896	Z5346	cmr/lysophospholipase L2 [Z5346]
plsC	-2.54	10.31	-1.35	10.99	0.0	9.64	0.0	0.00004629	0.00052830	0.04731771	0.57048880	A_07_P016768	c_3758	cmr/1-acyl-sn-glycerol-3-phosphate acyltransferase [c_3758]
plsC	-5.54	8.59	-1.34	9.26	0.1	7.92	0.1	0.00056796	0.00444873	0.04788164	0.58355412	A_07_P022764	b4018	cmr/1-acyl-sn-glycerol-3-phosphate acyltransferase [b4018]
pmbA	+4.04	9.05	+2.01	8.04	0.2	10.05	0.2	0.00022934	0.00239152	0.01973833	0.37743242	A_07_P003729	b4235	cmr/maturation of antibiotic MccB17, wtr fdl genes [b4235]
pnuA	+11.69	9.20	+3.55	7.42	0.2	10.97	0.4	0.00006848	0.00097674	0.02484991	0.31077710	A_07_P024008	b1603	cmr/pyridine nucleotide transhydrogenase, alpha subunit [b1603]
pnuB	+6.17	10.35	+2.67	9.01	0.2	11.68	0.1	0.00003750	0.00066782	0.00909934	0.26286239	A_07_P020644	b1602	cmr/pyridine nucleotide transhydrogenase, beta subunit [b1602]
pnuC	+3.67	9.59	+1.87	8.65	0.0	10.52	0.1	0.00010220	0.00129369	0.02123600	0.39932097	A_07_P022517	Z2597	cmr/pyridine nucleotide transhydrogenase beta subunit [Z2597]
pnuE	+2.68	9.40	+1.42	8.69	0.2	10.11	0.2	0.00139501	0.00889583	0.04016547	0.50231736	A_07_P063202	ECJ2388	cmr/pyridine nucleotide transhydrogenase beta subunit [ECJ2388]
poxA	+7.67	9.11	+2.90	7.64	0.1	10.57	0.0	0.00000107	0.00040227	0.00642792	0.22929411	A_07_P019883	b1253	cmr/DNA polymerase I, 3′→ 5′ exonuclease, 5′→ 3′ and 3′→ 5′ exonuclease [b1863]
polA	+5.69	9.16	+2.53	7.91	0.4	10.42	0.0	0.00019756	0.00208752	0.01968862	0.28125407	A_07_P012260	Z5398	cmr/DNA polymerase I, 3′→ 5′ polymerase [Z5398]
polB	-4.32	10.60	-2.11	11.66	0.0	9.55	0.1	0.00004989	0.00080150	0.00966443	0.31626912	A_07_P020889	b0660	cmr/DNA polymerase II [b0660]
polB	-5.65	10.10	-2.50	11.35	0.0	8.85	0.2	0.00004552	0.00075592	0.00445276	0.21708878	A_07_P006583	b1126	cmr/ATP-binding component of spermidine/putrescine transport [b1126]
potC	-4.03	11.77	-2.01	12.77	0.0	10.76	0.1	0.00009773	0.00128464	0.01238168	0.34657656	A_07_P007563	b1124	cmr/spermidine/putrescine transport system permease [b1124]
potD	-3.02	12.81	-1.60	12.01	0.0	13.60	0.1	0.00002098	0.00021689	0.00324121	0.45830783	A_07_P052411	b2762	cmr/Spermidine/putrescine binding periplasmic protein precursor [b2762]
potD	-3.71	13.51	-1.89	12.56	0.0	14.45	0.4	0.00008531	0.00063271	0.02340384	0.40307606	A_07_P042313	c_1398	cmr/Spermidine/putrescine-binding periplasmic protein precursor [c_1398]
potE	-2.95	12.95	-1.56	12.17	0.0	13.73	0.0	0.00022104	0.00227013	0.03391260	0.46790460	A_07_P063111	ECs1499	cmr/spermidine/putrescine periplasmic transport protein [ECs1499]
potG	+3.28	13.08	+1.35	11.85	0.1	14.23	0.2	0.00007682	0.00088465	0.01938516	0.30242604	A_07_P018919	b1123	cmr/spermidine/putrescine periplasmic transport protein [b1123]
potE	-4.75	8.29	-2.24	7.17	0.2	9.41	0.1	0.00008656	0.00095768	0.01425556	0.30190890	A_07_P009878	b0892	cmr/putrescine transport protein [b0892]
ppa	-3.11	10.40	-1.63	11.21	0.1	9.58	0.1	0.00023600	0.00235854	0.02680223	0.47521396	A_07_P003884	b4226	cmr/inorganic pyrophosphatase [b4226]
ppc	+30.73	9.84	+3.42	8.13	0.1	11.55	0.1	0.00000848	0.00029161	0.00318311	0.16546850	A_07_P008882	b3956	cmr/phosphoenolpyruvate carboxylase [b3956]
ppiA	+2.40	7.92	+1.26	7.32	0.2	8.52	0.0	0.00102340	0.00956166	0.04698020	0.56939502	A_07_P042261	z4143	cmr/prolyln peptidase dependent protein A [z4143]
ppiB	+2.37	8.13	+1.25	7.50	0.1	8.75	0.1	0.00088450	0.00632947	0.05002223	0.55451268	A_07_P008822	c_3420	cmr/Prolyln peptidase dependent protein B precursor [c_3420]
ppiD	-2.46	9.82	-1.30	10.47	0.1	9.17	0.1	0.00002263	0.00475860	0.05270387	0.60462826	A_07_P021316	b0441	cmr/putative protease maturation protein [b0441]
ppk	+5.31	10.56	+2.40	8.95	0.2	12.16	0.1	0.00005028	0.00088401	0.01262226	0.29657698	A_07_P015681	b2501	cmr/polyphosphate kinase [b2501]
ppn	+6.90	13.83	+2.79	9.22	0.0	15.22	0.1	0.00001047	0.00040033	0.00780234	0.24816162	A_07_P018562	b1702	cmr/phosphoenolpyruvate synthase [b1702]
ppqB	+2.91	11.79	+1.54	11.02	0.1	12.56	0.1	0.00031603	0.00292037	0.04634615	0.47210390	A_07_P005203	b0951	cmr/paraquat-inducible protein B [b0951]
prfB	-1.39	13.74	-1.76	14.62	0.0	12.86	0.0	0.00010010	0.00139340	0.02060340	0.43424364	A_07_P006421	b2891	cmr/peptide chain release factor RF-2 [b2891]
prfB	-3.45	14.18	-1.75	15.07	0.0	13.29	0.0	0.00010655	0.00145648	0.01538862	0.41945751	A_07_P018912	c_3422	cmr/peptide chain release factor RF-2 [c_3422]
prfC	-2.55	10.50	-1.35	11.18	0.1	9.83	0.0	0.00044656	0.00371993	0.04754129	0.57912663	A_07_P017557	b2475	cmr/peptide chain release factor RF-3 [b2475]
prfH	-13.26	10.15	-3.73	12.01	0.0	8.28	0.2	0.00000787	0.00028735	0.00028138	0.07137349	A_07_P003853	c_0182	cmr/Peptide chain release factor homolog [c_0182]
prfH	-7.03	10.87	-2.81	12.28	0.2	9.46	0.2	0.00003027	0.00060404	0.00230437	0.15912281	A_07_P007894	b0236	cmr/probable peptide chain release factor [b0236]
prfH	-5.49	9.44	-2.46	10.67	0.1	8.21	0.1	0.00008515	0.00060200	0.00484515	0.22543724	A_07_P042922	ECs0243	cmr/probable peptide chain release factor [ECs0243]
prfH	-5.85	9.40	-2.55	10.67	0.0	8.12	0.2	0.00003283	0.00062948	0.00394118	0.20614618	A_07_P051892	z0297	cmr/probable peptide chain release factor [Z0297]
prlA	-2.21	8.55	-1.14	9.12	0.1	7.98	0.2	0.04698882	0.02033244	0.27040509	0.62440167	A_07_P019451	b3915	cmr/prlmosomal protein N [b3915]
prlB	-3.63	15.80	-1.66	16.73	0.0	14.87	0.1	0.00008012	0.00121169	0.01484834	0.39376627	A_07_P011731	b4301	cmr/prlmosomal replication protein N [b4301]
prlB	+2.09	8.60	+1.06	8.07	0.0	9.13	0.1	0.04966575	0.02360192	0.36151569	0.68345971	A_07_P052340	z4716	cmr/probable phosphodiesterase [Z4716]
prlC	+2.68	8.92	+1.42	8.20	0.0	9.63	0.2	0.03105221	0.00716564	0.03969449	0.49996000	A_07_P007426	b3498	cmr/oligopeptidase A [b3498]
prlC	-2.60	8.92	-1.40	8.76	0.0	10.44	0.2	0.00102488	0.00266476	0.02494329	0.49492228	A_07_P011201	c_4297	cmr/Oligopeptidase A [c_4297]
prsA	-2.59	8.80	-1.37	9.48	0.1	8.11	0.3	0.00231201	0.01299546	0.04434769	0.50603830	A_07_P051897	z0303	cmr/gamma glutamate kinase [Z0303]
proP	-7.13	10.03	-2.83	11.45	0.1	8.61	0.0	0.00000966	0.00034948	0.00219008	0.15472773	A_07_P011292	b4111	cmr/low-affinity transport system; proline permease II [b4111]
proX	+3.30	8.35	+1.72	7.49	0.5	9.21	0.2	0.00339375	0.01752604	0.02839939	0.43621663	A_07_P001866	b2679	cmr/high-affinity transport system for glycine betaine and proline [b2679]
proX	+6.14	9.12	+2.62	7.81	0.1	10.43	0.4	0.00028293	0.00267394	0.00950512	0.36738571	A_07_P018970	c_3232	cmr/Glycine betaine-binding periplasmic protein precursor [c_3232]
prpR	-3.00	10.22	-1.59	11.01	0.2	9.43	0.5	0.00724441	0.03128128	0.02779786	0.48218990	A_07_P008344	b0310	cmr/regulator for pqo operon [b0310]
prpB	-2.48	11.21	-1.31	11.87	0.3	10.56	0.4	0.01517564	0.04324490	0.04818325	0.58238681	A_07_P015653	c_0450	cmr/Propionate catabolism operon Regulatory protein [c_0450]
psd	+2.93	12.19	+1.55	11.42	0.0	12.97	0.1	0.00023554	0.00236959	0.03443057	0.47109565	A_07_P011531	b1360	cmr/phosphatidylserine decarboxylase; phospholipid synthesis [b1360]
pspB	-8.68	10.15	-3.12	11.71	0.1	8.59	0.1	0.00008713	0.00118164	0.01164699	0.18852071	A_07_P014506	b1305	cmr/phage shock protein [b1305]
pspC	-23.79	10.29	-4.57	12.57	0.0	8.00	0.2	0.00000197	0.00007032	0.00003366	0.01709677	A_07_P014514	b1306	cmr/phage shock protein; activates phage shock-protein expression [b1306]
pspD	-2.57	8.31	-1.36	9.01	0.0	7.65	0.1	0.00057662	0.00452429	0.04644472	0.57476610	A_07_P014502	b1307	cmr/phage shock protein D [b1307]
pspE	+9.58	11.88	+3.26	10.25	0.1	13.51	0.1	0.00000951	0.00032326	0.00394636	0.18682143	A_07_P014522	b1308	cmr/phage shock protein [b1308]
pspE	-6.13	11.80	-2.62	10.49	0.1	13.11	0.1	0.00000861	0.00028231	0.00376372	0.17551347	A_07_P014520	b1309	cmr/phage shock protein [b1309]
pspF	+2.64	10.15	+1.40	9.45	0.0	10.85	0.2	0.01038926	0.03736651	0.04114964	0.55176551	A_07_P014500	b1310	cmr/psp operon transcriptional activator [b1310]
pspG	-3.69	9.26	-1.88	10.20	0.2	8.32	0.1	0.00015338	0.00174691	0.01347652	0.35552000	A_07_P008668	Q1532	cmr/hypothetical protein [Q1532]
pssA	+3.14	9.35	+1.65	8.52	0.1	10.17	0.0	0.00021753	0.00224136	0.03037560	0.44619145	A_07_P019829	b2585	cm

rpiI	-12.99	13.86	-3.70	15.71	0.0	12.01	0.1	0.00030295	0.00018751	0.00289900	0.05290698	A_07_P11735	b4203
rpiI	2.43	14.66	-1.28	15.30	0.0	14.02	0.1	0.00002181	0.00047685	0.00438365	0.60933675	A_07_P008588	b1985
rplL	-2.62	15.31	-1.39	16.00	0.0	14.61	0.2	0.00073808	0.00546585	0.04455369	0.57364664	A_07_P008995	b3986
rplM	-4.97	16.01	-2.21	17.10	0.0	14.86	0.4	0.00026424	0.00255553	0.00643727	0.26189630	A_07_P012630	b2231
rpiO	-2.84	16.24	-1.51	16.99	0.1	15.48	0.2	0.00053780	0.00427318	0.01455595	0.50932203	A_07_P012932	b3301
rpiP	-3.59	15.01	-1.84	15.93	0.1	14.09	0.1	0.00016091	0.00180958	0.01676575	0.39753012	A_07_P012994	b3313
rpiR	-7.84	15.58	-2.97	17.06	0.1	14.09	0.3	0.00035651	0.00606813	0.01591028	0.12979275	A_07_P012998	b3304
rpiS	-57.82	11.28	-5.85	14.21	0.0	8.35	0.2	0.00000037	0.00009117	0.00000064	0.00313333	A_07_P019906	b2606
rpiT	-13.99	12.99	-3.80	14.89	0.1	11.09	0.1	0.00003280	0.00018406	0.00020389	0.06791045	A_07_P018627	b1716
rpiU	-2.59	14.27	-1.37	14.96	0.0	13.58	0.0	0.00039793	0.00340481	0.04581682	0.57158979	A_07_P012406	b3186
rpiV	-3.33	16.14	-1.74	17.00	0.0	15.26	0.0	0.00015121	0.00141616	0.01276622	0.44692060	A_07_P013002	b3315
rpiW	-2.68	15.90	-1.38	16.88	0.0	15.50	0.1	0.00041717	0.00352927	0.04516124	0.57296535	A_07_P013020	b3318
rpiX	-2.97	14.71	-1.57	15.52	0.0	13.95	0.3	0.00121587	0.00800615	0.01438994	0.49193870	A_07_P012973	b3309
rpiY	-3.56	12.52	-1.83	13.44	0.1	11.61	0.0	0.00011537	0.00143243	0.01763941	0.40674887	A_07_P000722	b2185
rpiY	-3.44	12.31	-1.78	13.22	0.1	11.40	0.1	0.00031328	0.00157776	0.01969195	0.42353825	A_07_P001151	c_2722
rpmA	-7.69	15.06	-2.94	16.53	0.1	13.59	0.1	0.00000854	0.00030484	0.01648842	0.11505951	A_07_P012404	b3185
rpmB	-8.82	13.88	-3.14	15.45	0.0	12.31	0.1	0.00000614	0.00026402	0.00109693	0.10530688	A_07_P017127	b3627
rpmC	-14.11	15.18	-3.82	17.09	0.0	13.27	0.3	0.00001294	0.00037688	0.00019881	0.04968254	A_07_P012987	b3312
rpmD	-2.89	15.58	-1.53	16.34	0.0	14.81	0.2	0.00040961	0.00349668	0.03239809	0.49821559	A_07_P012940	b3302
rpmE	-15.71	14.41	-3.97	16.40	0.0	12.42	0.1	0.00000157	0.00015843	0.00013021	0.03796296	A_07_P019460	b3936
rpmG	-19.82	12.82	-4.31	14.98	0.0	10.67	0.1	0.00000096	0.00012946	0.00005145	0.02078823	A_07_P017123	b3626
rpmI	-2.31	13.82	-1.21	14.43	0.0	13.22	0.0	0.00075337	0.00513994	0.06246736	0.64215542	A_07_P018633	b1717
rpoA	-6.45	14.36	-2.69	15.70	0.0	13.01	0.2	0.00003704	0.00086202	0.02398888	0.17486590	A_07_P12909	b3295
rpoB	-15.32	11.00	-2.46	9.80	0.0	12.21	0.1	0.00039125	0.00061413	0.01272421	0.28610012	A_07_P008600	b3987
rpoC	-12.54	10.66	-1.35	9.99	0.1	11.33	0.3	0.00239874	0.01330065	0.04382431	0.53915572	A_07_P008605	b3988
rpoD	-9.19	14.00	-3.20	15.60	0.0	12.40	0.3	0.00003241	0.00071849	0.00094131	0.30013514	A_07_P000800	b3867
rpoE	-2.80	12.53	-1.49	13.28	0.0	11.79	0.1	0.00034383	0.00308094	0.03654281	0.52160671	A_07_P019770	b2573
rpoH	-11.68	10.87	-3.55	12.64	0.0	9.10	0.3	0.00002661	0.00015658	0.00450904	0.06192308	A_07_P007345	b3461
rpoN	-6.82	10.62	-2.77	9.24	0.0	12.01	0.1	0.00001245	0.00036986	0.00803735	0.24860511	A_07_P012490	b3202
rpoZ	-5.77	13.41	-2.13	14.68	0.0	12.15	0.0	0.00003016	0.00041839	0.00148300	0.20900641	A_07_P017387	b3449
rpsB	-3.51	12.45	-1.81	13.35	0.1	11.54	0.2	0.00030947	0.00286300	0.03818607	0.41017559	A_07_P006135	b2830
rpsA	-5.97	13.94	-2.58	15.23	0.0	12.65	0.3	0.00010968	0.00164511	0.00376619	0.20061224	A_07_P005002	b0911
rpsB	-5.42	13.71	-2.24	15.32	0.0	12.09	0.1	0.00000806	0.00029787	0.00019845	0.10041667	A_07_P002803	b0169
rpsC	-10.20	15.65	-3.35	17.32	0.0	13.97	0.1	0.00000614	0.00023797	0.00070015	0.08534551	A_07_P002806	b0174
rpsE	-3.62	16.69	-1.86	17.92	0.0	15.76	0.0	0.00008563	0.00116924	0.01650512	0.39543379	A_07_P012943	b3303
rpsF	-4.91	15.91	-2.11	16.96	0.1	14.86	0.0	0.00009806	0.00078246	0.00998612	0.31542057	A_07_P011720	b4200
rpsG	-7.56	15.42	-2.92	16.88	0.0	13.96	0.6	0.00044832	0.00370061	0.01801886	0.13990148	A_07_P017731	b3341
rpsH	-3.22	15.71	-1.66	16.51	0.1	14.87	0.1	0.00022048	0.00238337	0.02193832	0.41753772	A_07_P012967	b3306
rpsI	-20.66	12.29	-4.37	14.47	0.1	10.10	0.0	0.00000102	0.00012946	0.00000704	0.02000000	A_07_P012625	b3230
rpsK	-2.07	14.70	-1.05	15.23	0.1	14.18	0.1	0.00186577	0.00105143	0.08398875	0.70360000	A_07_P012916	b3297
rpsL	-3.91	15.89	-1.97	16.88	0.1	14.91	0.0	0.00005683	0.00098312	0.01315549	0.36272205	A_07_P017738	b3342
rpsM	-2.96	15.72	-1.56	16.50	0.0	14.94	0.2	0.00026059	0.00207927	0.03025407	0.48054583	A_07_P012963	b3307
rpsP	-3.55	16.51	-1.83	17.42	0.1	15.59	0.1	0.00057124	0.00190249	0.01813326	0.40959828	A_07_P019921	b3269
rpsQ	-29.87	14.39	-4.90	16.84	0.0	11.94	0.0	0.00000047	0.00009262	0.00001207	0.00904762	A_07_P012981	b3311
rpsR	-5.09	15.79	-2.35	16.96	0.0	14.62	0.0	0.00003332	0.00052262	0.00599848	0.24918206	A_07_P011729	b4202
rpsR	-4.70	15.87	-2.23	16.99	0.0	14.75	0.0	0.00003323	0.00050613	0.00779980	0.28691589	A_07_P012364	25811
rpsT	-17.42	12.57	-4.12	14.64	0.0	10.51	0.0	0.00000114	0.00013852	0.00008257	0.02869252	A_07_P010823	b0523
rpsU	-2.89	16.73	-1.53	17.49	0.0	15.96	0.1	0.00023851	0.00238617	0.03806937	0.55241080	A_07_P000059	b3065
rrmJ	-3.46	12.11	-1.79	13.00	0.0	11.21	0.4	0.00190268	0.01158862	0.06890194	0.41682759	A_07_P000609	b3179
rsmI	-3.80	10.15	-1.93	9.19	0.1	11.12	0.1	0.00008949	0.00120520	0.02194550	0.39084842	A_07_P008627	b3995
rsmA	-2.05	14.03	-1.03	14.55	0.0	13.52	0.1	0.00171829	0.01040141	0.08614979	0.75410605	A_07_P019761	b2572
rsmF	-2.00	12.24	-1.00	12.74	0.0	11.74	0.1	0.00294835	0.01578856	0.08979896	0.72486154	A_07_P002836	b0176
rsmE	-2.93	10.92	-1.54	10.41	0.0	11.43	0.1	0.00030717	0.00404204	0.01437042	0.47935745	A_07_P011872	b2946
rsuA	-6.08	11.71	-2.60	13.01	0.1	10.41	0.5	0.00035555	0.00315017	0.00361344	0.19823300	A_07_P000715	b2183
rsuB	-15.42	10.54	-4.67	12.88	0.0	8.21	0.2	0.00000158	0.00015880	0.00002610	0.01293559	A_07_P020768	b1627
rsuB	-13.20	9.87	-3.72	11.73	0.0	8.00	0.2	0.00000416	0.00022003	0.00027566	0.05293883	A_07_P020774	b1628
rsuC	-4.37	9.73	-2.13	10.79	0.0	8.63	0.1	0.00006644	0.00076475	0.00967652	0.31012220	A_07_P020776	b1629
rsuD	-2.61	8.14	-1.27	8.78	0.1	7.51	0.0	0.00078192	0.00570461	0.05484947	0.60985169	A_07_P020785	b1630
rsmB	-3.90	9.09	-1.96	10.07	0.1	8.11	0.0	0.00007063	0.00100790	0.01334667	0.36544468	A_07_P004749	b0859
rsmB	-3.07	8.94	-1.62	9.75	0.1	8.13	0.2	0.00039685	0.00340023	0.02800813	0.48297919	A_07_P004960	ECd0039
rsmB	-3.05	9.22	-1.61	10.00	0.1	8.39	0.2	0.00065310	0.00496738	0.02738758	0.47958826	A_07_P004615	25386
rusA	-4.22	7.93	-2.08	6.89	0.0	8.96	0.2	0.00037190	0.00419859	0.01837398	0.36152253	A_07_P016520	b0510
rutB	-3.21	10.93	-1.68	11.78	0.0	10.09	0.1	0.00018740	0.00201810	0.02443979	0.45971326	A_07_P001287	b1011
rutR	-4.52	12.16	-2.28	13.01	0.0	11.30	0.1	0.00010945	0.00155163	0.00860709	0.29908268	A_07_P001289	b1013
rvaA	-4.75	11.62	-2.25	12.74	0.0	10.49	0.1	0.00005118	0.00063372	0.00735201	0.28026634	A_07_P015985	b1861
rvaB	-3.72	11.37	-1.90	12.32	0.0	10.42	0.0	0.00007704	0.00108686	0.01514609	0.37788993	A_07_P015980	b1860
rvsC	-4.61	8.02	-1.27	8.66	0.0	7.39	0.2	0.00185209	0.01095520	0.05439605	0.60823463	A_07_P015994	b1863
rvsC	-3.01	9.01	-1.59	9.80	0.0	8.21	0.1	0.00136882	0.00876717	0.02835556	0.48149655	A_07_P015995	c_2277
rpoD	-8.52	10.50	-3.08	8.95	0.4	12.04	0.2	0.00018499	0.00199636	0.05056942	0.21226599	A_07_P010301	b0556
rpoD	-4.66	8.86	-1.79	7.96	0.2	9.75	0.4	0.00176155	0.01409657	0.05349135	0.41545139	A_07_P010301	b0556
sad	-2.68	9.31	-1.42	10.02	0.2	8.60	0.2	0.00140104	0.00893412	0.04147929	0.55437182	A_07_P020272	b1525
saeA	-2.56	9.79	-1.24	10.41	0.0	9.17	0.0	0.00006028	0.00498272	0.01862178	0.42512648	A_07_P014051	b1294
saeD	-2.61	8.27	-1.38	7.58	0.0	8.96	0.0	0.00039170	0.00336992	0.02413034	0.50983859	A_07_P014440	b1291
sbcB	-12.35	10.36	-3.63	12.17	0.1	8.55	0.1	0.00000227	0.00018406	0.00003791	0.05260000	A_07_P016297	c_3619
sbcB	-13.68	9.21	-4.88	8.27	0.2	10.15	0.6	0.00643344	0.02911415	0.02362805	0.40129850	A_07_P004967	23173
sbcB	-4.59	9.73	-2.20	8.43	0.1	10.83	0.3	0.00002663	0.00255163	0.01610645	0.33946652	A_07_P005542	EC2813
sbcB	-5.92	11.02	-2.57	9.74	0.0	12.30	0.2	0.00003061	0.00086019	0.01044334	0.27773649	A_07_P031971	c_2539
sbcC	-2.55	8.70	-1.35	8.03	0.1	9.37	0.1	0.00071852	0.00534863	0.04304573	0.57129539	A_07_P021099	b0307
sbcC	-2.49	8.73	-1.32	8.07	0.2	9.39	0.3	0.00436749	0.02122808	0.04726690	0.54382122	A_07_P051929	20495
sbcC	-2.13	8.83	-1.22	8.22	0.0	9.44	0.1	0.00081989	0.00590502	0.01262880	0.56162143	A_07_P021099	b0307
sbmA	-2.37	9.40	-1.24	10.03	0.0	8.78	0.1	0.00089127	0.00631227	0.01769552	0.42267319	A_07_P020999	b0077
sbp	-8.96	10.71	-3.16	12.30	0.1	9.13	0.3	0.00002716	0.00056519	0.00103944	0.10314839	A_07_P019364	b1917
sdhA	-19.53	12.16	-4.29	10.01	0.1	14.30	0.1	0.00000315	0.00049976	0.00008108	0.08653947	A_07_P015315	b0721
sdhB	-15.49	10.38	-3.95	8.40	0.2	12.36	0.0	0.00000404	0.00021622	0.00144817	0.11573604	A_07_P015706	20877
sdhA	-13.82	10.46	-4.79	8.57	0.0	12.36	0.1	0.00002104	0.00017963	0.00182230	0.23059649	A_07_P063661	EC4748
sdhB	-11.50	12.08	-3.52	10.12	0.1	13.84	0.3	0.00002511	0.00054532	0.00276740	0.15341549	A_07_P010119	b0724
sdhC	-61.49	10.90	-6.97	9.31	0.1	15.79	0.2	0.00000078	0.00012441	0.00000741	0.02877755	A_07_P010122	b0721
sdhD	-48.28	12.70	-6.59	9.91	0.1	15.51	0.0	0.00000045	0.00009262	0.00013021	0.03059701	A_07_P010127	b0722
sdiA	-3.82	10.19	-1.93	11.16	0.1	9.23	0.1	0.00014188	0.00166451	0.01415691	0.37653716	A_07_P014943	b1916
sdiA	-3.27	8.45	-1.71	9.31	0.1	7.60	0.0	0.00014761	0.00169545	0.02316552	0.45249380	A_07_P015369	c_2330
seaA	-3.13	9.11	-1.65	8.29	0.0	9.94	0.1	0.00022856	0.00238157	0.00450287	0.24419462	A_07_P021484	b0898
secB	-3.99	11.02	-1.99	10.03	0.1	12.02	0.2	0.00023457	0.00236134	0.02038809	0.37942080	A_07_P016888	b3609
secE	-13.77	12.74	-3.78	14.63	0.0	10.85	0.2	0.00000527	0.00024857	0.00022612	0.01005670	A_07_P015670	b1981
secG	-3.17	11.58	-1.67	12.41	0.1	10.75	0.0	0.00018880	0.00196311	0.02525407	0.46557377	A_07_P000590	b3175
sefD	-8.42	10.68	-3.07	9.15	0.0	12.23	0.1	0.00000557	0.00017868	0.01398868	0.21398868	A_07_P017884	b1764
sfbB	-12.61	9.04	-3.66	7.21	0.1	10.87	0.1	0.00000406	0.00021673	0.00225546	0.14204000	A_07_P004881	c_1238
sfbC	-7.14	8.36	-2.84	6.94	0.1	9.78	0.1	0.00000980	0.00032816	0.00736344	0.24460024	A_07_P004883	c_1237
sfbD	-7.30	9.24	-2.87	7.81	0.0	10.68	0.3	0.00000073	0.00010790	0.00681974	0.12554053	A_07_P004893	c_1240
sfhA	-1.98	10.81	-1.53	10.02	0.0	11.60	0.4	0.00152798	0.01130507	0.03176766	0.46796899	A_07_P015869	c_3579
sgbH	-48.97	8.39	-4.08	6.85	0.1	9.93	0.2	0.00003228	0.00068434	0.00514916	0.21538809	A_07_P016850	b3591
sgbU	-7.17	8.48	-2.84	7.06	0.2	9.90	0.1	0.00003941	0.00084369	0.00714939	0.24000000	A_07_P019878	c_4405
sgcA	-2.56	8.42	-1.57	7.64	0.3	9.20	0.1	0.00023600	0.00224332	0.01403323	0.47046425	A_07_P004040	b4832
sgcA	-3.25	8.33	-1.70	7.94	0.2	9.18	0.0	0.00037760	0.00327983	0.02860157	0.43854211	A_07_P004040	b4832
sgcA	-3.21	8.25	-1.68	7.41	0.1	9.10	0.1	0.00018430	0.00199457	0.02908807	0.43839234	A_07_P004040	b4832
sgcA	-2.08	8.29	-1.05	7.76	0.2	8.81	0.1	0.00387684	0.01948196	0.06587779	0.66221672	A_07_P004040	b4832
sgcA	-2.64	8.39	-1.40	7.69	0.3	9.09	0.2	0.00049667	0.00228824	0.04291931	0.51283764	A_07_P004040	b4832
sgcB	-2.84	7.68	-1.51	5.53	0.0	8.44	0.1	0.00035587	0.00315116	0.03642912	0.48196639	A_07_P010684	AAC-0205086
sgcC	-2.26	7.65	-1.18	7.06	0.0	8.24	0.1	0.00119934	0.00792050	0.05388274	0.57996458	A_07_P004046	b4834
sgcE	-2.21	8.20	-1.14	7.63	0.1	8.77	0.2	0.00388437	0.01628119	0.05830554	0.60260328	A_07_P004033	b4301
sgcF	-7.89	8.23	-2.98	6.74	0.0	9.72	0.1	0.00016455	0.00098013	0.00588812	0.22268585	A_07_P004054	b4305
sirA	-2.29	10.47	-1.20	11.07	0.1	9.87	0.2	0.00190163	0.01118642	0.04429169	0.44876561	A_07_P007289	b3470
sitB	-2.60	8.31	-1.38	9.00	0.1	7.62	0.0	0.00053668	0.00462179	0.04089856	0.57264040	A_07_P018673	c_1599
sitC	-6.57	8.31	-2.19	9.41	0.2	7.22	0.1	0.00015296	0.00174253	0.00859311	0.29997783	A_07_P018667	c_1598
sltp	-14.75	13.14	-4.88	11.20	0.0	15.08	0.4	0.00002119	0.00049283	0.00410873	0.12408045	A_07_P002847	b0178
slmA	-3.40	11.37	-1.77	12.25	0.2	10.48	0.1	0.00028714	0.00250768	0.02307996	0.43479361	A_07_P017348	b3641
sphA	-2.84	10.46	-1.51	9.70	0.5	11.21	0.4	0.00402288	0.02030744	0.03704291	0.48363207	A_07_P013860	20033
sll	-4.52	8.60	-2.18	7.51	0.3	9.68	0.1	0.00045930	0.00376654	0.01466596	0.34291005	A_07_P017645	b4392
sll	-4.63	8.40	-2.21	7.29	0.0	9.50	0.1	0.00006523	0.00075578	0.01936603	0.33737197	A_07_P017645	b4392
sll	-2.82	8.52	-1.50	7.77	0.2	9.27	0.3	0.00018243	0.00173564	0.01649564	0.48240608	A_07_P017645	b4392
sll	-3.43	8.37	-1.78	7.48	0.1	9.25	0.4	0.00221094	0.01228812	0.02649581	0.43924623	A_07_P017645	b4392
sll	-4.34	8.57	-2.12	7.51	0.1	9.63	0.1	0.00036907	0.00310347	0.01779045	0.35721243	A_07_P018845	25994
sll	-3.92	8.71	-1.97	7.73	0.1	9.70	0.1	0.00019993	0.00162551	0.02109256	0.38314651	A_07_P017645	b4392
slyD	-3.13	11.28	-1.65	12.10	0.1	10.45	0.1	0.00030114	0.00254576	0.02142026	0.47254879	A_07_P017773	b3349
smg	-7.83	9.79	-2.97	8.30	0.1	11.27	0.2	0.00002571	0.00055176	0.00597243	0.22281991	A_07_P014260	c_4045
smg	-4.58	9.26	-2.19	8.17	0.2	10.36	0.0	0.00036565	0.00310244	0.01624631	0.34006649	A_07_P012813	b3284
smg	-4.57	11.44	-2.19	10.34	0.3	12.53	0.2	0.00028876	0.00271092	0.03463610	0.34274172	A_07_P045882	24655
smpA	-2.22	10.33	-1.15	9.75	0.0	10.91	0.0	0.00091274	0.00644402	0.05185556	0.58734847	A_07_P037364	c_5472
smpA	-2.22	11.45	-3.61	13.26	0.1	9.65	0.1	0.00000323	0.00019540	0.00015887	0.05824742	A_07_P019965	b2617
smpB	-5.11	11.92	-2.36	13.10	0.0	10.74	0.1	0.00000818	0.00027514	0.00019178	0.24837766	A_07_P019980	b2620
sodA	-2.11	9.83	-1.08	9.30	0.0	10.37	0.2	0.00235409	0.01341751	0.06138512	0.62805556	A_07_P041367	c_4859
sodA	-2.05	8.39	-1.04	7.87	0.3	8.90	0.0	0.00682522	0.03483409	0.08453906	0.65413596	A_07_P019316	b3908
sodB	-12.35	13.05	-3.63	11.24	0.1	14.87	0.1	0.00000495	0.00022989	0.00337741	0.14396154	A_07_P018362	b1656
sodB	-9.14	13.39	-3.18	11.80	0.0	14.99	0.1	0.00000760	0.00028299	0.00428708	0.19288571	A_07_P018363	c_3650
sodC	-2.65	9.27	-1.41	8.67	0.2	10.08	0.0	0.00015138	0.00768106	0.06045605	0.50152756	A_07_P020863	b1646
sohA	-2.53	11.13	-1.22	11.74	0.1	10.52	0.1	0.00015232	0.00755844	0.06008966	0.62367374	A_07_P005370	b3129
soxR	-3.69	8.46	-1.88	9.41	0.1	7.52	0.2	0.00032764	0.00298169	0.01638814	0.39640012	A_07_P008959	b4063
spaB	-3.48	9.24	-1.80	10.14	0.0	8.34	0.0	0.00009606	0.00127387	0.00830212	0.41888117	A_07_P011831	b2937
speD	-2.46	10.23	-1.30	9.58	0.2	10.88	0.1	0.00122205	0.00803675	0.04623095	0.52716605	A_07_P002565	b0120
speE	-2.07	11.08	-1.05	10.56	0.0	11.61	0.1	0.00285369	0.01187413	0.06349657	0.63032156	A_07_P002568	b0121
speF	-31.28	10.03	-4.97	7.55	0.4	12.52	0.2	0.00000184	0.00053092	0.00013134	0.05717134	A_07_P000893	b0693
speG	-3.29	10.68	-1.72	11.54	0.1	9.82	0.0	0.00018617	0.00200758	0.02264946	0.45069630	A_07_P020551	b1584
srlA	-7.29	8.50	-2.87	7.66	0.0	9.33	0.0	0.00008053	0.00030484	0.00755158	0.23922724	A_07_P001960	b3702
srlA	-7.00	9.01	-2.81	7.61	0.2	10.42	0.2	0.00005698	0.00087614	0.00757304	0.24634298	A_07_P041662	c_3256
srlA_1	-5.17	8.61	-2.42	6.80	0.0	9.23	0.1	0.00019268	0.00156197	0.01247659	0.29538815	A_07_P041662	24005
srlB	-3.41	8.20	-1.23	6.58	0.2	9.81	0.1	0.00001661	0.00024603	0.00408881	0.18994100	A_07_P001966	b3704
srlE	-6.80	8.01	-2.76	6.43	0.1	9.59	0.3	0.00007600	0.00105418	0.00786003	0.24778000	A_07_P001965	c_3257
srlE	-8.67	8.39	-3.12	6.83	0.0	9.94	0.0	0.00001405	0.00039160	0.00488631	0.20961853	A_07_P001964	b2703
srlE_1	-5.89	9.39	-2.56	8.11	0.1	10.67	0.3	0.00000975	0.00128681	0.01055767	0.27657338	A_07_P041665	24007
srlR	-2.12	10.41	-1.08	9.87	0.1	10.95	0.1	0.00109722	0.01247948	0.06285124	0.62668144	A_07_P041666	c_3261
srlR	-2.02	10.52	-1.01	10.01	0.1	11.02	0.3	0.00818628	0.03195933	0.07343124	0.67228774	A_07_P001981	b2707
srmB	-2.03	8.91	-1.02	8.40	0.0	9.42	0.1	0.00251197	0.01391879	0.06843662	0.65472727	A_07_P030217	c_3100
ssb	-8.19	12.36	-3.03	13.87	0.0	10.84	0.2	0.00000644	0.00034618	0.00014874	0.12556087	A_07_P008940	b4059
sseA	-13.97	11.91	-3.80	10.77	0.0	13.82	0.1	0.00000354	0.00020330	0.00188707	0.12806034	A_07_P013661	b2521
sspB	-18.36	12.53	-4.20	14.63	0.0	10.43	0.2	0.00000430	0.00021258	0.00006479	0.02428317	A_07_P012616	b3229
sspB	-11.94	13.38	-3.58	15.17	0.0	11.60	0.1	0.00000385	0.00021100	0.00039557	0.06220000	A_07_P012612	b3228
sspB	-12.08	8.23	-4.08	7.70	0.1	8.76	0.1	0.00016893	0.00123602	0.06366644	0.63061752	A_07_P000895	b3880
sthA	-2.32	11.78	-1.22	13.17	0.1	14.39	0.1	0.00113183	0.00848030	0.05274136	0.57069416	A_07_P008514	b3962
stpA	-7.17	9.80	-2.84	11.22	0.1	8.38	0.1	0.00003581	0.00064177	0.00217700	0.15796209	A_07_P020199	b2669
suaA	-465.07	11.82	-48.86	9.77	0.0	13.87	0.0	0.00000002	0.00000000	0.00000000	0.00000000	A_07_P019349	b0726
suaB	+190.56	13.10	-7.57	9.32	0.0	16.89	0.0	0.00000005	0.00000702	0.00000002	0.00666667	A_07_P010511	b0727
suaC	-215.93	12.20	-7.75	8.32	0.1	16.07	0.3	0.00000042	0.00009262	0.00000017	0.00000000	A_07_P010519	b0728
suaD	-112.44	11.35	-6.81	7.94	0.0	14.75	0.1	0.00000009	0.00007032	0.00000588	0.00961538	A_07_P010515	b0729
sufS	-2.42	7.58	-1.37	6.95	0.2	8.22	0.1	0.00078968	0.00576446	0.01845024	0.53482525	A_07_P018852	b1680
sugE	-4.17	11.68	-2.06	12.51	0.1	10.65	0.1	0.00011609	0.00146033	0.03875125	0.33112284	A_07_P015585	c_5236
sugE	-3.50	9.51	-1.81	10.42	0.1	8.61	0.0	0.00010302	0.00132941	0.01884425	0.41790577	A_07_P048623	25755
sugE	-3.22	10.43	-1.69	11.27	0.2	9.58	0.0	0.00052132	0.00417053	0.02369313	0.45741818	A_07_P010613	b4148
sugE	-12.70	8.94	-3.67	10.77	0.1	7.11	0.2	0.00005115	0.00246468	0.00031123	0.05444444	A_07_P010614	b4148
surA	-13.68	11.15	-4.88	10.21	0.0	12.09	0.1	0.00000370	0.00012691	0.00032460	0.39970660	A_07_P010951	b0053
talA	-4.05	8.99	-2.60	10.29	0.

ucpA	+3.75	8.76	+1.77	11.90	0.2	9.71	0.1	0.00014851	0.01248158	0.39503348	A_07_P013388	b2426	cmr/putative oxidoreductase [b2426]
ucpA	-6.66	11.56	+2.60	10.26	0.1	12.86	0.3	0.00001673	0.00344253	0.00998823	0.27153713	A_07_P041260	c_3960
ugd	-2.12	8.93	-1.08	9.47	0.1	8.39	0.4	0.01072023	0.04597586	0.07569233	0.07488381	A_07_P042482	c_2555
ugd	-3.08	8.78	-1.62	9.92	0.1	7.97	0.0	0.00025117	0.00247311	0.02784189	0.47933881	A_07_P044992	c2190
ugpB	+2.10	8.16	+1.07	7.62	0.1	8.69	0.1	0.01171688	0.03260341	0.06134550	0.62918074	A_07_P018281	b3453
ugpC	+5.79	8.77	+2.53	7.50	0.0	10.03	0.1	0.00003709	0.00042882	0.03092576	0.28052243	A_07_P018267	b3450
uhpA	-2.14	8.24	-1.10	8.79	0.1	7.69	0.1	0.00168545	0.03026132	0.07457574	0.47428861	A_07_P017384	b3669
uhpB	-2.01	8.03	-1.01	8.53	0.2	7.52	0.1	0.00498562	0.02365876	0.09175686	0.72703573	A_07_P018979	c_4592
uhpB	-2.32	8.60	-1.21	9.21	0.0	7.99	0.1	0.00110634	0.00745321	0.06098006	0.63412814	A_07_P049827	25158
uhpT	-11.97	8.33	-3.58	10.12	0.0	6.54	0.2	0.00000521	0.00024641	0.00042069	0.06215686	A_07_P017270	b3666
uhpT	-15.24	8.58	-3.93	10.54	0.0	6.62	0.2	0.00000328	0.00018846	0.00019910	0.03912714	A_07_P018972	c_4590
ulaA	+3.34	8.00	+1.74	7.13	0.0	8.87	0.2	0.00028862	0.00278521	0.02734566	0.42416749	A_07_P011684	b4193
ulaB	-1.63	7.86	-1.86	6.93	0.0	8.79	0.1	0.00009842	0.00129131	0.02348114	0.40595688	A_07_P011689	b4194
ulaC	+3.52	8.43	+1.82	7.52	0.2	9.34	0.4	0.00144305	0.00907687	0.02514863	0.41113265	A_07_P011693	b4195
ulaD	+4.99	9.86	+2.32	8.70	0.3	10.99	0.3	0.00017918	0.00104924	0.01413314	0.32010266	A_07_P011696	b4196
umuC	-7.86	11.07	-2.96	12.56	0.1	9.58	0.2	0.00001924	0.00046180	0.00152630	0.12647368	A_07_P006875	b1184
umuD	-5.75	11.17	-2.52	12.44	0.1	9.91	0.4	0.00031350	0.00288486	0.00429005	0.21089172	A_07_P006883	b1183
ung	-2.35	10.48	-1.23	11.10	0.1	9.87	0.2	0.00210231	0.01220764	0.05778328	0.42132604	A_07_P041614	c_3105
upp	+3.35	11.65	+1.79	10.78	0.2	12.52	0.1	0.00003130	0.00258365	0.03704586	0.42305605	A_07_P013547	b2498
ung	-3.69	10.77	-1.88	11.71	0.0	9.83	0.1	0.00012370	0.00150616	0.03155196	0.39176000	A_07_P032443	c_2864
ung	-3.35	10.18	-1.74	11.06	0.1	9.31	0.1	0.00010132	0.00156505	0.02146627	0.46252949	A_07_P013884	b2319
uspA	+18.87	13.09	+4.24	10.97	0.0	15.21	0.1	0.00000154	0.00015822	0.00094385	0.08898204	A_07_P007413	b3495
uspA	+6.08	11.46	+2.60	10.42	0.0	12.74	0.4	0.00025879	0.00253067	0.03970084	0.26889085	A_07_P049374	24895
uspA	+16.76	12.63	+4.07	10.60	0.1	14.67	0.2	0.00006638	0.00027919	0.00119919	0.10260870	A_07_P049423	c_4293
uspB	-2.24	8.11	-1.16	8.69	0.0	7.53	0.2	0.00240954	0.01342731	0.06449962	0.65517522	A_07_P007456	b3494
uspD	-4.66	9.59	-2.22	8.48	0.0	10.70	0.2	0.00003950	0.00062943	0.01585302	0.31774019	A_07_P013921	b3923
uspE	+2.48	12.53	+1.31	11.87	0.1	13.18	0.1	0.00073767	0.00546135	0.06600156	0.53729970	A_07_P014645	b1333
uspF	-8.92	12.40	-4.24	9.28	0.1	15.52	0.2	0.00000300	0.00009047	0.00035399	0.02023810	A_07_P014857	b1376
usp	-2.10	10.19	-1.07	10.73	0.1	9.66	0.2	0.00316615	0.01597786	0.07801321	0.68084257	A_07_P005192	b0949
uvrA	-11.08	12.89	-3.47	14.63	0.0	11.16	0.0	0.00000168	0.00018867	0.00005212	0.07095563	A_07_P008913	b4058
uvrB	-17.33	12.77	-4.32	14.82	0.0	10.71	0.0	0.00000118	0.00014031	0.00008257	0.02708333	A_07_P033475	c_0860
uvrB	-10.36	11.85	-4.35	14.02	0.1	9.68	0.3	0.00000425	0.00022158	0.00004954	0.03973684	A_07_P004347	b0779
uvrD	-2.32	12.77	-1.21	13.38	0.1	12.16	0.1	0.00119933	0.00792050	0.06267093	0.64231615	A_07_P005932	b1813
uvrY	-2.60	9.76	-1.38	10.44	0.0	9.07	0.0	0.00038275	0.00316417	0.04315252	0.57268135	A_07_P014691	b1914
uxaA	+9.78	8.54	+3.29	6.89	0.3	10.18	0.4	0.00015651	0.00017268	0.00392785	0.18514970	A_07_P000185	b3091
uxaB	-10.01	10.01	-4.39	7.82	0.1	12.21	0.1	0.00000099	0.00012946	0.00067027	0.07861852	A_07_P014558	c_3849
uxaB	+2.02	7.79	+1.01	7.29	0.2	8.30	0.1	0.00335527	0.01719703	0.06908051	0.65647734	A_07_P020252	b1521
uxaB	+3.08	10.04	+1.62	9.23	0.0	10.85	0.1	0.00017018	0.00109860	0.01123603	0.41137631	A_07_P052450	22184
uxaC	+68.10	10.36	+6.08	7.32	0.0	13.41	0.2	0.00000026	0.00009047	0.00060606	0.02217766	A_07_P000188	b3092
uxuA	-2.09	12.04	-1.07	13.51	0.1	10.58	0.1	0.00572738	0.02585481	0.06631479	0.62806905	A_07_P004138	b4322
uxuB	+2.64	9.59	+1.40	8.89	0.1	10.29	0.1	0.00046247	0.00368935	0.04088669	0.50408771	A_07_P037204	c_5403
uxuB	+5.47	8.43	+2.40	6.03	0.1	9.65	0.0	0.00002361	0.00052497	0.01214950	0.29271557	A_07_P047511	25921
uxuD	-2.27	7.57	-1.18	8.16	0.1	6.98	0.3	0.00387920	0.01948761	0.06364849	0.64625403	A_07_P049559	25050
uxaF	-4.45	10.11	-2.15	11.19	0.2	9.04	0.2	0.00010408	0.00158449	0.03928862	0.30632851	A_07_P049579	25054
uxaQ	-2.13	10.92	-1.09	11.46	0.1	10.37	0.0	0.00170052	0.01588018	0.07439109	0.67452260	A_07_P049589	25056
uxaD	-2.23	9.67	-1.16	10.25	0.1	9.09	0.2	0.00308944	0.01612713	0.06923971	0.65788171	A_07_P049567	25052
uxaB	-3.95	10.33	-1.98	11.32	0.1	9.34	0.0	0.00006177	0.00092312	0.01288110	0.35762225	A_07_P049568	25054
uxaA	-5.50	9.78	-2.17	8.69	0.1	10.86	0.1	0.00008297	0.00114285	0.01625566	0.34369881	A_07_P001254	b1004
uxaB	-2.05	8.24	-1.03	8.76	0.1	7.73	0.0	0.00231608	0.01905206	0.08614217	0.71331126	A_07_P052450	22184
uxaC	+2.05	10.27	+1.04	9.23	0.1	11.30	0.1	0.00016587	0.01673301	0.06460307	0.64292818	A_07_P005838	b3792
uxaE	-4.92	8.78	-2.30	7.63	0.2	9.93	0.3	0.00019685	0.00208281	0.01448866	0.32223011	A_07_P005852	b3793
uxaR	-3.44	11.26	-1.78	12.15	0.0	10.37	0.6	0.00365541	0.02886436	0.02029980	0.43189189	A_07_P031985	c_2554
uxuR	-2.46	8.99	-1.30	9.64	0.2	8.34	0.2	0.00535958	0.02520008	0.04998857	0.58952809	A_07_P049860	23189
uxaR	+11.08	9.88	+3.47	8.15	0.3	11.62	0.3	0.00004725	0.00007751	0.00304688	0.16373014	A_07_P006300	b2866
xerC	-4.15	8.47	-2.05	7.44	0.3	9.50	0.1	0.00026409	0.00255163	0.01884718	0.38724010	A_07_P049869	23328
xerC	+3.40	8.25	+1.77	7.37	0.2	9.14	0.0	0.00002040	0.00012689	0.02665650	0.42094283	A_07_P005923	b3811
xerC	+3.71	8.73	+1.89	7.78	0.0	9.67	0.1	0.00012431	0.00150779	0.02270706	0.39362655	A_07_P018912	c_4732
xerC	+2.55	8.57	+1.35	7.90	0.0	9.25	0.4	0.00673249	0.03032285	0.04628871	0.53730428	A_07_P057791	EC4741
xerD	-4.65	11.57	-2.22	12.68	0.0	10.46	0.0	0.00003287	0.00062948	0.00805069	0.29006577	A_07_P006436	b1894
xisC	-2.79	9.74	-1.48	10.49	0.1	9.00	0.3	0.00260009	0.01422638	0.03663618	0.52190095	A_07_P006656	b1141
xisW	-2.01	8.47	-1.01	8.91	0.0	7.96	0.0	0.01058198	0.08947536	0.09475136	0.72463992	A_07_P051290	21425
xpkA	+2.61	8.52	+1.39	7.83	0.1	9.21	0.2	0.00096658	0.00676548	0.04173684	0.50831539	A_07_P007551	b3565
xpkG	+5.69	8.59	+2.51	7.34	0.0	9.85	0.1	0.00002521	0.00054604	0.01131512	0.28363057	A_07_P007561	b3567
xpkH	+2.96	8.16	+1.56	7.38	0.0	8.94	0.0	0.00030608	0.00215269	0.03349517	0.46776014	A_07_P007770	b3568
xseA	+2.21	9.17	+1.21	8.71	0.1	9.77	0.1	0.00199570	0.00746376	0.05217670	0.56692202	A_07_P010722	b0306
xseA	-3.36	8.34	-1.75	9.21	0.1	7.46	0.1	0.00020627	0.00215353	0.02049122	0.43672848	A_07_P010701	b0303
xseY	-3.78	8.39	-1.92	9.35	0.0	7.44	0.2	0.00027500	0.00260922	0.01445502	0.37951505	A_07_P010806	b0024
yahJ	-3.71	8.30	-1.89	9.25	0.1	7.36	0.2	0.00034713	0.00310171	0.01425889	0.35383538	A_07_P007770	b3568
yaiJ	-4.62	8.16	-2.21	9.26	0.1	7.05	0.1	0.00003979	0.00080974	0.03826791	0.29383747	A_07_P035723	c_0081
yaiJ	-3.61	8.05	-1.85	8.97	0.0	7.12	0.3	0.00037656	0.00237367	0.01418311	0.39757760	A_07_P035723	c_0081
yaiJ	-3.35	8.20	-1.74	9.07	0.0	7.33	0.1	0.00031143	0.00156640	0.02138112	0.46085526	A_07_P035723	c_0081
yaiJ	-3.45	8.26	-1.79	9.16	0.0	7.37	0.2	0.00035569	0.00270561	0.01918857	0.41973574	A_07_P035723	c_0081
yaiJ	-2.65	8.66	-1.44	10.56	0.1	9.63	0.3	0.00265329	0.01444445	0.04274517	0.56269231	A_07_P002479	b0102
yaiS	+3.26	13.25	+1.79	12.48	0.1	14.11	0.0	0.00024649	0.00207010	0.02872761	0.43812640	A_07_P002509	b0109
yaiEC	-16.14	11.63	-4.01	13.64	0.0	9.63	0.3	0.00000247	0.00017989	0.00015160	0.03568627	A_07_P035826	c_0166
yaiEC	-2.87	9.82	-1.52	10.58	0.0	9.06	0.3	0.00004368	0.00403583	0.03319741	0.50304162	A_07_P002599	b0127
yaiEH	-2.65	8.53	-1.60	9.23	0.1	7.83	0.1	0.00053348	0.00462179	0.02443140	0.56137815	A_07_P049187	20139
yaiEH	-2.85	8.58	-1.51	9.34	0.0	7.83	0.1	0.00042158	0.00355887	0.03397231	0.50792022	A_07_P002603	b0128
yaiEH	+3.12	11.01	+1.64	10.19	0.3	11.83	0.1	0.00074354	0.00549878	0.03095238	0.44873849	A_07_P035875	c_0180
yaiES	-2.08	8.33	-1.06	8.86	0.1	7.80	0.2	0.00562691	0.02612106	0.07888946	0.68480727	A_07_P002749	b0157
yaiaI	-2.30	9.47	-1.20	10.07	0.0	8.87	0.3	0.00560083	0.02721892	0.06394569	0.64268617	A_07_P002614	b0191
yaeQ	-4.90	9.31	-2.29	10.46	0.1	8.17	0.6	0.00129353	0.00840501	0.00704141	0.27218329	A_07_P002906	b0190
yafE	-2.23	7.76	-1.16	7.18	0.1	8.34	0.1	0.01534697	0.09050012	0.06420594	0.58916778	A_07_P041461	c_3247
yafJ	+3.20	10.71	+1.68	9.87	0.0	11.54	0.1	0.00009186	0.00204384	0.02927083	0.43847764	A_07_P007830	b2223
yafK	-4.56	10.12	-2.19	11.22	0.2	9.03	0.3	0.00003560	0.00285522	0.08664625	0.35112583	A_07_P007831	b2224
yafP	-2.87	9.72	-1.52	10.48	0.1	8.96	0.1	0.00031496	0.00260492	0.03413046	0.50769225	A_07_P007881	b2234
yafX	-3.70	8.92	-1.43	9.64	0.2	8.20	0.1	0.00116579	0.00776259	0.03972815	0.54291139	A_07_P007906	b2238
yahA	-4.70	8.61	-2.23	9.73	0.1	7.50	0.3	0.00190071	0.00203700	0.00777185	0.28657338	A_07_P008268	b0315
yahI	-2.42	8.11	-1.27	7.48	0.3	8.75	0.1	0.00367681	0.01485178	0.04551578	0.55159752	A_07_P008306	b0323
yahM	-8.28	9.60	-3.05	11.12	0.1	8.08	0.4	0.00012208	0.00148956	0.00138529	0.12513809	A_07_P008330	b0327
yahN	+2.56	8.40	+1.35	7.72	0.3	9.08	0.2	0.00131565	0.01635513	0.04560834	0.52032674	A_07_P008332	b0328
yaiA	-6.04	12.00	-2.60	13.29	0.1	10.70	0.2	0.00006558	0.00075621	0.03630391	0.19839161	A_07_P021060	b0389
yaiE	+2.00	10.61	+1.00	10.11	0.0	11.11	0.1	0.00275593	0.01466058	0.07028027	0.66108124	A_07_P021069	b0391
yaiI	+3.57	10.23	+1.84	9.32	0.5	11.15	0.0	0.00280370	0.01567775	0.02491044	0.40981191	A_07_P021047	b0387
yaiC	+5.81	9.66	+2.54	8.39	0.1	10.93	0.1	0.00025312	0.00248931	0.03107736	0.27662791	A_07_P021148	b0407
yaiK	-3.21	9.17	-1.68	10.01	0.3	8.33	0.1	0.00055515	0.00176235	0.02410950	0.45842095	A_07_P043862	20526
yBeA	-2.89	8.16	-1.53	8.92	0.2	7.39	0.3	0.00165493	0.01011555	0.03320263	0.49526223	A_07_P021388	b0456
yBeB	-2.04	11.71	+1.03	11.19	0.0	12.22	0.0	0.00166797	0.01017455	0.06464668	0.64319519	A_07_P021461	b0471
yBeC	-18.37	10.31	-4.20	12.41	0.1	8.21	0.2	0.00000232	0.00007963	0.00007668	0.02610364	A_07_P031201	c_0596
yBeL	-3.38	10.40	-1.76	11.28	0.1	9.52	0.0	0.00034082	0.00164165	0.02067518	0.45117080	A_07_P021498	b0479
yBeQ	-18.22	10.19	-4.19	12.29	0.1	8.10	0.3	0.00000120	0.00004031	0.00007514	0.02609651	A_07_P021524	b0483
yBeR	-2.00	9.95	-1.00	10.45	0.2	9.45	0.1	0.00785629	0.03156224	0.08869079	0.75180218	A_07_P021528	c_0604
yBeY	+3.89	10.54	+1.96	9.56	0.3	11.52	0.1	0.00035221	0.00314916	0.02107533	0.38131242	A_07_P021322	b0442
yBeY	-2.58	10.08	-1.37	10.76	0.1	9.39	0.2	0.00110048	0.00746320	0.04505462	0.57297254	A_07_P021380	b0453
yBbB	-2.26	8.50	-1.17	9.08	0.1	7.91	0.1	0.00111118	0.00747627	0.06408867	0.65726627	A_07_P016305	b0503
yBbJ	-2.51	8.97	-1.33	9.63	0.1	8.31	0.1	0.00605185	0.02768164	0.04560937	0.58814906	A_07_P016966	20661
yBbP	-2.65	10.56	-1.41	11.20	0.0	9.86	0.1	0.00051753	0.00415078	0.04243077	0.51914188	A_07_P031218	c_0609
yBbQ	+2.11	7.81	+1.07	7.27	0.1	8.35	0.0	0.00280697	0.01207770	0.06241941	0.62615224	A_07_P031226	c_0624
yBbT	+2.48	8.38	+1.31	7.72	0.3	9.03	0.2	0.00228766	0.01417346	0.04738440	0.54137881	A_07_P031224	c_0620
yBbW	+3.99	8.64	+2.00	7.64	0.2	9.63	0.0	0.00102124	0.00329812	0.01992312	0.27812201	A_07_P031241	b0511
yBcJ	-2.52	9.62	-1.33	10.28	0.1	8.95	0.1	0.00006508	0.00468214	0.04842749	0.58124252	A_07_P016429	b0528
yBcK	-2.00	7.74	-1.00	8.24	0.2	7.24	0.0	0.00348943	0.01791831	0.08974575	0.72491003	A_07_P016486	b0544
yBdD	+8.14	9.03	+3.03	7.52	0.0	10.55	0.1	0.00003024	0.00031697	0.00157800	0.21683951	A_07_P010317	ABE-0285033
yBdM	-3.07	7.84	-1.62	8.64	0.1	7.03	0.2	0.00002870	0.00482664	0.07235800	0.67842809	A_07_P016765	b0601
yBdN	-6.30	10.44	-2.65	11.80	0.0	9.21	0.2	0.00003467	0.00066547	0.03317645	0.18733337	A_07_P016768	b0602
yBeA	-6.69	11.85	-2.74	13.22	0.0	10.47	0.1	0.00001295	0.00015388	0.00267552	0.17433333	A_07_P016786	b0636
yBeB	-5.18	13.06	-2.37	14.24	0.0	11.87	0.0	0.00002209	0.00050688	0.00548979	0.24542666	A_07_P009752	b0637
yBeJ	+4.71	12.36	+2.39	10.38	0.4	14.33	0.4	0.00005553	0.00015017	0.01432365	0.33810651	A_07_P044091	20805
yBeL	+3.49	11.28	+1.80	10.38	0.3	12.18	0.0	0.00004323	0.00408647	0.02456866	0.41993569	A_07_P009784	b0643
yBeT	+5.55	10.76	+2.47	9.52	0.1	12.00	0.1	0.00002666	0.00056107	0.01849959	0.29152000	A_07_P009856	b0659
yBeZ	+5.08	10.88	+2.34	9.71	0.1	12.05	0.1	0.00003837	0.00057633	0.01838479	0.31567489	A_07_P009865	b0660
yBfA	-10.45	10.99	-3.39	12.38	0.0	9.19	0.1	0.00003048	0.00020738	0.00068274	0.08228346	A_07_P010014	b0699
yBfD	-2.98	8.56	-1.58	9.35	0.1	7.77	0.2	0.00079215	0.00534738	0.03022104	0.49051546	A_07_P010047	b0706
yBfE	-5.59	11.26	-2.48	12.50	0.1	10.02	0.3	0.00011380	0.00141969	0.00459551	0.22233003	A_07_P009941	b0685
yBfL	-3.36	10.65	-1.24	11.27	0.4	10.03	0.1	0.00915506	0.03859818	0.05869172	0.62609969	A_07_P010101	b0705
yBgA	-4.63	9.69	-2.21	10.80	0.1	8.58	0.3	0.00021131	0.00219159	0.08802401	0.29041379	A_07_P033376	c_0786
yBgC	-3.72	10.67	-1.90	11.62	0.1	9.72	0.2	0.00017992	0.00156227	0.01319018	0.35945160	A_07_P010338	b0736
yBgE	+6.55	8.89	+2.71	7.54	0.1	10.25	0.1	0.00001672	0.00042422	0.00861562	0.26038888	A_07_P010394	b0755
yBgI	+3.38	12.04	+1.76	11.16	0.1	12.92	0.1	0.00019438	0.00266018	0.02707081	0.42280706	A_07_P010460	b0750
yBgO	+2.52	7.59	+1.33	6.93	0.1	8.26	0.1	0.00066641	0.00492163	0.04467416	0.52681593	A_07_P010097	b0716
yBhC	+2.06	7.82	+1.04	7.30	0.0	8.34	0.1	0.00221545	0.01222132	0.06414710	0.62427197	A_07_P021991	20843
yBhF	+3.19	9.17	+1.67	8.33	0.1	10.00	0.0	0.00018500	0.00196636	0.02930787	0.43914616	A_07_P004422	b0794
yBhG	-2.86	9.71	-1.51	8.95	0.1	10.47	0.0	0.00037008	0.00325587	0.03018623	0.45948624	A_07_P004426	b0795
yBhH	-2.88	9.55	-1.51	8.92	0.0	10.32	0.1	0.00028726	0.00270003	0.03331364	0.50334933	A_07_P004392	b0788
yBhQ	+2.06	10.30	+1.04	9.78	0.1	10.82	0.3	0.00787293	0.02425364	0.06038570	0.64266483	A_07_P004406	b0791
yBhR	+2.57	7.65	+1.36	6.97	0.0	8.33	0.1	0.00464387	0.00389944	0.02942671	0.51257771	A_07_P004412	b0792
yBhR	-2.30	8.08	-1.20	7.48	0.3	8.68	0.1	0.00507532	0.02403884	0.05455222	0.58243504	A_07_P004575	21012
yBiB	+2.64	10.80	+1.40	11.12	0.1	12.54	0.0	0.00088109	0.00391373	0.04121761	0.50618565	A_07_P004455	b0800
yBiB	+2.11	9.89	+1.08	9.35	0.1	10.42	0.1	0.00206682	0.01184594	0.06138054	0.62361307	A_07_P004583	21021
yBiB	+3.91	11.20	+1.97	10.21	0.1	12.18	0.1	0.00012551	0.00151881	0.02074441	0.38243560	A_07_P004564	c_0884
yBiC	+6.89	9.26	+2.79	7.86	0.1	10.65	0.2	0.00003038	0.00084029	0.00778192	0.24800000	A_07_P042097	c_0885
yBiC	+2.76	9.23	+1.47	8.49	0.0	9.96	0.0	0.00039102	0.00272690	0.04842209	0.49408497	A_07_P004457	b0801
yBiH	+2.82	7.71	+1.50	6.96	0.2	8.46	0.4	0.00464410	0.02914177	0.03749174	0.48702145	A_07_P004412	b0796
yBiO	-10.60	9.25	-3.41	10.95	0.2	7.54	0.3	0.00010112	0.00061324	0.00184269	0.08175000	A_07_P004663	b0802
yBiO	-4.95	9.45	-2.31	10.61	0.1	8.30	0.0	0.00003464	0.00064547	0.04640324	0.26146030	A_07_P004491	b0808
yBiR	-3.57	9.62	-1.84	10.54	0.1	8.70	0.1	0.00011828	0.00145366	0.01769944	0.42739766	A_07_P004652	b0818
yBiS	-5.86	9.96	-2.55	11.23	0.0	8.68	0.1	0.00002003	0.00047140	0.03079529	0.32743033	A_07_P004547	b0819
yBiS	-7.94	11.46	-2.99	12.96	0.1	9.97	0.1	0.00000168	0.00005997	0.00150661	0.12617021	A_07_P042114	c_0905
yBiT	-13.08	10.33	-3.81	12.23	0.1	8.43	0.2	0.00000536	0.00024927	0.00020071	0.08061538	A_07_P004555	b0820
yBjG	-4.92	10.66	-2.47	11.40	0.0	7.93	0.1	0.00000029	0.00000947	0.00000191	0.00042671	A_07_P004660	b0841
yBjL	-13.79	9.98	-3.79	11.87	0.1	8.09	0.3	0.00000319	0.00001528	0.00022104	0.06971429	A_07_P004688	b0847
yBjM	-4.41	9.01	-2.14	10.08	0.1	7.94	0.2	0.00001329	0.00135236	0.00027782	0.30751579	A_07_P004692	b0848
yBjP	+2.75	9.25	+1.46	8.52	0.1	9.99	0.2	0.00074344	0.00549878	0.03845846	0.49387439	A_07_P052022	21095
yBjT	-17.58	8.55	-4.92	7.09	0.0	10.01	0.1	0.00000850	0.00003484	0.00633582	0.23071704	A_07_P004803	b0869
yBjT	+4.79	8.28	+2.26	7.15	0.1	9.41	0.0	0.00012396	0.00150701	0.01504330	0.33108895	A_07_P052027	21103
yBjX	-10.26	10.25	-3.17	11.83	0.0	8.66	0.1	0.00009618	0.00038503	0.00130434	0.10304027	A_07_P004829	b0873
yBjX	-10.40	11.93	-3.38	13.31	0.0	10.25	0.2	0.00003898	0.00031671	0.00062500	0.08132231	A_07_P042136	c_1012
ycaD	-2.72	8.10	-1.65	8.82	0.1	7.38	0.0	0.00032178	0.00017189	0.03952807	0.54119652	A_07_P032821	c_1037
ycaF	-2.17	8.30	-1.11	8.86	0.0	7.74	0.4	0.01126006	0.04507080	0.07058117	0.46302506	A_07_P033841	c_1052
ycaQ	-2.39	7.77	-1.26	8.40	0.1	7.14	0.3	0.00565887	0.01863115	0.05032239	0.61102257	A_07_P005026	b0916
ycbF	-3.80	11.49	-1.93	12.46	0.1	10.53	0.3	0.00054331	0.00376202	0.01509192	0.38690978	A_07_P005047	b0944
ycbG	+3.21	9.22	+1.68	8.38	0.0	10.06	0.3	0.00102251	0.00691416	0.02696369	0.43941729	A_07_P005226	b0956
ycbJ	+4.69	9.51	+2.23	8.39	0.0	10.62	0.1	0.00000403	0.00076197	0.01504914	0.18615251	A_07_P005252	b0959
ycbK	+2.36	12.56	+1.24	11.34	0.1	13.18	0.1	0.00093368	0.00638869	0.04984311	0.55340621	A_07_P005076	b0926
ycbQ	-4.77	8.51	-2.25	9.64	0.4	7.39	0.3	0.01125779	0.02832193	0.07436832	0.62260000	A_07_P005127	b0938
ycbZ	-2.34	8.48	-1.23	9.10	0.1	7.87	0.4	0.00895165	0.03790606	0.05635554	0.61664592	A_07_P005221	b0955
ycdC	-2.10	10.57	-1.07	11.91	0.1	9.24	0.1	0.00160576	0.01005584	0.06355442	0.69282585	A_07_P005305	b0968
ycdF	-2.63	11.21	-1.39	11.91	0.1	10.52	0.

yqjE	-3.38	7.93	-1.76	8.81	0.0	0.0	0.00015895	0.00179261	0.02108187	0.41771164	A_07_P018893	b1769			cmr/putative transport protein (b1769)
yqjF	-4.40	9.94	-2.14	11.01	0.1	0.87	0.0	0.00010058	0.00131088	0.00910990	0.30730326	A_07_P018898	b1770		cmr/putative DIDA-type transcriptional regulator (b1770)
yqjH	-2.04	7.85	-1.03	7.33	0.0	0.0	0.0	0.00279932	0.01409513	0.04842401	0.61303849	A_07_P018910	b1772		cmr/putative kinase (b1772)
yqjI	-2.09	7.90	-1.07	7.37	0.1	0.43	0.0	0.01782831	0.01667351	0.08623419	0.42651686	A_07_P018915	b1773		cmr/putative aldolase (b1773)
yqjM	-4.80	8.27	-2.26	9.40	0.1	0.0	0.0	0.00059907	0.00068943	0.00718941	0.27607317	A_07_P018930	b1728		cmr/conf, hypothetical protein (b1728)
yqjN	-14.67	9.96	-3.88	11.90	0.0	0.0	0.0	0.00000244	0.00017989	0.00017340	0.06475410	A_07_P018891	b1729		cmr/part of a kinase (b1729)
yqjN	-7.34	9.33	-2.88	10.76	0.0	0.0	0.0	7.89	0.2	0.00003225	0.00050974	0.00195312	0.35000074	A_07_P042351	c_2128
yqjR	-2.16	7.71	-1.16	8.30	0.0	0.0	7.13	0.1	0.00102437	0.00703146	0.00851880	0.65898595	A_07_P041169	c_2141	cmr/Hypothetical protein yqjR (c_2141)
yqjT	-2.88	8.69	-1.50	7.92	0.4	0.4	9.65	0.3	0.00648506	0.03005413	0.01676449	0.48353690	A_07_P018802	b1751	cmr/conf, hypothetical protein (b1751)
yreC	+2.67	12.15	+1.42	11.44	0.1	0.1	12.86	0.1	0.00057230	0.00447604	0.04046684	0.50126072	A_07_P015578	b1777	cmr/conf, hypothetical protein (b1777)
yreD	+6.39	9.49	+2.68	8.16	0.2	0.2	10.83	0.3	0.00086624	0.01254163	0.00880907	0.25973010	A_07_P015653	c_2185	cmr/Unknown protein from 20-page [c_2185]
yreE	+6.55	9.61	+2.71	8.26	0.3	0.3	10.97	0.1	0.00009798	0.00110728	0.00865346	0.25950476	A_07_P015663	c_2185	cmr/Unknown protein from 20-page [c_2185]
yreD	+6.96	9.96	+2.80	8.56	0.1	0.1	11.26	0.0	0.00001748	0.00044398	0.00763338	0.24728365	A_07_P015663	c_2185	cmr/Unknown protein from 20-page [c_2185]
yreG	+6.57	9.67	+2.72	8.31	0.0	0.0	11.03	0.0	0.00001155	0.00035443	0.00862282	0.25998092	A_07_P015663	c_2185	cmr/Unknown protein from 20-page [c_2185]
yreH	+5.41	8.97	+2.44	7.75	0.0	0.0	10.19	0.1	0.00053760	0.00353705	0.01234697	0.29450961	A_07_P015663	b1780	cmr/conf, hypothetical protein (b1780)
yreJ	+6.86	9.93	+2.78	8.54	0.0	0.0	11.32	0.1	0.00003710	0.00042882	0.00780014	0.24899396	A_07_P015663	c_2185	cmr/Unknown protein from 20-page [c_2185]
yreL	-5.77	8.93	-2.53	10.20	0.1	0.1	0.0	0.00002882	0.00003893	0.00410077	0.20877419	A_07_P015623	b1786		cmr/conf, hypothetical protein (b1786)
yreM	-2.52	9.51	-1.33	10.18	0.1	0.1	8.85	0.5	0.09300886	0.03809711	0.04903392	0.58528831	A_07_P044476	22826	cmr/conf,Unknown function [22826]
yreN	-1.59	8.99	-1.84	9.91	0.1	0.1	8.07	0.4	0.01404713	0.00090617	0.01813301	0.41004010	A_07_P044476	22826	cmr/conf,Unknown function [22826]
yreO	-2.36	9.59	-1.24	10.21	0.0	0.0	8.97	0.1	0.00070134	0.00524305	0.05895706	0.62548518	A_07_P044476	22826	cmr/conf,Unknown function [22826]
yreP	-1.73	9.34	-1.90	10.29	0.3	0.3	8.09	0.1	0.00049953	0.00366659	0.01436326	0.39125266	A_07_P044476	22826	cmr/conf,Unknown function [22826]
yreQ	-2.79	9.47	-1.48	10.21	0.0	0.0	8.73	0.3	0.00156881	0.00956658	0.03683626	0.52342058	A_07_P044476	22826	cmr/conf,Unknown function [22826]
yreX	-4.45	8.89	-2.15	9.92	0.2	0.2	7.81	0.1	0.00009161	0.00122184	0.00893864	0.30264516	A_07_P015638	b1789	cmr/conf, hypothetical protein (b1789)
yreY	-3.92	7.72	-1.55	8.50	0.0	0.0	6.95	0.1	0.00035922	0.00317256	0.01106214	0.49216572	A_07_P015689	b1799	cmr/putative transcriptional regulator LYSR-type [b1799]
yreZ	-3.70	10.73	-1.89	11.67	0.3	0.3	9.78	0.3	0.00155126	0.00957391	0.01610455	0.39310078	A_07_P015344	c_2276	cmr/Hypothetical protein ydiB [c_2276]
yreC	-2.00	7.22	-1.00	12.72	0.1	0.1	11.72	0.1	0.00122479	0.01688480	0.08985522	0.73473873	A_07_P015969	b1864	cmr/conf, hypothetical protein (b1864)
yreE	-19.50	10.48	-4.29	12.63	0.0	0.0	8.34	0.2	0.00000221	0.00017963	0.00005780	0.02275000	A_07_P015906	b1846	cmr/conf, hypothetical protein (b1846)
yreF	-39.05	14.00	-4.86	16.43	0.0	0.0	11.57	0.1	0.00000051	0.00009514	0.00001548	0.00386957	A_07_P015914	b1847	cmr/conf, hypothetical protein (b1847)
yreG	-7.96	14.53	-2.99	16.03	0.0	0.0	13.04	0.0	0.00000660	0.00027019	0.00149708	0.12809783	A_07_P015916	b1848	cmr/conf, hypothetical protein (b1848)
yreM	-5.81	8.65	-2.54	7.58	0.1	0.1	10.12	0.0	0.00000760	0.00045124	0.01097580	0.28878065	A_07_P015941	b1853	cmr/conf, hypothetical protein (b1853)
yreN	-8.04	10.22	-3.01	11.72	0.1	0.1	8.71	0.2	0.00001704	0.00042859	0.01146786	0.12697802	A_07_P015797	b1821	cmr/conf, hypothetical protein (b1821)
yreO	-11.82	9.54	-3.56	11.32	0.0	0.0	7.76	0.1	0.00003042	0.00020055	0.00400904	0.06133333	A_07_P015812	b1825	cmr/conf, hypothetical protein (b1825)
yreR	+3.69	8.95	+1.88	8.01	0.1	0.1	9.89	0.2	0.00024820	0.00245286	0.02301258	0.38958086	A_07_P015837	b1832	cmr/conf, hypothetical protein (b1832)
yreT	+4.64	10.48	+2.22	9.38	0.0	0.0	10.70	0.0	0.00007065	0.00018700	0.01581575	0.33817071	A_07_P015874	b1839	cmr/conf, hypothetical protein (b1839)
yreX	+2.46	12.07	+1.30	11.42	0.1	0.1	12.72	0.0	0.00068141	0.00511060	0.04629510	0.53711864	A_07_P014920	b1908	cmr/conf, hypothetical protein (b1908)
yreZ	-3.32	8.64	-1.73	8.50	0.1	0.1	7.77	0.1	0.00021092	0.00218866	0.02207752	0.44652023	A_07_P014947	b1917	cmr/putative ATP-binding component of a transport system [b1917]
yreF	-2.24	8.56	-1.16	9.15	0.0	0.0	7.98	0.2	0.02218984	0.01248185	0.06804497	0.65924154	A_07_P014960	b1915	cmr/conf, hypothetical protein (b1915)
yreI	-2.87	10.29	+1.52	9.53	0.0	0.0	11.05	0.1	0.00022703	0.00261488	0.03573425	0.47406336	A_07_P015203	c_2315	cmr/Ferritin-like protein [c_2315]
yreR	-4.37	7.85	-2.13	8.66	0.1	0.1	6.78	0.1	0.00005756	0.00088323	0.00952998	0.30872428	A_07_P016190	b1904	cmr/conf, hypothetical protein (b1904)
yreS	-4.81	9.20	-2.27	10.33	0.1	0.1	8.07	0.1	0.00004485	0.00075204	0.00724657	0.27703614	A_07_P016955	b1918	cmr/putative transport system permease protein [b1918]
yreS	-4.18	9.45	-2.06	10.48	0.0	0.0	8.42	0.2	0.00008669	0.00127819	0.01092797	0.33407767	A_07_P042434	c_2332	cmr/Hypothetical amino-acid ABC transporter permease protein yeeS [c_2332]
yreW	+21.52	11.02	+4.43	8.81	0.1	0.1	13.23	0.1	0.00000131	0.00014643	0.00065231	0.07790303	A_07_P015376	c_2344	cmr/Hypothetical protein yeeX [c_2344]
yreX	-20.90	10.61	-4.39	8.41	0.2	0.2	0.0	0.00003899	0.00031471	0.00073900	0.08143885	A_07_P015512	b1930		cmr/conf, hypothetical protein (b1930)
yreY	-2.58	8.17	-1.37	8.85	0.0	0.0	7.49	0.2	0.00112112	0.00848030	0.04622777	0.57398265	A_07_P052607	23055	cmr/conf, hypothetical protein (23055)
yreD	-5.89	10.04	-2.56	11.31	0.0	0.0	8.76	0.2	0.00003023	0.00060399	0.00388974	0.20553936	A_07_P041216	c_2381	cmr/Hypothetical protein yeeD [c_2381]
yreE	-9.53	9.13	-2.18	10.21	0.0	0.0	8.04	0.1	0.00005392	0.00088214	0.00869474	0.30511082	A_07_P015968	b1962	cmr/conf, hypothetical protein (b1962)
yreR	-3.48	8.11	-1.80	9.01	0.1	0.1	7.21	0.2	0.00031566	0.00269066	0.01873984	0.47936568	A_07_P015174	b1963	cmr/conf, hypothetical protein (b1963)
yreU	+6.43	11.09	+2.69	9.75	0.4	0.4	12.43	0.2	0.00036036	0.00254204	0.00873116	0.25981061	A_07_P042074	c_2385	cmr/Protein yeeU [c_2385]
yreW	-2.67	8.11	-1.41	8.84	0.1	0.1	7.43	0.1	0.00470099	0.00387034	0.04209540	0.59767207	A_07_P015203	b1969	cmr/putative 2-component transcriptional regulator [b1969]
yreZ	+2.17	7.64	+1.12	7.08	0.1	0.1	8.19	0.0	0.00013561	0.00867719	0.05818661	0.60150361	A_07_P015218	b1972	cmr/conf, hypothetical protein (b1972)
yreA	+3.07	8.05	+1.62	7.24	0.1	0.1	8.86	0.1	0.00042145	0.00155252	0.01452269	0.41303636	A_07_P015367	c_2536	cmr/putative fimbrial-like protein [c2311]
yreD	-4.11	10.34	-2.04	11.36	0.1	0.1	9.32	0.8	0.00858305	0.03670060	0.01210693	0.34650909	A_07_P015390	b2012	cmr/conf, hypothetical protein (b2012)
yreF	-2.67	7.88	-1.42	8.69	0.0	0.1	7.27	0.1	0.00040751	0.00395237	0.04162093	0.55418242	A_07_P015400	b2014	cmr/putative amino acid/peptide transport protein [b2014]
yreG	-7.02	8.34	-2.91	9.25	0.0	0.0	6.93	0.2	0.00003314	0.00062062	0.00232645	0.15831111	A_07_P015266	b1985	cmr/conf, hypothetical protein (b1985)
yreH	-3.29	9.56	-1.72	10.42	0.1	0.1	8.70	0.2	0.00025556	0.00246861	0.02122260	0.64708870	A_07_P015404	b2015	cmr/putative transcriptional regulator LYSR-type [b2015]
yreI	-3.53	12.17	-1.82	13.08	0.0	0.0	11.26	0.0	0.00008867	0.00129314	0.01784743	0.40901019	A_07_P015407	b2016	cmr/putative enzyme of sugar metabolism [b2016]
yreM	-2.64	13.81	-1.40	14.51	0.1	0.1	13.11	0.0	0.00000303	0.00046268	0.00410841	0.49379858	A_07_P015411	b2017	cmr/conf, hypothetical protein (b2017)
yreN	-3.87	9.57	-1.95	8.60	0.2	0.2	10.55	0.1	0.00032248	0.00234924	0.02122749	0.38510091	A_07_P002500	b2147	cmr/putative oxidoreductase [b2147]
yreO	-3.55	9.60	-1.83	8.99	0.2	0.2	10.82	0.1	0.00010317	0.00206751	0.02468280	0.49456037	A_07_P002500	b2147	cmr/putative oxidoreductase [b2147]
yreC	-19.66	8.75	-4.30	6.60	0.3	0.3	10.89	0.2	0.00000648	0.00027019	0.00083206	0.08451613	A_07_P032264	c_2701	cmr/Hypothetical sugar kinase yeeC [c_2701]
yreQ	-12.93	9.64	-3.60	7.84	0.0	0.0	11.44	0.1	0.00000295	0.00018751	0.00247265	0.14414815	A_07_P000603	b2172	cmr/putative oxidoreductase [b2172]
yreT	-10.84	9.68	-3.44	7.96	0.2	0.2	11.40	0.0	0.00000734	0.00028727	0.00306847	0.36410973	A_07_P003491	b2146	cmr/putative oxidoreductase [b2146]
yreW	-2.42	8.10	-1.28	8.74	0.1	0.1	7.46	0.1	0.00081209	0.00585149	0.05181098	0.60867679	A_07_P010506	ABE-0285016
yreX	+3.75	7.79	+1.91	6.84	0.1	0.1	8.74	0.0	0.00037840	0.00100102	0.02247586	0.39537430	A_07_P032368	c_2716	cmr/Hypothetical ABC transporter permease protein yeiE [c_2716]
yreZ	+2.98	7.79	+1.58	7.04	0.1	0.1	8.58	0.1	0.00026227	0.00251460	0.03137962	0.46473089	A_07_P000894	b2179	cmr/putative transport system permease protein [b2179]
yreD	-7.98	12.07	-3.00	13.07	0.0	0.0	10.57	0.0	0.00000645	0.00027019	0.00150025	0.12631016	A_07_P000703	b2181	cmr/conf, hypothetical protein (b2181)
yreE	-2.38	12.00	-1.25	12.63	0.1	0.1	11.38	0.0	0.00070870	0.00528303	0.05499441	0.61798858	A_07_P000713	b2187	cmr/conf, hypothetical protein (b2187)
yreM	-3.16	8.59	-1.11	9.15	0.2	0.2	8.04	0.1	0.00402018	0.00009316	0.07324129	0.84798954	A_07_P000756	b2188	cmr/putative sulfatase (b2188)
yreO	-2.85	8.57	-1.51	9.32	0.2	0.2	7.81	0.1	0.00085937	0.00618879	0.03479751	0.51204864	A_07_P000743	b2190	cmr/putative ATP-binding component of a transport system [b2190]
yrfA	-2.43	7.77	-1.28	8.41	0.2	0.2	7.13	0.2	0.02277378	0.01495299	0.05452566	0.80799142	A_07_P000838	b2230	cmr/conf, hypothetical protein (b2230)
yrfC	+5.62	9.31	+2.73	7.95	0.2	0.2	10.67	0.0	0.00003459	0.00064547	0.00845592	0.25700772	A_07_P000866	b2236	cmr/conf, hypothetical protein (b2236)
yrfW	-2.90	7.80	-1.53	7.03	0.0	0.0	8.57	0.1	0.00003459	0.00107254	0.01520262	0.47601202	A_07_P001021	b2247	cmr/putative racemase (b2247)
yrfZ	-2.35	7.62	-1.23	8.24	0.0	0.0	7.01	0.0	0.00072007	0.00535764	0.05971989	0.63903362	A_07_P001040	b2250	cmr/conf, hypothetical protein (b2250)
yrfB	+3.41	8.72	+1.77	7.83	0.0	0.0	9.60	0.3	0.00004165	0.00472975	0.01491197	0.41834604	A_07_P001104	b2263	cmr/putative enzyme (b2263)
yrfM	+2.42	8.03	+1.27	7.39	0.1	0.1	8.67	0.0	0.00083966	0.00602809	0.04843750	0.54705882	A_07_P001148	b2272	cmr/conf, hypothetical protein (b2272)
yrfN2	-2.14	8.69	-1.10	9.24	0.1	0.1	8.15	0.1	0.00015052	0.00957369	0.07573806	0.67482738	A_07_P001178	b2298	cmr/putative aminotransferase (b2298)
yrfbv	-2.00	9.94	-1.00	10.44	0.0	0.0	9.44	0.0	0.00168193	0.01060842	0.08738395	0.72528234	A_07_P001765	b2295	cmr/conf, hypothetical protein (b2295)
yrfcz	-2.12	12.36	-1.09	12.90	0.1	0.1	11.82	0.1	0.00107180	0.01150478	0.07608883	0.67384572	A_07_P001802	b2343	cmr/conf, hypothetical protein (b2343)
yrfdY	+2.05	9.70	+1.04	9.18	0.1	0.1	10.22	0.0	0.00175234	0.01056236	0.06543826	0.63911911	A_07_P001468	b2377	cmr/conf, hypothetical protein (b2377)
yrfeD	-3.86	8.80	-1.95	7.82	0.0	0.0	9.77	0.4	0.00060123	0.00511060	0.03178030	0.38837267	A_07_P001479	b2379	cmr/putative aminotransferase (b2379)
yrfeO	-3.36	9.37	-1.75	10.25	0.1	0.1	8.50	0.2	0.00037450	0.00202650	0.02078586	0.48469744	A_07_P042786	23601	cmr/conf, hypothetical protein (23601)
yrfeD	-5.22	9.25	-2.38	10.44	0.0	0.0	8.06	0.4	0.00047585	0.00388777	0.00558803	0.24472527	A_07_P000017	c_2935	cmr/Hypothetical protein yfeD [c_2935]
yrfeN	-2.98	10.85	-1.58	11.63	0.2	0.2	10.06	0.0	0.00018194	0.00482505	0.01003791	0.49884404	A_07_P000128	c_3006	cmr/putative sugar hydrolase [c3408]
yrfeM	-2.31	11.20	-1.21	11.81	0.0	0.0	10.60	0.1	0.00085981	0.00619919	0.03182419	0.43741287	A_07_P013411	b2471	cmr/conf, hypothetical protein (b2471)
yrfgC	-2.69	8.66	-1.43	7.95	0.0	0.0	9.37	0.2	0.00078572	0.00579337	0.03977277	0.49968051	A_07_P013324	b2494	cmr/conf, hypothetical protein (b2494)
yrfgC	-3.45	9.82	-1.79	8.92	0.2	0.2	10.71	0.2	0.00047399	0.00387863	0.02618394	0.45682508	A_07_P042608	c_3011	cmr/Hypothetical protein yfgC precursor [c_3011]
yrfgD	-4.09	8.44	-2.03	7.42	0.1	0.1	9.45	0.2	0.00018653	0.00194671	0.01953252	0.37503459	A_07_P013327	b2495	cmr/putative oxidoreductase [b2495]
yrfgB	+3.15	10.46	+1.66	9.63	0.1	0.1	11.29	0.0	0.00026388	0.00255503	0.03019817	0.44309413	A_07_P013579	b2504	cmr/conf, hypothetical protein (b2504)
yrfgI	-3.60	10.90	-1.85	11.82	0.2	0.2	9.97	0.4	0.00140012	0.00602801	0.07771833	0.40754745	A_07_P013587	b2506	cmr/putative membrane protein [b2506]
yrfhA	+2.02	9.09	+1.03	8.58	0.2	0.2	9.59	0.0	0.04807081	0.02324412	0.06948804	0.65868867	A_07_P019671	b2554	cmr/putative 2-component transcriptional regulator [b2554]
yrfhB	-7.30	9.87	-2.87	11.30	0.1	0.1	8.43	0.1	0.00001102	0.00034847	0.00200883	0.15516746	A_07_P019703	b2560	cmr/conf, hypothetical protein (b2560)
yrfbM	-2.07	8.39	-1.05	7.86	0.2	0.2	8.92	0.2	0.00427821	0.02098320	0.06588641	0.64168623	A_07_P003091	c_3043	cmr/Hypothetical lipoprotein yfbM precursor [c_3043]
yrfR	-5.43	9.31	-1.78	8.42	0.1	0.1	10.20	0.1	0.00021077	0.00218894	0.02693076	0.61621120	A_07_P019801	b2615	cmr/putative outer membrane protein [b2615]
yrfD	+4.84	11.34	+2.28	10.20	0.1	0.1	12.48	0.2	0.00007173	0.00102756	0.01467543	0.32614181	A_07_P019799	b2579	cmr/putative formate acetyltransferase [b2579]
yrfF	-5.39	10.78	-2.43	9.56	0.1	0.1	12.17	0.1	0.00002743	0.00056718	0.01246253	0.29549669	A_07_P019806	b2581	cmr/conf, hypothetical protein (b2581)
yrfH	-3.77	8.97	-1.92	9.92	0.1	0.1	8.01	0.0	0.00007984	0.00110942	0.01469195	0.38296358	A_07_P019847	b2593	cmr/conf, hypothetical protein (b2593)
yrfG	-10.64	9.88	-3.45	8.17	0.0	0.0	11.58	0.0	0.00000612	0.00026402	0.00313055	0.16482277	A_07_P019821	b2584	cmr/conf, hypothetical protein (b2584)
yrfJ	-3.26	11.45	-1.70	12.30	0.1	0.1	10.60	0.1	0.00018674	0.00199636	0.02320884	0.45168873	A_07_P019968	b2618	cmr/conf, hypothetical protein (b2618)
yrfyC	-3.01	9.96	-2.00	10.96	0.0	0.0	8.96	0.1	0.00186026	0.00812849	0.02139323	0.34560579	A_07_P019973	b2619	cmr/conf, hypothetical protein (b2619)
yrfyW	-2.24	8.95	-1.16	9.53	0.0	0.2	9.37	0.2	0.00285575	0.01528603	0.06735937	0.65695947	A_07_P020076	b2642	cmr/conf, hypothetical protein (b2642)
yrgeA	-4.87	8.90	-2.28	10.04	0.1	0.1	7.76	0.2	0.00058875	0.00887714	0.06690622	0.26905941	A_07_P010801	c_3263	cmr/Hypothetical sigma-54-dependent transcriptional regulator ygeA [c_3263]
ygeD	-2.77	9.41	-1.47	8.88	0.0	0.0	10.34	0.2	0.00078658	0.00572066	0.03747015	0.48714286	A_07_P020106	b2700	cmr/conf, hypothetical protein (b2700)
ygeF	-12.50	10.35	-4.12	9.69	0.1	0.1	11.01	0.3	0.00019664	0.00208096	0.01654789	0.39594225	A_07_P043074	23958	cmr/conf, hypothetical protein (23958)
ygeG	-2.48	10.24	+1.31	9.58	0.0	0.0	11.90	0.2	0.00160799	0.01002272	0.04653646	0.53793686	A_07_P020017	c_3268	cmr/Putative metallopeptidase ygeG [c_3268]
ygeV	+6.22	9.20	+2.64	7.88	0.2	0.2	10.52	0.1	0.00004863	0.00078769	0.00939669	0.26748835	A_07_P020189	b2667	cmr/conf, hypothetical protein (b2667)
ygeV	-2.68	8.18	-1.42	7.47	0.1	0.1	8.89	0.2	0.00085765	0.00619919	0.03994792	0.49995231	A_07_P041648	c_3216	cmr/Hypothetical transcriptional regulator ygeV [c_3216]
ygeW	-13.50	11.50	-3.76	12.97	0.1	0.1	9.22	0.2	0.00000834	0.00032373	0.00026232	0.05162500	A_07_P001825	b2670	cmr/conf, hypothetical protein (b2670)
ygeZ	-2.43	9.86	-1.28	10.50	0.2	0.2	9.22	0.1	0.00140512	0.00809048	0.05180437	0.82806443	A_07_P001883	b2682	cmr/conf, hypothetical protein (b2682)
ygbE	-2.08	8.87	-1.06	9.40	0.0	0.0	8.34	0.1	0.00244771	0.01351589	0.08117315	0.69493747	A_07_P020701	c_3316	cmr/conf, hypothetical protein (gb [c_3316]
ygbF	-2.09	8.88	-1.06	9.51	0.1	0.1	8.44	0.2	0.00446461	0.02195182	0.07831173	0.68365051	A_07_P002216	b2754	cmr/conf, hypothetical protein (b2754)
ygbI	+8.24	9.39	+3.04	7.87	0.1	0.1	10.91	0.0	0.00000670	0.00027042	0.00541559	0.21569620	A_07_P020675	c_3297	cmr/Hypothetical oxidoreductase ygbI [c_3297]
ygbK	+2.96	8.10	+1.57	7.32	0.1	0.1	8.88	0.1	0.00038466	0.00332667	0.03192276	0.46833480	A_07_P002127	b2756	cmr/putative dehydrogenase [b2756]
ygbM	+5.00	8.70	+2.32	7.54	0.2	0.2	9.86	0.1	0.00006080	0.00091422	0.01407393	0.32020231	A_07_P002131	b2737	cmr/conf, hypothetical protein (b2737)
ygbS	-2.84	9.64	-1.50	10.39	0.1	0.1	8.89	0.1	0.00035676	0.00238867	0.01526807	0.35126882	A_07_P002164	c_3342	cmr/Hypothetical protein ygbS [c_3342]
ygbT	-2.97	8.11	-1.57	8.89	0.1	0.1	7.32	0.1	0.00034761	0.00310252	0.03080412	0.49186013	A_07_P002234	b2757	cmr/conf, hypothetical protein (b2757)
ygbT	-2.17	10.26	-1.12	10.82	0.0	0.0	8.70	0.2	0.00208480	0.01200551	0.07413745	0.67506377	A_07_P002288	b2768	cmr/putative anti-terminator regulatory protein [b2768]
ygbT	-2.14	10.71	-1.10	11.26	0.2	0.2	10.17	0.2	0.00562680	0.02682374	0.07554560	0.67425737	A_07_P006031	b2807	cmr/conf, hypothetical protein (b2807)
ygeB	-3.01	8.79	-1.59	9.58	0.1	0.1	7.99	0.2	0.00061409	0.00472975	0.02874511	0.48365722	A_07_P006045	b2806	cmr/conf, hypothetical protein (b2806)
ygbR	+6.31	10.18	+2.66	8.85	0.1	0.1	11.51	0.0	0.00003727	0.00004168	0.00945567	0.26775180	A_07_P002424	b2795	cmr/conf, hypothetical protein (b2795)
ygbL	-4.74	10.38	-2.24	11.50	0.1	0.1	9.26	0.1	0.00003757	0.00066784	0.00762957	0.28609000	A_07_P002456	c_3383	cmr/Hypothetical protein ygbL [c_3383]
ygbQ	-3.40	7.99	-1.77	8.87	0.1	0.1	7.11	0.1	0.00012686	0.00153291	0.02052591	0.43377181	A_07_P006041	b2832	cmr/putative transport protein [b2832]
ygbX	-3.57	10.98	-1.84	11.90	0.2	0.2	10.07	0.4	0.00180250	0.01076579	0.01828260	0.39721139	A_07_P006257	b2855	cmr/putative 2-component transcriptional regulator [b2855]
ygbR	-13.72	9.88	-3.78	11.77	0.0	0.0	7.99	0.1	0.00000275	0.00018406	0.00023104	0.06429478	A_07_P006395	b2865	cmr/putative lipoprotein [b2865]
ygbT	+12.09	9.06	+3.60	7.26	0.1	0.1	10.85	0.0	0.00000330	0.00019671	0.00249428	0.14384615	A_07_P022831	c_3445	cmr/Xanthine dehydrogenase, FAD-binding subunit [c_3445]
ygbV	-2.66	8.27	-1.41	7.57	0.3	0.3	8.98	0.1	0.00189155	0.01161147	0.04064669	0.50229414	A_07_P006312	b2869	cmr/conf, hypothetical protein (b2869)
ygbX	-3.61	8.30	-1.81	8.37	0.1	0.1	8.37	0.1	0.00012294	0.00148808	0.01639629	0.39470948	A_07_P006525	b2912	cmr/putative ligase [b2912]
ygfM	+2.11	7.63	+1.07	7.09	0.1	0.1	8.16	0.0	0.00149146	0.00930330	0.02131020	0.42530218	A_07_P041709	c_3458	cmr/Hypothetical protein ygfM [c_3458]
ygfX	-4.06	11.03	-2.02	12.04	0.0	0.0	10.01	0.1	0.00006970	0.00100135	0.01189977	0.34566421	A_07_P006446	b2896	cmr/conf, hypothetical protein (b2896)
ygjD	-2.95	8.37	-1.56	9.15	0.0	0.0	7.59	0.1	0.00029740	0.00277514	0.03116501	0.49199599	A_07_P006296	b2920	cmr/Hypothetical transcriptional regulator [b2920]
ygjD	-3.62	9.60	-1.86	10.53	0.0	0.0	8.67	0.2	0.00019654	0.00208096	0.01654789	0.39594225	A_07_P032921	c_3512	cmr/Hypothetical protein ygjD [c_3512]
ygjE	-2.07	10.54	+0.05	10.01	0.1	0.1	10.59	0.1	0.00258242	0.01405162	0.06329052	0.62852268	A_07_P032931	c_3521	cmr/putative metallopeptidase ygjE [c_3521]
ygjG	+3.47	12.93	+1.79	12.03

yigM	-2.80	8.05	-1.49	8.79	0.1	7.30	0.0	0.00031181	0.00030100	0.03650152	0.52148820	A_07_P018941	b3827	cmr|orf, hypothetical protein b3827|
yigP	-3.41	12.93	-2.77	11.81	0.0	12.04	0.0	0.00003767	0.00013670	0.01935163	0.42799728	A_07_P018976	b3834	cmr|orf, hypothetical protein b3834|
yigZ	-2.46	10.44	-1.30	11.08	0.1	9.79	0.4	0.00057569	0.00024757	0.05218750	0.60193407	A_07_P041354	c_4795	cmr|Hypothetical protein yigZ|c_4795|
yihD	-57.91	10.37	-5.86	7.44	0.3	13.30	0.0	0.00000130	0.00014643	0.00009273	0.02807692	A_07_P019075	b3858	cmr|orf, hypothetical protein b3858|
yihI	-6.61	8.22	-1.85	7.30	0.1	9.15	0.1	0.00011937	0.00140287	0.02163922	0.40231838	A_07_P019308	b3866	cmr|orf, hypothetical protein b3866|
yihT	+2.25	7.47	+1.17	6.89	0.0	8.06	0.1	0.00126308	0.00826163	0.05349867	0.58483009	A_07_P019333	c_4827	cmr|Hypothetical protein yihT|c_4827|
yihX	-6.74	10.44	-2.75	9.06	0.1	11.82	0.0	0.00003153	0.00055443	0.00812309	0.20227597	A_07_P019305	b3865	cmr|putative phosphatase| b3865|
yiiY	+2.23	7.81	+1.16	7.23	0.1	8.39	0.1	0.00197782	0.01152289	0.05372726	0.58686057	A_07_P019210	b3886	cmr|tRNA processing exoribonuclease 6| b3886|
yiiD	+1.67	8.81	+0.80	7.91	0.2	9.71	0.3	0.00096774	0.00673864	0.02572927	0.41419223	A_07_P019315	b3888	cmr|putative acetyltransferase| b3888|
yiiD	+5.84	9.73	+2.55	8.46	0.3	11.01	0.2	0.00016870	0.00170389	0.01047764	0.27724570	A_07_P041954	c_4835	cmr|Hypothetical protein yiiD|c_4835|
yiiQ	+4.72	8.60	+2.24	7.48	0.1	9.72	0.0	0.00003410	0.00073284	0.01545697	0.31388209	A_07_P019377	b3920	cmr|orf, hypothetical protein b3920|
yiiS	+7.16	9.07	+2.84	7.65	0.1	10.49	0.0	0.00001394	0.00038090	0.00733450	0.24182590	A_07_P019426	c_4874	cmr|Hypothetical protein yiiS|c_4874|
yiiS	+6.97	8.51	+2.80	7.11	0.0	9.91	0.2	0.00002183	0.00050245	0.00760861	0.23698969	A_07_P019386	b3922	cmr|orf, hypothetical protein b3922|
yiiS	+3.84	8.65	+1.94	7.68	0.3	9.62	0.3	0.00113729	0.00761611	0.02170678	0.38787741	A_07_P047306	25467	cmr|Putative transcriptional protein| 25467|
yiiT	+6.12	10.22	+2.61	8.92	0.1	11.53	0.1	0.00002024	0.00047541	0.00902188	0.27166857	A_07_P047311	25468	cmr|putative regulator| 25468|
yiiT	+5.50	10.30	+2.46	8.97	0.0	11.42	0.2	0.00003758	0.00066784	0.01391883	0.29093023	A_07_P019431	c_4875	cmr|Hypothetical protein yiiT|c_4875|
yiiU	+2.41	12.47	+1.27	11.84	0.1	13.11	0.0	0.00087051	0.00626147	0.04843814	0.56462584	A_07_P019420	b3928	cmr|orf, hypothetical protein b3928|
yiiX	-2.42	9.73	-1.27	10.37	0.1	9.09	0.1	0.00092517	0.00650555	0.05448869	0.60885025	A_07_P052282	25492	cmr|orf, hypothetical protein 25492|
yiiX	-2.83	9.04	-1.50	9.79	0.0	8.29	0.0	0.00026444	0.00255555	0.03531563	0.51513850	A_07_P041984	c_4890	cmr|Hypothetical protein yiiX|c_4890|
yiiX	-2.52	7.77	-1.33	8.44	0.0	7.11	0.3	0.00215837	0.01228844	0.04795129	0.57963162	A_07_P019465	b3937	cmr|orf, hypothetical protein b3937|
yiiD	-3.06	10.03	-1.04	10.55	0.0	9.51	0.1	0.00177996	0.01065380	0.08304433	0.70338823	A_07_P052298	25525	cmr|orf, hypothetical protein 25525|
yiiD	-2.84	9.98	-1.50	10.73	0.0	9.22	0.1	0.00027919	0.00265270	0.03526169	0.51403704	A_07_P008525	b3964	cmr|orf, hypothetical protein b3964|
yiiF	-4.01	12.81	-2.01	11.80	0.1	13.81	0.1	0.00104344	0.00166295	0.03215951	0.34559957	A_07_P019476	c_4962	cmr|Hypothetical protein yiiF precursor|c_4962|
yiiF	-2.93	13.31	-1.55	14.11	0.4	12.56	0.2	0.01597063	0.03847863	0.03221016	0.49636986	A_07_P019499	b3994	cmr|orf, hypothetical protein b3994|
yiiAA	-8.67	9.50	-3.12	11.06	0.1	7.94	0.2	0.00001695	0.00042762	0.00118235	0.10892857	A_07_P008899	b4011	cmr|orf, hypothetical protein b4011|
yiiAB	-3.25	12.84	-1.17	13.43	0.1	12.26	0.3	0.00182888	0.01930226	0.06784166	0.65817171	A_07_P008704	b4012	cmr|orf, hypothetical protein b4012|
yiiAC	-2.90	11.51	-1.53	12.28	0.1	10.74	0.3	0.00128475	0.00835485	0.03164774	0.50452281	A_07_P008783	b4028	cmr|orf, hypothetical protein b4028|
yiiU	-2.91	9.61	-1.54	10.18	0.0	8.84	0.0	0.00023779	0.00238308	0.03218385	0.50116592	A_07_P008870	b4045	cmr|orf, hypothetical protein b4045|
yiiU	-5.06	10.82	-2.34	11.99	0.1	9.65	0.0	0.00002780	0.00057043	0.00612741	0.25057143	A_07_P037555	c_5016	cmr|Protein yiiU|c_5016|
yiiX2	+8.15	9.58	+3.03	8.06	0.2	11.09	0.3	0.00010056	0.00131084	0.00531564	0.21623310	A_07_P008923	b4056	cmr|orf, hypothetical protein b4056|
yiiX	-13.22	9.80	-3.74	11.66	0.1	7.93	0.4	0.00003444	0.00046547	0.00239832	0.05258824	A_07_P008942	b4060	cmr|orf, hypothetical protein b4060|
yiiX	-9.22	9.77	-3.20	11.37	0.1	8.17	0.0	0.00003791	0.00028715	0.00089092	0.10243213	A_07_P008952	c_5050	cmr|Hypothetical protein yiiX|c_5050|
yiiX	+8.16	10.05	+3.03	8.54	0.1	11.57	0.1	0.00001465	0.00039588	0.00548653	0.21595000	A_07_P037683	c_5063	cmr|Hypothetical protein yiiX|c_5063|
yiiX	+9.03	10.45	+3.17	8.87	0.0	12.04	0.2	0.00001032	0.00037778	0.00446130	0.19652661	A_07_P037683	c_5063	cmr|Hypothetical protein yiiX|c_5063|
yiiX	+6.25	10.06	+2.64	8.74	0.1	11.38	0.3	0.00013415	0.00158449	0.00938834	0.26771174	A_07_P037683	c_5063	cmr|Hypothetical protein yiiX|c_5063|
yiiX	+3.03	10.08	+1.60	9.28	0.1	10.88	0.0	0.00022626	0.00122270	0.02239012	0.45818813	A_07_P047279	25667	cmr|Hypothetical protein 25667|
yiiX	+6.90	10.18	+2.79	8.79	0.1	11.58	0.1	0.00001464	0.00038588	0.00793890	0.24848907	A_07_P037683	c_5063	cmr|Hypothetical protein yiiX|c_5063|
yiiX	+8.19	10.28	+3.03	8.76	0.0	11.79	0.0	0.00000608	0.00034653	0.00546313	0.21603015	A_07_P037683	c_5063	cmr|Hypothetical protein yiiX|c_5063|
yiiX	+7.32	9.40	+2.55	7.85	0.0	10.95	0.0	0.00160046	0.00988285	0.05635820	0.61675676	A_07_P008934	b4078	cmr|orf, hypothetical protein b4078|
yiiO	-3.31	9.53	-1.73	10.39	0.1	8.66	0.5	0.00382251	0.01927563	0.02397407	0.41213750	A_07_P008934	b4078	cmr|orf, hypothetical protein b4078|
yiiO	-2.20	9.75	-1.14	10.32	0.1	9.18	0.3	0.00145015	0.00910331	0.07175622	0.66653737	A_07_P008934	b4078	cmr|orf, hypothetical protein b4078|
yiiO	-2.59	9.56	-1.37	10.21	0.0	8.88	0.1	0.00084646	0.00408242	0.04152210	0.57151110	A_07_P008934	b4078	cmr|orf, hypothetical protein b4078|
yiiW	+3.33	9.90	+1.74	9.03	0.2	10.77	0.3	0.00034132	0.00184859	0.02763664	0.43008832	A_07_P037736	c_5093	cmr|ABC-type transport ATP-binding protein ylxA|c_5093|
yiiW	+3.90	7.99	+1.96	7.01	0.2	8.97	0.0	0.00017791	0.00196447	0.02066144	0.38329849	A_07_P037782	c_5119	cmr|Hypothetical protein yiiW|c_5119|
yiiX	+3.89	9.01	+1.96	8.04	0.0	9.99	0.7	0.00164440	0.02803982	0.02158885	0.38764840	A_07_P041409	b4131	cmr|orf, hypothetical protein b4131|
yiiZ	+3.07	8.54	+1.62	7.73	0.0	9.35	0.2	0.00042875	0.00360786	0.01486899	0.45229374	A_07_P047348	25729	cmr|orf, hypothetical protein 25729|
yiiZ	+1.52	8.69	+0.32	8.03	0.3	9.35	0.2	0.00420023	0.02105562	0.04631677	0.53819434	A_07_P011174	b4127	cmr|orf, hypothetical protein b4127|
yiiN	-3.25	8.55	-1.70	9.40	0.1	7.70	0.1	0.00028131	0.00266319	0.03304560	0.45128109	A_07_P011271	b4107	cmr|orf, hypothetical protein b4107|
yiiI	-2.41	10.90	-1.27	10.27	0.0	11.53	0.1	0.00180261	0.00691414	0.04862170	0.54752795	A_07_P011455	b4144	cmr|orf, hypothetical protein b4144|
yiiE	-2.26	8.84	-1.18	9.43	0.1	8.25	0.1	0.00101788	0.00700111	0.06542048	0.63154061	A_07_P011461	b4146	cmr|orf, hypothetical protein b4146|
yiiP	+2.11	8.61	+1.08	8.07	0.1	9.15	0.1	0.02188653	0.01242767	0.06240663	0.62661152	A_07_P011552	c_5245	cmr|Hypothetical protein yiiP precursor|c_5245|
yiiG	-13.38	9.63	-3.74	11.50	0.0	7.76	0.3	0.00001171	0.00035727	0.00027248	0.05296296	A_07_P011550	b4166	cmr|orf, hypothetical protein b4166|
yiiFN	+10.05	10.52	+3.33	8.85	0.0	12.18	0.2	0.00000687	0.00027532	0.00314992	0.17639361	A_07_P011660	b4188	cmr|orf, hypothetical protein b4188|
yiiFO	+14.67	12.48	+3.87	10.55	0.1	14.42	0.1	0.00000318	0.00019528	0.00148064	0.12364486	A_07_P035589	c_5277	cmr|Hypothetical lipoprotein yiiFO precursor|c_5277|
yiiFO	-14.12	10.76	+3.82	8.85	0.1	12.67	0.1	0.00000259	0.00018134	0.00177846	0.12500000	A_07_P011661	b4189	cmr|orf, hypothetical protein b4189|
yiiFO	+13.79	11.22	+3.79	9.33	0.0	13.12	0.1	0.00000251	0.00018118	0.00193311	0.12817021	A_07_P010658	b4189	cmr|orf, hypothetical protein b4189|
yiiFO	+10.73	10.81	+3.42	9.10	0.0	12.52	0.1	0.00000464	0.00034487	0.00313080	0.16511706	A_07_P048630	25796	cmr|orf, hypothetical protein 25796|
yiiJA	-8.94	12.38	-3.16	13.96	0.0	10.80	0.1	0.00000643	0.00027019	0.01007215	0.10484672	A_07_P037054	c_5332	cmr|Hypothetical protein yiiJA|c_5332|
yiiJA	-8.01	12.20	-3.00	13.71	0.0	10.70	0.0	0.00000679	0.00027353	0.01484815	0.13682704	A_07_P037312	b4234	cmr|putative alpha helix protein| b4234|
yiiKF	+110.93	12.08	+6.79	8.68	0.2	15.48	0.1	0.00000027	0.00009047	0.00006551	0.00962963	A_07_P037066	c_5342	cmr|Protein yiiKF|c_5342|
yiiKF	+37.72	10.37	+5.24	7.75	0.1	12.99	0.0	0.00000037	0.00009117	0.00035553	0.03948718	A_07_P001767	b4243	cmr|orf, hypothetical protein b4243|
yiiKF	-3.80	10.26	-1.92	11.22	0.1	9.29	0.3	0.00326649	0.03026649	0.04148412	0.37939196	A_07_P003851	b4261	cmr|orf, hypothetical protein b4261|
yiiQ3	-4.61	11.04	-2.21	12.15	0.0	9.94	0.0	0.00003565	0.00065418	0.00825394	0.29601367	A_07_P003856	b4262	cmr|orf, hypothetical protein b4262|
yiiR	+2.67	8.58	+1.42	7.88	0.5	9.29	0.7	0.07530978	0.03088024	0.04216693	0.52992008	A_07_P003863	b4263	cmr|orf, hypothetical protein b4263|
yiiR	+8.29	9.26	+3.05	7.74	0.0	10.79	0.3	0.00003867	0.00068020	0.00540604	0.21614213	A_07_P037716	c_5364	cmr|Putative protein yiiR|c_5364|
yiiQ2	-3.21	7.74	-1.68	8.58	0.3	6.90	0.1	0.00142501	0.00906660	0.02378247	0.41727717	A_07_P003927	b4277	cmr|orf, hypothetical protein b4277|
yiiH	+3.35	8.28	+1.74	7.41	0.2	9.15	0.2	0.00000056	0.00065408	0.02731707	0.42141201	A_07_P004016	b4298	cmr|putative lysex/synthase| b4298|
yiiN	-2.16	8.14	-1.11	7.58	0.2	8.70	0.0	0.00138414	0.01749276	0.06035910	0.61468005	A_07_P004061	b4307	cmr|orf, hypothetical protein b4307|
yiiNQ	+2.01	8.41	+1.00	7.91	0.1	8.91	0.0	0.00038579	0.01200683	0.06830793	0.65410058	A_07_P004061	b4307	cmr|orf, hypothetical protein b4307|
yiiR	-3.06	11.74	-1.61	12.55	0.1	10.94	0.2	0.00039615	0.01039887	0.02780170	0.48290996	A_07_P004068	b4308	cmr|putative frameshift| b4308|
yiiU	-2.99	9.58	-1.58	10.37	0.1	8.79	0.3	0.00032994	0.00300092	0.02955363	0.48869430	A_07_P004004	b4295	cmr|orf, hypothetical protein b4295|
yiiO	-2.42	9.09	-1.28	9.73	0.0	8.45	0.1	0.00070062	0.00234161	0.04574530	0.60955446	A_07_P004019	b4326	cmr|orf, hypothetical protein b4326|
yiiG	+7.58	8.91	+2.92	7.45	0.2	10.37	0.2	0.00001382	0.00039622	0.00636242	0.22869863	A_07_P004174	b4329	cmr|orf, hypothetical protein b4329|
yiiH	-4.60	7.92	+1.85	6.99	0.1	8.84	0.1	0.00017705	0.00193940	0.02184118	0.40184455	A_07_P004179	b4330	cmr|orf, hypothetical protein b4330|
yiiH	+2.07	7.34	+1.05	6.82	0.0	7.87	0.0	0.00195544	0.00981961	0.04462781	0.63672821	A_07_P037230	c_5410	cmr|Putative protein yiiH|c_5410|
yiiL	+19.38	10.47	+4.79	8.60	0.2	12.34	0.2	0.00000184	0.00023763	0.00328270	0.13418825	A_07_P004194	b4334	cmr|putative enzyme| b4334|
yiiM	+17.34	9.70	+4.13	7.64	0.1	11.76	0.3	0.00000967	0.00032448	0.00108121	0.09706215	A_07_P004201	b4335	cmr|orf, hypothetical protein b4335|
yiiP	-2.87	9.72	-1.52	10.48	0.1	8.96	0.5	0.00062849	0.02832506	0.04198355	0.56188261	A_07_P004217	b4338	cmr|orf, hypothetical protein b4338|
yiiS	+2.72	9.38	+1.44	8.66	0.1	10.10	0.0	0.00042084	0.00155445	0.03882485	0.49157277	A_07_P017462	b4353	cmr|orf, hypothetical protein b4353|
yiiT	+4.58	10.60	+2.19	9.51	0.0	11.70	0.4	0.00073661	0.00537873	0.01144774	0.33942590	A_07_P017585	b4380	cmr|orf, hypothetical protein b4380|
yiiX	+13.33	9.90	+4.75	9.03	0.0	10.77	0.1	0.00015728	0.00177863	0.02751905	0.42519821	A_07_P017627	b4391	cmr|putative ATP-binding component of a transport system| b4391|
yiiX	+13.40	9.91	+4.76	9.03	0.0	10.79	0.1	0.00013097	0.00156505	0.02612868	0.41636460	A_07_P017627	b4391	cmr|putative ATP-binding component of a transport system| b4391|
yiiX	+2.81	9.67	+1.49	8.92	0.0	10.41	0.0	0.00035715	0.00252641	0.03738604	0.48592715	A_07_P017627	b4391	cmr|putative ATP-binding component of a transport system| b4391|
yiiX	+2.44	9.76	+1.28	9.11	0.0	10.40	0.3	0.00238542	0.01327539	0.04703512	0.56010197	A_07_P017627	b4391	cmr|putative ATP-binding component of a transport system| b4391|
yiiN	+2.33	7.83	+1.22	7.22	0.3	8.44	0.1	0.00597726	0.02742014	0.05313661	0.57300000	A_07_P017684	b4437	cmr|orf, hypothetical protein b4437|
yiiN	-2.10	7.67	-1.07	8.21	0.0	7.14	0.2	0.00246713	0.01361462	0.08094385	0.69410675	A_07_P017688	b4358	cmr|putative oxidoreductase| b4358|
yiiN	-2.34	7.49	-1.22	8.10	0.1	6.87	0.1	0.00149103	0.00930164	0.05197500	0.62790360	A_07_P017688	b4358	cmr|putative oxidoreductase| b4358|
yiiQ	-2.52	7.22	-1.33	7.89	0.2	6.56	0.1	0.00085792	0.00611593	0.04927718	0.58512453	A_07_P042086	c_5444	cmr|Hypothetical protein yiiQ|c_5444|
yiiQ2	-2.88	7.53	-1.52	8.29	0.0	6.76	0.1	0.00018921	0.00285608	0.03816006	0.50683665	A_07_P017521	b4365	cmr|putative regulator| b4365|
yiiR	-3.67	10.52	-1.88	11.46	0.2	9.58	0.6	0.00546180	0.02545548	0.01692264	0.39647321	A_07_P017655	b4394	cmr|orf, hypothetical protein b4394|
yiiS	-14.63	11.16	-3.87	13.10	0.0	9.21	0.1	0.00000320	0.00037976	0.00016816	0.04223339	A_07_P007889	b0191	cmr|orf, hypothetical protein b0191|
yiiSP	+2.22	8.53	+1.15	7.96	0.0	9.11	0.1	0.00135330	0.00867719	0.05455142	0.59106693	A_07_P008226	b0307	cmr|orf, hypothetical protein b0307|
yiiqP	-4.99	8.26	-2.32	9.42	0.3	7.10	0.1	0.00002155	0.00222616	0.06648854	0.38327411	A_07_P008311	b0288	cmr|putative ferredoxin| b0288|
yiiqG	-2.62	7.88	-1.39	8.57	0.1	7.18	0.3	0.00404337	0.03063502	0.04454141	0.56966694	A_07_P043383	20363	cmr|orf, hypothetical protein 20363|
yiiqA	-2.28	7.58	-1.19	8.17	0.2	6.98	0.3	0.05095450	0.02409345	0.06461842	0.64918653	A_07_P008324	b0292	cmr|orf, hypothetical protein b0292|
yiiaB	-2.32	11.16	-1.21	11.76	0.1	10.55	0.3	0.00395919	0.01826240	0.06221418	0.60019008	A_07_P021391	b0457	cmr|orf, hypothetical protein b0457|
yiiaC	-17.67	11.77	-4.14	13.84	0.0	9.70	0.1	0.00001447	0.00015430	0.00008257	0.02765067	A_07_P021396	b0458	cmr|orf, hypothetical protein b0458|
yiiaC	-2.79	11.89	-1.48	12.63	0.3	11.15	0.5	0.01030143	0.04481409	0.03635226	0.52073343	A_07_P016365	b0515	cmr|orf, hypothetical protein b0515|
yiiA	+2.28	7.81	+1.19	7.21	0.1	8.40	0.3	0.00380146	0.01987507	0.05193832	0.58408801	A_07_P011240	c_3629	cmr|Hypothetical protein yiiA|c_3629|
yiiJ	+2.34	10.18	+1.22	9.57	0.2	10.79	0.1	0.00179234	0.01071324	0.02449919	0.50496956	A_07_P004644	b0818	cmr|putative transferase| b0818|
yiimS	+5.21	9.52	+2.41	8.31	0.0	10.72	0.1	0.00002644	0.00055821	0.01251588	0.30020772	A_07_P011189	b0991	cmr|suppresses fabA and its growth mutation| b0991|
yiimP	-3.45	12.20	-1.79	13.09	0.0	11.30	0.1	0.00000192	0.00019718	0.01982724	0.42586630	A_07_P010550	AB-028539	cmr|conserved protein| b0518|
yiimA	-2.33	9.09	-1.22	9.70	0.0	8.48	0.2	0.00141622	0.00903332	0.06005228	0.63148820	A_07_P040833	c_1397	cmr|Hypothetical protein yiimA|c_1397|
yiimC	-13.49	12.64	-3.75	14.52	0.0	10.76	0.2	0.00001087	0.00023028	0.00138268	0.05099360	A_07_P050485	21864	cmr|orf, hypothetical protein 21864|
yiimE	+2.33	7.73	+1.22	7.12	0.0	8.34	0.3	0.00012863	0.02574669	0.05407043	0.58291498	A_07_P006641	b1138	cmr|orf, hypothetical protein b1138|
yiimM	-2.42	9.34	-1.28	9.98	0.4	8.71	0.3	0.00461663	0.02205727	0.05466019	0.60946884	A_07_P006644	b1148	cmr|orf, hypothetical protein b1148|
yiimgA	-9.62	8.31	-3.27	9.68	0.1	9.94	0.1	0.00000952	0.00033026	0.00160770	0.18489614	A_07_P006777	b1165	cmr|orf, hypothetical protein b1165|
yiimgB	-13.87	10.55	-4.79	8.65	0.2	12.44	0.1	0.00000533	0.00024927	0.00187246	0.12617391	A_07_P018831	c_1609	cmr|Hypothetical protein yiimgB|c_1609|
yiimgC	-2.99	8.66	-1.58	9.45	0.3	7.87	0.4	0.00435791	0.02130114	0.02872015	0.48412206	A_07_P006807	b1171	cmr|orf, hypothetical protein b1171|
yiimgC	-2.31	13.07	-1.21	13.67	0.0	12.46	0.2	0.00176142	0.01050197	0.06117550	0.61620329	A_07_P006812	b1172	cmr|orf, hypothetical protein b1172|
yiimyA	+3.65	8.29	+1.87	7.36	0.3	9.22	0.1	0.00012607	0.00022398	0.02936310	0.42187853	A_07_P014457	b1295	cmr|orf, hypothetical protein b1295|
yiimz	-4.06	10.96	-2.02	11.97	0.1	9.95	0.1	0.00012115	0.00140461	0.01178385	0.34942283	A_07_P014612	b1330	cmr|orf, hypothetical protein b1330|
yiimz	-2.45	9.31	-1.29	9.95	0.1	8.68	0.3	0.00080634	0.00582985	0.05248807	0.60334676	A_07_P014640	b1332	cmr|orf, hypothetical protein b1332|
yiimK	-3.04	9.27	-1.60	10.08	0.3	8.47	0.5	0.07060223	0.03442367	0.05139372	0.48494715	A_07_P014801	b1360	cmr|orf, hypothetical protein b1360|
yiibC	-3.19	8.10	-1.67	8.93	0.4	7.26	0.2	0.02275949	0.01490408	0.02472180	0.46061538	A_07_P009344	b1410	cmr|orf, hypothetical protein b1410|
yiibE	-2.47	8.42	-1.35	7.76	0.2	9.07	0.3	0.00308822	0.01205139	0.04688262	0.53956213	A_07_P009348	b1382	cmr|orf, hypothetical protein b1382|
yiibH	-3.63	8.83	-1.86	7.10	0.0	10.56	0.3	0.00039233	0.00337350	0.02389926	0.40242761	A_07_P034809	c_1829	cmr|Hypothetical protein yiibH|c_1829|
yiiC	-2.34	8.50	-1.74	9.37	0.7	7.63	0.0	0.09661277	0.04011225	0.02136751	0.44148294	A_07_P048215	22327	cmr|Putative protein| 22327|
yiiC2	-4.22	7.86	+1.28	7.22	0.2	8.49	0.0	0.00105148	0.00716564	0.04688897	0.54725546	A_07_P009361	b1450	cmr|orf, hypothetical protein b1450|
yiieH	-5.73	9.74	-2.52	11.00	0.1	8.49	0.0	0.00002969	0.00059792	0.00425877	0.20384006	A_07_P022070	b1524	cmr|putative glutaminase| b1524|
yiieI	-5.98	8.80	-2.58	10.09	0.0	7.51	0.0	0.00003842	0.00064639	0.00273503	0.20092466	A_07_P022076	c_1948	cmr|Alkylhalo-dehydrogenase-like protein yiieI|c_1948|
yiieJ	-2.44	11.30	-1.29	11.94	0.0	10.65	0.5	0.00398886	0.03944965	0.05279726	0.60346013	A_07_P022079	b1526	cmr|putative transcriptional regulator VSR-type| b1526|
yiieN	-3.70	14.20	-1.89	15.14	0.0	13.25	0.1	0.00003555	0.00135201	0.01541286	0.39138710	A_07_P022080	b1583	cmr|orf, hypothetical protein b1583|
yiiYO	+2.61	9.92	+1.39	9.22	0.1	10.61	0.2	0.00097747	0.00679238	0.04199441	0.51054826	A_07_P022053	b1586	cmr|orf, hypothetical protein b1586|
yiiY	+10.61	8.58	+3.41	6.88	0.3	10.28	0.3	0.00005408	0.00084291	0.00271039	0.16775244	A_07_P022044	b1587	cmr|putative transcriptional regulator| b1587|
yiiZ	-23.39	9.52	+6.53	7.25	0.1	10.80	0.1	0.00000072	0.00011611	0.00005436	0.07066116	A_07_P042301	c_1977	cmr|Putative dimethyl sulfoxide reductase chain yiiZ|c_1977|
yiiY1	+10.30	10.39	+4.70	8.54	0.3	10.24	0.1	0.00003415	0.00039421	0.02146612	0.13637097	A_07_P022075	b1588	cmr|putative oxidoreductase, major subunit| b1588|
yiiYG	+33.16	9.85	+5.05	7.32	0.3	12.37	0.0	0.00000201	0.00017324	0.00025915	0.06689655	A_07_P022076	b1589	cmr|putative oxidoreductase, Fe-S subunit| b1589|
yiiYH	+4.67	9.30	+2.22	8.19	0.2	10.41	0.2	0.00015253	0.00137122	0.01918397	0.31482466	A_07_P022082	b1590	cmr|putative DMSO reductase anchor subunit| b1590|
yiiYL	-2.95	10.89	-1.56	11.67	0.2	10.10	0.2	0.00106584	0.00726611	0.01123603	0.49128871	A_07_P022069	b1595	cmr|putative transcriptional regulator VSR-type| b1595|
yiiYM	-6.02	11.30	-2.59	12.49	0.4	9.90	0.6	0.00202157	0.01127718	0.03370563	0.20154671	A_07_P022061	b1596	cmr|putative transport protein| b1596|
yiiYA	+7.56	8.92	+2.99	7.42	0.0	10.41	0.1	0.00000713	0.00028183	0.00586636	0.22201923	A_07_P018674	b1725	cmr|orf, hypothetical protein b1725|
yiiYC	-2.50	10.36	-1.32	10.92	0.1	9.80	0.2	0.00087216	0.00426908	0.04988979	0.59841154	A_07_P018685	b1727	cmr|putative phosphatase| b1727|
yiiYA	+3.64	8.83	+1.86	7.90	0.1	9.76	0.1	0.00013197	0.00157032	0.02150864	0.40012973	A_07_P018811	b1753	cmr|orf, hypothetical protein b1753|
yiiYB	-7.57	8.56	-2.92	7.10	0.0	10.03	0.1	0.00003093	0.00033349	0.00636623	0.22831435	A_

21898	+5.20	10.31	+2.38	9.12	0.4	11.50	0.0	0.00046787	0.00384652	0.01294207	0.30186667	A_07_P05610	21898	cmr/putative tail component of prophage CP-933X [21898]
21915	+3.23	8.62	+1.69	7.77	0.0	9.67	0.1	0.00002634	0.00331393	0.02876411	0.43804453	A_07_P05856	21915	cmr/putative tail protein [21915]
21957	-7.97	9.94	-2.99	11.44	0.1	8.44	0.1	0.00001162	0.00005586	0.00151423	0.12613757	A_07_P05726	21957	cmr/transposase for 6629 [21957]
22005	-3.46	12.34	-1.79	13.24	0.2	11.45	0.0	0.00022142	0.00224711	0.01933269	0.41910668	A_07_P052791	22005	cmr/conf Unknown function [22005]
22047	-2.31	7.79	-1.21	8.40	0.4	7.19	0.1	0.01088098	0.04430319	0.06243394	0.64561880	A_07_P050858	22047	cmr/unknown protein encoded by prophage CP-933D [22047]
22049	+2.09	8.22	+1.06	7.68	0.0	8.75	0.0	0.00143325	0.00903332	0.06264551	0.42619683	A_07_P047614	22049	cmr/unknown protein encoded by prophage CP-933D [22049]
22074	-3.06	11.17	-1.61	11.98	0.1	10.36	0.0	0.00023775	0.00224211	0.02812520	0.48139435	A_07_P047987	22074	cmr/putative O-encoded protein within CP-933D [22074]
22076	-2.07	11.19	-1.05	11.71	0.1	10.67	0.3	0.00896989	0.03796606	0.08048336	0.69279934	A_07_P047930	22076	cmr/putative O-encoded protein within CP-933D [22076]
22080	-6.35	11.39	-3.23	13.00	0.1	9.77	0.1	0.00006602	0.00026402	0.00093369	0.30000500	A_07_P047717	22080	cmr/putative O-encoded protein within CP-933D [22080]
22096	-4.88	9.32	-2.29	10.47	0.8	8.18	0.4	0.00896545	0.03795432	0.00737297	0.28038647	A_07_P047778	22096	cmr/unknown protein encoded within prophage CP-933D [22096]
22099	-2.32	8.63	-1.21	9.24	0.0	8.03	0.4	0.00802699	0.03479868	0.06138632	0.60477632	A_07_P047969	22099	cmr/unknown protein encoded within prophage CP-933D [22099]
22115	-2.44	11.51	-1.28	12.15	0.3	10.87	0.0	0.00340604	0.01755883	0.05406568	0.60713980	A_07_P047851	22115	cmr/unknown protein encoded within prophage CP-933D [22115]
22119	-2.79	8.95	-1.48	9.69	0.0	8.21	0.1	0.00031673	0.00302754	0.03845749	0.52120671	A_07_P047868	22119	cmr/unknown protein encoded within prophage CP-933D [22119]
22133	+2.73	7.74	+1.45	7.01	0.1	8.46	0.1	0.00054284	0.00430634	0.03873857	0.49508870	A_07_P047956	22133	cmr/putative capsid assembly protein of prophage CP-933D [22133]
22136	+7.12	8.71	+2.87	7.28	0.4	10.15	0.0	0.00034178	0.00208384	0.00673596	0.23431718	A_07_P047913	22136	cmr/putative major capsid protein of prophage [22136]
22142	-4.24	11.49	-2.09	12.54	0.2	10.45	0.5	0.00230006	0.01293914	0.03084731	0.33290648	A_07_P047939	22142	cmr/putative tail component of prophage CP-933D [22142]
22144	-3.46	10.59	-1.77	11.48	0.3	9.71	0.2	0.00110061	0.00744323	0.02074568	0.43432611	A_07_P047949	22144	cmr/putative tail component of prophage CP-933D [22144]
22181	-2.10	7.92	-1.07	8.45	0.2	7.38	0.1	0.00335803	0.01821120	0.07676778	0.68439294	A_07_P048026	22181	cmr/conf Unknown function [22181]
22199	-1.29	8.72	-1.19	9.31	0.1	8.12	0.0	0.00120913	0.00861948	0.06463301	0.64955577	A_07_P048039	22199	cmr/conf, hypothetical protein [22199]
22201	-2.58	7.68	-1.37	8.37	0.1	7.00	0.1	0.00072185	0.00536584	0.04526613	0.57196629	A_07_P048050	22201	cmr/putative fimbrial chaperone protein [22201]
22249	-4.07	10.32	-2.02	11.33	0.2	9.30	0.2	0.00022214	0.00234886	0.01178608	0.34814259	A_07_P048091	22249	cmr/conf Unknown function [22249]
22274	-2.66	7.29	-1.30	7.94	0.2	6.64	0.2	0.00388476	0.01948807	0.05176670	0.60081121	A_07_P048560	22274	cmr/conf Unknown function [22274]
22290	-2.53	9.37	-1.34	10.03	0.3	8.70	0.3	0.00618767	0.02918013	0.04918026	0.57993119	A_07_P052464	22290	cmr/ orf, hypothetical protein [22290]
22297	-3.16	10.95	-1.11	11.51	0.1	10.40	0.0	0.00176850	0.01061556	0.07406504	0.42707507	A_07_P048613	22297	cmr/conf Unknown function [22297]
22298	-3.24	9.03	-1.70	9.88	0.1	8.18	0.1	0.00010883	0.00188113	0.02156707	0.45470588	A_07_P048360	22298	cmr/conf Unknown function [22298]
22309	-3.26	10.61	-1.70	11.46	0.2	9.76	0.0	0.00040741	0.00347035	0.02316946	0.45201983	A_07_P048362	22309	cmr/conf Unknown function [22309]
22318	-2.37	9.38	-1.18	9.97	0.0	8.79	0.1	0.00097375	0.00676511	0.06642594	0.65609159	A_07_P048390	22318	cmr/putative phosphatidate cytidiltransferase [22318]
22360	+15.65	9.68	+3.97	7.69	0.5	11.66	0.1	0.00004699	0.00080150	0.00147075	0.31443026	A_07_P048200	22360	cmr/putative capsid protein of prophage CP-933X [22360]
22361	+30.94	10.57	+4.39	8.37	0.0	12.76	0.1	0.00000101	0.00012946	0.00068280	0.07904612	A_07_P048291	22361	cmr/putative capsid assembly protein of prophage CP-933X [22361]
22391	+2.75	7.66	+1.46	6.93	0.2	8.38	0.5	0.01117959	0.04532019	0.03978532	0.49905558	A_07_P048371	22391	cmr/unknown protein encoded within prophage CP-933X [22391]
22394	-2.56	8.98	-1.35	9.66	0.1	8.31	0.4	0.00669880	0.03101731	0.07604617	0.57874003	A_07_P048386	22394	cmr/unknown protein encoded within prophage CP-933X [22394]
22446	+5.51	9.38	+2.46	8.15	0.0	10.61	0.1	0.00002566	0.00058702	0.01189914	0.26908262	A_07_P048452	22446	cmr/conf Unknown function [22446]
22511	-3.59	7.59	-1.37	8.27	0.3	6.90	0.3	0.00455836	0.02208209	0.04411204	0.56833061	A_07_P048103	22511	cmr/conf Unknown function [22511]
22519	+2.81	8.30	+1.49	7.55	0.3	9.05	0.1	0.00188050	0.01111606	0.03704268	0.48398168	A_07_P048109	22519	cmr/conf Unknown function [22519]
22519	+2.85	8.59	+1.51	7.84	0.2	9.35	0.2	0.00072050	0.00535832	0.03415282	0.48012911	A_07_P048110	22519	cmr/conf Unknown function [22519]
22519	+3.57	8.78	+1.84	7.87	0.1	9.70	0.1	0.00010471	0.00158871	0.02419842	0.40158051	A_07_P048110	22519	cmr/conf Unknown function [22519]
22519	+3.43	8.63	+1.78	7.74	0.2	9.52	0.1	0.00028452	0.00267907	0.02428620	0.41760848	A_07_P048110	22519	cmr/conf Unknown function [22519]
22519	+2.89	8.46	+1.53	7.69	0.1	9.23	0.1	0.00051701	0.00415078	0.05123158	0.47601717	A_07_P048110	22519	cmr/conf Unknown function [22519]
22546	+5.70	10.27	+2.51	9.01	0.0	11.52	0.0	0.00001616	0.00040859	0.01138275	0.28491256	A_07_P048121	22546	cmr/anthranilate synthase component I [22546]
22547	-78.24	10.63	-6.26	7.49	0.2	13.78	0.1	0.00000031	0.00008117	0.00004646	0.01750800	A_07_P048129	22547	cmr/anthranilate synthase component I [22547]
22560	-2.37	8.99	-1.25	9.61	0.0	8.37	0.4	0.00622109	0.02760512	0.05326989	0.61206338	A_07_P048137	22560	cmr/conf Unknown function [22560]
22561	-4.65	8.98	-2.22	10.09	0.1	7.87	0.2	0.00088551	0.00516924	0.03806560	0.29052752	A_07_P048163	22561	cmr/putative transposase [22561]
22581	+2.10	8.53	+1.07	7.99	0.0	9.07	0.2	0.00323716	0.01692654	0.04474439	0.69427965	A_07_P048486	22581	cmr/putative oxidoreductase component [22581]
22622	+2.02	7.57	+1.01	7.06	0.2	8.07	0.1	0.00496808	0.02360192	0.06989647	0.66053421	A_07_P048415	22622	cmr/partial beta-D-glucuronidase [22622]
22664	+9.09	9.47	+1.63	8.66	0.0	10.28	0.1	0.00028702	0.00256768	0.01138084	0.45119635	A_07_P048420	22664	cmr/conf Unknown function [22664]
22754	+6.34	9.46	+2.66	8.12	0.4	10.79	0.1	0.00024821	0.00245286	0.00890307	0.26053903	A_07_P048434	22754	cmr/ orf, hypothetical protein [22754]
22756	-3.29	10.51	-1.72	11.37	0.2	9.65	0.1	0.00041677	0.00352927	0.02167792	0.45130291	A_07_P052541	22756	cmr/putative phosphatase [22756]
22804	-3.59	9.04	-1.84	9.96	0.1	8.12	0.2	0.00037460	0.00325950	0.03790566	0.41563861	A_07_P048458	22804	cmr/unknown protein encoded within 6629 [22804]
22806	-5.84	8.21	-2.54	9.48	0.2	6.94	0.2	0.00036208	0.00092690	0.00490976	0.20872221	A_07_P048461	22806	cmr/putative transposase [22806]
22810	+2.01	7.57	+1.01	7.07	0.2	8.08	0.0	0.00588623	0.02711293	0.07203324	0.66113842	A_07_P048469	22810	cmr/putative kinase [22810]
22952	-2.31	9.41	-1.21	10.01	0.2	8.81	0.3	0.00689202	0.03114951	0.06317922	0.61154667	A_07_P048645	22952	cmr/putative tail assembly protein of prophage CP-933T [22952]
22992	-3.08	9.46	-1.06	9.99	0.0	8.93	0.2	0.00266545	0.01468562	0.08308877	0.70338536	A_07_P048645	22992	cmr/putative tail assembly protein of prophage CP-933T [22992]
22992	-2.08	9.55	-1.06	10.08	0.1	9.02	0.0	0.00170315	0.01003706	0.08222497	0.69973671	A_07_P048645	22992	cmr/putative tail assembly protein of prophage CP-933T [22992]
22994	-5.78	8.98	-2.53	10.24	1.0	7.71	0.0	0.00796442	0.03456223	0.00412792	0.20897106	A_07_P048649	22994	cmr/unknown protein encoded by prophage CP-933T [22994]
23058	-2.32	8.45	-1.22	9.05	0.0	7.84	0.4	0.00573883	0.02652733	0.06132277	0.64432863	A_07_P048705	23058	cmr/putative outer membrane protein [23058]
23077	-2.03	8.48	-1.02	8.99	0.1	7.97	0.1	0.00228837	0.01563917	0.08830260	0.71999481	A_07_P048736	23077	cmr/putative tail fiber component J of prophage [23077]
23108	-3.24	8.10	-1.70	8.95	0.0	7.26	0.4	0.02238414	0.01327294	0.02249134	0.45209011	A_07_P048815	23108	cmr/unknown protein encoded within prophage CP-933U [23108]
23144	-5.17	8.83	-2.37	10.02	0.0	7.65	0.3	0.00016033	0.00180431	0.00584667	0.24612299	A_07_P048923	23144	cmr/conf Unknown function [23144]
23159	-6.61	8.83	-2.72	10.19	0.1	7.47	0.3	0.00006774	0.00099132	0.00374962	0.17668388	A_07_P048945	23159	cmr/putative outer membrane receptor for iron compound [23159]
23162	-4.87	9.25	-2.28	10.39	0.1	8.11	0.2	0.00011107	0.00139729	0.00755158	0.27210784	A_07_P048951	23162	cmr/IS629 transposase [23162]
23272	-3.16	8.06	-1.11	8.62	0.2	7.50	0.0	0.00272215	0.01411500	0.07946601	0.67272520	A_07_P049154	23272	cmr/conf Unknown function [23272]
23297	-6.73	9.65	-2.75	11.02	0.0	8.27	0.4	0.00016650	0.00177268	0.00255526	0.17068610	A_07_P049211	23297	cmr/putative transposase for 6629 [23297]
23311	+2.01	7.14	+1.01	6.63	0.0	7.64	0.3	0.00668311	0.03061948	0.07234688	0.67215339	A_07_P049236	23311	cmr/putative tail fiber protein of prophage CP-933V [23311]
23313	-3.62	7.89	-1.85	8.81	0.7	6.96	0.1	0.00585062	0.03060453	0.01690739	0.39070641	A_07_P052645	23313	cmr/putative tail component of prophage CP-933V [23313]
23314	-2.16	9.85	-1.11	10.41	0.2	9.30	0.1	0.00366138	0.01863115	0.07488226	0.67348571	A_07_P049250	23314	cmr/putative tail component of prophage CP-933V [23314]
23345	-2.59	10.23	-1.37	10.92	0.2	9.55	0.2	0.00204731	0.01196594	0.04136522	0.57138600	A_07_P049326	23345	cmr/putative antitermination protein Q for prophage CP-933V [23345]
23349	+3.21	7.46	+1.68	6.62	0.1	8.30	0.1	0.00024910	0.00245579	0.02920614	0.43789224	A_07_P049345	23349	cmr/putative DNA methyltransferase encoded within prophage CP-933V [23349]
23357	-3.16	8.05	-1.11	8.60	0.1	7.49	0.3	0.00425830	0.02005508	0.07271659	0.66833941	A_07_P049373	23357	cmr/putative regulatory protein C0 of prophage CP-933V [23357]
23364	-4.39	11.96	-2.14	13.02	0.0	10.89	0.0	0.00004116	0.00076900	0.00948234	0.30908903	A_07_P049400	23364	cmr/putative host killing protein Kil of prophage [23364]
23366	-2.20	13.22	-1.14	13.79	0.0	12.65	0.1	0.00108449	0.00737341	0.07120173	0.66449318	A_07_P049406	23366	cmr/putative recombination protein Bet of prophage CP-933V [23366]
23367	-3.41	10.02	-1.77	10.90	0.1	9.13	0.6	0.00573842	0.02652733	0.02110391	0.43891678	A_07_P049415	23367	cmr/putative exonuclease of prophage CP-933V [23367]
23390	-2.22	10.20	-1.15	10.78	0.3	9.62	0.1	0.00420035	0.02079385	0.06737960	0.65669560	A_07_P049451	23390	cmr/putative hydrolase [23390]
23392	-2.78	10.43	-1.47	11.17	0.3	9.70	0.4	0.00785007	0.03417298	0.03540333	0.51419742	A_07_P049464	23392	cmr/putative isomerase-decarboxylase [23392]
23603	-3.53	8.75	-1.82	9.66	0.3	7.84	0.6	0.00544210	0.02545048	0.01278675	0.48224520	A_07_P049727	23603	cmr/ orf, hypothetical protein [23603]
23618	-2.64	8.86	-1.29	9.51	0.0	8.22	0.1	0.00060040	0.00465408	0.05349530	0.60461594	A_07_P049758	23618	cmr/conf Unknown function [23618]
23657	-3.21	10.57	-1.68	11.43	0.1	9.73	0.4	0.00227837	0.01284168	0.05030849	0.46362653	A_07_P049781	23657	cmr/ orf, hypothetical protein [23657]
23673	-4.22	11.32	-2.08	12.36	0.0	10.28	0.0	0.00094505	0.00075371	0.01062373	0.32731898	A_07_P049804	23673	cmr/putative transcriptional regulator LYSR-type [23673]
23689	-3.25	9.82	-1.37	10.41	0.4	9.24	0.0	0.00879758	0.03733178	0.06496583	0.65648194	A_07_P049823	23689	cmr/conf Unknown function [23689]
23767	-2.14	7.41	-1.10	7.96	0.1	6.86	0.1	0.00220077	0.01257968	0.07423663	0.67130959	A_07_P049845	23767	cmr/conf Unknown function [23767]
23783	-5.15	11.43	-2.36	12.61	0.1	10.25	0.3	0.00022077	0.00218894	0.00834660	0.24691648	A_07_P049860	23783	cmr/putative dimethyl sulfoxide reductase subunit C [23783]
23799	-19.27	12.94	-4.27	15.07	0.0	10.80	0.6	0.00005595	0.00086270	0.00060034	0.02173573	A_07_P049878	23799	cmr/putative ATP synthase beta subunit [23799]
23799	-11.35	12.95	-3.50	14.70	0.0	11.20	0.1	0.00000440	0.00022561	0.00049162	0.07166667	A_07_P049878	23799	cmr/putative ATP synthase beta subunit [23799]
23799	-14.91	13.06	-3.90	15.01	0.0	11.11	0.4	0.00003974	0.00046811	0.00016070	0.04216667	A_07_P049878	23799	cmr/putative ATP synthase beta subunit [23799]
23799	-10.38	13.63	-3.38	15.31	0.1	11.94	0.0	0.00000550	0.00025298	0.00059193	0.08304000	A_07_P049878	23799	cmr/putative ATP synthase beta subunit [23799]
23799	-13.64	13.07	-3.77	14.96	0.1	11.19	0.4	0.00003645	0.00035821	0.00024835	0.05147727	A_07_P049878	23799	cmr/putative ATP synthase beta subunit [23799]
23866	+2.33	7.82	+1.22	7.21	0.0	8.43	0.0	0.00072265	0.00536671	0.05097624	0.55889276	A_07_P049912	23866	cmr/conf Unknown function [23866]
23923	-6.63	10.02	-2.73	11.39	0.1	8.66	0.0	0.00004402	0.00039147	0.00277058	0.17659919	A_07_P049961	23923	cmr/conf Unknown function [23923]
23924	-10.93	10.43	-3.45	12.16	0.0	8.71	0.2	0.00008821	0.00030062	0.00055005	0.07721143	A_07_P049971	23924	cmr/putative transposase [23924]
23925	-6.12	9.22	-2.61	10.53	0.1	7.92	0.1	0.00002323	0.00052262	0.00316271	0.19778169	A_07_P049976	23925	cmr/putative transposase [23925]
23931	+2.77	10.76	+1.47	10.03	0.1	11.50	0.1	0.00051332	0.00412930	0.03796098	0.49147905	A_07_P049986	23931	cmr/unknown protein encoded by prophage CP-933Y [23931]
23934	-2.62	10.29	-1.39	10.99	0.2	9.59	0.3	0.00416615	0.02038523	0.06221481	0.56080920	A_07_P049994	23934	cmr/unknown protein encoded by prophage CP-933Y [23934]
23974	+3.58	8.28	+1.84	7.36	0.3	9.20	0.0	0.00055956	0.00439729	0.02445249	0.40609705	A_07_P049390	23974	cmr/conf Unknown function [23974]
24061	-5.99	9.59	-2.58	10.88	0.4	8.29	0.0	0.00022775	0.00238308	0.00338030	0.19828070	A_07_P050170	24061	cmr/ orf, hypothetical protein [24061]
24127	-3.12	9.21	-1.64	10.03	0.0	8.39	0.2	0.00041747	0.00352993	0.02594131	0.47107266	A_07_P050257	24127	cmr/ orf, hypothetical protein [24127]
24191	-2.57	8.69	-1.36	8.78	0.2	8.60	0.2	0.00168657	0.01026417	0.04577990	0.57196825	A_07_P050584	24191	cmr/type III secretion apparatus protein [24191]
24237	+3.59	9.26	+1.84	8.34	0.1	10.18	0.0	0.00012509	0.00151602	0.02431847	0.40429778	A_07_P052774	24237	cmr/putative oxidoreductase [24237]
24268	+12.89	8.63	+3.68	6.78	0.3	10.47	0.1	0.00001937	0.00066342	0.02110693	0.13473565	A_07_P050673	24268	cmr/ orf,hypothetical protein [24268]
24269	+8.45	8.87	+3.08	7.33	0.1	10.41	0.0	0.00003604	0.00026402	0.00589654	0.21340626	A_07_P050678	24269	cmr/ orf,hypothetical protein [24269]
24270	+4.93	7.25	+2.30	6.60	0.1	8.90	0.1	0.00004527	0.00075578	0.01440903	0.32181542	A_07_P050685	24270	cmr/putative ATP-binding protein of ABC transport system [24270]
24315	-2.92	9.15	-1.55	9.92	0.1	8.37	0.0	0.00027664	0.00261738	0.03237134	0.49606689	A_07_P050721	24315	cmr/unknown protein encoded by ISc828 [24315]
24324	-3.78	8.55	-1.68	9.29	0.4	7.81	0.4	0.00981572	0.04086162	0.03508829	0.51436685	A_07_P050757	24324	cmr/putative transposase [24324]
24332	-2.22	9.33	-1.15	9.91	0.2	8.76	0.2	0.00439947	0.02145764	0.06897929	0.60739104	A_07_P050797	24332	cmr/putative cytotoxin [24332]
24338	-2.38	7.39	-1.25	8.01	0.1	6.76	0.3	0.00315817	0.01659066	0.06575033	0.62104651	A_07_P050796	24338	cmr/unknown protein encoded by ISc828 [24338]
24340	-2.99	11.84	-1.58	12.63	0.0	11.05	0.1	0.00023061	0.00234535	0.02969246	0.48838174	A_07_P050803	24340	cmr/unknown protein encoded by ISc828 [24340]
24343	+2.89	10.23	+1.53	9.46	0.2	10.99	0.2	0.00100833	0.00746025	0.03532012	0.47652286	A_07_P050808	24343	cmr/ orf, hypothetical protein [24343]
24382	-3.76	8.57	-1.46	9.30	0.0	7.84	0.0	0.00029237	0.00276664	0.03895112	0.53012400	A_07_P050926	24382	cmr/putative iron compound-binding protein of ABC transporter [24382]
24385	-2.15	8.50	-1.10	9.05	0.0	7.95	0.0	0.00117500	0.00780071	0.07548717	0.67411798	A_07_P050944	24385	cmr/putative ATP-binding protein of ABC transporter family [24385]
24400	-7.15	12.51	-2.84	13.93	0.1	11.09	0.2	0.00003155	0.00062713	0.00214727	0.16018779	A_07_P050959	24400	cmr/conf Unknown function [24400]
24400	-6.07	13.15	-2.60	14.45	0.0	11.85	0.0	0.00001417	0.00039205	0.00353023	0.19779359	A_07_P050959	24400	cmr/conf Unknown function [24400]
24400	-7.15	12.78	-2.84	14.20	0.0	11.36	0.0	0.00000915	0.00032668	0.00217734	0.15870370	A_07_P050959	24400	cmr/conf Unknown function [24400]
24400	-14.02	14.32	-3.81	15.21	1.0	11.40	0.1	0.00014814	0.00092289	0.00050289	0.05064103	A_07_P050959	24400	cmr/conf Unknown function [24400]
24400	-5.26	13.12	-2.39	14.32	0.0	11.93	0.1	0.00003295	0.00062963	0.00545795	0.24137640	A_07_P050959	24400	cmr/conf Unknown function [24400]
24487	+5.63	7.93	+2.49	6.68	0.0	9.17	0.1	0.00002721	0.00056519	0.01141197	0.28473851	A_07_P050601	24487	cmr/putative phosphotransferase system enzyme subunit [24487]
24488	+5.27	8.90	+2.40	7.70	0.1	10.10	0.0	0.00003468	0.00064547	0.01312055	0.30377941	A_07_P050610	24488	cmr/putative phosphotransferase system enzyme subunit [24488]
24501	-43.14	11.60	-5.43	14.32	0.0	8.89	0.1	0.00000036	0.00009117	0.00000191	0.00333333	A_07_P050934	24501	cmr/ orf,hypothetical protein [24501]
24799	+2.56	10.75	+1.36	10.07	0.2	11.43	0.4	0.00889363	0.03805312	0.06445706	0.52780882	A_07_P050275	24799	cmr/putative DNA processing protein [24799]
24801	+5.90	9.04	+2.56	7.76	0.2	10.32	0.0	0.00002926	0.00059064	0.01058877	0.27763067	A_07_P046078	24801	cmr/putative ATP-dependent DNA helicase [24801]
24803	+4.15	8.17	+2.05	7.14	0.1	9.20	0.2	0.00012748	0.00177863	0.03897863	0.38388889	A_07_P046088	24803	cmr/putative ATP-dependent DNA helicase [24803]
24858	+3.65	7.69	+1.87	6.75	0.5	8.62	0.2	0.00028709	0.00270503	0.02469588	0.40252594	A_07_P046176	24858	cmr/putative enzyme [24858]
24859	+8.25	9.44	+3.04	7.92	0.2	10.96	0.0	0.00003132	0.00038273	0.00518681	0.21637204	A_07_P046184	24859	cmr/ orf,hypothetical protein [24859]
24860	+4.72	8.72	+2.24	7.60	0.1	9.84	0.1	0.00007976	0.00110927	0.01515067	0.33452655	A_07_P046186	24860	cmr/conf Unknown function [24860]
24862	+10.49	8.54	+3.42	6.83	0.0	10.25	0.0	0.00000312	0.00019442	0.00131484	0.16511785	A_07_P046200	24862	cmr/conf Unknown function [24862]
24863	+9.39	8.48	+3.23	6.87	0.1	10.10	0.1	0.00005005	0.00027756	0.00410379	0.19002941	A_07_P046205	24863	cmr/putative 3-oxoacyl- [24863]
24864	+5.78	8.39	+2.53	7.13	0.2	9.66	0.2	0.00014265	0.00165628	0.01076220	0.27773049	A_07_P046210	24864	cmr/conf Unknown function [24864]
24874	+4.14	9.22	+2.05	8.20	0.7	10.25	0.1	0.00671012	0.01604959	0.01930005	0.37329238	A_07_P046227	24874	cmr/putative regulator [24874]
24875	+3.25	7.91	+1.70	7.06	0.2	8.76	0.2	0.00006286	0.00466639	0.02887195	0.43876448	A_07_P046232	24875	cmr/putative phosphotransferase system enzyme subunit [24875]
24876	+3.29	8.11	+1.72	7.25	0.3	8.97	0.3	0.00175494	0.01056991	0.02832124	0.43779352	A_07_P046239	24876	cmr/putative phosphotransferase system enzyme subunit [24876]
24883	-2.23	10.50	-1.16	11.08	0.1	9.92	0.1	0.00122702	0.00806608	0.06743616	0.65640074	A_07_P046368	24883	cmr/conf Unknown function [24883]
24945	+3.49	8.92	+1.80	8.02	0.2	9.82	0.2	0.00016479	0.00207754	0.02547467	0.41219658	A_07_P046434	24945	cmr/conf Unknown function [24945]
24950	-2.16	10.37	-1.11	10.93	0.2	9.82	0.1	0.00396114	0.01981073	0.07214939	0.66818824	A_07_P046440	24950	cmr/conf Unknown function [24950]
24982	-2.14	11.50	-1.10	12.05	0.1	10.95	0.2	0.00420686	0.02083600	0.07376708	0.67963705	A_07_P046615	24982	cmr/putative membrane-associated adenosylcobalamin-dependent ribonucleotide reductase [24982]
24999	-2.84	7.95	-1.50	8.70	0.1	7.20	0.3	0.00165772	0.01011988	0.03399962	0.50786528	A_07_P046884	24999	cmr/conf Unknown function [24999]
25220	-3.25	7.74	-1.17	8.32	0.1	7.15	0.1	0.00185523	0.00965642	0.06814660	0.65862492	A_07_P046946	25220	cmr/putative fimbrial protein [25220]
25339	-2.08	9.97	-1.05	10.49	0.1	9.44	0.1	0.00223722	0.01305298	0.08182355	0.69747158	A_07_P050821	25339	cmr/conf Unknown function [25339]
25522	-2.32	11.96	-1.21	12.56	0.1	11.35	0.1	0.00136510	0.00836488	0.06247078	0.64157860	A_07_P047570	25522	cmr/putative hypacrucin [25522]
25523	-4.42	11.64	-2.15	12.72	0.1	10.57	0.3	0.00026220	0.00255135	0.00928227	0.30701681	A_07_P047573	25523	cmr/putative citrate permease [25523]
25613	+2.38	8.21	+1.25	7.58	0.3	8.83	0.1	0.00686642	0.02252189	0.05018293	0.55161183	A_07_P047325	25613	cmr/putative L-arginine 1-P-reductase [25613]
25618	-2.07	7.56	-1.05	8.09	0.1	7.03	0.2	0.00312010	0.01642355	0.08203887	0.68817297	A_07_P047247