Ali et. al, Supplementary microarray data

AGILENT PROBE ID	This is the name of the probe as given by Agilent, the manufacturer of the array. The array employed here is the commercially available "E. coli" array with the catalog/design number 020097.
POSITION OF PROBE START IN BL21(DE3) GENOME	This indicates the nucleotide at which the sequence of the oligonucleotide probe on the array begins on the BL21(DE3) genome using the numbering scheme used for Genbank file CP001509.3
LOCUS ID IN BL21(DE3) GENOME	The locus ID of the gene to which the probe is specific using the names present in the CP001509.3 genbank annotation
GENE NAME	the common shorthand name of the gene
ALTERNATIVE GENE NAME	an alternative gene name
FOLD CHANGE FIVE POINT FIVE	the observed fold change (average Cy3 signal vs. Cy5 signal) when transcripts from the 5.5 expressing strain (Cy3) is compared to the empty plasmid strain (Cy5). **Boxes highlighted in RED are transcripts that displayed increased levels after expression of 5.5. Blue indicates decreased transcript levels.**
FOLD CHANGE HNS (1to64)	the observed fold change (average Cy3 signal vs. Cy5 signal) when transcripts from the truncated H-NS expressing strain (Cy3) is compared to the empty plasmid strain (Cy5). **Boxes highlighted in RED are transcripts that displayed increased levels after expression of H-NS truncation (amino acids 1-64). Blue indicates decreased transcript levels.**
GENE PRODUCT DESCRIPTION	a brief description of gene function
PROBE IDENTITY TO BL21 SEQUENCE	The sequence of each probe was compared to the BL21(DE3) genome using BLAST and the percent identity of the probe to the genome sequence is shown. Probes with less than 90% identity are shaded in gray.

AGILENT PROBE ID	POSITION OF PROBE START IN BL21(DE3) GENOME	LOCUS ID IN BL21(DE3) GENOME	GENE NAME	ALTERNATIVE GENE NAME	FOLD CHANGE FIVE POINT FIVE	FOLD CHANGE HNS (1to64)	GENE PRODUCT DESCRIPTION	PROBE IDENTITY TO BL21 SEQUENCE
A_07_P010704	2239	ECD_00002	thrA	thrA	16.89		bifunctional aspartokinase I/homoserine dehydrogenase I	98.33
A_07_P010763	13645	ECD_00014	dnaK	dnaK	-6.1	7.97	molecular chaperone DnaK	100
A_07_P010766	14299	ECD_00015	dnaJ	dnaJ	-5.77	4.41	chaperone Hsp40, co-chaperone with DnaK	100
A_07_P049110	19719	ECD_00020	-	Z0020	12.09	11.68	hypothetical protein	96.67
A_07_P059386	21024	ECD_00021	-	ECs0022	11.85	14.13	putative usher protein	96.49
A_07_P010806	25391	ECD_00028	yaaY	yaaY	3.46	2.9	hypothetical protein	100
A_07_P011063	87973	ECD_00078	leuO	leuO	25.89	9.18	leucine transcriptional activator	100
A_07_P002766	184515	ECD_00160	degP	degP		-4.06	serine endoprotease (protease Do), membrane-associated	100
A_07_P002875	207787	ECD_00181	rnhB	rnhB		-4.25	ribonuclease HII	96.67
A_07_P003008	240913	ECD_00209	yafT	yafT	20.99	8.41	predicted aminopeptidase	100
A_07_P048086	242905	ECD_00213	yhhI-1	Z2254	13.31	22.64	predicted transposase	91.67
A_07_P007845	250885	ECD_00221	dinJ	dinJ		3.42	predicted antitoxin of YafQ-DinJ toxin-antitoxin system	98.33
A_07_P007889	258005	ECD_00230	ykfJ	ykfJ		5.16	hypothetical protein	100
A_07_P051892	258300	ECD_00231	prfH	prfH		3.02	peptide chain release factor 2	98.33
A_07_P008129	273639	ECD_00246	yagU	yagU		4.27	conserved inner membrane protein	96.43
A_07_P008155	280135	ECD_00251	yagY	matC	8.46	2.99	hypothetical protein	100
A_07_P008156	280679	ECD_00252	yagZ	matB	26.07	13.23	hypothetical protein	100
A_07_P008164	281004	ECD_00253	ykgK	matA	16.15	8.86	predicted regulator	100
A_07_P008172	282828	ECD_00255	ykgM	ykgM	5.33		50S ribosomal protein L31	100
A_07_P053817	285630	ECD_00256	eaeH	ECs0336	3.07	2.36	attaching and effacing protein, pathogenesis factor	95
A_07_P008206	288030	ECD_00259	ykgI	ykgI	11.52	11.69	hypothetical protein	100
A_07_P008213	288389	ECD_00260	ykgC	ykgC	7.8	4.86	pyridine nucleotide-disulfide oxidoreductase	100
A_07_P008225	291575	ECD_00262	ykgE	ykgE		6.93	predicted oxidoreductase	100
A_07_P008226	293013	ECD_00263	ykgF	ykgF	6.24	9.91	predicted amino acid dehydrogenase with NAD(P)-binding domain and ferric	100
A_07_P008233	293846	ECD_00264	ykgG	ykgG		3.76	predicted transporter	100
A_07_P008239	294152	ECD_00265	-	b0309	11.78	6.49	hypothetical protein	100
A_07_P008244	294438	ECD_00266	ykgH	ykgH	37.6	22.27	predicted inner membrane protein	100
A_07_P008268	303028	ECD_00271	yahA	yahA	8.17	3.25	predicted DNA-binding transcriptional regulator	100
A_07_P043691	305052	ECD_00274	yahD	yahD		6.32	predicted transcriptional regulator with ankyrin domain	100
A_07_P008292	307795	ECD_00276	yahF	yahF		3.53	predicted acyl-CoA synthetase with NAD(P)-binding domain and succinyl-Co	95
A_07_P008325	314395	ECD_00281	yahL	yahL		9.09	hypothetical protein	100
A_07_P008330	315181	ECD_00282	yahM	yahM	8.24		hypothetical protein	100
A_07_P031022	325372	ECD_00290	codB	codB		-3.45	cytosine transporter	100
A_07_P008378	326517	ECD_00291	codA	codA		-3.4	cytosine deaminase	100
A_07_P020975	356048	ECD_00320	-	b0370	4.96		hypothetical protein	100
A_07_P020980	357379	ECD_00321	yaiT	yaiT	5.97	2.48	conserved hypothetical protein	100
A_07_P021023	366031	ECD_00329	yaiB	iraP		7.19	hypothetical protein	100
A_07_P021254	415222	ECD_00379	cyoE	cyoE	3.09		protoheme IX farnesyltransferase	100
A_07_P051941	415466	ECD_00380	cyoD	cyoD	3.41		cytochrome o ubiquinol oxidase subunit IV	98.33
A_07_P021406	449205	ECD_00411	hha	hha	19.84	16.51	modulator of gene expression, with H-NS	100
A_07_P021411	449448	ECD_00412	ybaJ	ybaJ	18.23	30.73	hypothetical protein	100
A_07_P041529	481167	ECD_00436	ybaS	ybaS		4.38	predicted glutaminase	95

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A_07_P016279	496982	ECD_00449	ybbC	ybbC	21.76	70.12	hypothetical protein	100
A_07_P016283	497678	ECD_00450	ylbH	ylbH	78.56	59.99	conserved protein, rhs-like protein	100
A_07_P016287	497938	ECD_00451	ybbD	ybbD	96.84	41.68	hypothetical protein	100
A_07_P016340	506775	ECD_00460	ybbV	b0510		3.46	hypothetical protein	100
A_07_P016343	508166	ECD_00461	allP	ybbW	7.29	12.61	predicted allantoin transporter	100
A_07_P016349	509459	ECD_00462	allB	allB	13.52	7.87	allantoinase	100
A_07_P016437	527782	ECD_00480	sfmA	sfmA	4.05	5.21	predicted fimbrial-like adhesin protein	100
A_07_P016452	532001	ECD_00483	sfmH	sfmH		3.49	predicted fimbrial-like adhesin protein	100
A_07_P016465	533141	ECD_00485	fimZ	fimZ		3.13	predicted DNA-binding transcriptional regulator	98.33
A_07_P056700	535652	ECD_00488	-	ECs0805	5.14	-3.28	conserved hypothetical protein	95.65
A_07_P035397	537042	ECD_00493	emrE	emrE		4.67	multidrug efflux protein	96.67
A_07_P016486	538964	ECD_00494	ybcK	ybcK	4.19	5.97	predicted recombinase	100
A_07_P016493	539918	ECD_00495	ybcL	ybcL	14.78	17.05	predicted kinase inhibitor	100
A_07_P016496	540652	ECD_00496	ybcM	ybcM	7.51	5.48	predicted DNA-binding transcriptional regulator	100
A_07_P053132	543243	ECD_00503	#N/A	ECs3104	1.84	5.59	#N/A	91.67
A_07_P016781	598807	ECD_00574	ahpC	ahpC	3.05	2.07	alkyl hydroperoxide reductase, C22 subunit	100
A_07_P015809	617765	ECD_00593	cspE	cspC	2.82	7.99	cold shock protein E	87.5
A_07_P009714	620855	ECD_00598	ybeF	ybeF	5.36	2.12	predicted DNA-binding transcriptional regulator	100
A_07_P044030	636835	ECD_00613	ybeQ	Z0793	4.96	13.83	PSEUDOGENE - hypothetical - similar to b0644	100
A_07_P009794	637591	ECD_00614	ybeR	ybeR		8.17	hypothetical protein	100
A_07_P010017	691084	ECD_00658	rhsC	rhsC		4.69	rhsC element core protein RshC	100
A_07_P010028	691388	ECD_00659	ybfB	ybfB	12.89	13.5	predicted inner membrane protein	100
A_07_P010033	693075	ECD_00660	ybfO	ybfO	3.11	4.31	conserved protein, rhs-like protein	100
A_07_P063004	693636	ECD_00661	ybfC	ECs0730	10.7	10.47	hypothetical protein	98.33
A_07_P010326	695687	ECD_00665	yhhI-3	ybfQ	45.9	36.71	PSEUDOGENE - hypothetical - similar to b3484 (transposase)	97.87
A_07_P010047	697433	ECD_00666	ybfD	ybfD	16.72	13.76	hypothetical protein	95
A_07_P063010	697703	ECD_00667	ybgA	ECs0732	2.33	4.48	hypothetical protein	98.25
A_07_P046286	712162	ECD_00680	gltA	gltA	6.85		citrate synthase	100
A_07_P010185	731548	ECD_00692	cydA	cydA	1.92	4.28	cytochrome d terminal oxidase, subunit I	100
A_07_P053006	756222	ECD_10010	-	ECs3004	6.64	-3.17	hypothetical protein	98.31
A_07_P053004	756383	ECD_10011	-	ECs3003	5.59	-3.46	hypothetical protein	98.33
A_07_P052976	758422	ECD_10016	cIII	ECs2998		-3.34	antitermination protein	98.33
A_07_P062064	761231	ECD_10023	cII	ECs1187	4.15	-2.49	antitermination protein	100
A_07_P043403	761862	ECD_10024	O	Z0311		-3.02	DNA replication protein	100
A_07_P056737	763739	ECD_10026	ren	ECs0813		-4.54	ren exclusion protein	96.67
A_07_P055902	764046	ECD_10027	Q	ECs3501		-4.12	late gene regulator	100
A_07_P016554	767160	ECD_10033	-	ybcV	3.42	2.71	putative envelope protein	98.28
A_07_P016559	767853	ECD_10034	-	ybcW	9.9	2.16	hypothetical protein	100
A_07_P030399	770716	ECD_10036	A	c_3173	8.19	-3.29	DNA packaging protein	100
A_07_P050550	771203	ECD_10037	W	Z1884	6.05	-2.98	head-tail joining protein	94.92
A_07_P050567	774681	ECD_10041	E	Z1888		4.06	capsid component	100
A_07_P033485	805415	ECD_00754	ybhM	ybhM		4.52	conserved inner membrane protein	93.33

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A_07_P004515	832802	ECD_00779	dps	dps	-3.72		DNA protection during starvation conditions	100
A_07_P004620	859037	ECD_00800	yliE	yliE	9.97	3.3	conserved inner membrane protein	98.33
A_07_P033669	884964	ECD_00839	-	c_0961	5.23	7.64	putative phage tail protein	96.43
A_07_P005092	991081	ECD_00933	ompF	ompF	3.64	7.33	outer membrane porin 1a (Ia;b;F)	100
A_07_P005137	1003362	ECD_00942	ycbQ	ycbQ	5.54	16.98	predicted fimbrial-like adhesin protein	100
A_07_P005145	1004171	ECD_00943	ycbR	ycbR	3.33	3.14	predicted periplasmic pilin chaperone	100
A_07_P005180	1011227	ECD_00950	ycbW	ycbW		5.22	hypothetical protein	100
A_07_P005192	1016701	ECD_00953	uup	uup		-3.64	fused predicted transporter subunits of ABC superfamily: ATP-binding comp	100
A_07_P005216	1021211	ECD_00958	fabA	fabA		-4.5	3-hydroxydecanoyl-ACP dehydratase	100
A_07_P005240	1025561	ECD_00962	sulA	sulA	18.38		SOS cell division inhibitor	100
A_07_P005282	1034058	ECD_00971	yccW	yccW		-3.44	predicted methyltransferase	100
A_07_P005364	1051126	ECD_00987	ymcA	gfcD	-1.5	4.66	hypothetical protein	100
A_07_P005392	1055863	ECD_00992	cspG	cspG		14.67	DNA-binding transcriptional regulator	100
A_07_P001189	1056304	ECD_00993	sfa	ymcE		3.7	cold shock protein	100
A_07_P010343	1056458	ECD_00994	gnsA	gnsA		3.73	predicted regulator of phosphatidylethanolamine synthesis	100
A_07_P001226	1067118	ECD_01002	yccD	cbpM		3.91	modulator of CbpA co-chaperone	100
A_07_P001235	1067630	ECD_01003	cbpA	cbpA		7.09	curved DNA-binding protein, DnaJ-like protein that functions as a co-chaper	100
A_07_P001240	1069460	ECD_01004	yccE	yccE	22.94	71.67	hypothetical protein	98.33
A_07_P033937	1070934	ECD_01005	agp	c_1138	2.42	4.8	glucose-1-phosphatase/inositol phosphatase	98.33
A_07_P001401	1104442	ECD_01035	csgF	csgF	5.94		predicted transport protein	100
A_07_P001409	1104832	ECD_01036	csgE	csgE	5.76	3.08	predicted transport protein	100
A_07_P001412	1105190	ECD_01037	csgD	csgD	9.39	4.69	DNA-binding transcriptional activator in two-component regulatory system	100
A_07_P001417	1106897	ECD_01038	csgB	csgB	29.45	12.07	curlin nucleator protein, minor subunit in curli complex	100
A_07_P060575	1107317	ECD_01039	csgA	ECs1420	5.04	2.38	cryptic curlin major subunit	87.5
A_07_P001429	1107766	ECD_01040	csgC	csgC	3.97	2.28	predicted curli production protein	100
A_07_P001431	1108211	ECD_01041	ymdA	ymdA	3.19		hypothetical protein	100
A_07_P001504	1123335	ECD_01056	yceP	bssS		10.03	hypothetical protein	98.33
A_07_P001568	1133712	ECD_01069	flgB	flgB		3.92	flagellar basal-body rod protein B	98.33
A_07_P001612	1142462	ECD_01078	flgK	flgK		-7.08	flagellar hook-associated protein K	100
A_07_P001620	1143460	ECD_01079	flgL	flgL		-7.77	flagellar hook-associated protein L	100
A_07_P006752	1199967	ECD_01135	ycgW	elbA	8.43	28.24	hypothetical protein	98.33
A_07_P006759	1201044	ECD_01136	ycgX	ycgX		4.07	hypothetical protein	100
A_07_P006771	1204123	ECD_01139	ycgZ	ycgZ		3.7	hypothetical protein	100
A_07_P006777	1204342	ECD_01140	ymgA	ymgA	5.48	6.2	hypothetical protein	100
A_07_P041114	1205014	ECD_01142	ymgC	ABR-0081754	17.63	27.13	hypothetical protein	96.43
A_07_P006792	1206951	ECD_01143	ycgG	ycgG		3.44	conserved inner membrane protein	100
A_07_P010359	1207300	ECD_01144	ymgF	ymgF	3.64	7.51	hypothetical protein	100
A_07_P006798	1209099	ECD_01145	ycgH	b1169	113	50.42	PSEUDOGENE - in frame stop - similar to b4491	100
A_07_P006821	1212497	ECD_01149	minE	minE	5.53		cell division topological specificity factor MinE	100
A_07_P006827	1213210	ECD_01150	minD	minD	3.68		membrane ATPase of the MinC-MinD-MinE system	100
A_07_P006864	1217874	ECD_01157	hlyE	hlyE	12.82	11.17	PSEUDOGENE - in frame stop - similar to b1182	100
A_07_P007124	1280369	ECD_01213	hns	hns	4.64	3.13	global DNA-binding transcriptional dual regulator H-NS	96.55

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A_07_P007151	1288346	ECD_01217	oppA	oppA	8.74		oligopeptide transporter subunit	100
A_07_P007157	1289352	ECD_01218	oppB	oppB	13.29		oligopeptide permease ABC transporter membrane protein	100
A_07_P007165	1289870	ECD_01219	oppC	oppC	16.36		oligopeptide transporter subunit	100
A_07_P007166	1290957	ECD_01220	oppD	oppD	8.89		oligopeptide transporter ATP-binding component	100
A_07_P007204	1297534	ECD_01227	yciA	yciA	7.87	-3.16	predicted hydrolase	96.67
A_07_P007225	1300373	ECD_01231	yciE	yciE	30.47	17.92	hypothetical protein	100
A_07_P007235	1301672	ECD_01233	yciG	yciG		3.92	hypothetical protein	100
A_07_P014396	1329664	ECD_01260	osmB	osmB	1.78	5.4	lipoprotein	100
A_07_P058509	1356689	ECD_01286	ycjM	ECs1886		3.51	predicted glucosyltransferase	100
A_07_P058535	1369403	ECD_01297	ycjW	ECs1899		3.59	predicted DNA-binding transcriptional regulator	95
A_07_P062776	1389249	ECD_01315	abgA	ECs1922		-3.84	predicted peptidase, aminobenzoyl-glutamate utilization protein	98.33
A_07_P014705	1397439	ECD_01322	intR	intR	5.25	2.45	integrase	100
A_07_P014742	1402708	ECD_01331	sieB	sieB	5.36	5.6	phage superinfection exclusion protein	100
A_07_P014748	1402865	ECD_01332	ydaF	b1354	6.1	3.4	predicted protein	90
A_07_P016531	1403267	ECD_01334	-	essD	6.04	2.42	putative Lysozyme	94.55
A_07_P014792	1406508	ECD_01339	trkG	trkG	35.82	60.64	potassium transporter subunit	96.67
A_07_P014801	1406860	ECD_01340	ynaK	ynaK	2.75	4.57	conserved hypothetical protein	100
A_07_P038648	1408034	ECD_01343	-	c_1594	2.6	3.57	conserved hypothetical protein	100
A_07_P030273	1408248	ECD_01344	-	c_3147	4.62	4.65	conserved hypothetical protein	95.56
A_07_P014850	1408754	ECD_01345	pinR	pinR	3.37	4.42	predicted site-specific recombinase	98.33
A_07_P014851	1409718	ECD_01346	ynaE	ynaE	5.84	11.9	predicted DNA-binding transcriptional regulator	100
A_07_P058811	1412343	ECD_01348	ompN	ECs1999	10.28	9.09	outer membrane pore protein N, non-specific	100
A_07_P009130	1430378	ECD_01362	ydbD	ydbD		3.54	hypothetical protein	98.18
A_07_P009133	1431454	ECD_01363	ynbA	ynbA		3.5	predicted inner membrane protein	100
A_07_P009140	1432269	ECD_01364	ynbB	ynbB	3.56	5.66	predicted CDP-diglyceride synthase	100
A_07_P009204	1448270	ECD_01379	ydcI	ydcI		-3.44	predicted DNA-binding transcriptional regulator	100
A_07_P048121	1481156	ECD_01412	yncH	Z2264	3.49	6.33	hypothetical protein	100
A_07_P009372	1485904	ECD_01414	rhsE	rhsE		13.51	rhsE element core protein RshE	100
A_07_P009376	1486342	ECD_01415	ydcD	ydcD	52.67	313.28	hypothetical protein	100
A_07_P009383	1487253	ECD_01416	-	b1458	20.29	61.58	hypothetical protein	100
A_07_P009389	1487603	ECD_01417	-	yncI	6.55	14.86	hypothetical protein	100
A_07_P009396	1488838	ECD_01419	ydcE	pptA	8.34	18.76	4-oxalocrotonate tautomerase	100
A_07_P009499	1512192	ECD_01440	osmC	osmC		3.14	osmotically inducible, stress-inducible membrane protein	100
A_07_P009584	1538466	ECD_01457	ydeO	ydeO	9.99	10.1	predicted DNA-binding transcriptional acfivator	98.33
A_07_P009587	1539328	ECD_01458	-	yneN	9.66	13.88	hypothetical protein	100
A_07_P009593	1539784	ECD_01459	ydeP	ydeP	25.93	8.97	predicted oxidoreductase	100
A_07_P009596	1542360	ECD_01460	ydeQ	ydeQ	8.4	6.63	predicted fimbrial-like adhesin protein	100
A_07_P020327	1573574	ECD_01495	ydeI	ydeI		3.88	hypothetical protein	100
A_07_P020333	1574114	ECD_01496	ydeJ	ydeJ		10.03	competence damage-inducible protein A	100
A_07_P020361	1580485	ECD_01502	ydfJ	b1543	7.82	3.69	predicted transporter	100
A_07_P038191	1583930	ECD_01505	-	c_1471	6.72	6.25	conserved hypothetical protein	98.33
A_07_P030282	1584813	ECD_01507	-	c_3149	40.78	46.17	conserved hypothetical protein	98.33

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A_07_P020626	1618282	ECD_01568	ydgE	mdtI		6.49	multidrug efflux system transporter	100
A_07_P044393	1618533	ECD_01569	ydgF	Z2594		3.2	multidrug efflux system transporter	96.61
A_07_P054884	1637113	ECD_01584	uidC	ECs2322		5.25	predicted outer membrane porin protein	100
A_07_P042333	1680667	ECD_01626	sodB	sodB		4.93	superoxide dismutase, Fe	98.25
A_07_P018430	1700315	ECD_01644	ydhZ	ydhZ	3.26	2.47	hypothetical protein	100
A_07_P018508	1718065	ECD_01660	ydiN	ydiN		3.71	predicted transporter	98.33
A_07_P018523	1721462	ECD_01663	ydiF	ydiF		3.06	fused predicted acetyl-CoA:acetoacetyl-CoA transferase: alpha subunit/beta	100
A_07_P018534	1722901	ECD_01665	ydiP	ydiP		3.66	predicted DNA-binding transcriptional regulator	93.33
A_07_P018587	1735979	ECD_01676	ydiV	ydiV		3.08	hypothetical protein	100
A_07_P018627	1743939	ECD_01685	rplT	rplT		3.01	50S ribosomal protein L20	100
A_07_P018633	1744365	ECD_01686	rpmI	rpmI		3.45	50S ribosomal protein L35	100
A_07_P018641	1745313	ECD_01688	thrS	thrS	3.57	2.14	threonyl-tRNA synthetase	100
A_07_P018654	1749339	ECD_01689	-	b1721	6.94	8.87	PSEUDOGENE - arpB - b1720	100
A_07_P018674	1753008	ECD_01694	yniA	yniA		3.16	predicted phosphotransferase/kinase	100
A_07_P018698	1756937	ECD_01699	ydjO	ydjO	7.25	10.75	hypothetical protein	100
A_07_P018721	1763166	ECD_01704	celD	chbR	6.27	3.41	DNA-binding transcriptional dual regulator	100
A_07_P018739	1765948	ECD_01707	celA	chbB		5.81	N,N'-diacetylchitobiose-specific enzyme IIB component of PTS	100
A_07_P018898	1798540	ECD_01739	ydjF	ydjF	6.99	6.22	predicted DNA-binding transcriptional regulator	100
A_07_P018910	1800784	ECD_01741	ydjH	ydjH		5.03	predicted kinase	100
A_07_P018915	1801371	ECD_01742	ydjI	ydjI		4.02	predicted aldolase	100
A_07_P018919	1802245	ECD_01743	ydjJ	ydjJ		3.09	predicted oxidoreductase, Zn-dependent and NAD(P)-binding	100
A_07_P015590	1808057	ECD_01748	gapA	gapA	-3.12	3.17	glyceraldehyde-3-phosphate dehydrogenase	100
A_07_P021405	1814431	ECD_01753	yeaH	maa	8.2	4.91	hypothetical protein	100
A_07_P015616	1816036	ECD_01754	yeaI	yeaI	11.62	5.15	predicted diguanylate cyclase	100
A_07_P015721	1835854	ECD_01776	yeaY	yeaY	2.2	-3.36	predicted lipoprotein	100
A_07_P015761	1843553	ECD_01784	sdaA	sdaA		-3.34	L-serine deaminase I	100
A_07_P009684	1853049	ECD_01793	cspC	cspE	7.56	3.39	stress protein, member of the CspA-family	87.5
A_07_P015812	1854109	ECD_01795	yebO	yebO		3.21	hypothetical protein	96.67
A_07_P016041	1903021	ECD_01844	torY	torY		5.18	TMAO reductase III (TorYZ), cytochrome c-type subunit	100
A_07_P015227	1947966	ECD_01889	yodB	yodB	2.33	4.43	predicted cytochrome	100
A_07_P015234	1949475	ECD_01890	yeeI	mtfA	3.61		hypothetical protein	100
A_07_P015265	1962654	ECD_01895	yeeN	yeeN	3.85	8.02	hypothetical protein	100
A_07_P053639	1973124	ECD_01904	insD	ECs0288	3.51	5.99	IS2 insertion element transposase InsAB'	89.19
A_07_P015420	1986407	ECD_01921	hisG	hisG		8.75	ATP phosphoribosyltransferase	96.55
A_07_P015421	1987174	ECD_01922	hisD	hisD		10.03	histidinol dehydrogenase	100
A_07_P015429	1989155	ECD_01923	hisC	hisC		5.96	histidinol-phosphate aminotransferase	100
A_07_P015435	1990215	ECD_01924	hisB	hisB		3.71	imidazole glycerol-phosphate dehydratase/histidinol phosphatase	96.49
A_07_P015440	1990754	ECD_01925	hisH	hisH		3.51	imidazole glycerol phosphate synthase subunit HisH	96.67
A_07_P062811	1991473	ECD_01926	hisA	ECs2825		3.29	1-(5-phosphoribosyl)-5-[(5- phosphoribosylamino)methylideneamino] imida	100
A_07_P055562	1994420	ECD_01930	ugd	ECs2829	25.54		UDP-glucose 6-dehydrogenase	96.55
A_07_P015470	1995726	ECD_01931	gnd	gnd	3.18		6-phosphogluconate dehydrogenase	98.33
A_07_P055651	1998157	ECD_01932	manB	ECs2853	13.98	7.06	Phosphomannomutase	100

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A_07_P032034	2016357	ECD_01951	wcaK	wcaK		3.51	predicted pyruvyl transferase	100
A_07_P032038	2017901	ECD_01952	wzxC	wzxC		3.83	colanic acid exporter	100
A_07_P015554	2019142	ECD_01953	wcaJ	wcaJ		5.33	predicted UDP-glucose lipid carrier transferase	95
A_07_P015565	2022266	ECD_01955	cpsB	cpsB		6.52	mannose-1-phosphate guanyltransferase	98.21
A_07_P003030	2023603	ECD_01956	wcaI	wcaI		11.6	predicted glycosyl transferase	100
A_07_P003032	2024966	ECD_01957	wcaH	gmm		7.33	GDP-mannose mannosyl hydrolase	98.33
A_07_P003038	2025980	ECD_01958	wcaG	fcl		11.26	bifunctional GDP-fucose synthetase: GDP-4-dehydro-6-deoxy-D-mannose ep	100
A_07_P063301	2026627	ECD_01959	gmd	ECs2858		6.51	GDP-D-mannose dehydratase, NAD(P)-binding	98.31
A_07_P045078	2027592	ECD_01960	wcaF	wcaF		10.78	predicted acyl transferase	98.31
A_07_P003051	2027981	ECD_01961	wcaE	wcaE		19.46	predicted glycosyl transferase	100
A_07_P003060	2028812	ECD_01962	wcaD	wcaD	16.63	43.54	predicted colanic acid polymerase	98.33
A_07_P003061	2030763	ECD_01963	wcaC	wcaC		4.51	predicted glycosyl transferase	96.67
A_07_P045081	2031353	ECD_01964	wcaB	wcaB		6.65	predicted acyl transferase	98.33
A_07_P003074	2031687	ECD_01965	wcaA	wcaA		10.16	predicted glycosyl transferase	100
A_07_P003081	2034807	ECD_01967	wzb	wzb		3.62	protein-tyrosine phosphatase	100
A_07_P032067	2036143	ECD_01968	wza	c_2589		12.91	lipoprotein required for capsular polysaccharide translocation through the o	98.18
A_07_P003154	2060046	ECD_01981	yegO	mdtB		3.64	multidrug efflux system, subunit C	89.47
A_07_P003195	2066192	ECD_02013	-	b2084	4.35	7.12	conserved hypothetical protein; putative exported protein	100
A_07_P003199	2066354	ECD_02014	yegR	yegR	5.52	8.27	hypothetical protein	100
A_07_P045133	2068051	ECD_02016	gatR	gatR		3.25	PSEUDOGENE -galactol utilization repressor - b2089	95
A_07_P003211	2069363	ECD_04281	insB-29	b2090	4.24		IS1 protein InsB	100
A_07_P003220	2069886	ECD_02017	gatD	gatD	3.12		galactitol-1-phosphate dehydrogenase, Zn-dependent and NAD(P)-binding	100
A_07_P003225	2070808	ECD_02018	gatC	gatC	2.34	3.79	galactitol-specific enzyme IIC component of PTS	100
A_07_P003229	2072182	ECD_02019	gatB	gatB	5.33	6.46	galactitol-specific enzyme IIB component of PTS	100
A_07_P003233	2072547	ECD_02020	gatA	gatA	6.19	5.22	galactitol-specific enzyme IIA component of PTS	100
A_07_P042502	2072918	ECD_02021	gatZ	gatZ	3.63		putative tagatose 6-phosphate kinase 1	100
A_07_P003356	2100085	ECD_02048	yehL	yehL		19.04	predicted transporter subunit: ATP-binding component of ABC superfamily	100
A_07_P055787	2101568	ECD_02049	yehM	ECs2928		5.75	hypothetical protein	98.33
A_07_P003491	2129251	ECD_02075	yeiT	yeiT	1.99	4.51	predicted oxidoreductase	100
A_07_P003507	2132732	ECD_02078	mglA	mglA	4.3	2.07	fused methyl-galactoside transporter subunits of ABC superfamily: ATP-bind	100
A_07_P000722	2177537	ECD_02115	rplY	rplY		3.51	50S ribosomal protein L25	100
A_07_P001070	2260884	ECD_02182	yfbH	arnD		-3.36	hypothetical protein	100
A_07_P001133	2273869	ECD_02196	elaD	elaD	4.31	5.89	predicted enzyme	98.33
A_07_P001148	2275604	ECD_02198	yfbM	yfbM		3.97	predicted enzyme	100
A_07_P013721	2291462	ECD_02212	nuoB	nuoB	3.46		NADH dehydrogenase subunit B	100
A_07_P013728	2292021	ECD_02213	nuoA	nuoA	3.01		NADH dehydrogenase subunit A	100
A_07_P013976	2341027	ECD_02262	yfcTU	yfcU	5.03		predicted outer membrane export usher protein	96.67
A_07_P053274	2351064	ECD_02269	yfdF	ECs3228	6.21	5.44	PSEUDOGEN - similar to b2345	92.59
A_07_P014013	2352091	ECD_02271	insA-18	yfdF	5.73	8.51	IS1 protein InsA	93.33
A_07_P014116	2358656	ECD_02277	emrY	emrY	4.52	4.58	predicted multidrug efflux system	100
A_07_P014123	2360159	ECD_02278	emrK	emrK	4.45	2.98	EmrKY-TolC multidrug resistance efflux pump, membrane fusion protein con	100
A_07_P014130	2362046	ECD_02279	evgA	evgA	20.68	15.46	DNA-binding response regulator in two-component regulatory system with	100

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A_07_P014135	2365796	ECD_02280	evgS	evgS	6.62	1.69	hybrid sensory histidine kinase in two-component regulatory system with Ev	100
A_07_P014141	2367623	ECD_02282	yfdV	yfdV	16.91	8.1	predicted transporter	100
A_07_P014150	2368203	ECD_02283	yfdU	oxc		4.76	hypothetical protein	100
A_07_P014154	2370045	ECD_02284	yfdW	frc	6.27	10.42	formyl-coenzyme A transferase	100
A_07_P014160	2371821	ECD_02285	yfdX	yfdX		3.35	hypothetical protein	100
A_07_P030085	2421826	ECD_02332	yfeY	yfeY	1.72	-4.85	hypothetical protein	100
A_07_P013411	2455852	ECD_02362	yffB	yffB		4.45	hypothetical protein	100
A_07_P013443	2462429	ECD_02369	nlpB	bamC	5.25	-3.93	lipoprotein	100
A_07_P013551	2486440	ECD_02391	purM	purM		-3.41	phosphoribosylaminoimidazole synthetase	96.67
A_07_P013578	2493816	ECD_02396	yfgG	yfgG	3.22	12.95	hypothetical protein	100
A_07_P013581	2494730	ECD_02397	yfgH	yfgH		6.46	predicted outer membrane lipoprotein	100
A_07_P019755	2574136	ECD_02464	rseC	rseC		-3.62	RseC protein involved in reduction of the SoxR iron-sulfur cluster	98.33
A_07_P019758	2574622	ECD_02465	rseB	rseB		-3.93	periplasmic negative regulator of sigmaE	100
A_07_P041262	2632786	ECD_02518	gabT	gabT	-3.97		4-aminobutyrate aminotransferase	98
A_07_P020199	2638271	ECD_02525	stpA	stpA		18.89	DNA binding protein, nucleoid-associated	100
A_07_P009676	2642703	ECD_02531	nrdE	pagP	24.62	11.64	ribonucleotide-diphosphate reductase alpha subunit	100
A_07_P030555	2645572	ECD_02533	proV	proV		6.77	glycine betaine transporter subunit	98.33
A_07_P001861	2646019	ECD_02534	proW	proW		3.54	glycine betaine transporter subunit	100
A_07_P030557	2647364	ECD_02535	proX	proX	18.79		glycine betaine transporter subunit	93.33
A_07_P055986	2665904	ECD_02552	srlA	ECs3559		6.04	glucitol/sorbitol-specific enzyme IIC component of PTS	100
A_07_P002256	2719879	ECD_02607	cysH	cysH		-5.17	phosphoadenosine phosphosulfate reductase	96.67
A_07_P000282	2763426	ECD_02642	sdaB	b3111		-3.36	L-serine deaminase II	87.76
A_07_P006006	2774572	ECD_02653	fucI	fucI	4.02		L-fucose isomerase	96.67
A_07_P006090	2794543	ECD_02669	ptr	ptrA		-3.51	protease III	100
A_07_P006347	2845290	ECD_02709	yqeC	yqeC	5.93	2.59	hypothetical protein	100
A_07_P045631	2846335	ECD_02710	ygfJ	ygfJ		3.32	hypothetical protein	96.67
A_07_P056285	2867665	ECD_02724	recJ	ECs3764		-3.43	ssDNA exonuclease, 5' -> 3'-specific	98.33
A_07_P006489	2880337	ECD_02736	gcvH	gcvH	3.39		glycine cleavage system protein H	100
A_07_P011811	2908449	ECD_02763	cmtA	cmtA		5.31	predicted fused mannitol-specific PTS enzymes: IIB component/IIC compone	100
A_07_P012057	3000905	ECD_02861	yghS	yghS	12.3	9.78	predicted protein with nucleoside triphosphate hydrolase domain	100
A_07_P012065	3001698	ECD_02862	yghT	yghT		4.8	predicted protein with nucleoside triphosphate hydrolase domain	100
A_07_P012269	3039508	ECD_02899	ygiZ	ygiZ		7.44	conserved inner membrane protein	100
A_07_P012364	3057631	ECD_02918	yqiI	yqiI	13.84	5.21	hypothetical protein	100
A_07_P012366	3057929	ECD_02919	glgS	glgS		3.94	glycogen synthesis protein GlgS	100
A_07_P012375	3058760	ECD_02920	yqiJ	yqiJ	3.31	6.48	predicted inner membrane protein	100
A_07_P059659	3128810	ECD_02982	tdcD	ECs3995	21.32	4.04	propionate kinase/acetate kinase C, anaerobic	98.33
A_07_P000306	3130049	ECD_02983	tdcC	tdcC	10.08	3.55	L-threonine/L-serine transporter	100
A_07_P000312	3131598	ECD_02984	tdcB	tdcB	14.83	8.24	threonine dehydratase	100
A_07_P000316	3132563	ECD_02985	tdcA	tdcA	17.57	7.58	DNA-binding transcriptional activator	100
A_07_P058949	3133718	ECD_02986	tdcR	ECs3999		3.04	DNA-binding transcriptional activator	96.67
A_07_P059662	3134558	ECD_02987	yhaB	ECs4000	2.27	5.63	hypothetical protein	95
A_07_P000434	3156386	ECD_03009	yraH	yraH		7.88	predicted fimbrial-like adhesin protein	98.21

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A_07_P063488	3157128	ECD_03010	yraI	ECs4021	6.16		predicted periplasmic pilin chaperone	96.67
A_07_P000590	3190802	ECD_03040	secG	secG	40.49		protein-export membrane protein	100
A_07_P012734	3262623	ECD_03111	yhdA	csrD		-3.68	conserved inner membrane protein	100
A_07_P012787	3274099	ECD_03122	envR	envR		3.34	DNA-binding transcriptional regulator	96.67
A_07_P013047	3317435	ECD_03175	gspC	gspC	6.13	3.28	general secretory pathway component, cryptic	100
A_07_P017847	3352288	ECD_03215	yhfC	tsgA		4.6	hypothetical protein	98.33
A_07_P017874	3359104	ECD_03220	yhfL	yhfL		6.07	conserved secreted peptide	100
A_07_P018236	3446114	ECD_03293	yhhZ	yhhZ	27.33	35.16	hypothetical protein	100
A_07_P018241	3446414	ECD_03294	yrhA	yrhA	23.5	21.06	hypothetical protein	100
A_07_P041848	3447354	ECD_03295	yrhB	yrhB	9.14	6.02	hypothetical protein	96.67
A_07_P016274	3485596	ECD_03331	rhsB	rhsD	89.48	228.19	rhsB element core protein RshB	96.88
A_07_P007353	3486054	ECD_03332	yhhH	yhhH	21.2	29.08	hypothetical protein	100
A_07_P054163	3487608	ECD_03334	yhhI	ECs0602	18.21	12.17	predicted transposase	94.64
A_07_P007380	3493529	ECD_03338	yhiJ	yhiJ	14.01	11.68	hypothetical protein	100
A_07_P007381	3495399	ECD_03339	yhiKL	b3489	11.75	31.07	hypothetical protein	100
A_07_P007460	3514326	ECD_03353	yhiS	yhiS	4.07	5.25	hypothetical protein	100
A_07_P007464	3515520	ECD_03354	slp	slp	5.82	13.84	outer membrane lipoprotein	100
A_07_P007468	3516337	ECD_03355	yhiF	dctR	4.36	2.24	predicted DNA-binding ranscriptional regulator	100
A_07_P007477	3517378	ECD_03357	hdeB	hdeB	3.68	3.61	acid-resistance protein	100
A_07_P007483	3517755	ECD_03358	hdeA	hdeA	3.09	4.25	stress response protein acid-resistance protein	100
A_07_P007490	3518317	ECD_03359	hdeD	hdeD	3.04	4.79	acid-resistance membrane protein	100
A_07_P007494	3520015	ECD_03360	yhiE	gadE	103.36	18.09	DNA-binding transcriptional activator	100
A_07_P007508	3525150	ECD_03363	yhiW	gadW	12.62	1.75	DNA-binding transcriptional activator	100
A_07_P007513	3526371	ECD_03364	gadX	gadX	65.58	50.69	DNA-binding transcriptional dual regulator	100
A_07_P007516	3528537	ECD_03365	gadA	gadA		4.22	glutamate decarboxylase A, PLP-dependent	100
A_07_P007703	3581732	ECD_03405	yiaG	yiaG	3.66		predicted transcriptional regulator	100
A_07_P007706	3582297	ECD_03406	cspA	cspA		3.54	major cold shock protein	100
A_07_P007744	3589631	ECD_03415	yiaB	yiaB		3.42	conserved inner membrane protein	100
A_07_P016870	3618921	ECD_03440	yiaU	yiaU	8.49	6.01	predicted DNA-binding transcriptional regulator	100
A_07_P016907	3629357	ECD_03448	rhsA	rhsA	4.42	4.24	rhsA element core protein RshA	100
A_07_P016913	3629605	ECD_03449	yibA	yibA	3.42	7.2	lyase containing HEAT-repeat protein	93.33
A_07_P016918	3630833	ECD_03450	yibJ	yibJ	23.05	30.9	predicted Rhs-family protein	100
A_07_P016924	3631545	ECD_03451	yibG	yibG	23.71	22.66	hypothetical protein	100
A_07_P052196	3634782	ECD_03453	yibI	yiaW		3.42	predicted inner membrane protein	86.67
A_07_P049535	3641304	ECD_03459	-	Z5028	5.03	6.29	conserved hypothetical protein	93.33
A_07_P017019	3658437	ECD_03473	yibD	yibD	16.91	6.57	predicted glycosyl transferase	100
A_07_P039781	3666611	ECD_03480	waaV	waaV	5.64	2.41	putative beta1,3-glucosyltransferase	100
A_07_P039787	3667504	ECD_03481	waaW	c_4450	6.79	3.38	UDP-galactose:(Galactosyl) LPS alpha1,2-galactosyltransferase	98.33
A_07_P017198	3691582	ECD_03508	trmH	trmH		-3.9	tRNA (Guanosine-2'-O-)-methyltransferase	100
A_07_P039883	3705963	ECD_03517	-	c_4492	11.01	13.33	ShiA-like protein	100
A_07_P039893	3707284	ECD_03519	-	c_4494	18.89	6.44	putative transcriptional regulator	100
A_07_P039898	3709535	ECD_03520	-	c_4495	17.23	7.54	conserved hypothetical protein	98.33

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A_07_P039905	3710277	ECD_03521	-	c_4496	28.82	7.05	conserved hypothetical protein	100
A_07_P038017	3716273	ECD_03528	-	c_5198	8.35	12.41	PSEUDOGENE - in frame stop - transposase (fragment)	96.67
A_07_P048749	3720380	ECD_03532	-	L7023	24.22	7.22	hypothetical protein	96.43
A_07_P055150	3721457	ECD_03535	ykgN	ECs2648	4.1	2.03	predicted IS protein	100
A_07_P007989	3722353	ECD_03536	insI	insI	4.81		IS30 transposase	100
A_07_P036562	3722847	ECD_03537	-	c_3677	4.05		putative uncharacterized protein, yeeV-like protein	100
A_07_P017232	3726269	ECD_03542	yicK	setC	9.64	3.64	predicted sugar efflux system	100
A_07_P057595	3731302	ECD_03548	yicO	ECs4601		4.26	predicted xanthine/uracil permease	96.72
A_07_P017261	3732999	ECD_03549	ade	ade		14.47	cryptic adenine deaminase	100
A_07_P017334	3749432	ECD_03564	yidL	yidL		3.23	predicted DNA-binding transcriptional regulator	100
A_07_P017370	3755916	ECD_03570	ibpA	ibpA		3.85	heat shock chaperone	100
A_07_P057646	3778874	ECD_03592	tnaA	tnaA	4.83		tryptophanase/L-cysteine desulfhydrase, PLP-dependent	98.33
A_07_P005540	3794847	ECD_03607	bglG	bglG	98.84	8.72	transcriptional antiterminator of the bgl operon	98.33
A_07_P005587	3806567	ECD_03617	atpG	atpG	5.14		F0F1 ATP synthase subunit gamma	100
A_07_P005591	3808084	ECD_03618	atpA	atpA	4.43		F0F1 ATP synthase subunit alpha	100
A_07_P005596	3808799	ECD_03619	atpH	atpH	5.84		F0F1 ATP synthase subunit delta	100
A_07_P005604	3809624	ECD_03620	atpF	atpF	4.04		F0F1 ATP synthase subunit B	100
A_07_P005607	3809862	ECD_03621	atpE	atpE	6.84		F0F1 ATP synthase subunit C	100
A_07_P005662	3823889	ECD_04285	insJ-6	rbsD		-4.64	IS150 hypothetical protein	100
A_07_P005669	3825311	ECD_03635	rbsA	rbsA	4.45	-9.39	fused D-ribose transporter subunits of ABC superfamily: ATP-binding compo	100
A_07_P005727	3842569	ECD_03647	ilvM	ilvM	9.24		acetolactate synthase II, small subunit	100
A_07_P039071	3844794	ECD_03649	ilvD	ilvD	22.74		dihydroxy-acid dehydratase	88.33
A_07_P005880	3877312	ECD_03677	hemY	hemY		-3.46	predicted protoheme IX synthesis protein	98.33
A_07_P005885	3878608	ECD_03678	hemX	hemX		-3.51	predicted uroporphyrinogen III methylase	100
A_07_P050009	3893867	ECD_03693	-	Z5334	16.57	8.41	conserved hypothetical protein	100
A_07_P057752	3894270	ECD_03694	-	ECs4747	22.84	6.7	conserved hypothetical protein	100
A_07_P005951	3895380	ECD_03696	yigF	yigF	15.82	26.34	conserved inner membrane protein	98.28
A_07_P005960	3895817	ECD_03697	yigG	yigG	31.86	36.83	predicted inner membrane protein	100
A_07_P019225	3985888	ECD_03774	yiiE	yiiE	11.69	14.4	predicted transcriptional regulator	100
A_07_P019227	3986440	ECD_03775	yiiF	yiiF	6.45	5.09	hypothetical protein	100
A_07_P047071	3994453	ECD_03781	yiiG	yiiG		4.2	hypothetical protein	92.98
A_07_P047084	4001066	ECD_03786	-	Z5444		4.24	putative glycoporin	98.33
A_07_P057873	4009036	ECD_03794	sodA	ECs4834	-1.63	3.08	superoxide dismutase, Mn	95
A_07_P019439	4029741	ECD_03817	hslV	hslV	-3.54	3.15	ATP-dependent protease peptidase subunit	100
A_07_P034350	4084911	ECD_03856	tufB	c_4111	3.08	2.57	protein chain elongation factor EF-Tu (duplicate of tufA)	98.33
A_07_P008595	4088770	ECD_03862	rplL	rplL	3.46		50S ribosomal protein L7/L12	100
A_07_P008728	4128344	ECD_03889	arpA	arpA	7.66	3.89	PSEUDOGENE - arpA - regulator of Acetyl-CoA synthetase - similar to b4017	100
A_07_P008773	4143279	ECD_03898	yjbE	yjbE		4.13	hypothetical protein	100
A_07_P008811	4152888	ECD_03906	malE	malE		3.77	maltose ABC transporter periplasmic protein	100
A_07_P008822	4156153	ECD_03908	lamB	lamB	1.67	6.46	maltoporin precursor	100
A_07_P047260	4159545	ECD_03910	yjbI	yjbI	7.17	3.17	hypothetical protein	91.67
A_07_P047264	4167172	ECD_03918	zur	yjbK	1.31	3.14	DNA-binding transcriptional repressor, Zn(II)-binding	100

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A_07_P008880	4167880	ECD_03919	yjbL	yjbL	10.53	12.11	hypothetical protein	98.31
A_07_P047270	4168580	ECD_03920	yjbM	Z5646	6.97	7.15	hypothetical protein	100
A_07_P008972	4189273	ECD_03938	yjcF	yjcF	8.57	9.91	PSEUDOGENE - yjcF - similar to b4066	96.67
A_07_P011282	4236227	ECD_03980	yjdA	yjdA		3.85	conserved protein with nucleoside triphosphate hydrolase domain	100
A_07_P011370	4258973	ECD_03997	yjdI	yjdI		3.01	hypothetical protein	100
A_07_P011380	4259844	ECD_03999	yjdK	yjdK	7.68	5.1	hypothetical protein	100
A_07_P011393	4263616	ECD_04002	cadA	cadA	29.6		lysine decarboxylase 1	100
A_07_P011396	4266018	ECD_04003	cadB	cadB	5.26		predicted lysine/cadaverine transporter	100
A_07_P011404	4267680	ECD_04004	cadC	cadC	19.12	3.42	DNA-binding transcriptional activator	98.33
A_07_P011431	4275967	ECD_04010	fxsA	fxsA	-2.17	3.8	inner membrane protein	96.67
A_07_P011443	4278003	ECD_04012	groES	groS	-4.19	7.48	co-chaperonin GroES	100
A_07_P011446	4279243	ECD_04013	groEL	groL	-2.43	4.35	chaperonin GroEL	98.33
A_07_P047353	4280841	ECD_04015	yjeJ	yjeJ	6.97	8.18	hypothetical protein	98.33
A_07_P011513	4291728	ECD_04028	yjeM	yjeM		3.1	predicted transporter	100
A_07_P011571	4306527	ECD_04038	miaA	miaA		3.12	tRNA delta(2)-isopentenylpyrophosphate transferase	100
A_07_P011623	4316983	ECD_04048	yjfI	yjfI		5.56	hypothetical protein	100
A_07_P011630	4317307	ECD_04049	yjfJ	yjfJ		4.87	predicted transcriptional regulator effector protein	100
A_07_P061590	4318358	ECD_04050	yjfK	ECs5159		3.99	hypothetical protein	100
A_07_P011636	4318747	ECD_04051	yjfL	yjfL		5.83	conserved inner membrane protein	100
A_07_P010658	4323081	ECD_04056	yjfO	yjfO	4.28		hypothetical protein	100
A_07_P011720	4331777	ECD_04067	rpsF	rpsF		4.63	30S ribosomal protein S6	98.33
A_07_P011721	4332295	ECD_04068	priB	priB	2.01	4.39	primosomal replication protein N	100
A_07_P011729	4332426	ECD_04069	rpsR	rpsR	2.32	3.89	30S ribosomal protein S18	100
A_07_P011745	4341386	ECD_04077	ytfA	ytfA	9.24	3.81	predicted transcriptional regulator	100
A_07_P003811	4387962	ECD_04119	yjgL	yjgL	4.89	5.13	hypothetical protein	96.67
A_07_P047400	4390530	ECD_04122	yjgM	Z5868		13.55	predicted acetyltransferase	100
A_07_P003831	4392255	ECD_04123	yjgN	yjgN	6.23	11.94	conserved inner membrane protein	98.33
A_07_P003888	4406629	ECD_04134	idnK	idnK		4.25	D-gluconate kinase, thermosensitive	100
A_07_P003901	4409912	ECD_04137	yjgW	b4274	8.13	3.06	predicted protein	100
A_07_P003924	4412584	ECD_04140	insG	insG		-3.72	IS4 predicted transposase	100
A_07_P003926	4415372	ECD_04141	yjhB	yjhB	1.32	13.09	predicted transporter	100
A_07_P003931	4416588	ECD_04142	yjhC	yjhC	9.7	14.42	predicted oxidoreductase	100
A_07_P003942	4417281	ECD_04144	yjhE	yjhE	6.36		PSEUDOGENE -similar to b4282; predicted membrane protein	100
A_07_P003998	4432042	ECD_04160	insA-25	insA	4.57	3.43	IS1 protein InsA	93.33
A_07_P005381	4432560	ECD_04161	insB-25	insB	5.09	1.85	PSEUDOGENE - IS1 insB - interrupted by in-frame stop	96.55
A_07_P004083	4447449	ECD_04178	yjhA	nanC	3.12	5.44	N-acetylnuraminic acid outer membrane channel protein	100
A_07_P004086	4449910	ECD_04179	fimB	fimB	3.85	5.61	PSEUDOGENE - nterrupted by IS1; recombinase involved in phase variation;	92.59
A_07_P004095	4451827	ECD_04182	fimE	fimE	3.98	4.87	tyrosine recombinase/inversion of on/off regulator of fimA	100
A_07_P004109	4453885	ECD_04185	fimC	fimC		3.86	chaperone, periplasmic	100
A_07_P047520	4464843	ECD_04194	yjiC	yjiC	19.98	10.5	hypothetical protein	100
A_07_P004159	4466346	ECD_04195	yjiD	yjiD	47.42	10.99	DNA replication/recombination/repair protein	100
A_07_P017421	4483429	ECD_04211	mcrC	mcrC	22.15		5-methylcytosine-specific restriction enzyme McrBC, subunit McrC	98.25

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A_07_P017427	4484609	ECD_04212	mcrB	mcrB	21.44	4.13	5-methylcytosine-specific restriction enzyme McrBC, subunit McrB	98.21
A_07_P037247	4486097	ECD_04213	yjiW	yjiW	7.3	5.33	hypothetical protein	98.33
A_07_P017518	4520927	ECD_04241	yjjP	yjjP		3.98	predicted inner membrane protein	100
A_07_P042086	4522272	ECD_04242	yjjQ	yjjQ	17.84	10.46	predicted DNA-binding transcriptional regulator	100