

ORF start and unique ID in ERGO		Common gene name	Gene essentiality assertions				Swiss-Prot ID and Functional Description		alias	Functional category	ERI
start			gene	E/N	length	transposon insertions	assertion error	SP_ID			
190	REC00001	<i>thrL</i>	?	21	-	-	P03059	Thr operon leader peptide	b0001	RCD	0.00
337	REC00002	<i>thrA</i>	N	820	101, 130, 218, 291, 315, 401	-	P00561	Bifunctional aspartokinase/homoserine dehydrogenase I	b0002	AAM	0.78
2801	REC00003	<i>thrB</i>	X	310	291, 309	-	P00547	Homoserine kinase (EC 2.7.1.39)	b0003	AAM	0.56
3734	REC00004	<i>thrC</i>	N	428	167, 222, 317, 384	-	P00934	Threonine synthase (EC 4.2.3.1)	b0004	NCM	0.81
5234	REC00005	<i>yaaX</i>	N	98	23, 49	-	P75616	Hypothetical protein yaaX precursor	b0005	UNC	0.00
6459	REC04286	<i>yaaA</i>	N	258	69	-	P11288	Protein yaaA	b0006	UNC	0.25
7959	REC04287	<i>yaaJ</i>	N	476	81, 225, 311	-	P30143	Putative transporter yaaJ	b0007	UNC	0.50
8238	REC00008	<i>talB</i>	N	317	48, 78, 114, 183	-	P30148	Transaldolase B (EC 2.2.1.2)	b0008	CHM	0.78
9306	REC00009	<i>mog</i>	E	195	-	< 0.1	P28694	Molybdopterin biosynthesis mog protein	b0009	NCM	0.63
10494	REC04288	<i>yaaH</i>	N	188	27, 103, 170	-	P28695	Hypothetical protein yaaH	b0010	UNC	0.03
11356	REC04289	<i>yaaW</i>	N	237	49, 80, 109, 221, 226	-	P75617	Hypothetical protein yaaW	b0011	UNC	0.13
11786	REC04290	<i>yaaI</i>	N	134	64, 88	-	P28696	Hypothetical protein yaaI precursor	b0013	UNC	0.00
12163	REC00014	<i>dnaK</i>	E	638	9, 581	< 0.001	P04475	Chaperone protein dnaK	b0014	PMS	1.00
14168	REC00015	<i>dnaJ</i>	N	376	97, 154, 199, 250, 328, 335, 347	-	P08622	Chaperone protein dnaJ	b0015	PMS	1.00
15445	REC06563	<i>dnaX</i>	N	370	19, 107, 223, 295, 339	-	P08409	Putative transposase insL for insertion sequence element IS186A/	b0016	UNC	0.00
16960	REC04292	<i>hokC</i>	N	69	40	-	P22982	HokC protein	b0018.1	UNC	0.00
17489	REC00019	<i>nhaA</i>	N	388	42, 62, 99, 128, 158, 183, 205, 255, 261, 296, 307, 342, 376, 385	-	P13738	Na(+)/H(+) antiporter 1	b0019	MTR	0.28
18715	REC00020	<i>nhaR</i>	N	301	24, 52, 112, 134, 244, 264	-	P10087	Transcriptional activator protein nhaR	b0020	RCD	0.03
20314	REC06564	<i>insB1</i>	N	167	58	-	P03830	Insertion element IS1 1/5/6 protein insB	b0021	PHT	0.00
20508	REC06565	<i>insA</i>	E	91	-	< 0.2	P03827	Insertion element IS1 1/2/3/5/6 protein insA	b0022	PHT	0.00
21078	REC04295	<i>ipsT</i>	E	87	71	< 0.2	P02378	30S ribosomal protein S20	b0023	PMS	0.78
21181	REC00024	<i>yaaY</i>	?	72	-	-	P75620	Hypothetical protein yaaY	b0024	UNC	0.00
21407	REC00025	<i>ribF</i>	E	313	-	< 0.001	P08391	Riboflavin biosynthesis protein ribF	b0025	NCM	0.94
22391	REC06566	<i>ileS</i>	E	938	-	< 0.001	P00956	Isoleucyl-tRNA synthetase (EC 6.1.1.5)	b0026	PMS	1.00
25207	REC00027	<i>lspA</i>	E	164	-	< 0.3	P00804	Lipoprotein signal peptidase (EC 3.4.23.36)	b0027	PMS	0.97
25826	REC00028	<i>fkpB</i>	N	149	54, 105	-	P22563	FKBP-type 16 kDa peptidyl-prolyl cis-trans isomerase (EC 5.2.1.8)	b0028	PMS	0.34
26277	REC00029	<i>ispH*</i>	E	313	203	< 0.05	P22565	Isoprenyl pyrophosphate lyase (EC 5.4.1.13)	b0029	LPC	0.75
27293	REC00030	<i>yaaF</i>	N	304	98, 181, 186, 246, 248	-	P22564	Hypothetical protein yaaF	b0030	UNC	0.41
28374	REC00031	<i>dapB</i>	E	273	-	< 0.1	P04036	Dihydrodipicolinate reductase (EC 1.3.1.26)	b0031	AAM	0.84
29651	REC00032	<i>carA</i>	N	382	186, 219, 304, 326	-	P00907	Carbamoyl-phosphate synthase small chain (EC 6.3.5.5)	b0032	AAM	0.81
30817	REC00033	<i>carB</i>	N	1073	111, 121, 148, 193, 588, 596, 732, 802, 933	-	P00968	Carbamoyl-phosphate synthase large chain (EC 6.3.5.5)	b0033	AAM	0.81
34195	REC00034	<i>caiF</i>	N	166	63, 94, 110, 120, 159, 166	-	Q47081	Transcriptional activator protein caiF	b0034	UNC	0.00
35392	REC04296	<i>caiE</i>	N	203	150, 188, 202	-	P39206	Carnitine operon protein caiE	b0035	UNC	0.00
36270	REC04297	<i>caiD</i>	N	297	3, 52, 70, 105, 266, 281	-	P31551	Carnitine racemase (EC 5.-.-.-)	b0036	AAM	0.19
37839	REC04298	<i>caiC</i>	N	522	355, 435, 478	-	P31552	Probable crotonobetaine/carnitine-CoA ligase (EC 6.3.2.-)	b0037	UNC	0.19
39115	REC04299	<i>caiB</i>	N	405	56, 95, 148, 204, 229, 256, 300, 346, 355	-	P31572	L-carnitine dehydratase (EC 4.2.1.89)	b0038	AAM	0.00
40386	REC04300	<i>caiA</i>	N	380	52, 196, 301, 354	-	P31571	Probable carnitine operon oxidoreductase caiA (EC 1.3.99.-)	b0039	UNC	0.41
41931	REC04301	<i>caiT</i>	N	504	15, 38, 159, 196, 320, 350, 407	-	P31553	Probable carnitine transporter	b0040	UNC	0.00
42367	REC00041	<i>fixA</i>	N	268	35, 56, 57, 85	-	P31573	FixA protein	b0041	UNC	0.44
43188	REC00042	<i>fixB</i>	N	313	28, 245	-	P31574	FixB protein	b0042	UNC	0.25
44180	REC00043	<i>fixC</i>	N	428	26, 30, 43, 138, 164, 161, 167, 223, 313, 409	-	P31575	FixC protein	b0043	UNC	0.34
45463	REC00044	<i>fixX</i>	N	95	66	-	P31576	Ferredoxin-like protein	b0044	UNC	0.13
45807	REC00045	<i>yaaU</i>	N	443	117, 179, 320, 422	-	P31679	Hypothetical metabolite transport protein yaaU	b0045	UNC	0.22
47246	REC00046	<i>yabF</i>	N	176	150	-	P31577	Putative NAD(P)H oxidoreductase yabF (EC 1.6.99.-)	b0046	UNC	0.19
47769	REC00047	<i>kefC</i>	N	620	3, 25, 81, 102, 121, 231, 327, 359, 415, 442, 474	-	P03819	Glutathione-regulated potassium-efflux system protein kefC	b0047	MTR	0.16
49823	REC00048	<i>folA</i>	E	159	-	< 0.2	P00379	Dihydrofolate reductase (EC 1.5.1.3)	b0048	NCM	0.69
51222	REC04302	<i>apaH</i>	N	280	84, 205	-	P05637	Bis(5'-nucleosyl)-tetraphosphatase, symmetrical (EC 3.6.1.41)	b0049	NCM	0.25
51606	REC04303	<i>apaG</i>	N	125	18, 60	-	P05636	ApaG protein	b0050	UNC	0.31
52430	REC04304	<i>ksgA</i>	N	273	1, 29, 123, 187	-	P06992	Dimethyladenosine transferase (EC 2.1.1.-)	b0051	NAM	1.00
53416	REC04305	<i>pdxA</i>	N	329	86, 90, 194, 212, 267, 320	-	P19624	4-hydroxythreonine-4-phosphate dehydrogenase (EC 1.1.1.262)	b0052	NCM	0.50
54702	REC04306	<i>suzA</i>	N	428	152, 274, 293, 347, 405	-	P21202	Survival protein surA precursor (EC 5.2.1.8)	b0053	UNC	0.53
57109	REC04307	<i>imp</i>	E	784	767	< 0.001	P31554	Organic solvent tolerance protein precursor	b0054	UNC	0.47
57364	REC00055	<i>djIA</i>	N	271	1, 10, 76, 105, 188, 252	-	P31680	DnaJ-like protein djIA	b0055	PMS	0.09
58474	REC00056	<i>yabP</i>	N	216	17, 37, 59, 66, 142, 205	-	P39220	Hypothetical protein yabP	b0056	UNC	0.00
59121	REC00057	<i>yabQ</i>	N	52	10	-	P39221	Hypothetical protein yabQ	b0057	UNC	0.00
60346	REC04308	<i>rluA</i>	E	219	-	< 0.05	P39219	Ribosomal large subunit pseudouridine synthase A (EC 4.2.1.70)	b0058	NAM	0.25
63264	REC04309	<i>hepA</i>	N	968	40, 73, 107, 225, 253, 301, 335, 429, 443, 483	-	P23852	RNA polymerase associated protein	b0059	UNC	0.25
65780	REC04310	<i>poLB</i>	N	783	119, 129, 169, 173, 206, 396, 427, 518, 575, 658, 737	-	P21189	DNA polymerase II (EC 2.7.7.7)	b0060	NAM	0.06
66550	REC04311	<i>araD</i>	N	231	9, 37, 160	-	P08203	L-ribulose-5-phosphate 4-epimerase (EC 5.1.3.4)	b0061	CHM	0.22
68337	REC04312	<i>araA</i>	N	500	255, 312, 377, 440, 454	-	P08202	L-arabinose isomerase (EC 5.3.1.4)	b0062	CHM	0.13
70048	REC04313	<i>araB</i>	N	566	22, 73, 75, 130, 190, 215, 227, 276, 288, 310, 462, 467	-	P08204	L-ribulokinase (EC 2.7.1.16)	b0063	CHM	0.06
70387	REC00064	<i>araC</i>	N	292	102, 265	-	P03021	Arabinose operon regulatory protein	b0064	RCD	0.16
71351	REC00065	<i>yabI</i>	N	254	12, 58	-	P30149	Hypothetical protein yabI	b0065	UNC	0.16
72927	REC04314	<i>thiQ</i>	N	232	66, 78, 215	-	P31548	Thiamine transport ATP-binding protein thiQ	b0066	MTR	0.38
74521	REC04315	<i>thiP</i>	N	536	55, 75, 223, 227, 303, 359, 529	-	P31549	Thiamine transport system permease protein thiP	b0067	MTR	0.19
75480	REC04316	<i>tbpA</i>	N	327	34, 185, 249	-	P31550	Thiamine-binding periplasmic protein precursor	b0068	MTR	0.31
77299	REC04317	<i>yabN</i>	N	551	43, 54, 109, 147, 276, 395, 424	-	P33595	Hypothetical protein yabN	b0069	UNC	0.13
77621	REC00070	<i>setA</i>	N	392	316	-	P31675	Sugar efflux transporter A	b0070	MTR	0.13
79453	REC04318	<i>leuD</i>	N	201	29, 79, 166, 185, 194	-	P30126	3-isopropylmalate dehydratase small subunit (EC 4.2.1.33)	b0071	AAM	0.78
80864	REC04319	<i>leuC</i>	N	466	8, 22, 116, 217, 361, 423, 458	-	P30127	3-isopropylmalate dehydratase large subunit (EC 4.2.1.33)	b0072	AAM	0.78
81961	REC04320	<i>leuB</i>	N	364	167, 235	-	P30125	3-isopropylmalate dehydrogenase (EC 1.1.1.85)	b0073	AAM	0.81
83529	REC04321	<i>leuA</i>	N	523	31, 66, 125, 213, 293, 392, 453	-	P09151	2-isopropylmalate synthase (EC 4.1.3.12)	b0074	AAM	0.78
83708	REC04322	<i>leuL</i>	N	28	6, 16	-	P09149	Leu operon leader peptide	b0075	RCD	0.00
84191	REC00076	<i>leuO</i>	N	373	76, 158, 307, 349	-	P10151	Probable activator protein in leuABCD operon	b0076	UNC	0.25
85540	REC00077	<i>ilvI</i>	N	604	61, 87, 126, 162, 345, 434, 602	-	P00893	Acetolactate synthase isozyme III large subunit (EC 4.1.3.18)	b0077	AAM	0.78
87357	REC00078	<i>ilvH</i>	N	163	32, 85, 138, 143	-	P00894	Acetolactate synthase isozyme III small subunit (EC 4.1.3.18)	b0078	AAM	0.69
87860	REC00079	<i>fruL</i>	?	28	-	-	P22183	Very hypothetical fruR/shi operon leader peptide	b0079	UNC	0.00
88028	REC00080	<i>fruR</i>	N	334	63, 104	-	P21186	Fructose repressor	b0080	RCD	0.16
89634	REC00081	<i>mraZ</i>	N	152	37	-	P22188	Protein mraZ	b0081	UNC	0.50
90094	REC00082	<i>mraW</i>	E	313	-	< 0.05	P18595	S-adenosyl-methyltransferase mraW (EC 2.1.1.-)	b0082	RCD	1.00
91032	REC00083	<i>ftsL</i>	E	121	-	< 0.3	P22187	Cell division protein ftsL	b0083	RCD	0.13
91413	REC00084	<i>ftsI</i>	E	588	-	< 0.001	P04286	Peptidoglycan synthetase ftsI precursor	b0084	LPC	0.91
93166	REC00085	<i>murE</i>	E	495	405	< 0.01	P22188	UDP-N-acetylmuramoylalanine-D-glutamate--2,6-diaminopimelate ligase	b0085	LPC	0.97
94650	REC00086	<i>murF</i>	N	452	217	-	P11880	UDP-N-acetylmuramoylalanine-D-glutamate-2,6-diaminopimelate--D-ribitol ligase	b0086	LPC	0.91
96002	REC00087	<i>mraY</i>	N	360	89	-	P15876	Phospho-N-acetylmuramoyl-pentapeptide-transferase (EC 2.7.8.1)	b0087	LPC	0.97
97087	REC00088	<i>murD</i>	E	438	27, 102	< 0.05	P14900	UDP-N-acetylmuramoylalanine--D-glutamate ligase (EC 6.3.2.9)	b0088	LPC	0.97
98403	REC00089	<i>ftsW</i>	E	414	-	< 0.1	P16457	Cell division protein ftsW	b0089	RCD	0.88

99644	REC00090	<i>murG</i>	E	355	-	< 0.2	P17443	UDP-N-acetylglucosamine--N-acetylmuramyl-(Pentapeptide) pyro	b0090	LPC	0.97
100765	REC00091	<i>murC</i>	E	491	-	< 0.001	P17952	UDP-N-acetylmuramate--alanine ligase (EC 6.3.2.8)	b0091	LPC	0.97
102233	REC00092	<i>ddlB</i>	E	306	-	n.d.	P07862	D-alanine-D-alanine ligase B (EC 6.3.2.4)	b0092	LPC	0.91
103155	REC00093	<i>ftsQ</i>	E	276	-	n.d.	P06136	Cell division protein ftsQ	b0093	RCD	0.41
103982	REC00094	<i>ftsA</i>	E	420	-	n.d.	P06137	Cell division protein ftsA	b0094	RCD	0.81
105305	REC00095	<i>ftsZ</i>	E	383	-	n.d.	P06138	Cell division protein ftsZ	b0095	RCD	0.97
106557	REC00096	<i>lpxC</i>	?	305	7, 58		P07652	UDP-3-O-[3-hydroxymyristoyl] N-acetylglucosamine deacetylase (I	b0096	LPC	0.59
107630	REC00097	<i>secM</i>	E	195	-	< 0.05	P10409	Secretion monitor precursor	b0097	RCD	0.00
108279	REC00098	<i>secA</i>	E	901	839, 861, 870	< 0.001	P10408	Preprotein translocase secA subunit	b0098	PMS	1.00
111044	REC00099	<i>mutT</i>	N	129	38, 79		P08337	Mutator mutT protein (EC 3.6.1.-)	b0099	NAM	0.50
111698	REC04323		?	44	8, 12		P75643	FROM BASES 105245 TO 117678 (SECTION 9 OF 400) OF THE	b0100	UNC	0.00
111846	REC04324	<i>yacG</i>	?	65	57, 61		P36681	Hypothetical protein yacG	b0101	UNC	0.28
112599	REC04325	<i>yacF</i>	N	247	123		P36680	Hypothetical protein yacF	b0102	UNC	0.06
113219	REC04326	<i>coaE</i>	E	206	193	< 0.1	P36679	Dephospho-CoA kinase (EC 2.7.1.24)	b0103	NCM	0.94
113444	REC00104	<i>guaC</i>	N	347	7, 73, 119, 143, 157, 212, 312		P15344	GMP reductase (EC 1.6.6.8)	b0104	NCM	0.34
115724	REC04328	<i>hofC</i>	N	400	19, 39, 156, 234, 348		P36646	Protein transport protein hofC	b0106	UNC	0.56
117099	REC04329	<i>hofB</i>	N	461	96, 138, 181, 345		P36645	Protein transport protein hofB	b0107	UNC	0.16
117549	REC04330	<i>ppdD</i>	N	146	36, 36, 61		P36647	Prepilin peptidase dependent protein D precursor	b0108	UNC	0.06
118645	REC04331	<i>nadC</i>	N	297	114		P30011	Nicotinate-nucleotide pyrophosphorylase [carboxylating] (EC 4.2.4.2)	b0109	NCM	0.69
118733	REC00110	<i>ampD</i>	N	183	18, 65, 117, 176		P13016	AmpD protein	b0110	UNC	0.34
119281	REC00111	<i>ampE</i>	N	284	110, 200, 213, 266, 276		P13017	AmpE protein	b0111	UNC	0.00
121551	REC04332	<i>aroP</i>	N	457	68, 229, 253, 273, 295, 327, 348		P15993	Aromatic amino acid transport protein aroP	b0112	MTR	0.03
122092	REC00113	<i>pdhR</i>	N	254	186		P06957	Pyruvate dehydrogenase complex repressor	b0113	RCD	0.47
123017	REC00114	<i>aceE</i>	N	887	126, 168, 194, 253, 453, 470, 525, 564, 599, 614, 673, 687, 748, 796		P06958	Pyruvate dehydrogenase E1 component (EC 1.2.4.1)	b0114	CHM	0.38
125695	REC00115	<i>aceF</i>	E	630	-	< 0.0001	P06959	Dihydroliipoamide acetyltransferase component of pyruvate dehydri	b0115	NCM	0.72
127912	REC00116	<i>lpdA</i>	E	474	-	< 0.01	P00391	Dihydroliipoamide dehydrogenase (EC 1.8.1.4)	b0116	CHM	0.84
131260	REC04333	<i>yacH</i>	N	617	26, 120, 143, 144, 192, 204, 313, 480, 547		P36682	Hypothetical protein yacH	b0117	UNC	0.03
131615	REC00118	<i>acnB</i>	N	865	695, 712, 774, 777, 650		P36683	Aconitate hydratase 2 (EC 4.2.1.3)	b0118	CHM	0.38
134340	REC00119	<i>yacl</i>	N	136	67, 123		P45567	Hypothetical protein yacl	b0119	UNC	0.06
135582	REC04334	<i>speD</i>	N	264	97, 140, 144, 202, 208		P09159	S-adenosylmethionine decarboxylase proenzyme (EC 4.1.1.50)	b0120	MSM	0.13
136464	REC04335	<i>speE</i>	N	288	38, 87		P09158	Spermidine synthase (EC 2.5.1.16)	b0121	AAM	0.38
137040	REC04336	<i>yacC</i>	E	156	-	< 0.2	P23838	Hypothetical protein yacC precursor	b0122	UNC	0.00
137083	REC00123	<i>cueO</i>	N	516	24, 32, 146, 161, 242, 321, 321, 392, 405		P36649	Blue copper oxidase cueO precursor	b0123	UNC	0.41
141225	REC04337	<i>gcd</i>	N	796	20, 23, 157, 181, 578, 601, 644, 694		P15877	Glucose dehydrogenase [pyroloquinoline-quinone] (EC 1.1.99.17)	b0124	CHM	0.73
141419	REC00125	<i>hpt</i>	N	182	10, 17, 89, 96, 143		P36766	Hypoxanthine phosphoribosyltransferase (EC 2.4.2.8)	b0125	NCM	0.15
142670	REC04338	<i>yadF</i>	E	220	-	< 0.05	P36857	Protein yadF	b0126	UNC	0.66
142779	REC00127	<i>yadG</i>	N	308	19, 124, 157, 225, 238		P36879	Hypothetical ABC transporter ATP-binding protein yadG	b0127	UNC	0.50
143702	REC00128	<i>yadH</i>	N	256	21, 43, 194		P36880	Hypothetical protein yadH	b0128	UNC	0.41
144577	REC00129	<i>yadI</i>	E	146	-	< 0.2	P36881	Putative PTS system IIA component yadI (EC 2.7.1.69)	b0129	UNC	0.00
145081	REC00130	<i>yadE</i>	N	409	35, 146, 378		P31666	Hypothetical protein yadE precursor	b0130	UNC	0.25
146694	REC04339	<i>panD</i>	N	126	23, 23, 89		P31664	Aspartate 1-decarboxylase precursor (EC 4.1.1.11)	b0131	AAM	0.63
146968	REC00132	<i>yadD</i>	N	300	134, 135, 153, 227, 273, 277		P31665	Hypothetical protein yadD	b0132	UNC	0.00
148795	REC04340	<i>panC</i>	N	146	283		P31663	Pantoate-beta-alanine ligase (EC 6.3.2.1)	b0133	NCM	0.75
149601	REC04341	<i>panB</i>	N	264	198		P31057	3-methyl-2-oxobutanoate hydroxymethyltransferase (EC 2.1.2.11)	b0134	NCM	0.75
150953	REC04342	<i>yadC</i>	N	412	33, 89, 206, 273, 278, 317, 372		P31058	Hypothetical fibrial-like protein yadC precursor	b0135	UNC	0.00
151599	REC04343	<i>yadK</i>	N	198	18, 36, 49, 84, 100, 104, 124, 133, 178		P37016	Protein yadK	b0136	UNC	0.00
152231	REC04344	<i>yadL</i>	N	201	33, 49, 145, 150, 180		P37017	Hypothetical protein yadL precursor	b0137	UNC	0.00
152854	REC04345	<i>yadM</i>	N	203	71, 125, 132, 183, 199		P37018	Hypothetical protein yadM precursor	b0138	UNC	0.00
154262	REC04346	<i>htrE</i>	N	865	53, 66, 116, 184, 199, 232, 267, 300, 315, 330, 337, 361, 389, 395, 425, 457		P33129	Outer membrane usher protein htrE precursor	b0139	UNC	0.06
156201	REC04347	<i>ecpD</i>	N	246	221		P31218	Chaperone protein ecpD precursor	b0140	UNC	0.06
156883	REC04348	<i>yadN</i>	N	194	171		P37050	Hypothetical fibrial-like protein yadN precursor	b0141	UNC	0.00
157732	REC04349	<i>folK</i>	E	159	-	< 0.1	P26281	2-amino-4-hydroxy-6-hydroxymethylidihydropteridine pyrophospho	b0142	NCM	0.84
159093	REC04350	<i>pcnB</i>	N	454	32, 39, 144, 247, 303, 350		P13685	Poly(A) polymerase (EC 2.7.7.19)	b0143	NAM	0.97
160112	REC04351	<i>yadB</i>	N	308	41, 79, 151, 266		P27305	Hypothetical protein yadB	b0144	UNC	1.00
160604	REC04352	<i>dksA</i>	N	151	34, 50		P18274	DnaK suppressor protein	b0145	UNC	0.47
161486	REC04353	<i>sfsA</i>	N	234	87, 124, 162, 165, 166, 172, 194, 210, 217		P18273	Sugar fermentation stimulation protein A	b0146	UNC	0.38
162040	REC04354	<i>ligT</i>	N	179	91, 127, 141, 179		P37025	2'-5' RNA ligase (EC 6.5.1.-)	b0147	NAM	0.38
162060	REC00148	<i>hrpB</i>	N	824	38, 255, 271, 492, 655, 754, 785, 794		P37024	ATP-dependent helicase hrpB	b0148	NAM	0.38
164730	REC00149	<i>mrcB</i>	N	844	19, 30, 110, 178, 229, 284, 295, 389, 433, 593, 840		P02919	Penicillin-binding protein 1B	b0149	LPC	0.59
167484	REC00150	<i>fhua</i>	N	747	45, 135, 204, 213, 291, 321, 331, 413, 519, 554, 571, 653, 672		P06971	Ferrichrome-iron receptor precursor	b0150	MTR	0.31
169778	REC00151	<i>fhuc</i>	N	265	46, 79, 191		P07821	Ferrichrome transport ATP-binding protein fhuc	b0151	MTR	0.69
170575	REC00152	<i>fhud</i>	N	296	248		P07822	Ferrichrome-binding periplasmic protein precursor	b0152	MTR	0.16
171462	REC00153	<i>fhub</i>	N	660	15, 43, 125, 126, 169, 212, 284, 342, 350, 547		P06972	Ferrichrome transport system permease protein fhub	b0153	MTR	0.69
174882	REC04355	<i>hemL</i>	E	426	-	< 0.01	P23893	Glutamate-1-semialdehyde 2,1-aminomutase (EC 5.4.3.8)	b0154	NCM	0.75
175107	REC00155	<i>eriC</i>	N	473	107, 137, 172, 230, 261, 333, 401, 415		P37019	Voltage-gated ClC-type chloride channel eriC	b0155	MTR	0.47
176610	REC00156	<i>yadR</i>	N	114	39		P37026	Hypothetical protein yadR	b0156	UNC	0.66
177624	REC04356	<i>yadS</i>	?	207	151		P37027	Hypothetical protein yadS	b0157	UNC	0.41
178462	REC04357	<i>btuF</i>	N	266	168, 214, 254		P37028	Vitamin B12 transport protein btuF precursor	b0158	MTR	0.44
179153	REC04358	<i>mtn</i>	E	232	14	< 0.05	P24247	MTA/SAH nucleosidase	b0159	MSM	0.53
179237	REC00160	<i>dgt</i>	N	505	122, 241, 260, 313, 337, 359, 486		P15723	Deoxyguanosinetriphosphate triphosphohydrolase (EC 3.1.5.1)	b0160	NCM	0.47
180884	REC00161	<i>degP</i>	N	474	48, 135, 262, 309, 356, 382, 441		P09376	Protease do precursor (EC 3.4.21.-)	b0161	PMS	0.94
182445	REC00162	<i>cdar</i>	N	391	8, 18, 90, 124, 290, 388		P37047	Carbohydrate diacid regulator	b0162	RCD	0.16
184095	REC04359	<i>yaeH</i>	N	128	21		P37048	Hypothetical protein yaeH	b0163	UNC	0.03
185000	REC04360	<i>yaeI</i>	N	247	30, 40, 64, 73, 127, 164, 228		P37049	Hypothetical protein yaeI	b0164	UNC	0.25
185947	REC04362	<i>dapD</i>	E	274	-	< 0.01	P03948	2,3,4,5-tetrahydropteridine-2-carboxylate N-succinyltransferase (EC	b0166	AAM	0.53
188650	REC04363	<i>glnD</i>	E	890	-	< 0.001	P27249	[Protein-PilI] uridylyltransferase (EC 2.7.7.59)	b0167	SMC	0.38
189506	REC04364	<i>map</i>	E	264	222, 239	< 0.01	P07906	Methionine aminopeptidase (EC 3.4.11.18)	b0168	PMS	1.00
189874	REC00169	<i>tpsB</i>	E	241	-	< 0.05	P02351	30S ribosomal protein S2	b0169	PMS	1.00
190857	REC00170	<i>tsf</i>	E	283	-	< 0.01	P02997	Elongation factor Ts	b0170	PMS	1.00
191855	REC00171	<i>pyrH</i>	E	241	-	< 0.1	P29464	Uridylate kinase (EC 2.7.4.-)	b0171	NCM	0.94
192872	REC00172	<i>frr</i>	E	185	-	< 0.2	P16174	Ribosome recycling factor	b0172	PMS	1.00
193521	REC00173	<i>dxr</i>	E	398	-	< 0.01	P45568	1-deoxy-D-xylulose 5-phosphate reductoisomerase (EC 1.1.1.267)	b0173	LPC	0.78
194903	REC00174	<i>uppS</i>	E	253	28, 154	< 0.2	Q47675	Undecaprenyl pyrophosphate synthetase (EC 2.5.1.31)	b0174	NCM	0.97
195785	REC00175	<i>cdsA</i>	E	249	244	< 0.1	P06466	Phosphatidate cytidylyltransferase (EC 2.7.7.41)	b0175	LPC	0.94
196546	REC00176	<i>ecfE</i>	N	450	34, 236, 297		P37764	Protease ecfE (EC 3.4.24.-)	b0176	PMS	0.94
197928	REC00177	<i>yaeT</i>	E	810	-	< 0.001	P39170	Unknown protein from 2D-page spots M62/M63/O3/O9/T35 precu	b0177	UNC	0.59
200482	REC00178	<i>hlpA</i>	N	161	12, 62		P11457	Histone-like protein HLP-1 precursor	b0178	UNC	0.09
200971	REC00179	<i>lpxD</i>	?	341	24		P21645	UDP-3-O-[3-hydroxymyristoyl] glucosamine N-acyltransferase (EC	b0179	LPC	0.59
202101	REC00180	<i>fabZ</i>	E	151	-	< 0.3	P21774	(3R)-hydroxymyristoyl[acyl carrier protein] dehydratase (EC 4.2.1.	b0180	LPC	0.81
202560	REC00181	<i>lpxA</i>	E	262	-	< 0.05	P10440	Acyl[acyl-carrier-protein]-UDP-N-acetylglucosamine O-acyltransf	b0181	LPC</	

208621	REC00185	<i>acca</i>	E	319	-	< 0.01	P30867	Acetyl-coenzyme A carboxylase carboxyl transferase subunit alpha	b0185	LPC	0.75
209679	REC00186	<i>ldcC</i>	N	713	67, 95, 121, 127, 150, 181, 219, 233, 337, 392, 402, 499, 680		P52095	Lysine decarboxylase, constitutive (EC 4.1.1.18)	b0186	AAM	0.09
211850	REC00187	<i>yaeR</i>	N	138	32		P52096	Hypothetical protein yaeR	b0187	UNC	0.53
212331	REC00188	<i>mesJ</i>	E	432	14	< 0.0001	P52097	Putative cell cycle protein mesJ	b0188	UNC	0.97
213938	REC04365	<i>rof</i>	N	86	38		P52098	Rof protein	b0189	UNC	0.03
214143	REC06749	<i>yaeP</i>	?	72	-		P52099	Hypothetical protein yaeP		UNC	0.03
214291	REC00190	<i>yaeQ</i>	N	181	90, 172		P52100	Hypothetical protein yaeQ	b0190	UNC	0.06
214833	REC00191	<i>yaeJ</i>	N	140	20, 100		P40711	Hypothetical protein yaeJ	b0191	UNC	0.22
215269	REC00192	<i>cutF</i>	N	236	90, 124, 148, 159, 190, 208		P40710	Copper homeostasis protein cutF precursor	b0192	UNC	0.03
217057	REC04366	<i>yaeF</i>	N	292	60, 83, 92, 136, 250, 269, 275		P37056	Hypothetical lipoprotein yaeF precursor	b0193	UNC	0.00
218775	REC04367	<i>proS</i>	E	572	564	< 0.001	P16659	Prolyl-tRNA synthetase (EC 6.1.1.15)	b0194	PMS	1.00
219594	REC04368	<i>yaeB</i>	?	235	24		P28634	Hypothetical protein yaeB	b0195	UNC	0.22
219995	REC04369	<i>rcsF</i>	N	134	12, 40, 62, 97		P28633	Protein rcsF	b0196	SMC	0.00
220928	REC04370	<i>yaeC</i>	N	271	176, 216, 224, 235		P28635	Putative lipoprotein yaeC precursor	b0197	UNC	0.69
221621	REC04371	<i>yaeE</i>	N	217	20, 119, 184, 205		P31547	Hypothetical ABC transporter permease protein yaeE	b0198	UNC	0.69
222645	REC04372	<i>abc</i>	N	343	3, 17, 67, 286		P30750	ATP-binding protein abc	b0199	UNC	0.97
222833	REC00200	<i>yaeD</i>	N	191	24, 34, 104		P31546	Hypothetical protein yaeD	b0200	UNC	0.75
229167	REC00201	<i>dkgB</i>	N	267	54, 95, 106, 132, 133, 184, 188, 236, 242, 252		P30863	2,5-diketo-D-gluconic acid reductase B (EC 1.1.1.-)	b0207	CHM	0.53
230881	REC04373	<i>yafC</i>	N	304	53, 87, 93, 109, 158, 195, 208, 231, 249, 283, 287		P30864	Hypothetical transcriptional regulator yafC	b0208	UNC	0.72
231122	REC00203	<i>yafD</i>	N	266	15, 47, 113, 261		P30865	Hypothetical protein yafD	b0209	UNC	0.09
231926	REC00204	<i>yafE</i>	E	207	-	< 0.2	P30866	Hypothetical protein yafE	b0210	UNC	0.13
233955	REC04374	<i>mltD</i>	N	452	63, 109, 180, 196, 253, 326		P23931	Membrane-bound lytic murein transglycosylase D precursor (EC 3	b0211	LPC	0.38
234782	REC04375	<i>gloB</i>	N	251	224		Q47677	Probable hydroxyacylglutathione hydrolase (EC 3.1.2.6)	b0212	UNC	0.81
234798	REC00207	<i>yafS</i>	N	246	41, 53, 193, 198		P75672	Hypothetical protein yafS	b0213	UNC	0.28
236002	REC04376	<i>rnhA</i>	E	155	42, 72	< 0.2	P00647	Ribonuclease HI (EC 3.1.26.4)	b0214	NAM	0.56
236067	REC00209	<i>dnaQ</i>	E	243	138, 240	< 0.05	P03007	DNA polymerase III, epsilon chain (EC 2.7.7.7)	b0215	NAM	0.75
237335	REC00210	<i>yafT</i>	N	261	5, 47, 102, 248		P77339	Hypothetical lipoprotein yafT precursor	b0217	UNC	0.00
239084	REC04377	<i>yafU</i>	N	112	45		P77354	Hypothetical protein yafU	P77358	UNC	0.00
239154	REC06766	<i>yhhI</i>	N	74	66		Q47678	H repeat-associated protein in rhsB-pit intergenic region (orf-h), YhhI protein	b0219	UNC	0.00
240189	REC04378	<i>yafV</i>	N	256	25, 67, 93, 126, 146, 175, 191, 203, 226, 246		Q47679	Hypothetical protein yafV	b0219	UNC	0.75
240343	REC00213	<i>ivy</i>	N	157	31, 98, 143		P45502	Inhibitor of vertebrate lysozyme precursor	b0220	MSM	0.00
243339	REC04379	<i>yafH</i>	N	826	18, 42, 118, 403, 431, 528, 583, 647		Q47146	Hypothetical protein yafH	b0221	UNC	0.25
243543	REC00215	<i>lpcA</i>	N	192	25, 49, 161		P51001	Phosphoheptose isomerase (EC 5.-.-.-)	b0222	CHM	0.38
244327	REC00216	<i>yafJ</i>	N	255	69, 102		Q47147	Hypothetical protein yafJ	b0223	UNC	0.25
245805	REC04380	<i>yafK</i>	N	246	21, 52, 175, 229		Q47148	Hypothetical protein yafK precursor	b0224	UNC	0.13
246239	REC04381	<i>yafQ</i>	?	92	1		Q47149	Hypothetical protein yafQ	b0225	UNC	0.19
246502	REC04382	<i>dinJ</i>	N	86	30, 31		Q47150	DNA-damage-inducible protein J	b0226	UNC	0.06
246712	REC00220	<i>yafL</i>	N	249	6, 30, 53, 106, 115, 165, 184, 203		Q47151	Hypothetical lipoprotein yafL precursor	b0227	UNC	0.09
247637	REC00221	<i>yafM</i>	N	165	61, 69, 136		Q47152	Hypothetical protein yafM	b0228	UNC	0.16
250042	REC00223	<i>mbhA</i>	N	261	105, 138, 150, 202, 204		Q47154	MbhA protein	b0230	UNC	0.22
250097	REC04383	<i>fhiA</i>	N	579	330, 439		Q47153	FhiA protein	b0229	UNC	0.13
250898	REC00224	<i>dinP</i>	N	351	45, 78, 236		Q47155	DNA-damage-inducible protein P	b0231	UNC	0.59
252005	REC00225	<i>yafN</i>	N	97	30, 31		Q47156	Hypothetical protein yafN	b0232	UNC	0.00
252301	REC00226	<i>yafO</i>	N	132	52, 53		Q47157	Hypothetical protein yafO	b0233	UNC	0.00
252709	REC00227	<i>yafP</i>	N	150	13, 122, 127, 141		Q47158	Hypothetical acetyltransferase yafP (EC 2.3.1.-)	b0234	UNC	0.25
253467	REC00228	<i>ykfJ</i>	N	88	27, 46		P75675	Hypothetical protein ykfJ	b0235	UNC	0.31
253702	REC00229	<i>prfH</i>	N	166	31, 74, 150		P28369	Peptide chain release factor homolog	b0236	UNC	0.09
255716	REC04384	<i>pepD</i>	N	485	36, 59, 269, 277, 361, 442, 452		P15288	Aminoacyl-histidine dipeptidase (EC 3.4.13.3)	b0237	PMS	0.16
255977	REC00231	<i>gpt</i>	?	152	122		P00501	Xanthine-guanine phosphoribosyltransferase (EC 2.4.2.22)	b0238	NCM	0.22
256527	REC00232	<i>yafA</i>	N	414	18, 79, 118, 215, 250, 296, 363, 372		P04335	Hypothetical protein yafA	b0239	UNC	0.03
257829	REC00233	<i>crl</i>	N	133	12, 88		P24251	Curlin genes transcriptional activatory protein	b0240	RCD	0.03
259324	REC04385	<i>phoE</i>	N	351	37, 38, 114, 202, 207, 294		P02932	Outer membrane pore protein E precursor	b0241	SMC	0.00
259612	REC00235	<i>proB</i>	N	367	253, 320		P07005	Glutamate 5-kinase (EC 2.7.2.11)	b0242	AAM	0.75
260727	REC00236	<i>proA</i>	N	417	90, 103, 181, 214, 267, 282, 315		P07004	Gamma-glutamyl phosphate reductase (EC 1.2.1.41)	b0243	AAM	0.75
262893	REC04386	<i>ykfI</i>	E	113	-	< 0.2	P77692	Hypothetical protein ykfI	b0245	UNC	0.00
263231	REC04387	<i>yafW</i>	N	105	86		Q47684	Hypothetical protein yafW	b0246	UNC	0.00
263956	REC06618	<i>ykgG</i>	N	158	17, 52, 64, 86, 99, 101, 122		Q47685	Putative radC-like protein ykgG	b0247	UNC	0.00
264430	REC04388	<i>yafX</i>	N	152	24, 59, 152		P75676	Hypothetical protein yafX	b0248	UNC	0.03
264767	REC04389	<i>ykfF</i>	N	79	34		P75677	Hypothetical protein ykfF	b0249	UNC	0.00
265311	REC04390	<i>ykfB</i>	N	155	54, 145		P77162	Hypothetical protein ykfB precursor	b0250	UNC	0.00
266191	REC04391	<i>yafY</i>	N	285	16		P77365	Hypothetical transcriptional regulator yafY	b0251	UNC	0.03
267244	REC04392	<i>yafZ</i>	N	278	1, 57, 65, 69, 84, 236		P77206	Hypothetical protein yafZ	b0252	UNC	0.03
268187	REC04393	<i>ykfA</i>	N	288	6, 10, 44, 75, 87, 135, 178		P75678	Hypothetical protein ykfA	b0253	UNC	0.00
269406	REC04394	<i>perR</i>	N	297	63, 107, 162, 249		Q57083	Peroxide resistance protein perR	b0254	RCD	0.06
269466	REC00246	<i>insN1</i>	N	134	16, 53		P75679	Transposase insN for insertion sequence element IS911A	b0255	PHT	0.56
269827	REC00247	<i>insI1</i>	N	383	47, 179, 202, 217, 238, 250, 280, 281, 301, 306, 327, 351, 361		P37246	Transposase insI for insertion sequence element IS30B/C/D	b0256	PHT	0.22
271054	REC00248		N	141	13, 26, 64, 74, 118, 120		P75680	FROM BASES 263572 TO 274477 (SECTION 23 OF 400) OF THIB0257	b0257	UNC	0.56
272086	REC00249	<i>ykfC</i>	N	376	45, 61, 133, 138		Q47688	Hypothetical protein ykfC	b0258	UNC	0.19
274341	REC06619		N	338	11, 32, 75, 116, 141, 187		P03837	Transposase insH for insertion sequence element IS5	b0259	PHT	0.34
274525	REC00251	<i>mmuP</i>	N	475	39, 63, 107, 114, 144, 171, 173, 240, 284, 366, 421, 459		Q47689	Probable S-methylmethionine permease	b0260	UNC	0.13
275939	REC00252	<i>mmuM</i>	N	310	65, 80		Q47690	Homocysteine S-methyltransferase (EC 2.1.1.10)	b0261	AAM	0.16
278038	REC04396	<i>afuC</i>	N	352	136, 175, 176, 223, 319		P37009	Putative ferric transport ATP-binding protein afuC	b0262	UNC	0.16
278400	REC04397	<i>afuB</i>	N	120	35, 62, 83, 110		P75681	Putative ferric transport system permease protein afuB	b0263	UNC	0.47
278905	REC04398		N	167	89		Q47302	Insertion element IS1 2/3 protein insB	b0264	PHT	0.00
279099	REC04399		E	91	-	0.31	P03827	Insertion element IS1 1/2/3/5/6 protein insA	b0265	PHT	0.00
279592	REC06782		N	114	14, 96		Q57247	HYPOTHETICAL 12.9 kDa PROTEIN	b0266	UNC	0.56
279986	REC04400	<i>yagB</i>	N	125	35, 69, 95		P37008	Hypothetical protein yagB	b0266	UNC	0.00
281207	REC04401	<i>yagA</i>	N	384	4, 33, 79, 110, 150, 348		P37007	Hypothetical protein yagA	b0267	UNC	0.56
281481	REC00259	<i>yagE</i>	N	309	148, 168, 235		P75682	Hypothetical protein yagE	b0268	UNC	0.84
282425	REC00260	<i>yagF</i>	N	655	2, 90, 177, 199, 559, 598, 620, 635		P77596	Hypothetical protein yagF	b0269	UNC	0.78
284619	REC00261	<i>yagG</i>	E	460	5	< 0.01	P75683	Hypothetical symporter yagG	b0270	UNC	0.00
286013	REC00262	<i>yagH</i>	E	536	233, 532	< 0.001	P77713	Putative beta-xylosidase (EC 3.2.1.37)	b0271	UNC	0.13
288386	REC04402	<i>yagI</i>	N	252	19, 77, 196, 208, 227		P77300	Hypothetical transcriptional regulator yagI	b0272	UNC	0.38
289529	REC04403	<i>argF</i>	N	334	3, 187, 259		P06960	Ornithine carbamoyltransferase chain F (EC 2.1.3.3)	b0273	AAM	0.84
290376	REC06620	<i>insB3</i>	N	167	126		Q47302	Insertion element IS1 2/3 protein insB	b0274	PHT	0.00
290570	REC06621		X	91	-		P03827	Insertion element IS1 1/2/3/5/6 protein insA	b0275	PHT	0.00
290724	REC00267	<i>yagJ</i>	N	243	140, 168, 233, 235		P77169	Hypothetical protein yagJ	b0276	UNC	0.00
292172	REC04406	<i>yagK</i>	N	208	50, 74, 113, 140, 156		P77657	Hypothetical protein yagK	b0277	UNC	0.03
293142	REC04407	<i>yagL</i>	N	232	41, 85, 134, 224		P77607	Hypothetical protein yagL	b0278	UNC	0.00
294023	REC06622	<i>yagM</i>	N	284	18, 191		P71296	Hypothetical protein yagM	b0279	UNC	0.00
294803	REC06623	<i>yagN</i>	N	146	24, 106, 115		P71297	Hypothetical protein yagN	b0280	UNC	0.00
296320	REC06624	<i>intF</i>	N	466	91, 151, 228, 308, 387		P71298	Putative prophage CP4-6 integrase	b0281	UNC	0.00

297015	REC04408	yagP	N	136	74	P75684	Hypothetical protein yagP	b0282	UNC	0.72
297950	REC04409	yagQ	N	318	83, 248	P77183	Hypothetical protein yagQ	b0283	UNC	0.13
300158	REC04410	yagR	N	732	174, 266, 341, 412, 448, 539, 656, 670, 680, 708	P77489	Putative xanthine dehydrogenase yagR, molybdenum binding subunit	b0284	UNC	0.22
301111	REC04411	yagS	E	318	-	P77324	Putative xanthine dehydrogenase yagS, FAD binding subunit (EC	b0285	UNC	0.16
301797	REC04412	yagT	N	229	20, 47, 61, 78, 102	P77165	Putative xanthine dehydrogenase yagT iron-sulfur binding subunit	b0286	UNC	0.19
302215	REC00275	yagU	N	204	-	P77262	Hypothetical protein yagU	b0287	UNC	0.06
303406	REC06625	ykgJ	?	109	104	P71300	Hypothetical protein ykgJ	b0288	UNC	0.13
304474	REC04413	yagV	E	251	228	P77263	Hypothetical protein yagV precursor	b0289	UNC	0.00
306041	REC04414	yagW	N	547	2, 48, 82, 125, 189, 304, 325, 368, 426	P77694	Hypothetical protein yagW	b0290	UNC	0.00
308556	REC04415	yagX	N	841	158, 172, 362, 428, 505, 555, 610, 722, 733, 748, 841	P77802	Hypothetical protein yagX precursor	b0291	UNC	0.00
309250	REC04416	yagY	N	222	53, 134	P77188	Hypothetical protein yagY precursor	b0292	UNC	0.00
309895	REC04417	yagZ	N	195	2, 10, 81, 117, 145	P77264	Hypothetical protein yagZ precursor	b0293	UNC	0.00
310560	REC06626	ykgK	N	196	144, 177	P71301	Hypothetical protein ykgK	b0294	UNC	0.00
311336	REC06627	ykgL	?	75	-	P56257	Hypothetical protein ykgL	b0295	UNC	0.00
312001	REC06628	rpmE2	?	87	-	P71302	50S ribosomal protein L31 type B	b0296	PMS	0.41
313581	REC00281	eeah	N	295	35, 69, 195, 250	P36943	Attaching and effacing protein homolog precursor	b0297	UNC	0.00
314506	REC06629	insE1	E	102	-	P77681	Transposase insE for insertion sequence IS3A/B/C/D/E/FA/FB	b0298	PHT	0.56
314811	REC06630	insF1	N	288	99, 287	P05822	Transposase insF for insertion sequence IS3A/B/C/D/E/FA	b0299	PHT	0.56
316393	REC04418	ykgA	X	239	-	P77601	Hypothetical transcriptional regulator ykgA	b0300	UNC	0.22
317526	REC00286		X	89	-	P75686	FROM BASES 311709 TO 323910 (SECTION 27 OF 400) OF THI	b0302	UNC	0.00
317552	REC04419	ykgB	X	200	-	P75685	Hypothetical protein ykgB	b0301	UNC	0.06
319252	REC04421	ykgC	N	450	22, 81, 103, 106, 136, 157, 163, 223	P77212	Probable pyridine nucleotide-disulfide oxidoreductase ykgC	b0302	UNC	0.38
319451	REC00289	ykgD	N	284	16, 31, 173, 195, 246, 280	P77379	Hypothetical transcriptional regulator ykgD	b0305	UNC	0.34
320832	REC00290	ykgE	N	239	13, 18, 145	P77252	Hypothetical protein ykgE	b0306	UNC	0.19
321562	REC00291	ykgF	N	475	148, 152, 252, 301, 362	P77536	Putative electron transport protein ykgF	b0307	UNC	0.22
322829	REC00292	ykgG	N	282	154, 176, 184, 224	P77433	Hypothetical protein ykgG	b0308	UNC	0.19
324588	REC04423	ykgH	N	222	129	P77180	Hypothetical protein ykgH	b0310	UNC	0.00
326471	REC04424	betA	N	556	11, 20, 202, 339, 540	P17444	Choline dehydrogenase (EC 1.1.99.1)	b0311	AAM	0.31
327957	REC04425	betB	N	490	263, 356, 403	P17445	Betaine aldehyde dehydrogenase (EC 1.2.1.8)	b0312	AAM	0.31
328558	REC04426	betI	N	195	57, 107	P17446	Regulatory protein betI	b0313	RCD	0.19
328687	REC00298	betT	N	677	105, 140, 157, 216, 347, 515, 523, 588, 648	P17447	High-affinity choline transport protein	b0314	MTR	0.31
331595	REC00299	yahA	N	362	41, 114, 131, 141, 164, 181, 262, 274, 285, 299	P21514	Hypothetical protein yahA	b0315	UNC	0.31
333657	REC04427	yahB	N	310	9, 59, 155, 285	P77700	Hypothetical transcriptional regulator yahB	b0316	UNC	0.06
334246	REC04428	yahC	N	165	9, 119	P77219	Hypothetical protein yahC	b0317	UNC	0.00
334504	REC00302	yahD	N	201	19, 43, 120, 132, 149, 186	P77736	Hypothetical ANK-repeats protein yahD	b0318	UNC	0.44
335149	REC00303	yahE	N	287	11, 84, 181, 192	P77297	Hypothetical protein yahE	b0319	UNC	0.00
336002	REC00304	yahF	E	515	21, 21	P77187	Hypothetical protein yahF	b0320	UNC	0.69
337549	REC00305	yahG	N	472	17, 253, 271, 431, 455	P77221	Hypothetical protein yahG	b0321	UNC	0.00
338993	REC00306	yahH	E	106	-	P75690	Hypothetical protein yahH	b0322	UNC	0.00
339389	REC00307	yahI	N	316	101, 208	P77624	Carbamate kinase-like protein yahI	b0323	UNC	0.25
340349	REC00308	yahJ	N	460	36, 95, 278	P77554	Hypothetical protein yahJ	b0324	UNC	0.09
342108	REC00309	yahK	N	349	3, 35, 113, 220, 316	P75691	Hypothetical zinc-type alcohol dehydrogenase-like protein yahK	b0325	UNC	0.31
343400	REC00310	yahL	N	271	30, 117, 160, 262	P77393	Hypothetical protein yahL	b0326	UNC	0.00
344598	REC00311	yahM	N	91	30, 60	P75692	Hypothetical protein yahM	b0327	UNC	0.00
345561	REC04429	yahN	N	223	11, 21, 69, 147, 155, 222	P75693	Hypothetical protein yahN	b0328	UNC	0.31
345708	REC00313	yahO	N	91	20	P75694	Hypothetical protein yahO precursor	b0329	UNC	0.00
347667	REC04430	prpR	N	528	82, 89, 114, 151, 244, 404	P77743	Propionate catabolism operon regulatory protein	b0330	RCD	0.59
347906	REC00315	prpB	N	296	40, 45, 82, 123, 199, 282	P77541	Probable methylsuccinate lyase (EC 4.1.3.30)	b0331	UNC	0.41
349188	REC04431		N	148	124, 146	P06941	Hypothetical protein b0332	b0332	UNC	0.00
349236	REC00317	prpC	N	389	172, 259, 352	P31660	2-methylcitrate synthase (EC 4.1.3.31)	b0333	CHM	0.41
350439	REC00318	prpD	N	483	68, 96, 127, 211, 303, 447	P77243	2-methylcitrate dehydratase (EC 4.2.1.79)	b0334	CHM	0.16
351930	REC00319	prpE	N	628	44, 50, 357, 499, 606	P77495	Propionate-CoA ligase (EC 6.2.1.17)	b0335	CHM	0.19
354146	REC00320	codB	N	419	105, 120, 269, 304, 378	P25525	Cytosine permease	b0336	MTR	0.09
355395	REC00321	codA	N	427	225, 372	P25524	Cytosine deaminase (EC 3.5.4.1)	b0337	NCM	0.22
357914	REC04432	cynR	N	299	43, 115, 132, 155, 213	P27111	Cyn operon transcriptional activator	b0338	RCD	0.31
358023	REC00323	cynT	N	219	60, 149, 158	P17582	Carbonic anhydrase (EC 4.2.1.1)	b0339	MSM	0.66
358713	REC00324	cynS	E	156	-	P00816	Cyanate hydratase (EC 4.2.1.104)	b0340	MSM	0.16
359216	REC00325	cynX	N	384	221, 283	P17583	Cyanate transport protein cynX	b0341	MTR	0.03
361084	REC04433	laca	N	203	5, 20, 24, 38, 67, 89, 200	P07464	Galactoside O-acetyltransferase (EC 2.3.1.18)	b0342	CHM	0.44
362403	REC04434	lacY	N	417	20, 64, 123, 184, 204, 227, 250, 273, 293, 307, 341, 378, 393, 404	P02920	Lactose permease	b0343	MTR	0.00
365529	REC04435	lacZ	N	1024	10, 162, 214, 237, 295, 315, 396, 420, 461, 663, 886, 1014, 1020	P00722	Beta-galactosidase (EC 3.2.1.23)	b0344	CHM	0.09
366734	REC04436	lacI	N	302	132, 138	P03023	Lactose operon repressor	b0345	RCD	0.00
367758	REC04437	mphR	N	315	211, 276	P77569	Mhp operon transcriptional activator	b0346	RCD	0.03
367835	REC00331	mhpA	N	554	5, 23, 35, 132, 159, 236, 301, 302, 358, 424	P77397	3-(3-hydroxy-phenyl)propionate hydroxylase (EC 1.14.13.-)	b0347	MSM	0.34
369501	REC00332	mhpB	N	314	53, 131, 250, 290, 312	P54711	2,3-dihydroxyphenylpropionate 1,2-dioxygenase (EC 1.13.11.-)	b0348	MSM	0.00
370400	REC00333	mhpC	N	309	13, 221, 233	P77044	2-hydroxy-6-ketono-2,4-dienedioic acid hydrolase (EC 3.7.1.-)	b0349	MSM	0.16
371333	REC00334	mhpD	N	271	37, 90, 138, 186, 222	P77608	2-keto-4-pentenoate hydratase (EC 4.2.1.-)	b0350	MSM	0.19
372145	REC00335	mhpF	N	316	40, 123, 139, 177, 226, 244	P77580	Acetaldehyde dehydrogenase (EC 1.2.1.10)	b0351	CHM	0.06
373092	REC00336	mhpE	N	337	45, 212	P51020	4-hydroxy-2-oxovalerate aldolase (EC 4.1.3.-)	b0352	MSM	0.06
374638	REC00337	mhpT	N	418	-	P77589	Putative 3-hydroxyphenylpropionic acid transporter	b0353	UNC	0.13
375879	REC00338	yaiL	N	218	-	P51024	Hypothetical protein yaiL	b0354	UNC	0.06
377592	REC04438	yaiM	N	277	-	P51025	Hypothetical protein yaiM	b0355	UNC	0.16
378795	REC04439	adhC	N	369	61, 84, 181, 230	P25437	Alcohol dehydrogenase class III (EC 1.1.1.1) (EC 1.2.1.1)	b0356	CHM	0.59
379126	REC04440	yaiN	E	98	-	P55756	Hypothetical protein yaiN	b0357	UNC	0.00
380066	REC04441	yaiO	N	257	17, 60, 126, 129, 194, 246	Q47534	Hypothetical protein yaiO	b0358	UNC	0.00
380511	REC04442		?	147	-	P75697	FROM BASES 379180 TO 389460 (SECTION 33 OF 400) OF THI	b0359	UNC	0.03
380530	REC06641	insC6	N	136	20, 20	P19776	Transposase insC for insertion element IS2A/D/F/H/I/K	b4272	PHT	0.56
380898	REC06642	insD6	X	301	-	P19777	Transposase insD for insertion element IS2A/D/F/H/I/K	b4273	PHT	0.56
382114	REC04443		X	128	-	P75698	FROM BASES 379180 TO 389460 (SECTION 33 OF 400) OF THI	b0362	UNC	0.00
383159	REC04444	yaiP	X	398	-	Q47536	Hypothetical protein yaiP	b0363	UNC	0.00
383693	REC04445	yaiS	E	136	-	P71311	Hypothetical protein yaiS	b0364	UNC	0.00
384399	REC00349	tauA	N	339	226, 318	Q47537	Taurine-binding periplasmic protein precursor	b0365	MTR	0.28
385431	REC00350	tauB	N	255	102	Q47538	Taurine transport ATP-binding protein tauB	b0366	MTR	0.69
386195	REC00351	tauC	N	275	41, 150	Q47539	Taurine transport system permease protein tauC	b0367	MTR	0.41
387019	REC00352	tauD	N	283	38, 158, 208	P37610	Alpha-ketoglutarate-dependent taurine dioxygenase (EC 1.14.11.1)	b0368	AAM	0.13
388984	REC04446	hemB	E	335	-	P15002	Delta-aminolevulinic acid dehydratase (EC 4.2.1.24)	b0369	NCM	0.78
389390	REC04447		N	89	34	P77362	FROM BASES 379180 TO 389460 (SECTION 33 OF 400) OF THI	b0370	UNC	0.00
389475	REC00355	yaiT	N	486	46, 72, 151, 167, 241, 268, 430	P77199	Hypothetical protein yaiT precursor	b0371	UNC	0.00
391829	REC06643	insF5	E	288	43	P05823	Transposase insF for insertion sequence IS3A/B/C/D/E/FA	b2089	PHT	0.56
392134	REC06644	insE5	E	102	-	P77682	Transposase insE for insertion sequence IS3A/B/C/D/E/FA/FB	b2088	PHT	0.56
392239	REC00358	yaiU	N	467	14, 31, 87, 110, 164, 224, 272, 273, 390, 454	P75700	Hypothetical protein yaiU	b0374	UNC	0.00
393685	REC00359	yaiV	N	222	15, 221	P77723	Hypothetical protein yaiV	b0375	UNC	0.00

395511	REC04450	ampH	N	385	31, 50, 77, 273	P46127	Penicillin-binding protein ampH	b0376	PMS	0.28	
395863	REC00361	sbmA	N	406	51, 106, 129, 171, 175, 246, 320, 380	P24212	SbmA protein	b0377	UNC	0.16	
397096	REC00362	yaiW	N	384	20, 329	P77562	Hypothetical protein yaiW	b0378	UNC	0.03	
398557	REC04451	yaiY	E	102	72	< 0.3	P77669	Hypothetical protein yaiY	b0379	UNC	0.00
398685	REC00364	yaiZ	N	114	45		P77273	Hypothetical protein yaiZ	b0380	UNC	0.00
400147	REC04452	ddlA	N	364	117, 214, 242, 329, 339		P23844	D-alanine-D-alanine ligase A (EC 6.3.2.4)	b0381	LPC	0.91
400610	REC00366	yaiB	?	86			P21831	Hypothetical protein yaiB	b0382	UNC	0.00
400902	REC00367	phoA	N	494	1, 109, 378, 421		P00634	Alkaline phosphatase precursor (EC 3.1.3.1)	b0383	MSM	0.28
402487	REC00368	psiF	N	112	56, 88		P27295	Phosphate starvation-inducible protein psiF precursor	b0384	UNC	0.03
402927	REC00369	yaiC	N	371	77, 151, 176		P21830	Hypothetical protein yaiC	b0385	UNC	0.13
404868	REC00371	yaiI	N	192	101	< 0.05	P52088	Hypothetical protein yaiI	b0387	UNC	0.38
404868	REC04453	proC	E	269	77		P00373	Pyrraline-5-carboxylate reductase (EC 1.5.1.2)	b0386	AAM	0.81
405629	REC00372	aroL	N	174	9, 51, 92, 174		P08329	Shikimate kinase II (EC 2.7.1.71)	b0388	AAM	0.81
406203	REC00373	yaiA	N	63	33		P08366	Hypothetical protein yaiA	b0389	UNC	0.81
406652	REC00374	aroM	N	225	12, 136		P08403	AroM protein	b0390	UNC	0.00
407401	REC00375	yaiE	N	94	44		P36768	Hypothetical protein yaiE	b0391	UNC	0.09
407893	REC00376	ykiA	N	93	37, 69		P75704	Hypothetical protein ykiA	b0392	UNC	0.00
409230	REC00378	yajF	N	348	2, 49, 71, 89, 113		P23917	Hypothetical protein yajF	b0394	UNC	0.19
409243	REC04454	rdgC	N	303	4, 29, 48, 98		P36767	Recombination associated protein rdgC	b0393	UNC	0.19
410255	REC00379		?	80	-		P77351	FROM BASES 400349 TO 411796 (SECTION 35 OF 400) OF THIS	b0395	UNC	0.00
411705	REC04455	araJ	N	394	199, 215, 324, 366		P23910	Protein araJ precursor	b0396	UNC	0.00
414977	REC04456	sbcC	N	1048	204, 278, 289, 376, 442, 487, 518, 522, 579, 758, 808, 878		P13458	Exonuclease sbcC	b0397	NAM	0.31
416176	REC04457	sbcD	N	400	74, 85, 124, 327		P13457	Nuclease sbcCD subunit D	b0398	NAM	0.41
416366	REC00383	phoB	N	229	5, 44, 81, 115, 134, 178, 217		P08402	Phosphate regulon transcriptional regulatory protein phoB	b0399	RCD	0.75
417113	REC00384	phoR	N	431	63, 117, 275, 292		P08400	Phosphate regulon sensor protein phoR (EC 2.7.3.-)	b0400	MSM	0.69
418815	REC00385	brnQ	N	439	96, 165, 252, 268, 321, 363, 426		P37011	Branched-chain amino acid transport system II carrier protein	b0401	MTR	0.34
420210	REC00386	proY	N	457	41, 152, 158, 227, 295, 345, 413		P77327	Proline-specific permease proY	b0402	MTR	0.09
421739	REC00387	malZ	N	605	86, 246, 304, 323, 347, 351, 460, 477, 507, 542, 594		P21517	Maltodextrin glucosidase (EC 3.2.1.20)	b0403	CHM	0.28
424142	REC04458	yajB	N	193	5, 54, 156		P21515	Hypothetical protein yajB	b0404	UNC	0.06
424235	REC00389	queA	N	356	256		P21516	S-adenosylmethionine:tRNA ribosyltransferase-isomerase (EC 5.-	b0405	NAM	0.84
425361	REC00390	tgt	N	375	218, 300, 332		P19675	Queue tRNA-ribosyltransferase (EC 2.4.2.29)	b0406	NAM	0.91
426511	REC00391	yajC	?	110	-		P19677	Hypothetical protein yajC	b0407	UNC	0.78
426871	REC00392	secD	E	615	-	< 0.0001	P19673	Protein-export membrane protein secD	b0408	PMS	0.88
428729	REC00393	secF	E	323	-	< 0.05	P19674	Protein-export membrane protein secF	b0409	PMS	0.75
429829	REC00394	yajD	N	115	35, 101		P19678	Hypothetical protein yajD	b0410	UNC	0.00
431237	REC04459	tsx	N	294	18, 69, 163, 224, 243, 269, 288		P22786	Nucleoside-specific channel-forming protein tsx precursor	b0411	MTR	0.03
432135	REC04460	yajI	N	199	44, 55		P46122	Hypothetical lipoprotein yajI precursor	b0412	UNC	0.00
432226	REC00397	ybaD	?	149	19		P25538	Hypothetical protein ybaD	b0413	UNC	0.72
432679	REC00398	ribD	E	367	-	< 0.001	P25539	Riboflavin biosynthesis protein ribD	b0414	NCM	0.84
433871	REC00399	ribH	E	156	-	< 0.1	P25540	6,7-dimethyl-8-ribityllumazine synthase (EC 2.5.1.9)	b0415	NCM	0.84
434361	REC00400	nusB	E	139	-	< 0.1	P04381	N utilization substance protein B	b0416	RCD	0.88
434858	REC00401	thiL	E	325	-	< 0.01	P77785	Thiamine-monophosphate kinase (EC 2.7.4.16)	b0417	NCM	0.47
435813	REC00402	pppA	E	172	-	< 0.2	P18200	Phosphatidylglycerophosphatase A (EC 3.1.3.27)	b0418	LPC	0.31
437431	REC04461	yajO	N	348	170, 175, 237, 280, 299, 303		P77735	Hypothetical oxidoreductase yajO (EC 1.-.-.-)	b0419	UNC	0.41
439401	REC04462	dxs	E	620	-	< 0.0001	P77488	1-deoxy-D-xylulose 5-phosphate synthase (EC 4.1.3.37)	b0420	NCM	0.88
440325	REC04463	ispA	E	299	-	< 0.05	P22939	Geranyltranstransferase (EC 2.5.1.10)	b0421	LPC	0.84
440567	REC04464	xseB	?	80	-		P22938	Oxerythronuclease VII small subunit (EC 3.1.11.6)	b0422	NAM	0.16
440773	REC00407	thiI	N	482	245, 325		P77718	Thiamine biosynthesis protein thiI	b0423	NCM	0.34
442871	REC04465	thiJ	N	198	133		Q46948	4-methyl-5(B-hydroxyethyl)-thiazole monophosphate biosynthesis	b0424	NCM	0.22
443739	REC04466	panE	N	303	4, 24, 48, 84, 88, 156, 170		P77728	2-dehydropanoate 2-reductase (EC 1.1.1.169)	b0425	NCM	0.38
443889	REC00410	yajQ	N	169	30		P77482	Protein yajQ	b0426	UNC	0.25
445896	REC04467	yajR	N	456	78, 129, 407		P77726	Hypothetical transport protein yajR	b0427	UNC	0.66
446929	REC04468	cyoE	N	296	6, 98, 193, 276		P18404	Protochrome IX farnesyltransferase (EC 2.5.1.-)	b0428	NCM	0.59
447270	REC04469	cyoD	E	109	-	< 0.3	P18403	Cytochrome O ubiquinol oxidase protein cyoD	b0429	BEN	0.28
447884	REC04470	cyoC	N	204	128		P18402	Cytochrome O ubiquinol oxidase subunit III (EC 1.10.3.-)	b0430	BEN	0.56
449865	REC04471	cyoB	N	663	67, 99, 308, 381, 483, 487, 545, 615		P18401	Ubiquinol oxidase polypeptide I (EC 1.10.3.-)	b0431	BEN	0.56
450834	REC04472	cyoA	N	315	17, 22, 66, 68, 128, 239, 271		P18400	Ubiquinol oxidase polypeptide II precursor (EC 1.10.3.-)	b0432	BEN	0.44
452769	REC04473	ampG	N	491	136, 154, 266, 333, 335, 363, 442, 485		P36670	AmpG protein	b0433	UNC	0.31
453493	REC04474	yajG	N	226	197		P36671	Hypothetical lipoprotein yajG precursor	b0434	UNC	0.03
453663	REC00419	bolA	N	116	16, 92, 97		P15298	BolA protein	b0435	UNC	0.31
454357	REC00420	tig	N	432	98, 145, 206, 276, 387		P22257	Trigger factor	b0436	UNC	0.97
455901	REC00421	c1pP	N	207	22, 91, 132		P19245	ATP-dependent Clp protease proteolytic subunit (EC 3.4.21.92)	b0437	PMS	0.97
456650	REC00422	c1pX	N	424	100, 159, 177, 187, 215, 220, 228, 328, 351		P33138	ATP-dependent Clp protease ATP-binding subunit clpX	b0438	PMS	0.97
458112	REC00423	lon	N	784	276, 362, 363, 438, 484, 587		P08177	ATP-dependent protease La (EC 3.4.21.53)	b0439	PMS	0.78
460675	REC00424	hupB	N	90	40, 42, 60		P02341	DNA-binding protein HU-beta	b0440	RCD	0.81
461139	REC00425	ppiD	N	623	4, 166, 374, 495		P77241	Peptidyl-prolyl cis-trans isomerase D (EC 5.2.1.8)	b0441	PMS	0.56
463161	REC00426	ybaV	E	123	-	< 0.2	P77415	Hypothetical protein ybaV precursor	b0442	UNC	0.13
463626	REC00427	ybaW	N	132	44, 91, 107		P77712	Hypothetical protein ybaW	b0443	UNC	0.03
464771	REC04475	ybaX	N	231	2, 84, 197, 203		P77756	Hypothetical protein ybaX	b0444	UNC	0.63
466536	REC04476	ybaE	N	566	51, 52, 185, 208, 397		P46890	Hypothetical protein ybaE	b0445	UNC	0.00
466624	REC00430	cof	N	276	63		P46891	Cof protein	b0446	UNC	0.19
467520	REC00431	ybaO	N	181	53		P54986	Hypothetical transcriptional regulator ybaO	b0447	UNC	0.44
468095	REC00432	mdIA	N	590	9, 50, 129, 310, 340, 387		P77265	Multidrug resistance-like ATP-binding protein mdIA	b0448	MTR	0.91
468860	REC00433	mdIB	N	593	76, 83, 298, 424, 487, 506		P75706	Multidrug resistance-like ATP-binding protein mdIB	b0449	MTR	0.91
471822	REC00434	glnK	N	112	53, 59		P38504	Nitrogen regulatory protein P-II 2	b0450	SMC	0.66
472190	REC00435	amtB	N	428	75, 160, 165, 253, 287		P37905	Probable ammonium transporter	b0451	UNC	0.66
474385	REC04477	tesB	N	286	13, 15, 90, 155, 225		P23911	Acyl-CoA thioesterase II (EC 3.1.2.-)	b0452	LPC	0.34
474603	REC00437	ybaY	N	190	14, 54		P77717	Hypothetical protein ybaY precursor	b0453	UNC	0.22
475595	REC04478	ybaZ	N	129	103		P75707	Hypothetical protein ybaZ	b0454	UNC	0.16
475896	REC00439	ybaA	E	117	-	< 0.2	P09161	Hypothetical protein ybaA	b0456	UNC	0.06
477847	REC04479	y1aB	N	518	18, 52, 71, 96, 321, 325, 448, 482		P77473	Hypothetical protein y1aB	b0457	UNC	0.31
478514	REC04480	y1aC	N	169	7, 85, 98, 157		P77523	Hypothetical protein y1aC	b0458	UNC	0.00
479142	REC04481	maa	N	183	3, 42, 50, 73, 94, 108, 182		P77791	Maltose O-acetyltransferase (EC 2.3.1.79)	b0459	CHM	0.25
479532	REC04482	haa	N	72	10, 50		P23870	Haemolysin expression modulating protein	b0460	RCD	0.00
479932	REC04483	ybaJ	N	124	3, 4, 73, 74		P37611	Hypothetical protein ybaJ	b0461	UNC	0.00
483627	REC04484	acrB	N	1049	1, 71, 187, 198, 331, 444, 501, 515, 572, 582, 656, 658, 723, 770, 850, 859		P31224	Acriflavine resistance protein B	b0462	PMS	0.75
484843	REC04485	acrA	N	397	20, 87, 107, 188, 204, 343		P31223	Acriflavine resistance protein A precursor	b0463	PMS	0.47
484985	REC00447	acrR	N	215	43, 157, 173		P34000	Potential acrAB operon repressor	b0464	UNC	0.31
485760	REC00448	kefA	N	1120	214, 412, 661, 739, 750, 769, 793, 918, 990, 1052		P77338	Potassium efflux system kefA	b0465	UNC	0

491316	REC00453	<i>dnax</i>	E	643	-	< 0.001	P06710	DNA polymerase III subunit tau (EC 2.7.7.7)	b0470	NAM	1.00
493300	REC00454	<i>ybaB</i>	N	109	19		P17577	Hypothetical protein ybaB	b0471	UNC	0.44
493629	REC00455	<i>recR</i>	N	201	14, 153		P12727	Recombination protein recR	b0472	UNC	0.88
494344	REC00456	<i>htpG</i>	N	624	123, 149, 248, 312, 339, 395, 410, 437, 459, 495, 575		P10413	Chaperone protein htpG	b0473	SMC	0.66
496399	REC00457	<i>ack</i>	E	214	-	< 0.05	P05082	Adenylyl kinase (EC 2.7.4.3)	b0474	MSM	1.00
497279	REC00458	<i>hemH</i>	E	320	-	< 0.01	P23871	Ferrocyclase (EC 4.99.1.1)	b0475	NCM	0.78
499197	REC00488	<i>aes</i>	N	319	107, 118, 163, 215, 244, 273		P23872	Acetyl esterase (EC 3.1.1.-)	b0476	LPC	0.31
499349	REC00460	<i>gsk</i>	N	434	45, 48, 61, 125, 300, 384		P22937	Inosine-guanosine kinase (EC 2.7.1.73)	b0477	NCM	0.03
502462	REC00489	<i>ybaL</i>	N	558	10, 18, 59, 169, 195, 232, 323, 350		P39830	Hypothetical protein ybaL	b0478	UNC	0.38
503920	REC00490	<i>fsr</i>	N	406	69, 285, 357, 371		P52067	Fosmidomycin resistance protein	b0479	UNC	0.22
504138	REC00463	<i>ushA</i>	N	550	171, 173, 330, 412, 427, 443, 507		P07024	Protein ushA precursor	b0480	NCM	0.41
506306	REC04491	<i>ybaK</i>	N	159	97		P37175	Protein ybaK	b0481	UNC	0.47
507304	REC04492	<i>ybaP</i>	E	264	229	< 0.1	P77301	Hypothetical protein ybaP	b0482	UNC	0.06
507388	REC00466	<i>ybaQ</i>	E	131	-	< 0.3	P77303	Hypothetical protein ybaQ	b0483	UNC	0.28
510603	REC04493	<i>copA</i>	N	834	139, 180, 361, 419, 653, 666, 791		Q59385	Copper-transporting P-type ATPase (EC 3.6.3.4)	b0484	MTR	0.84
510865	REC00468	<i>ybaS</i>	N	310	310		P77454	Probable glutaminase ybaS (EC 3.5.1.2)	b0485	UNC	0.41
511800	REC00469	<i>ybaT</i>	N	430	124, 191, 225, 236, 278, 400		P77400	Hypothetical transport protein ybaT	b0486	UNC	0.34
513217	REC00470	<i>cueR</i>	?	135	-		P77565	Transcriptional regulator cueR	b0487	RCD	0.44
514080	REC00494	<i>ybbJ</i>	N	151	26, 82, 97, 138		P75709	Hypothetical protein ybbJ	b0488	UNC	0.28
514997	REC00495	<i>ybbK</i>	N	305	48, 119, 231		P77367	Hypothetical protein ybbK	b0489	UNC	0.66
515143	REC00473	<i>ybbL</i>	N	225	1, 59, 82, 99, 118, 138, 152, 194, 210		P77279	Hypothetical ABC transporter ATP-binding protein ybbL	b0490	UNC	0.97
515780	REC00474	<i>ybbM</i>	N	268	26, 37, 74, 101, 124, 165, 186, 187, 243		P77307	Hypothetical protein ybbM	b0491	UNC	0.25
517539	REC00496	<i>ybbN</i>	N	296	56, 207		P77395	Hypothetical protein ybbN	b0492	UNC	0.97
518373	REC00497	<i>ybbO</i>	N	269	183		P77388	Hypothetical oxidoreductase ybbO (EC 1.-.-.-)	b0493	UNC	0.47
518957	REC00478	<i>ybbA</i>	N	228	87, 147		P31219	Hypothetical ABC transporter ATP-binding protein ybbA	b0495	UNC	0.97
518989	REC00498	<i>tesA</i>	N	208	52, 137, 152		P29679	Acyl-CoA thioesterase I precursor (EC 3.1.2.-) (EC 3.1.1.5)	b0494	LPC	0.31
519640	REC00479	<i>ybbP</i>	N	804	117, 229, 352, 491, 629, 787		P77504	Hypothetical protein ybbP	b0496	UNC	0.25
522485	REC00480	<i>rhdD</i>	N	1426	17, 26, 79, 203, 286, 331, 511, 516, 619, 1035, 1089, 1166, 1202, 1227, 1252		P16919	RhdS protein precursor	b0497	UNC	0.03
526805	REC00481	<i>ybbC</i>	E	122	-	< 0.3	P33668	Hypothetical protein ybbC precursor	b0498	UNC	0.00
527173	REC00482	<i>ybbD</i>	N	236	52, 119, 186		P77759	FROM BASES 522240 TO 533123 (SECTION 46 OF 400) OF THIB0499	b0499	UNC	0.00
527864	REC00483	<i>ybbD</i>	?	86	12		P33669	Hypothetical protein ybbD	b0500	UNC	0.00
528163	REC00484	<i>ybbE</i>	N	63	24		P75710	FROM BASES 522240 TO 533123 (SECTION 46 OF 400) OF THIB0501	b0501	UNC	0.00
529276	REC00499	<i>ybbF</i>	N	135	64, 94, 124		P77688	FROM BASES 522240 TO 533123 (SECTION 46 OF 400) OF THIB0502	b0502	UNC	0.00
530450	REC004500	<i>ybbB</i>	N	364	20, 51, 261, 290, 352		P33667	Hypothetical protein ybbB	b0503	UNC	0.06
531445	REC004501	<i>ybbS</i>	N	308	175		P77702	Hypothetical transcriptional regulator ybbS	b0504	UNC	0.03
531675	REC00488	<i>a11A</i>	E	160	-	< 0.1	P77731	Ureidoglycolate hydrolase (EC 3.5.3.19)	b0505	NCM	0.19
532235	REC00489	<i>a11R</i>	N	271	85, 107, 132, 151, 262		P77734	Negative regulator of allantoin and glyoxylate utilization operons	b0506	RCD	0.03
533140	REC00490	<i>gc1</i>	N	593	157, 243, 330, 336, 532, 543		P30146	Glyoxylate carboligase (EC 4.1.1.47)	b0507	CHM	0.13
534934	REC00491	<i>hyi</i>	N	258	89		P30147	Hydroxypruvate isomerase (EC 5.3.1.22)	b0508	CHM	0.25
535810	REC00492	<i>glxR</i>	N	292	5, 5, 28, 40, 45, 55, 74, 130, 229, 270		P77161	2-hydroxy-3-oxopropionate reductase (EC 1.1.1.1.60)	b0509	CHM	0.47
536720	REC00493	<i>ybbV</i>	N	92	82, 87		P75711	Hypothetical protein ybbV	b0510	UNC	0.00
536998	REC00494	<i>ybbW</i>	N	437	58, 69, 125, 155, 270		P75712	Putative allantoin permease	b0511	UNC	0.22
538371	REC00495	<i>a11B</i>	N	453	229, 273, 288, 340		P77671	Allantoinase (EC 3.5.2.5)	b0512	NCM	0.59
539783	REC00496	<i>ybbY</i>	N	435	72, 99, 121, 143, 198, 266, 340, 372, 406		P77328	Putative purine permease ybbY	b0513	UNC	0.03
541112	REC00497	<i>glxK</i>	N	381	361		P77364	Glycerate kinase 1 (EC 2.7.1.31)	b0514	CHM	0.38
543270	REC04502	<i>y1bA</i>	N	261	21, 36, 67, 90, 95, 109, 129, 137, 146, 187, 227		P75713	Hypothetical protein y1bA	b0515	UNC	0.19
544516	REC04503	<i>a11C</i>	N	411	1, 123, 126, 205, 214, 268, 324, 365, 394		P77425	Allantoate amidohydrolase (EC 3.5.3.-)	b0516	NCM	0.31
545587	REC04504	<i>a11D</i>	N	349	256		P77555	Ureidoglycolate dehydrogenase (EC 1.1.1.154)	b0517	NCM	0.13
545904	REC00501	<i>fdxA</i>	N	555	43, 45, 67, 89, 304, 449		Q47208	Protein fdxA	b0518	UNC	0.00
547838	REC00502	<i>y1bE</i>	N	333	19, 88		P77129	Hypothetical protein y1bE	b0519	UNC	0.00
548850	REC00503	<i>y1bF</i>	E	271	20	< 0.05	P77518	Hypothetical protein y1bF	b0520	UNC	0.00
549662	REC00504	<i>arcC</i>	E	297	-	< 0.05	P37306	Carbamate kinase (EC 2.7.2.2)	b0521	MSM	0.25
551817	REC04505	<i>purK</i>	N	355	9, 84, 271, 311		P09029	Phosphoribosylaminoimidazole carboxylase ATPase subunit (EC 2.4.1.15)	b0522	NCM	0.78
552323	REC04506	<i>purE</i>	N	169	77		P09028	Phosphoribosylaminoimidazole carboxylase catalytic subunit (EC 2.4.1.15)	b0523	NCM	0.78
553163	REC04507	<i>lpxH</i>	E	240	19	< 0.1	P43341	UDP-2,3-diacetylglucosamine hydrolase (EC 3.6.1.-)	b0524	CHM	0.31
553660	REC04508	<i>ppiB</i>	E	164	-	< 0.3	P23869	Peptidyl-prolyl cis-trans isomerase B (EC 5.2.1.8)	b0525	PMS	0.84
553834	REC00509	<i>cysS</i>	E	461	-	< 0.001	P21888	CysteinyI-tRNA synthetase (EC 6.1.1.16)	b0526	PMS	1.00
555776	REC04509	<i>ybcI</i>	?	173	19		P45570	Hypothetical protein ybcI	b0527	UNC	0.03
556117	REC04510	<i>ybcJ</i>	?	77	-		P45571	Hypothetical protein ybcJ	b0528	UNC	0.06
556964	REC04511	<i>fo1D</i>	N	288	36		P24186	Fo1D bifunctional protein	b0529	MSM	1.00
557402	REC00513	<i>sfmA</i>	N	191	19, 60, 85, 120, 188		P77660	Sfm fibrillar protein, A chain precursor	b0530	SMC	0.00
558197	REC00514	<i>sfmC</i>	N	230	105, 174, 198		P77249	Chaperone protein sfmC precursor	b0531	PMS	0.00
558920	REC00515	<i>sfmD</i>	N	867	181, 218, 229, 229, 247, 254, 279, 295, 319, 376, 500, 553, 561, 721, 844		P77468	Outer membrane usher protein sfmD precursor	b0532	SMC	0.06
561565	REC00516	<i>sfmH</i>	X	325	-		P75715	SfmH protein precursor	b0533	UNC	0.00
562553	REC00517	<i>sfmF</i>	N	171	85, 145, 170		P38052	Fimbrial-like protein sfmF precursor	b0534	SMC	0.00
563703	REC04512	<i>fmZ</i>	N	210	21, 51, 65, 100, 103, 130, 170, 195		P21502	Fimbriae Z protein	b0535	SMC	0.03
565195	REC00520	<i>intD</i>	X	186	25		P77528	FROM BASES 555801 TO 565933 (SECTION 49 OF 400) OF THIB0538	b0538	UNC	0.00
565201	REC04513	<i>intD</i>	N	387	52, 246, 283, 298, 345, 378		P24218	Prophage DLP12 integrase	b0537	PHT	0.03
565584	REC04514	<i>intD</i>	X	87	-		P75717	EXONUCLEASE (EC 3.1.1.11.3)	b0539	NAM	0.00
566056	REC00282	<i>insE3</i>	E	102	-	< 0.1	P77681	Transposase insE for insertion sequence IS3A/B/C/D/E/FA/IB	b0540	PHT	0.56
566361	REC00283	<i>insF3</i>	N	288	55, 65, 114, 148, 157, 173, 189, 235, 241, 271		P05822	Transposase insF for insertion sequence IS3A/B/C/D/E/FA/IB	b0541	PHT	0.56
567333	REC00524	<i>emrE</i>	?	45	-		P75718	FROM BASES 565876 TO 576392 (SECTION 50 OF 400) OF THIB0542	b0542	UNC	0.00
567538	REC00525	<i>emrE</i>	N	110	10, 76		P23895	EmrE protein	b0543	MTR	0.44
568125	REC00526	<i>ybcK</i>	N	508	35, 126, 188, 500		P77698	Hypothetical protein ybcK	b0544	UNC	0.03
570116	REC00527	<i>ybcL</i>	N	183	13, 29, 30, 60, 72, 91, 108, 137		P77368	Protein ybcL precursor	b0545	UNC	0.28
570677	REC00528	<i>ybcM</i>	N	285	4, 98, 174, 213, 220		P77634	Hypothetical transcriptional regulator ybcM	b0546	UNC	0.09
571689	REC00529	<i>ybcN</i>	E	151	-	< 0.05	Q47269	Hypothetical protein ybcN in lambdaoid DLP12 prophage region	b0547	UNC	0.00
572144	REC00530	<i>ninE</i>	?	56	-		Q47270	Protein ninE homolog from lambdaoid prophage DLP12	b0548	UNC	0.00
572307	REC00531	<i>ybcO</i>	E	96	-	< 0.1	Q47271	Hypothetical protein ybcO in lambdaoid DLP12 prophage region	b0549	UNC	0.00
572594	REC00532	<i>rusA</i>	E	120	25	< 0.05	P40116	Crossover junction endonuclease rusA (EC 3.1.22.-)	b0550	NAM	0.00
573179	REC00533	<i>ybcQ</i>	N	127	36, 72, 101		Q47274	Antitermination protein Q homolog from lambdaoid prophage DLP12	b0551	UNC	0.00
574976	REC06491	<i>intD</i>	N	338	61		P03837	Transposase insH for insertion sequence element IS5	b0552	PHT	0.34
576108	REC04516	<i>nmpC</i>	N	375	44, 44, 152, 237, 312, 323		P21420	Outer membrane porin protein nmpC precursor	b0553	SMC	0.03
576621	REC00536	<i>essD</i>	N	71	6, 32, 61		P77242	Lysis protein S homolog from lambdaoid prophage DLP12	b0554	UNC	0.00
576836	REC00537	<i>ybcS</i>	N	165	14, 37, 62, 73, 88, 102, 117, 136		P78285	Probable lysozyme from lambdaoid prophage DLP12 (EC 3.2.1.17)	b0555	UNC	0.09
577330	REC00538	<i>rxpD</i>	N	153	6, 78, 109, 137		P75719	Putative Rz endopeptidase from lambdaoid prophage DLP12 (EC 3.4.21.5)	b0556	UNC	0.00
578116	REC04517	<i>borD</i>	N	97	20, 90		P77330	Bor protein homolog from lambdaoid prophage DLP12 precursor	b0557	UNC	0.00
578859	REC04518	<i>ybcV</i>	E	150	-	< 0.05	P77398	Hypothetical protein ybcV	b0558	UNC	0.00
579103	REC00541	<i>ybcW</i>	?	68	6		P75720	Hypothetical protein ybcW precursor	b0559	UNC	0.00
580057	REC00542	<i>nohB</i>	N	181	38, 77, 160		P31062	Prophage QSR' DNA packaging protein NU1 homolog	b0560	UNC	0.00
580577	REC00543	<i>tfad</i>	N	247	16, 23, 38, 71, 93, 123, 176		P77699	Tail fiber assembly protein homolog from lambdaoid prophage DLP12	b0561	UNC	0.06
581806	REC04519	<i>ybcY</i>	N	143	67, 101, 143		P77460	Hypothetical protein ybcY precursor	b0562	UNC	0.00

582098	REC06493	<i>ylcE</i>	?	61	-	P77087	Hypothetical protein <i>ylcE</i>	b0563	UNC	0.00
582904	REC00545	<i>appY</i>	E	249	-	P05052	AppY protein	b0564	UNC	0.03
584856	REC04520	<i>ompT</i>	N	317	10, 49, 66, 124, 135, 150, 161, 178, 206, 211, 237, 260, 261, 308	P09169	Protease VII precursor (EC 3.4.21.87)	b0565	PMS	0.06
586131	REC04521	<i>envY</i>	N	253	119, 152, 239	P10805	Porin thermoregulatory protein <i>envY</i>	b0566	RCD	0.00
587204	REC04522	<i>ycbH</i>	N	296	16, 51, 64, 80, 120, 278	P37325	Hypothetical protein <i>ycbH</i> precursor	b0567	UNC	0.00
590177	REC04523	<i>nfrA</i>	N	990	2, 38, 206, 245, 375, 547, 664, 928, 988	P31600	Bacteriophage N4 adsorption protein A precursor	b0568	PHT	0.00
592401	REC04524	<i>nfrB</i>	N	745	36, 194, 231, 391, 416, 453, 480, 502, 509, 541, 568, 594, 665, 676, 678	P31599	Bacteriophage N4 adsorption protein B	b0569	PHT	0.03
593993	REC04525	<i>cusS</i>	N	480	56, 170, 291, 374, 408	P77485	Sensor kinase <i>cusS</i> (EC 2.7.3.-)	b0570	UNC	0.53
594666	REC04526	<i>cusR</i>	N	227	13, 91, 95, 212	P77380	Transcriptional regulatory protein <i>cusR</i>	b0571	SMC	0.56
594823	REC00553	<i>cusC</i>	N	457	74, 120, 147, 224, 286, 303, 427	P77211	Probable outer membrane lipoprotein <i>cusC</i> precursor	b0572	UNC	0.25
596354	REC00554	<i>cusX</i>	N	110	93, 108	P77214	Hypothetical protein <i>cusX</i> precursor	b0573	UNC	0.00
596702	REC00555	<i>cusB</i>	N	407	83, 95, 164, 234, 249, 285, 320	P77239	Putative copper efflux system protein <i>cusB</i> precursor	b0574	UNC	0.13
597937	REC00556	<i>cusA</i>	N	1047	47, 109, 151, 491, 735, 798, 875, 910, 974	P38054	Putative cation efflux system protein <i>cusA</i>	b0575	UNC	0.28
601182	REC00557	<i>pheP</i>	N	458	5, 184, 206, 309, 323, 442	P24207	Phenylalanine-specific permease	b0576	MTR	0.00
603886	REC04527	<i>ybdG</i>	N	415	17, 60, 94, 221, 228, 371, 377	P39455	Hypothetical protein <i>ybdG</i>	b0577	UNC	0.16
604647	REC04528	<i>nfnB</i>	N	217	24, 98, 169, 194	P38489	Oxygen-insensitive NAD(P)H nitroreductase (EC 1.-.-.-) (EC 1.6.99.6)	b0578	NCM	0.25
605109	REC04529	<i>ybdF</i>	N	122	38, 63	P39454	Hypothetical protein <i>ybdF</i>	b0579	UNC	0.09
605422	REC04530	<i>ybdJ</i>	N	82	73	P77506	Hypothetical protein <i>ybdJ</i>	b0580	UNC	0.00
606606	REC04531	<i>ybdK</i>	N	372	26, 184, 325	P77213	Hypothetical protein <i>ybdK</i>	b0581	UNC	0.13
606960	REC06780	<i>hokE</i>	N	83	13, 69	P77091	HokE protein	b0582	UNC	0.00
607288	REC00016		N	370	5, 10, 37, 49, 162	P08409	Putative transposase <i>insL</i> for insertion sequence element IS186A	b0582	UNC	0.00
609311	REC04532	<i>entD</i>	N	209	7, 103, 175	P19925	Enterobactin synthetase component D	b0583	UNC	0.22
611717	REC04533	<i>lepA</i>	N	746	145, 277, 306, 324, 351, 357, 365, 395, 519, 563, 696	P05825	Ferrienterobactin receptor precursor	b0584	MTR	0.06
612038	REC00566	<i>fes</i>	N	374	12, 36, 129, 338	P13039	Enterocelin esterase	b0585	NCM	0.03
613156	REC06664	<i>ybdZ</i>	?	75	-	P18393	Hypothetical protein <i>ybdZ</i>	b0586	UNC	0.09
613380	REC00567	<i>entF</i>	N	1293	100, 103, 138, 195, 248, 268, 324, 349, 633, 636, 744, 756, 880, 897, 127	P11454	Enterobactin synthetase component F	b0586	RCD	0.16
617477	REC00568	<i>lepE</i>	N	377	1, 89, 170, 198, 213, 283, 284, 350, 369	P26266	Ferric enterobactin transport protein <i>lepE</i>	b0587	MTR	0.00
619422	REC04534	<i>lepC</i>	N	271	74, 172, 230	P23878	Ferric enterobactin transport ATP-binding protein <i>lepC</i>	b0588	MTR	0.81
620411	REC04535	<i>lepG</i>	X	330	237	P23877	Ferric enterobactin transport system permease protein <i>lepG</i>	b0589	MTR	0.69
621412	REC04536	<i>lepD</i>	N	334	91, 114, 177, 256	P23876	Ferric enterobactin transport system permease protein <i>lepD</i>	b0590	MTR	0.69
621523	REC00572	<i>ybdA</i>	X	416	-	P24077	Hypothetical membrane protein P43	b0591	UNC	0.09
623733	REC04537	<i>lepB</i>	E	318	-	P14609	Ferrienterobactin-binding periplasmic protein precursor	b0592	MTR	0.13
624108	REC00574	<i>entC</i>	N	391	33, 94, 158, 164, 231, 306, 351, 383	P10377	Isochorismate synthase <i>entC</i> (EC 5.4.99.6)	b0593	NCM	0.34
625293	REC00575	<i>entE</i>	N	536	38, 39, 115, 121, 234, 348, 479	P10378	2,3-dihydroxybenzoate-AMP ligase (EC 6.3.2.-)	b0594	MSM	0.25
626917	REC00576	<i>entB</i>	N	285	77, 139, 258	P15048	Isochorismatase (EC 3.3.2.1)	b0595	NCM	0.19
627774	REC00577	<i>entA</i>	N	248	37, 92, 136, 181	P15047	2,3-dihydro-2,3-dihydroxybenzoate dehydrogenase (EC 1.3.1.28)	b0596	NCM	0.13
628523	REC00578	<i>ybdB</i>	N	137	17, 54	P15050	Hypothetical protein <i>ybdB</i>	b0597	UNC	0.28
629117	REC00579	<i>cstA</i>	N	701	33, 66, 304, 321, 374, 594, 645, 696	P15078	Carbon starvation protein A	b0598	SMC	0.41
631405	REC06665	<i>ybdD</i>	?	65	-	P23518	Hypothetical protein <i>ybdD</i>	b0599	UNC	0.03
632700	REC04538	<i>ybdH</i>	N	362	10, 183	P45579	Hypothetical oxidoreductase <i>ybdH</i> (EC 1.1.-.-)	b0599	UNC	0.22
632809	REC00581	<i>ybdL</i>	N	386	175	P77806	Hypothetical aminotransferase <i>ybdL</i> (EC 2.6.1.-)	b0600	UNC	0.84
634599	REC04539	<i>ybdM</i>	N	209	29, 47, 84	P77174	Hypothetical protein <i>ybdM</i>	b0601	UNC	0.09
635792	REC04540	<i>ybdN</i>	N	406	52, 109, 206, 254, 339	P77216	Hypothetical protein <i>ybdN</i>	b0602	UNC	0.09
636841	REC04541	<i>ybdO</i>	N	300	7, 65, 150	P77746	Hypothetical transcriptional regulator <i>ybdO</i>	b0603	UNC	0.72
637856	REC04542	<i>dsbG</i>	N	268	15, 47, 53, 68, 79, 106, 147, 184	P77202	Thiol:disulfide interchange protein <i>dsbG</i> precursor	b0604	UNC	0.06
638168	REC00586	<i>ahpC</i>	N	187	62, 167	P26427	Alkyl hydroperoxide reductase C22 protein (EC 1.6.4.-)	b0605	MSM	0.78
638946	REC00587	<i>ahpF</i>	N	531	2, 38, 80, 86, 132, 142, 225	P35340	Alkyl hydroperoxide reductase subunit F (EC 1.6.4.-)	b0606	MSM	0.28
641090	REC04543	<i>ybdQ</i>	N	142	25, 31	P39177	Unknown protein from 2D-page	b0607	UNC	0.13
641311	REC00589	<i>ybdR</i>	N	412	6, 88, 141, 151, 175, 350	P77316	Hypothetical zinc-type alcohol dehydrogenase-like protein <i>ybdR</i>	b0608	UNC	0.59
642630	REC00590		?	153	14, 153	P75725	FROM BASES 635836 TO 651340 (SECTION 56 OF 400) OF THIOBACILLUM	b0609	UNC	0.00
643190	REC04544	<i>rnk</i>	N	136	9, 35	P40679	Regulator of nucleoside diphosphate kinase	b0610	RCD	0.16
644226	REC04545	<i>rna</i>	N	268	189, 267	P21338	Ribonuclease I precursor (EC 3.1.27.6)	b0611	NAM	0.00
645803	REC04546	<i>ci t T</i>	N	487	6, 167, 326, 349, 382, 399, 413, 433, 458, 461	P77405	Citrate carrier	b0612	MTR	0.09
646732	REC04547	<i>ci t G</i>	N	292	50, 251, 257	P77231	2-(5'-triphosphoribosyl)-3'-dephosphocoenzyme-A synthase (EC 4.6.1.15)	b0613	NCM	0.13
647258	REC04548	<i>ci t X</i>	N	183	106, 128	P77563	Apo-citrate lyase phosphoribosyl-dephospho-CoA transferase (EC 2.3.1.34)	b0614	CHM	0.06
648794	REC04549	<i>ci t F</i>	N	510	144, 170, 222, 388, 405, 495	P75726	Citrate lyase alpha chain (EC 4.1.3.6) (EC 2.8.3.10)	b0615	CHM	0.09
649728	REC04550	<i>ci t E</i>	N	307	26, 128, 210, 307	P77710	Citrate lyase beta chain (EC 4.1.3.6) (EC 4.1.3.34)	b0616	CHM	0.38
650006	REC04551	<i>ci t D</i>	N	98	35	P77618	Citrate lyase acyl carrier protein	b0617	MTR	0.09
651166	REC04552	<i>ci t C</i>	N	381	13, 60, 93, 218, 287	P77390	[Citrate [pro-3S]-lyase] ligase (EC 6.2.1.22)	b0618	CHM	0.09
651458	REC00600	<i>dpiB</i>	N	552	19, 23, 63, 82, 137, 266, 288, 389, 505, 517	P77510	Sensor kinase <i>dpiB</i> (EC 2.7.3.-)	b0619	SMC	0.16
653085	REC00601	<i>dpiA</i>	N	226	147	Q54149	Transcriptional regulatory protein <i>dpiA</i>	b0620	SMC	0.09
655191	REC04553	<i>drcC</i>	N	461	20, 57, 209, 232, 312, 379	Q47134	Anaerobic C4-dicarbonylate transporter <i>drcC</i>	b0621	MTR	0.06
655780	REC00603	<i>crcA</i>	N	186	29, 41, 55, 80, 155	P37001	CrcA protein	b0622	UNC	0.00
656515	REC00604	<i>cspE</i>	N	69	52	P36997	Cold shock-like protein <i>cspE</i>	b0623	UNC	0.72
657161	REC04554	<i>crcB</i>	E	127	-	P37002	Protein <i>crcB</i>	b0624	UNC	0.16
657254	REC00606	<i>ybeM</i>	?	75	-	P39874	HYPOTHETICAL PROTEIN YBEM	b0625	UNC	0.00
657478	REC00607	<i>ybeM</i>	N	187	107, 109, 123	P39874	Hypothetical protein <i>ybeM</i>	b0626	UNC	0.75
658170	REC00608	<i>tatE</i>	?	67	-	P25895	Sec-independent protein translocase protein <i>tatE</i>	b0627	PMS	0.03
659439	REC04555	<i>lipA</i>	N	321	20, 32, 200	P25845	Lipoic acid synthetase	b0628	NCM	0.69
660448	REC04556	<i>ybeF</i>	N	266	1, 11, 83, 105, 217, 225	P30979	Hypothetical transcriptional regulator <i>ybeF</i>	b0629	UNC	0.72
661435	REC04557	<i>lipB</i>	N	191	25, 27, 63, 149	P30976	Lipoate-protein ligase B (EC 6.-.-.-)	b0630	NCM	0.56
661865	REC04558	<i>ybeD</i>	N	87	25	P30977	Hypothetical protein <i>ybeD</i>	b0631	UNC	0.19
663186	REC04559	<i>dacA</i>	N	403	70, 76, 151, 175, 193, 269, 353, 394	P04287	Penicillin-binding protein 5 precursor (EC 3.4.16.4)	b0632	LPC	0.72
664413	REC04560	<i>rlpA</i>	N	362	85, 95, 179, 342	P10100	Rare lipoprotein A precursor	b0633	UNC	0.63
665536	REC04561	<i>mrdB</i>	E	370	332	P15035	Rod shape-determining protein <i>rodA</i>	b0634	RCD	0.72
667440	REC04562	<i>mrdA</i>	E	633	561	P08150	Penicillin-binding protein 2	b0635	LPC	0.69
667938	REC04563	<i>ybeA</i>	E	155	-	P05850	Hypothetical protein <i>ybeA</i>	b0636	UNC	0.66
668151	REC04564	<i>ybeB</i>	N	69	31	P05848	Hypothetical protein <i>ybeB</i>	b0637	UNC	0.88
669130	REC04565	<i>cobC</i>	N	203	8, 109	P52086	Alpha-ribazole-5'-phosphate phosphatase (EC 3.1.3.-)	b0638	NCM	0.47
669795	REC04566	<i>nadD</i>	N	213	130	P52085	Nicotinate-nucleotide adenyltransferase (EC 2.7.7.18)	b0639	NCM	0.75
670828	REC04567	<i>hoIA</i>	E	343	-	P28630	DNA polymerase III, delta subunit (EC 2.7.7.7)	b0640	NAM	0.53
671409	REC04568	<i>rlpB</i>	E	193	186	P10101	Rare lipoprotein B precursor	b0641	UNC	0.19
674006	REC04569	<i>leuS</i>	E	860	732	P07813	Leucyl-tRNA synthetase (EC 6.1.1.4)	b0642	PMS	1.00
674241	REC00624	<i>ybeL</i>	?	160	129, 158	P46129	Hypothetical protein <i>ybeL</i>	b0643	UNC	0.03
675776	REC04570	<i>ybeQ</i>	N	327	30, 36, 74, 90, 93, 295	P77234	Hypothetical protein <i>ybeQ</i>	b0644	UNC	0.34
675934	REC00626	<i>ybeR</i>	N	235	63, 101, 120, 133, 157, 196, 234	P77627	Hypothetical protein <i>ybeR</i>	b0645	UNC	0.00
676638	REC00627	<i>ybeS</i>	N	475	22, 65, 100, 143, 212, 243, 333, 355, 432	P77381	Hypothetical J-domain protein <i>ybeS</i>	b0646	UNC	0.00
678629	REC04571	<i>ybeT</i>	N	184	18, 55, 59, 82, 84, 91, 105, 130, 137, 158	P77296	Hypothetical protein <i>ybeT</i>	b0647	UNC	0.00
678731	REC00629	<i>ybeU</i>	N	235	1, 72, 98, 141, 143, 168, 221	P77427	Hypothetical protein <i>ybeU</i>	b0648	UNC	0.00
679435	REC00630	<i>ybeV</i>	N	483	29, 70, 149, 163, 237, 388, 404, 474	P77359	Hypothetical J-domain protein <i>ybeV</i>	b0649	UNC	0.00
682616	REC04572	<i>hscC</i>	N	556	17, 20, 65, 102	P77319	Chaperone protein <i>hscC</i>	b0650	UNC	0.06
683635	REC04573	<i>ybeK</i>	N	311	127, 193, 211, 287, 291	P41409	Hypothetical protein <i>ybeK</i>	b0651	UNC	0.41
684478	REC04574	<i>gl t L</i>	E	241	-	P41076	Glutamate/aspartate transport ATP-binding protein <i>gl t L</i>	b0652	MTR	0.69

685152	REC04575	<i>gl tK</i>	E	224	1, 221	< 0.05	P41075	Glutamate/aspartate transport system permease protein gltK	b0653	MTR	0.25
685892	REC04576	<i>gl tJ</i>	N	246	37, 86, 146, 183, 219		P41074	Glutamate/aspartate transport system permease protein gltJ	b0654	MTR	0.13
686970	REC04577	<i>gl tI</i>	N	302	32, 201, 272		P37902	Glutamate/aspartate periplasmic binding protein precursor	b0655	MTR	0.16
688236	REC06525		N	338	148, 213, 222, 329		P03837	Transposase insH for insertion sequence element IS5	b0656	PHT	0.34
690104	REC04579	<i>Int</i>	X	512	-		P23930	Apolipoprotein N-acyltransferase (EC 2.3.1.-)	b0657	LPC	0.69
691007	REC04580	<i>corC</i>	N	292	-	< 0.2	P77392	Magnesium and cobalt efflux protein corC	b0658	MTR	0.97
691564	REC04581	<i>ybeY</i>	E	155	-		P77385	Hypothetical protein ybeY	b0659	UNC	0.88
692640	REC04582	<i>ybeZ</i>	N	359	226, 238, 321		P77349	PhoH-like protein	b0660	UNC	0.69
694178	REC04583	<i>yIeA</i>	N	474	217, 235, 362, 371, 447		P77645	Hypothetical protein yIeA	b0661	UNC	0.84
694324	REC00643	<i>ubiF</i>	N	391	249, 256, 297, 344		P75728	2-oxoprenyl-3-methyl-6-methoxy-1,4-benzoquinol hydroxylase (EC 1.10.3.2)	b0662	NCM	0.03
695581	REC00644		N	111	2, 36		P75729	FROM BASES 685948 TO 696574 (SECTION 60 OF 400) OF THIB	b0663	UNC	0.00
696065	REC00646		?	39	-		P75731	FROM BASES 685948 TO 696574 (SECTION 60 OF 400) OF THIB	b0669	UNC	0.00
696185	REC00647		?	50	-		P75732	FROM BASES 685948 TO 696574 (SECTION 60 OF 400) OF THIB	b0671	UNC	0.00
698400	REC04584	<i>asnB</i>	N	554	37, 78, 135, 401, 512		P22106	Asparagine synthetase B [glutamine-hydrolyzing] (EC 6.3.5.4)	b0674	AAM	0.34
699549	REC04585	<i>nagD</i>	N	250	22, 98, 108, 128, 147		P15302	NagD protein	b0675	UNC	0.28
700817	REC04586	<i>nagC</i>	N	406	70, 190, 374, 392		P15301	N-acetylglucosamine repressor	b0676	RCD	0.41
701974	REC04587	<i>nagA</i>	N	382	107, 194, 309		P15300	N-acetylglucosamine-6-phosphate deacetylase (EC 3.5.1.25)	b0677	CHM	0.66
702834	REC04588	<i>nagB</i>	N	266	33, 161, 207		P09375	Glucosamine-6-phosphate isomerase (EC 3.5.99.6)	b0678	CHM	0.34
703167	REC00653	<i>nagE</i>	N	648	122, 141, 153, 177, 216, 354, 417, 431		P09323	PTS system, N-acetylglucosamine-specific IIBC component (EC 2.7.1.39)	b0679	CHM	0.47
705316	REC00654	<i>glnS</i>	E	554	223	< 0.001	P00962	Glutamyl-tRNA synthetase (EC 6.1.1.18)	b0680	PMS	0.25
707557	REC00655	<i>ybfM</i>	N	468	65, 162, 334, 357, 462		P75733	Hypothetical protein ybfM	b0681	UNC	0.03
709013	REC00656	<i>ybfN</i>	E	108	-	< 0.3	P75734	Hypothetical lipoprotein ybfN precursor	b0682	UNC	0.00
709869	REC04589	<i>fur</i>	N	148	39, 104		P06975	Ferric uptake regulation protein	b0683	RCD	0.72
709914	REC06925	<i>ybfJ</i>	N	84	32, 40		P46146	Hypothetical protein ybfJ	b0684	UNC	0.00
710688	REC04590	<i>fldA</i>	N	176	38		P23243	Flavodoxin 1	b0684	CHM	0.31
711190	REC04591	<i>ybfE</i>	N	120	41, 42		P75735	Hypothetical protein ybfE	b0685	UNC	0.00
712025	REC04592	<i>ybfF</i>	N	254	33, 68, 162, 219		P75736	Putative esterase/lipase ybfF (EC 3.1.-.-)	b0686	UNC	0.25
712210	REC00661	<i>seqA</i>	E	181	-	< 0.1	P36658	SeqA protein	b0687	RCD	0.06
712781	REC00662	<i>pym</i>	N	546	17, 41, 99, 170, 236, 256, 286		P36938	Phosphoglucosyltransferase (EC 5.4.2.2)	b0688	CHM	0.44
714635	REC00663	<i>ybfP</i>	N	164	38, 49, 88, 126, 142		P75737	Hypothetical lipoprotein ybfP precursor	b0689	UNC	0.00
715532	REC04593	<i>ybfG</i>	?	120	86		P37003	Hypothetical protein ybfG	b0690	UNC	0.03
715928	REC04594	<i>ybfH</i>	N	105	26, 49, 100		P37004		b0691	UNC	0.00
717488	REC04595	<i>potE</i>	N	439	270, 331, 363, 401, 407, 422		P24170	Putrescine-ornithine antiporter	b0692	MTR	0.09
719683	REC04596	<i>speF</i>	N	732	15, 44, 65, 104, 112, 148		P24169	Ornithine decarboxylase, inducible (EC 4.1.1.17)	b0693	AAM	0.13
719806	REC06791	<i>ybfK</i>	N	85	30, 67		P46121	Hypothetical protein ybfK	b0694	UNC	0.00
720956	REC04597	<i>kdpE</i>	N	225	152, 197, 210		P21866	KDP operon transcriptional regulatory protein kdpE	b0694	SMC	0.41
723637	REC04598	<i>kdpD</i>	N	894	127, 150, 193, 740, 854		P21865	Sensor protein kdpD (EC 2.7.3.-)	b0695	SMC	0.47
724202	REC04599	<i>kdpC</i>	?	190	15		P03961	Potassium-transporting ATPase C chain (EC 3.6.3.12)	b0696	SMC	0.44
726259	REC04600	<i>kdpB</i>	N	682	53, 120, 234, 387, 397, 467, 545, 632, 659		P03960	Potassium-transporting ATPase B chain (EC 3.6.3.12)	b0697	SMC	0.44
727955	REC04601	<i>kdpA</i>	N	557	165, 194, 285, 469, 536		P03959	Potassium-transporting ATPase A chain (EC 3.6.3.12)	b0698	SMC	0.44
728357	REC00673	<i>ybfA</i>	N	68	20, 36		P28913	Hypothetical protein ybfA precursor	b0699	UNC	0.00
728806	REC00674	<i>rhcS</i>	N	1397	104, 180, 209, 213, 248, 304, 342, 381, 436, 449, 487, 495, 527, 545, 582	< 0.3	P16918	RhcS protein precursor	b0700	UNC	0.00
732999	REC00676	<i>ybfB</i>	E	108	85	< 0.3	P28914	Hypothetical protein ybfB	b0702	UNC	0.00
733443	REC00677	<i>ybfO</i>	N	477	262, 269, 308, 358, 359, 413		P77779	Hypothetical protein ybfO	b0703	UNC	0.00
734873	REC00678	<i>ybfC</i>	E	189	8	< 0.1	P28915	Hypothetical protein ybfC precursor	b0704	UNC	0.00
735668	REC06741	<i>ybfD</i>	X	84	-		Q9ZBC8	H repeat-associated protein in rhcS 3'region	b0705	UNC	0.00
736327	REC00679	<i>ybfL</i>	N	285	46, 75, 150, 207, 216, 230, 267, 292		P75741	H REPEAT-ASSOCIATED PROTEIN IN RHSC-PHRB INTERGENE	b0706	UNC	0.00
737315	REC00680	<i>ybfD</i>	N	253	20, 50, 84, 88, 131, 161, 214		P28916	H REPEAT-ASSOCIATED protein ybfD	b0706	UNC	0.00
738224	REC00681	<i>ybgA</i>	X	169	-		P24252	Hypothetical protein ybgA	b0707	UNC	0.06
738730	REC00682	<i>phxB</i>	E	472	435	< 0.001	P00914	Deoxyribodipyrimidine photolase (EC 4.1.99.3)	b0708	NAM	0.38
741779	REC04602	<i>ybgH</i>	N	493	77, 138, 198, 332, 345, 473		P75742	Hypothetical transporter ybgH	b0709	UNC	0.31
742050	REC00684	<i>ybgI</i>	N	247	18, 113		P75743	Hypothetical protein ybgI	b0710	UNC	0.34
742816	REC00685	<i>ybgJ</i>	N	218	67, 84, 92, 116, 157, 199		P75744	Hypothetical protein ybgJ	b0711	UNC	0.38
743466	REC00686	<i>ybgK</i>	N	310	31, 54, 92, 128, 162, 263		P75745	Hypothetical protein ybgK	b0712	UNC	0.34
744388	REC00687	<i>ybgL</i>	X	244	167		P75746	Protein ybgL	b0713	UNC	0.34
745158	REC00688	<i>nei</i>	X	263	-		P50465	Endonuclease VIII (EC 3.2.-.-)	b0714	NAM	0.06
747037	REC04603	<i>abrB</i>	N	363	28, 124, 155, 165, 234		P75747	AbrB protein	b0715	UNC	0.16
748232	REC04604	<i>ybgO</i>	N	362	100, 187, 188, 312, 341		P75748	Hypothetical protein ybgO precursor	b0716	UNC	0.03
748930	REC04605	<i>ybgP</i>	E	242	-	< 0.05	P75749	Hypothetical fibrial chaperone ybgP precursor	b0717	UNC	0.00
751401	REC04606	<i>ybgQ</i>	N	818	2, 110, 134, 150, 212, 295, 327, 431, 542, 551, 564, 591, 800		P75750	Hypothetical outer membrane usher protein ybgQ precursor	b0718	UNC	0.06
752018	REC04607	<i>ybgD</i>	?	188	11, 177		P37909	Hypothetical fibrial-like protein ybgD precursor	b0719	UNC	0.00
753691	REC04608	<i>gltA</i>	E	405	53, 158, 187, 404		P00891	Citrate synthase (EC 4.1.3.7)	b0720	CHM	0.69
754400	REC00695	<i>sdhC</i>	N	129	60		P10446	Succinate dehydrogenase cytochrome B-556 subunit	b0721	CHM	0.28
754783	REC00696	<i>sdhD</i>	N	115	70		P10445	Succinate dehydrogenase hydrophobic membrane anchor protein	b0722	CHM	0.34
755130	REC00697	<i>sdhA</i>	N	588	57, 210, 220, 368, 511		P10444	Succinate dehydrogenase flavoprotein subunit (EC 1.3.99.1)	b0723	SMC	0.78
756912	REC00698	<i>sdhB</i>	N	238	63, 140, 215		P07014	Succinate dehydrogenase iron-sulfur protein (EC 1.3.99.1)	b0724	SMC	0.72
757687	REC00699		N	86	7, 34, 58		P75752	FROM BASES 747061 TO 762127 (SECTION 65 OF 400) OF THIB	b0725	UNC	0.00
757929	REC00700	<i>sucA</i>	E	933	74	< 0.001	P07015	2-oxoglutarate dehydrogenase E1 component (EC 1.2.4.-)	b0726	CHM	0.59
760745	REC00701	<i>sucB</i>	E	405	-	< 0.01	P07016	Dihydrolipoamide succinyltransferase component of 2-oxoglutarate	b0727	CHM	0.72
762237	REC00702	<i>sucC</i>	N	388	49, 70, 139, 275, 336		P07460	Succinyl-CoA synthetase beta chain (EC 6.2.1.5)	b0728	CHM	0.69
763403	REC00703	<i>sucD</i>	N	289	28, 68, 75, 168, 195		P07459	Succinyl-CoA synthetase alpha chain (EC 6.2.1.5)	b0729	CHM	0.69
765098	REC04609	<i>farR</i>	N	240	81, 120, 150		P13669	Fatty acyl responsive regulator	b0730	RCD	0.19
765207	REC00705	<i>hrsA</i>	N	658	27, 96, 646		P54745	HRSA protein (EC 2.7.1.69)	b0731	CHM	0.47
767201	REC00706	<i>ybgG</i>	N	877	25, 188, 212, 244, 262, 349, 360, 387, 430, 474, 581, 627, 709, 765, 856		P54746	Hypothetical protein ybgG	b0732	UNC	0.19
770678	REC00707	<i>cydA</i>	E	523	-	< 0.01	P11026	Cytochrome D ubiquinol oxidase subunit I (EC 1.10.3.-)	b0733	BEN	0.63
772265	REC00708	<i>cydB</i>	E	379	-	< 0.01	P11027	Cytochrome D ubiquinol oxidase subunit II (EC 1.10.3.-)	b0734	BEN	0.59
773398	REC06667	<i>ybgT</i>	?	44	31		P56100	Protein ybgT	b0735	UNC	0.09
773532	REC00709	<i>ybgE</i>	N	97	28, 51, 92		P37343	Protein ybgE	b0735	UNC	0.03
773975	REC0										

790252	REC04615	galT	N	348	31, 88, 117, 267, 268, 323	P09148	Galactose-1-phosphate uridylyltransferase (EC 2.7.7.10)	b0758	CHM	0.16	
791278	REC04616	galE	N	338	16, 33, 140, 163, 266	P09147	UDP-glucose 4-epimerase (EC 5.1.3.2)	b0759	CHM	0.84	
793011	REC04617	modF	N	490	93, 115, 238, 260, 285, 293, 338, 465, 479	P31060	Putative molybdenum transport ATP-binding protein modF	b0760	UNC	0.09	
793867	REC04618	modE	N	262	224	P46930	Transcriptional regulator modE	b0761	RCD	0.13	
793996	REC00729	ybhT	?	49	-	P75759	Hypothetical protein ybhT precursor	b0762	UNC	0.00	
794312	REC00730	modA	N	257	104	P37329	Molybdate-binding periplasmic protein precursor	b0763	MTR	0.66	
795085	REC00731	modB	N	229	9, 48, 172, 204, 213	P09834	Molybdenum transport system permease protein modB	b0764	MTR	0.50	
795777	REC00732	modC	N	352	33, 52	P09833	Molybdenum transport ATP-binding protein modC	b0765	MTR	0.34	
797654	REC04619	ybhA	E	272	3	< 0.05	P21829	Hypothetical protein ybhA	b0766	UNC	0.66
797809	REC00734	ybhE	N	331	50, 156, 254	P52697	Hypothetical protein ybhE	b0767	UNC	0.25	
799861	REC04620	ybhD	N	338	20, 89, 114, 141, 152, 209, 289	P52696	Hypothetical transcriptional regulator ybhD	b0768	UNC	0.25	
799982	REC00736	ybhH	N	350	92, 104, 156, 193, 248, 284, 332	P75762	Hypothetical protein ybhH	b0769	UNC	0.28	
801110	REC00737	ybhI	N	477	83, 121, 147, 235, 245, 292, 324, 383, 417, 433, 469, 473	P75763	Hypothetical protein ybhI	b0770	UNC	0.28	
802702	REC00738	ybhJ	N	761	87, 100, 158	P75764	Hypothetical protein ybhJ	b0771	UNC	0.59	
806504	REC04621	ybhC	N	427	107, 128, 167, 243, 316, 340, 384	P46130	Putative lipoprotein ybhC precursor	b0772	UNC	0.00	
807132	REC04622	ybhB	N	158	45, 46	P12994	Protein ybhB	b0773	UNC	0.28	
808480	REC04623	bioA	N	429	68, 413	P12995	Adenosylmethionine-8-amino-7-oxononanoate aminotransferase (b0774	b0774	NCM	0.66	
808567	REC00742	bioB	N	346	95, 287, 340	P12996	Biotin synthase (EC 2.8.1.6)	b0775	NCM	0.72	
809604	REC00743	bioF	N	384	23, 166, 227, 283, 347, 348	P12998	8-amino-7-oxononanoate synthase (EC 2.3.1.47)	b0776	NCM	0.66	
810745	REC00744	bioC	N	251	138, 214	P12999	Biotin synthesis protein bioC	b0777	NCM	0.47	
811493	REC00745	bioD	N	225	90, 127, 221	P13000	Dethiobiotin synthetase (EC 6.3.3.3)	b0778	NCM	0.69	
812749	REC00746	uvrB	N	673	21, 91, 316, 347, 419, 504, 601, 611	P07025	Excinuclease ABC subunit B	b0779	NAM	0.94	
815870	REC04624	ybhK	N	302	112, 175	P75767	Hypothetical protein ybhK	b0780	UNC	0.41	
816267	REC00748	moaA	N	329	105, 147, 217, 220	P30745	Molybdenum cofactor biosynthesis protein A	b0781	NCM	0.63	
817278	REC00749	moaB	N	170	93, 158	P30746	Molybdenum cofactor biosynthesis protein B	b0782	NCM	0.41	
817793	REC00750	moaC	N	161	21, 142, 142	P30747	Molybdenum cofactor biosynthesis protein C	b0783	NCM	0.66	
818271	REC00751	moaD	N	81	24, 28, 34, 46, 73	P30748	Molybdopterin converting factor subunit 1	b0784	NCM	0.19	
818518	REC00752	moaE	N	150	19	P30749	Molybdopterin converting factor subunit 2	b0785	NCM	0.56	
819107	REC00753	ybhL	N	234	78, 117, 165, 166	P75768	Hypothetical protein ybhL	b0786	UNC	0.38	
820016	REC00754	ybhM	N	237	49, 178, 169, 190, 234	P75769	Hypothetical protein ybhM	b0787	UNC	0.00	
821721	REC04625	ybhN	E	318	185	< 0.01	P75770	Hypothetical protein ybhN	b0788	UNC	0.22
822962	REC04626	ybhO	N	413	91, 130, 170, 177, 388	P75771	Hypothetical protein ybhO	b0789	UNC	0.63	
823720	REC04627	ybhP	N	253	174	P75772	Hypothetical protein ybhP	b0790	UNC	0.25	
823853	REC00758	ybhQ	E	136	-	< 0.2	P75773	Hypothetical protein ybhQ	b0791	UNC	0.00
825331	REC04628	ybhR	N	368	86, 173, 236, 355	P75774	Hypothetical protein ybhR	b0792	UNC	0.38	
826475	REC04629	ybhS	N	377	11, 251, 265, 293, 328, 377	P75775	Hypothetical protein ybhS	b0793	UNC	0.31	
828219	REC04630	ybhF	N	583	68, 141, 147, 219, 489	P75776	Hypothetical ABC transporter ATP-binding protein ybhF	b0794	UNC	0.63	
829195	REC04631	ybhG	N	332	17, 29, 87, 163, 208	P75777	Hypothetical membrane protein ybhG	b0795	UNC	0.53	
829878	REC04632	ybiH	N	227	71, 96, 150	P41037	Hypothetical transcriptional regulator ybiH	b0796	UNC	0.09	
830095	REC00764	rhlE	N	454	12, 25, 114	P25888	Putative ATP-dependent RNA helicase rhlE	b0797	UNC	0.88	
832173	REC04633	ybiA	E	160	-	< 0.2	P30176	Hypothetical protein ybiA	b0798	UNC	0.06
832293	REC00766	dinG	N	716	322, 330, 304	P27296	Probable ATP-dependent helicase dinG	b0799	UNC	0.47	
834471	REC00767	ybiB	N	320	101, 228, 251	P30177	Hypothetical protein ybiB	b0800	UNC	0.78	
835574	REC00768	ybiC	N	361	37, 40, 48, 186, 265, 324	P30178	Hypothetical oxidoreductase ybiC (EC 1.1.1.-)	b0801	UNC	0.19	
837148	REC04634	ybiJ	?	86	-	P41038	Hypothetical protein ybiJ precursor	b0802	UNC	0.00	
837679	REC04635	ybiI	N	88	39	P41039	Hypothetical protein ybiI	b0803	UNC	0.03	
838486	REC04636	ybiX	N	237	170, 211	P75779	Hypothetical protein ybiX	b0804	UNC	0.09	
840754	REC04637	ybiL	N	760	7, 79, 95, 178, 363, 401, 431, 484, 641, 732	P75780	Probable tonB-dependent receptor ybiL precursor	b0805	UNC	0.25	
841423	REC04638	ybiM	N	134	21	P75781	Hypothetical protein ybiM	b0806	UNC	0.00	
841474	REC00774	ybiN	N	335	122, 179, 261	P75782	Hypothetical protein ybiN	b0807	UNC	0.66	
844838	REC04639	ybiO	N	786	59, 139, 260, 340, 374, 653	P75783	Hypothetical protein ybiO	b0808	UNC	0.88	
845686	REC04640	glnQ	N	240	11, 113	P10346	Glutamine transport ATP-binding protein glnQ	b0809	MTR	0.44	
846342	REC04641	glnP	E	219	-	< 0.1	P10345	Glutamine transport system permease protein glnP	b0810	MTR	0.31
847227	REC04642	glnH	N	248	161, 186	P10344	Glutamine-binding periplasmic protein precursor	b0811	MTR	0.69	
848134	REC04643	dps	N	167	56, 150	P27430	DNA protection during starvation protein	b0812	UNC	0.25	
849320	REC04644	ybiF	N	295	18, 178, 239, 258	P36545	Hypothetical transport protein ybiF	b0813	UNC	0.25	
849673	REC00781	ompX	N	171	30, 77, 100, 141	P36546	Outer membrane protein X precursor	b0814	SMC	0.00	
851820	REC04645	ybiP	N	527	14, 57, 159, 377, 409, 440, 469, 497	P75785	Hypothetical protein ybiP	b0815	UNC	0.06	
851894	REC00783	?	?	89	30	P75786	FROM BASES 851828 TO 863593 (SECTION 74 OF 400) OF THI	b0816	UNC	0.00	
852406	REC00784	mntR	E	155	-	< 0.1	P75787	Transcriptional regulator mntR	b0817	RCD	0.19
852870	REC00785	ybiR	N	372	112, 207, 248, 252, 268, 370	P75788	Hypothetical protein ybiR	b0818	UNC	0.13	
854967	REC04646	ybiS	N	306	11, 61, 166, 184	P75789	Protein ybiS precursor	b0819	UNC	0.69	
855186	REC00787	ybiT	N	530	75, 310, 386, 426, 479	P75790	Hypothetical ABC transporter ATP-binding protein ybiT	b0820	UNC	0.88	
858284	REC04647	ybiU	N	421	9, 64, 87, 140, 174, 249, 263, 337, 408	P75791	Hypothetical protein ybiU	b0821	UNC	0.00	
859251	REC04648	ybiV	N	271	180, 229	P75792	Hypothetical protein ybiV	b0822	UNC	0.66	
861829	REC04649	ybiW	N	810	14, 94, 303, 393, 438, 464, 529, 544, 607, 631, 647, 669, 688, 700, 741, 7	P75793	Putative formate acetyltransferase 3 (EC 2.3.1.54)	b0823	UNC	0.22	
862761	REC04650	ybiY	N	308	33, 157	P75794	Putative pyruvate formate-lyase 3 activating enzyme (EC 1.97.1.4)	b0824	UNC	0.28	
862793	REC00792	fsaA	N	244	118	P78055	Fructose-6-phosphate aldolase 1 (EC 4.1.2.-)	b0825	CHM	0.06	
864352	REC04651	moaB	N	249	1, 82, 141, 210	P12282	Molybdopterin biosynthesis protein moeB	b0826	NCM	0.75	
865587	REC04652	moaA	N	411	128, 207	P12281	Molybdopterin biosynthesis protein moeA	b0827	NCM	0.66	
865791	REC00795	ybiK	N	321	152, 181, 232, 267	P37595	Putative L-asparaginase precursor (EC 3.5.1.1)	b0828	UNC	0.19	
866776	REC00796	yliA	N	612	54, 77, 187, 212, 284, 359, 418	P75796	Hypothetical ABC transporter ATP-binding protein yliA	b0829	UNC	0.34	
868634	REC00797	yliB	N	512	9, 367, 480	P75797	Putative binding protein yliB precursor	b0830	UNC	0.56	
870190	REC00798	yliC	N	306	17, 93, 115, 140, 226, 263	P75798	Hypothetical ABC transporter permease protein yliC	b0831	UNC	0.69	
871113	REC00799	yliD	N	303	31, 102, 207, 272, 272	P75799	Hypothetical ABC transporter permease protein yliD	b0832	UNC	0.63	
872202	REC00800	yliE	N	782	23, 27, 338, 397, 418, 474, 485, 554, 581, 648, 739	P75800	Hypothetical protein yliE	b0833	UNC	0.00	
874558	REC00801	yliF	N	442	60, 373	P75801	Hypothetical membrane protein yliF	b0834	UNC	0.03	
877258	REC04653	yliG	E	441	9	< 0.01	P75802	Hypothetical protein yliG	b0835	UNC	0.66
877471	REC00803	yliH	N	127	62, 119	P75803	Hypothetical protein yliH	b0836	UNC	0.00	
877965	REC00804	yliI	N	371	12, 118	P75804	Hypothetical protein yliI precursor	b0837	UNC	0.19	
879709	REC04654	yliJ	N	210	143, 199	P75805	Hypothetical GST-like protein yliJ	b0838	UNC	0.44	
879950	REC00806	dacC	N	400	70, 101, 118, 162, 187, 211, 285, 343, 373	P08506	Penicillin-binding protein 6 precursor (EC 3.4.16.4)	b0839	LPC	0.72	
881957	REC04655	deoR	N	252	70, 186, 219	P06217	Deoxyribose operon repressor	b0840	NAM	0.09	
882611	REC04656	ybjG	N	198	7, 90	P75806	Hypothetical protein ybjG	b0841	UNC	0.16	
882896	REC00809	cmr	N	410	199, 331, 338	Q46966	Multidrug translocase mdmA	b0842	MTR	0.03	
884453	REC04657	ybjH	N	94	92	P75808	Hypothetical protein ybjH precursor	b0843	UNC	0.00	
885327	REC04658	ybjI	N	262	30, 87, 169, 216	P75809	Protein ybjI	b0844	UNC	0.66	
886562	REC04659	ybjJ	N	402	132, 367	P75810	Hypothetical protein ybjJ	b0845	UNC	0.19	
886646	REC00813	ybjK	E	178	164	< 0.2	P75811	Hypothetical protein ybjK	b0846	UNC	0.03
889042	REC04660	ybjL	N	561	38, 122, 147, 200, 429, 481	P75812	Hypothetical membrane protein ybjL	b0847	UNC	0.13	
889312	REC00815	ybjM	N	125	4, 96	P75813	Hypothetical protein ybjM	b0848	UNC	0.00	
889976	REC04661	grxA	?	85	-	P00277	Glutaredoxin 1	b0849	BEN	0.06	
890136	REC00817	ybjC	E	95	7	0.34	P46119	Hypothetical protein ybjC	b0850	UNC	0.00

890407	REC00818	<i>nfsA</i>	N	240	14, 43, 115, 167		P17117	Oxygen-insensitive NADPH nitroreductase (EC 1.-.-.)	b0851	NCM	0.25
891190	REC00819	<i>rimK</i>	N	300	4, 22, 194, 269		P17116	Ribosomal protein S6 modification protein	b0852	PMS	0.22
892180	REC00820	<i>ybjN</i>	?	158	11		P75815	Hypothetical protein ybjN	b0853	UNC	0.00
893007	REC00821	<i>potF</i>	N	370	90, 159, 329		P31133	Putrescine-binding periplasmic protein precursor	b0854	MTR	0.66
894133	REC00822	<i>potG</i>	N	404	29, 81, 256, 295, 371, 397		P31134	Putrescine transport ATP-binding protein potG	b0855	MTR	0.50
895357	REC00823	<i>potH</i>	N	317	95		P31135	Putrescine transport system permease protein potH	b0856	MTR	0.22
896307	REC00824	<i>potI</i>	N	281	187, 274		P31136	Putrescine transport system permease protein potI	b0857	MTR	0.25
897212	REC00825	<i>ybjO</i>	N	162	48, 89, 131		P75816	Hypothetical protein ybjO	b0858	UNC	0.00
897741	REC00826	<i>ybjF</i>	N	375	125, 209, 262, 338		P75817	Hypothetical RNA methyltransferase ybjF (EC 2.1.1.-)	b0859	UNC	0.72
899798	REC04662	<i>artJ</i>	N	243	140, 231		P30860	Arginine-binding periplasmic protein 2 precursor	b0860	MTR	0.38
900757	REC04663	<i>artM</i>	N	222	28, 61, 86, 112, 132		P30862	Arginine transport system permease protein artM	b0861	MTR	0.16
901473	REC04664	<i>artQ</i>	N	238	30, 64, 111, 114, 198, 235, 237		P30861	Arginine transport system permease protein artQ	b0862	MTR	0.66
902211	REC04665	<i>artI</i>	N	243	92, 195, 202		P30859	Arginine-binding periplasmic protein 1 precursor	b0863	MTR	0.34
902957	REC04666	<i>artP</i>	N	242	26, 209		P30858	Arginine transport ATP-binding protein artP	b0864	MTR	0.09
903690	REC04667	<i>ybjP</i>	E	171	147	< 0.1	P75818	Putative lipoprotein ybjP precursor	b0865	UNC	0.00
903816	REC00833	<i>ybjQ</i>	E	107	-	< 0.3	P75819	Hypothetical protein ybjQ	b0866	UNC	0.19
904136	REC00834	<i>ybjR</i>	E	276	-	< 0.05	P75820	Probable N-acetylmuramoyl-L-alanine amidase ybjR (EC 3.5.1.28)	b0867	UNC	0.34
906012	REC04668	<i>ybjS</i>	E	349	-	< 0.01	P75821	Hypothetical protein ybjS	b0868	UNC	0.25
907535	REC04669	<i>ybjT</i>	N	486	41, 282, 325		P75822	Hypothetical protein ybjT	b0869	UNC	0.31
908517	REC04670	<i>ltaE</i>	N	333	26, 36, 164, 213		P75823	Low-specificity L-threonine aldolase (EC 4.1.2.5)	b0870	AAM	0.47
910272	REC04671	<i>poxB</i>	N	572	110, 112, 198, 249, 295, 528, 551, 563		P07001	Pyruvate dehydrogenase [cytochrome] (EC 1.2.2.2)	b0871	CHM	0.22
911373	REC04672	<i>hcr</i>	N	322	41, 69, 223, 257, 299		P75824	NADH oxidoreductase hcr (EC 1.-.-.-)	b0872	UNC	0.09
913043	REC04673	<i>hcp</i>	N	552	138, 286		P75825	Prismane protein homolog	b0873	UNC	0.09
914128	REC04674	<i>ybjE</i>	N	315	39, 140, 149, 264		P75826	Hypothetical protein ybjE	b0874	UNC	0.13
915270	REC04675	<i>aqpZ</i>	N	231	4, 13, 21, 152		P48838	Aquaporin Z	b0875	MTR	0.22
915696	REC00843	<i>ybjD</i>	N	552	63, 77, 144, 154, 169, 189		P75828	Hypothetical protein ybjD	b0876	UNC	0.03
918343	REC04676	<i>ybjX</i>	N	330	46, 63, 133		P75829	Hypothetical protein ybjX	b0877	UNC	0.16
918431	REC00845	<i>macA</i>	N	380	34, 63, 87, 122, 135, 308		P75830	Macrolide-specific efflux protein macA precursor	b0878	MTR	0.38
919570	REC00846	<i>macB</i>	N	648	16, 56, 109, 191, 564		P75831	Macrolide-specific ABC-type efflux carrier	b0879	MTR	0.75
921813	REC04677	<i>cspD</i>	N	74	65		P24245	Cold shock-like protein cspD	b0880	SMC	0.72
922136	REC00848	<i>yljA</i>	E	106	91	0.32	P75832	Protein yljA	b0881	UNC	0.44
922487	REC00849	<i>clpA</i>	N	758	45, 87, 130, 272, 353, 521, 550, 713		P15716	ATP-dependent clp protease ATP-binding subunit clpA	b0882	PMS	0.75
925666	REC04678	<i>infA</i>	?	72	-		P02998	Translation initiation factor IF-1	b0884	UNC	0.97
926655	REC04679	<i>aat</i>	N	234	6, 38		P23885	Leucyl/phenylalanyl-tRNA--protein transferase (EC 2.3.2.-)	b0885	NAM	0.44
928418	REC04680	<i>cydC</i>	E	573	528	< 0.001	P23886	Transport ATP-binding protein cydC	b0886	MTR	0.34
930185	REC04681	<i>cydD</i>	E	588	-	< 0.001	P29018	Transport ATP-binding protein cydD	b0887	MTR	0.31
931273	REC04682	<i>trxB</i>	N	321	60, 112, 117, 158, 224, 236		P09625	Thioredoxin reductase (EC 1.6.4.5)	b0888	MSM	1.00
931818	REC00855	<i>lrp</i>	N	164	4, 23, 46, 84, 142		P19494	Leucine-responsive regulatory protein	b0889	RCD	0.47
932447	REC00856	<i>ftsK</i>	N	1329	750, 803, 847, 928, 931, 1008, 1050, 1113, 1159, 1187, 1290		P46889	Cell division protein ftsK	b0890	RCD	0.81
936592	REC00857	<i>lolA</i>	N	204	38		P39178	Outer-membrane lipoproteins carrier protein precursor	b0891	LPC	0.19
937217	REC00858	<i>ycaJ</i>	N	447	37, 53, 139, 182, 289, 334, 410		P45526	Hypothetical protein ycaJ	b0892	UNC	0.72
938651	REC00859	<i>serS</i>	E	430	-	< 0.01	P09156	Seryl-tRNA synthetase (EC 6.1.1.11)	b0893	PMS	1.00
940269	REC00860	<i>dmsA</i>	N	785	24, 55, 308, 404, 668, 716		P18775	Anaerobic dimethyl sulfoxide reductase chain A precursor (EC 1.8	b0894	BEN	0.16
942637	REC00861	<i>dmsB</i>	N	205	52, 170		P18776	Anaerobic dimethyl sulfoxide reductase chain B	b0895	BEN	0.16
943256	REC00862	<i>dmsC</i>	N	287	53, 228		P18777	Anaerobic dimethyl sulfoxide reductase chain C	b0896	BEN	0.00
944780	REC04683	<i>ycaC</i>	E	208	-	< 0.1	P21367	Protein ycaC	b0897	UNC	0.13
945094	REC00864	<i>ycaD</i>	N	382	146, 207, 325, 357		P21503	Hypothetical protein ycaD	b0898	UNC	0.56
946260	REC00865	<i>ycaM</i>	N	540	61, 107, 151, 167, 293, 341, 518, 530, 537		P75835	Hypothetical transporter ycaM	b0899	UNC	0.00
948791	REC04684	<i>ycaN</i>	N	302	31, 32, 64, 78, 138, 169, 209, 254, 270, 284		P75836	Hypothetical transcriptional regulator ycaN	b0900	UNC	0.72
948891	REC00867	<i>ycaK</i>	N	196	28, 33, 79, 108, 169		P43340	Putative NAD(P)H oxidoreductase ycaK (EC 1.6.99.-)	b0901	UNC	0.22
950303	REC04685	<i>pflA</i>	N	246	23, 205		P09374	Pyruvate formate-lyase 1 activating enzyme (EC 1.97.1.4)	b0902	CHM	0.31
952777	REC04686	<i>pflB</i>	N	760	159, 168, 209, 371, 403, 434, 479		P09373	Formate acetyltransferase 1 (EC 2.3.1.54)	b0903	CHM	0.22
953689	REC04687	<i>focA</i>	N	285	7, 28, 120, 171, 245		P21501	Probable formate transporter 1	b0904	UNC	0.19
955864	REC04688	<i>ycaO</i>	N	589	6, 54, 151, 277, 278, 349, 389, 565, 575		P75838	Hypothetical protein ycaO	b0905	UNC	0.13
955985	REC00872	<i>ycaP</i>	N	230	45, 155		P75839	Hypothetical protein ycaP	b0906	UNC	0.16
956876	REC00873	<i>serC</i>	N	362	123, 191, 233, 283		P23721	Phosphoserine aminotransferase (EC 2.6.1.52)	b0907	NCM	0.56
958035	REC00874	<i>aroA</i>	N	427	29, 53, 175, 252, 402, 426		P07638	3-phosphoshikimate 1-carboxyvinyltransferase (EC 2.5.1.19)	b0908	AAM	0.88
959463	REC00875	<i>ycaL</i>	N	262	24, 99, 210		P43674	Putative metalloprotease ycaL (EC 3.4.24.-)	b0909	UNC	0.13
960424	REC00876	<i>cmk</i>	E	227	-	< 0.1	P23863	Cytidylate kinase (EC 2.7.4.14)	b0910	NCM	0.88
961218	REC00877	<i>xpsA</i>	N	557	475		P02349	30S ribosomal protein S1	b0911	PMS	0.97
963051	REC00878	<i>ihfB</i>	N	94	42		P08756	Integration host factor beta-subunit	b0912	NAM	0.44
963465	REC00879	<i>ycaI</i>	N	780	98, 98, 215, 381, 541, 575, 613, 675, 717		P37443	Hypothetical protein ycaI	b0913	UNC	0.56
965844	REC00880	<i>msbA</i>	E	582	-	< 0.01	P27299	Probable transport ATP-binding protein msbA	b0914	UNC	0.91
967589	REC00881	<i>lpxK</i>	E	328	-	< 0.01	P27300	Tetraacyldisaccharide 4'-kinase (EC 2.7.1.130)	b0915	LPC	0.53
968612	REC00882	<i>ycaQ</i>	N	410	207, 244, 304, 313		P75843	Hypothetical protein ycaQ	b0916	UNC	0.22
969896	REC00883	<i>ycaR</i>	?	60	-		P75844	Protein ycaR	b0917	UNC	0.28
970075	REC00884	<i>kdsB</i>	E	248	-	< 0.05	P04951	3-deoxy-manno-octulosonate cytidyltransferase (EC 2.7.7.38)	b0918	CHM	0.53
970975	REC00885	<i>ycbJ</i>	N	297	78, 140, 209, 258, 264		P75845	Hypothetical protein ycbJ	b0919	UNC	0.00
972624	REC04689	<i>ycbC</i>	N	259	33, 74		P36565	Hypothetical protein ycbC	b0920	UNC	0.22
972760	REC00887	<i>smtA</i>	N	261	93, 103, 139, 142, 201		P36566	Protein smtA	b0921	UNC	0.09
973542	REC00888	<i>mukF</i>	E	440	-	< 0.001	P36567	MukF protein	b0922	UNC	0.06
974872	REC00889	<i>mukE</i>	E	225	-	< 0.05	P22524	MukE protein	b0923	UNC	0.06
975549	REC00890	<i>mukB</i>	E	1486	-	< 0.001	P22523	Cell division protein mukB	b0924	RCD	0.06
980270	REC00891	<i>ycbB</i>	N	615	62, 205, 262, 550, 611		P22525	Hypothetical protein ycbB	b0925	UNC	0.22
982298	REC00892	<i>ycbK</i>	E	182	-	< 0.1	P75848	Hypothetical protein ycbK	b0926	UNC	0.22
982873	REC00893	<i>ycbL</i>	N	215	3, 112		P75849	Hypothetical protein ycbL	b0927	UNC	0.81
984932	REC04690	<i>aspC</i>	N	396	147, 260, 294, 385		P00509	Aspartate aminotransferase (EC 2.6.1.1)	b0928	AAM	0.25
986205	REC04691	<i>ompF</i>	N	362	6, 49, 70, 98, 118, 133, 263		P02931	Outer membrane protein F precursor	b0929	SMC	0.06
988208	REC04692	<i>asns</i>	E	466	-	< 0.001	P17242	Asparaginyl-tRNA synthetase (EC 6.1.1.22)	b0930	PMS	0.50
989579	REC04693	<i>pncB</i>	N	400	49, 85, 119, 139, 157, 180, 201, 247, 321, 397		P18133	Nicotinyl phosphoribosyltransferase (EC 2.4.2.11)	b0931	NCM	0.31
989845	REC00898	<i>pepN</i>	N	870	76, 81, 182, 462, 556, 753, 841, 850		P04825	Aminopeptidase N (EC 3.4.11.2)	b0932	PMS	0.53
993267	REC04694	<i>ssuB</i>	N	255	112, 255		P38053	Putative aliphatic sulfonates transport ATP-binding protein ssuB	b0933	UNC	0.25
994100	REC04695	<i>ssuC</i>	N	278	18, 71, 138, 177, 244, 258		P75851	Putative aliphatic sulfonates transport permease protein ssuC	b0934	UNC	0.34
995211	REC04696	<i>ssuD</i>	N	381	154, 204, 270, 324		P80645	Alkanesulfonate monooxygenase (EC 1.1.-.-)	b0935	MSM	0.22
996209	REC04697	<i>ssuA</i>	N	333	89, 153		P75853	Putative aliphatic sulfonates binding protein precursor	b0936	UNC	0.25
996735	REC04698	<i>ssuE</i>	N	191	145		P80644	NAD(P)H-dependent FMN reductase (EC 1.6.8.1)	b0937	BEN	0.25
997082	REC00904	<i>ycbQ</i>	N	182	50, 58, 98, 173		P75855	Hypothetical fimbrial-like protein ycbQ precursor	b0938	UNC	0.03
997713	REC00905	<i>ycbR</i>	N	233	11, 98, 103, 168, 224		P75856	Hypothetical fimbrial chaperone ycbR precursor	b0939	UNC	0.00
998439	REC00906	<i>ycbS</i>	N	866	14, 184, 188, 188, 210, 240, 242, 259, 272, 292, 347, 408, 445, 477, 642		P75857	Hypothetical outer membrane usher protein ycbS precursor	b0940	UNC	0.06
1001030	REC00907	<i>ycbT</i>	N	356	6, 74, 85, 129, 245, 325		P75858	Hypothetical fimbrial-like protein ycbT precursor	b0941	UNC	0.00
1002112	REC00908	<i>ycbU</i>	N	180	82		P75859	Hypothetical fimbrial-like protein ycbU precursor	b0942	UNC	0.00
1002614	REC00909	<i>ycbV</i>	N	187	63, 109		P75860	Hypothetical fimbrial-like protein ycbV precursor	b0943	UNC	0.00
1003143	REC00910	<i>ycbF</i>	N	245	17, 182		P40876	Hypothetical fimbrial chaperone ycbF precursor	b0944	UNC	0.00

1003991	REC00911	<i>pyrD</i>	N	336	11, 56, 79, 157, 207, 225, 301, 328	P05021	Dihydroorotate dehydrogenase (EC 1.3.3.1)	b0945	NCM	0.84
1005139	REC00912	<i>ycbW</i>	N	192	37, 49, 189	P75862	Hypothetical protein ycbW	b0946	UNC	0.03
1006823	REC04699	<i>ycbX</i>	N	369	46, 136, 154, 164, 200, 221, 242	P75863	Hypothetical protein ycbX	b0947	UNC	0.16
1007067	REC00914	<i>ycbY</i>	N	702	12, 20, 53, 56, 205, 464, 546, 552	P75864	Hypothetical protein ycbY	b0948	UNC	0.56
1009187	REC00915	<i>uup</i>	N	635	6, 121, 160, 236, 336, 374, 397, 493	P43672	ABC transporter ATP-binding protein uup	b0949	MTR	0.88
1011224	REC00916	<i>pqiA</i>	N	417	69, 274, 319, 322	P43670	Paraquat-inducible protein A	b0950	UNC	0.13
1012482	REC00917	<i>pqiB</i>	N	546	126, 158, 250	P43671	Paraquat-inducible protein B	b0951	UNC	0.16
1014134	REC00918	<i>ymbA</i>	N	182	25, 26, 66, 125	P75866	Hypothetical protein ymbA	b0952	UNC	0.06
1014938	REC00919	<i>rmf</i>	?	55	-	P22986	Ribosome modulation factor	b0953	PMS	0.06
1015693	REC04700	<i>fabA</i>	E	172	-	P18391	3-hydroxydecanoyl-[acyl-carrier-protein] dehydratase (EC 4.2.1.60)	b0954	LPC	0.31
1017522	REC04701	<i>ycbZ</i>	N	586	29, 41, 64, 149, 181, 253, 276, 310, 331, 509	P75867	Putative protease La homolog (EC 3.4.21.-)	b0955	UNC	0.78
1017708	REC00922	<i>ycbG</i>	N	150	32, 77, 85	P45569	Hypothetical protein ycbG	b0956	UNC	0.06
1019276	REC04702	<i>ompA</i>	N	346	47	P02934	Outer membrane protein A precursor	b0957	SMC	0.47
1020142	REC04703	<i>suLA</i>	N	169	10, 82, 108, 124, 159	P08846	Cell division inhibitor	b0958	RCD	0.03
1020361	REC00925	<i>yccR</i>	N	209	21, 40, 79, 195	P75869	Hypothetical protein yccR	b0959	UNC	0.19
1023115	REC04704	<i>yccS</i>	N	720	128, 133, 330, 364, 452, 514, 533, 567, 678	P75870	Hypothetical protein yccS	b0960	UNC	0.22
1023571	REC04705	<i>yccF</i>	N	148	93, 125	P37065	Hypothetical protein yccF	b0961	UNC	0.09
1023694	REC00928	<i>heID</i>	N	684	68, 73, 275, 332, 340, 452, 519	P15038	Helicase IV (EC 3.6.1.-)	b0962	NAM	0.06
1026247	REC04706	<i>mgsA</i>	E	155	-	P37066	Methylglyoxal synthase (EC 4.2.3.3)	b0963	CHM	0.38
1026996	REC04707	<i>yccT</i>	N	220	22, 47, 119	P75873	Hypothetical protein yccT precursor	b0964	UNC	0.06
1027088	REC00931	<i>yccU</i>	E	164	162	P75874	Protein yccU	b0965	UNC	0.31
1027995	REC04708	<i>yccV</i>	N	122	79	P75875	Hypothetical protein yccV	b0966	UNC	0.16
1029105	REC04709	<i>yccW</i>	N	367	166, 232, 309, 366	P75876	Hypothetical protein yccW	b0967	UNC	0.56
1029287	REC00934	<i>yccX</i>	N	92	48	P75877	Putative acylphosphatase (EC 3.6.1.7)	b0968	UNC	0.50
1029948	REC04710	<i>yccK</i>	X	128	-	P45572	Hypothetical protein yccK	b0969	UNC	0.13
1030641	REC04711	<i>yccA</i>	N	219	29, 53, 90	P06967	Hypothetical protein yccA	b0970	UNC	0.22
1031362	REC00937	<i>hyaA</i>	E	372	-	P19928	Hydrogenase-1 small chain precursor (EC 1.18.99.1)	b0972	BEN	0.16
1032477	REC00938	<i>hyaB</i>	N	597	34, 100, 293	P19927	Hydrogenase-1 large chain (EC 1.18.99.1)	b0973	BEN	0.19
1034289	REC00939	<i>hyaC</i>	E	235	-	P19929	Probable Ni/Fe-hydrogenase 1 B-type cytochrome subunit	b0974	UNC	0.09
1034993	REC00940	<i>hyaD</i>	E	195	174, 176	P19930	Hydrogenase 1 maturation protease (EC 3.4.24.-)	b0975	BEN	0.00
1035577	REC00941	<i>hyaE</i>	N	132	74, 127	P19931	Hydrogenase-1 operon protein hyaE	b0976	UNC	0.00
1035972	REC00942	<i>hyaF</i>	N	285	59, 94	P19932	Hydrogenase-1 operon protein hyaF	b0977	UNC	0.00
1036963	REC00943	<i>appC</i>	N	514	82, 148, 183, 193, 353, 399, 423, 506	P26459	Cytochrome BD-II oxidase subunit I (EC 1.10.3.-)	b0978	BEN	0.25
1038519	REC00944	<i>appB</i>	N	378	23, 94, 211, 272	P26458	Cytochrome BD-II oxidase subunit II (EC 1.10.3.-)	b0979	BEN	0.03
1039840	REC00945	<i>appA</i>	N	432	127, 151	P07102	Periplasmic appA protein precursor	b0980	MSM	0.03
1043433	REC04712	<i>etk</i>	N	726	3, 140, 223, 474, 542, 580, 623	P38134	Tyrosine-protein kinase etk (EC 2.7.1.112)	b0981	SMC	0.31
1043911	REC04713	<i>etp</i>	N	152	9, 42, 152	P75880	Low molecular weight protein-tyrosine-phosphatase etp (EC 3.1.3.1)	b0982	CHM	0.59
1045026	REC04714	<i>yccZ</i>	N	379	41, 68, 88, 216, 272, 324	P75881	Putative polysaccharide export protein yccZ precursor	b0983	UNC	0.16
1047168	REC04715	<i>ymcA</i>	N	698	17, 213, 311, 598, 696	P75882	Hypothetical lipoprotein ymcA precursor	b0984	UNC	0.03
1047914	REC04716	<i>ymcB</i>	N	248	17, 51, 57, 122, 144, 168, 244	P75883	Hypothetical protein ymcB precursor	b0985	UNC	0.00
1048555	REC04717	<i>ymcC</i>	N	214	34, 82, 84, 129, 151	P75884	Hypothetical lipoprotein ymcC precursor	b0986	UNC	0.00
1048985	REC04718	<i>ymcD</i>	E	107	-	P75885	Hypothetical protein ymcD	b0987	UNC	0.00
1049250	REC00953	<i>insB4</i>	E	167	-	P57998	Insertion element IS1 4 protein insB	b0988	PHT	0.03
1050398	REC06609	<i>cspH</i>	?	70	-	P56253	Cold shock-like protein cspH	b0989	UNC	0.00
1050684	REC06610	<i>cspG</i>	N	70	3, 23, 44, 65	Q47130	Cold shock-like protein cspG	b0990	UNC	0.72
1051070	REC00954	<i>sfa</i>	N	76	23, 46, 55	P52634	Sfa protein	b0991	UNC	0.00
1051293	REC06673	<i>gnsA</i>	N	56	30	P52635	GnsA protein	b0992	UNC	0.00
1052585	REC04719	<i>yccM</i>	N	357	73, 168, 291, 327	P52636	Putative electron transport protein yccM	b0992	UNC	0.25
1055371	REC04720	<i>torS</i>	N	904	6, 109, 138, 280, 310, 362, 393, 437	P39453	Sensor protein torS (EC 2.7.3.-)	b0993	SMC	0.06
1055484	REC00957	<i>torT</i>	N	342	115, 289	P38683	Periplasmic protein torT precursor	b0994	MSM	0.03
1057177	REC04721	<i>torR</i>	E	230	-	P38684	TorCAD operon transcriptional regulatory protein torR	b0995	SMC	0.06
1057307	REC00959	<i>torC</i>	N	390	56, 80, 297, 337	P33226	Cytochrome c-type protein torC	b0996	SMC	0.06
1058479	REC00960	<i>torA</i>	N	848	36, 80, 195, 348, 737, 779, 831	P33225	Trimethylamine-N-oxide reductase 1 precursor (EC 1.6.6.9)	b0997	SMC	0.06
1061022	REC00961	<i>torD</i>	E	199	186	P36662	Chaperone protein torD	b0998	SMC	0.03
1062078	REC04722	<i>yccD</i>	E	101	-	P36660	Hypothetical protein yccD	b0999	UNC	0.00
1062998	REC04723	<i>cbpA</i>	N	306	18, 111	P36659	Curved DNA-binding protein	b1000	UNC	0.34
1063259	REC00964	<i>yccE</i>	N	418	21, 168, 393	P36661	Hypothetical protein yccE	b1001	UNC	0.00
1064808	REC00965	<i>app</i>	N	413	23	P19926	Glucose-1-phosphatase precursor (EC 3.1.3.10)	b1002	MSM	0.00
1066314	REC04724	<i>yccJ</i>	?	75	-	P46131	Hypothetical protein yccJ	b1003	UNC	0.00
1066931	REC04725	<i>wzba</i>	N	198	-	P30849	Flavoprotein wzba	b1004	UNC	0.34
1067141	REC00968	<i>yedF</i>	?	76	-	Q9Z260	ORF, HYPOTHETICAL PROTEIN	b1005	UNC	0.00
1069128	REC04726	<i>yedG</i>	N	464	125, 143, 172, 182, 254, 311, 381	P75892	Putative purine permease yedG	b1006	UNC	0.47
1069541	REC04727	<i>yedH</i>	N	152	33, 91, 126, 137	P75893	Putative flavin:NADH reductase yedH (EC 1.6.8.-)	b1007	MSM	0.28
1070178	REC04728	<i>yedI</i>	N	196	11, 150	P75894	Putative NADH dehydrogenase/NAD(P)H nitroreductase yedI (EC 1.6.1.3)	b1008	UNC	0.13
1070988	REC04729	<i>yedJ</i>	N	266	32	P75895	Hypothetical protein yedJ	b1009	UNC	0.13
1071382	REC04730	<i>yedK</i>	E	128	-	P75896	Hypothetical protein yedK	b1010	UNC	0.81
1072128	REC04731	<i>yedL</i>	E	244	233	P75897	Hypothetical isochorismatase family protein yedL	b1011	UNC	0.34
1073234	REC04732	<i>yedM</i>	N	382	92, 266, 334	P75898	Putative monooxygenase yedM	b1012	UNC	0.13
1073465	REC00976	<i>yedC</i>	N	212	70, 153	P75899	Hypothetical transcriptional regulator yedC	b1013	UNC	0.28
1078105	REC04733	<i>putA</i>	N	1320	13, 17, 42, 230, 285, 363, 410, 428, 521, 610, 751, 770, 814, 823, 973, 987	P09546	Bifunctional putA protein	b1014	AAM	0.53
1078528	REC00978	<i>putP</i>	N	502	74, 151, 202, 287	P07117	Sodium/proline symporter	b1015	MTR	0.44
1080570	REC00979	-	N	39	17	P75901	Hypothetical protein ycdN	b1016	UNC	0.00
1080677	REC00980	<i>yedN</i>	N	243	92	P75901	Hypothetical protein ycdN	b1017	UNC	0.16
1081466	REC00981	<i>yedO</i>	N	375	171, 184, 354	P75902	Protein ycdO	b1018	UNC	0.13
1082599	REC00982	<i>yedB</i>	N	423	19, 53, 149, 207, 320, 375	P31545	Hypothetical protein ycdB precursor	b1019	UNC	0.16
1084215	REC00983	<i>phoH</i>	N	354	20, 183, 234, 327	P31544	PhoH protein	b1020	UNC	0.69
1085742	REC04734	<i>yedP</i>	N	137	78, 108, 127	P75904	Hypothetical protein ycdP	b1021	UNC	0.00
1087069	REC04735	<i>yedQ</i>	N	441	11, 69, 110, 205, 266, 292, 298, 332, 343, 370, 396, 412, 440	P75905	Hypothetical protein ycdQ	b1022	UNC	0.38
1089080	REC04736	<i>yedR</i>	N	672	24, 61, 85, 120, 165, 194, 202, 254, 260, 276, 299, 329, 652	P75906	Hypothetical lipoprotein ycdR precursor	b1023	UNC	0.06
1091512	REC04737	<i>yedS</i>	N	807	135, 256, 358, 379, 433, 710, 762, 799	P75907	Hypothetical protein ycdS precursor	b1024	UNC	0.03
1092099	REC00988	<i>yedT</i>	N	452	13, 31, 58, 158, 235, 272, 283, 307, 365, 374, 413, 424	P75908	Hypothetical protein ycdT	b1025	UNC	0.59
1094364	REC06639	<i>insF4</i>	N	288	73, 103, 144, 175, 262	P05822	Transposase insF for insertion sequence IS3A/B/C/D/E/FA	b1026	PHT	0.56
1094669	REC06640	<i>insE4</i>	E	102	-	P77681	Transposase insE for insertion sequence IS3A/B/C/D/E/FA/FB	b1027	PHT	0.56
1094746	REC00991	-	N	107	12, 68	P75909	ORF_ID:O230#4	b1028	UNC	0.00
1095066	REC00992	<i>yedU</i>	N	328	27, 165, 196, 238, 270	P75910	Hypothetical protein ycdU	b1029	UNC	0.00
1096171	REC00993	-	N	83	67, 76	P75911	FROM BASES 1094678 TO 1105023 (SECTION 95 OF 400) OF T	b1030	UNC	0.00
1097070	REC00995	<i>yedW</i>	E	325	72	P75913	Putative 2-hydroxyacid dehydrogenase ycdW	b1033	UNC	0.25
1098102	REC00996	<i>yedX</i>	E	245	-	P75914	Hypothetical protein ycdX precursor	b1034	UNC	0.06
1098863	REC00997	<i>yedY</i>	N	184	38	P75915	Hypothetical protein ycdY	b1035	UNC	0.03
1099471	REC00998	<i>yedZ</i>	E	179	-	P75916	Hypothetical protein ycdZ	b1036	UNC	0.03
1100907	REC04740	<i>csgG</i>	N	277	2, 12, 47, 91, 228, 230	P52103	Curli production assembly/transport component csgG precursor	b1037	UNC	0.00
1101350	REC04741	<i>csgF</i>	N	138	31	P52104	Curli production assembly/transport component csgF precursor	b1038	UNC	0.00

1101764	REC04742	<i>csgE</i>	E	129	-	< 0.2	P52105	Curli production assembly/transport component csgE precursor	b1039	UNC	0.00
1102419	REC04743	<i>csgD</i>	N	216	101, 171		P52106	Probable csgAB operon transcriptional regulatory protein	b1040	UNC	0.06
1103174	REC01003	<i>csgB</i>	N	151	15, 27, 68, 114, 127		P39828	Minor curlin subunit precursor	b1041	SMC	0.03
1103670	REC01004	<i>csgA</i>	N	151	18, 52, 142		P28307	Major curlin subunit precursor	b1042	SMC	0.00
1104184	REC01005	<i>csgC</i>	N	110	71		P52107	Putative curli production protein csgC precursor	b1043	UNC	0.00
1104637	REC01006	<i>ymdA</i>	X	103	-		P75917	Hypothetical protein ymdA precursor	b1044	UNC	0.00
1105043	REC01007	<i>ymdB</i>	N	177	174		P75918	Hypothetical protein ymdB	b1045	UNC	0.28
1105518	REC01008	<i>ymdC</i>	N	493	16, 155, 162, 210, 356, 404, 450, 473		P75919	Hypothetical protein ymdC	b1046	UNC	0.63
1108164	REC04744	<i>mdoC</i>	N	385	15, 58, 79, 119, 165, 208, 262, 340		P75920	Glucans biosynthesis protein mdoC	b1047	CHM	0.03
1108558	REC01010	<i>mdoG</i>	N	511	201, 203, 241, 295, 334, 357, 467		P33136	Periplasmic glucans biosynthesis protein mdoG precursor	b1048	CHM	0.13
1110086	REC01011	<i>mdoH</i>	N	847	57, 167, 220, 377, 377, 470, 484, 661		P33137	Periplasmic glucans biosynthesis protein mdoH	b1049	CHM	0.16
1112802	REC01012	<i>yceK</i>	N	75	29		P45806	Hypothetical protein yceK precursor	b1050	UNC	0.00
1113407	REC04745	<i>msyB</i>	E	125	-	< 0.3	P25738	Acidic protein msyB	b1051	UNC	0.00
1113532	REC04746	?	?	32	-		P75923	FROM BASES 1104966 TO 1115945 (SECTION 96 OF 400) OF T	b1052	UNC	0.00
1114713	REC04747	<i>yceE</i>	N	408	11, 175, 202, 225, 340, 366		P25744	Hypothetical transport protein yceE	b1053	UNC	0.81
1115805	REC04748	<i>htrB</i>	N	306	43		P24187	Lipid A biosynthesis lauroyl acyltransferase (EC 2.3.1.-)	b1054	LPC	0.50
1116030	REC01017	<i>yceA</i>	N	350	25, 31, 75, 160, 267, 300, 348		P24188	Hypothetical protein yceA	b1055	UNC	0.63
1117699	REC04749	<i>yceI</i>	N	191	28, 123		P37904	Protein yceI precursor	b1056	UNC	0.44
1118269	REC04750	<i>yceJ</i>	N	188	140		P75925	Cytochrome b561 homolog 2	b1057	UNC	0.31
1118670	REC04751	<i>yceO</i>	?	46	-		P75926	Hypothetical protein yceO	b1058	UNC	0.00
1119809	REC04752	<i>soIA</i>	N	372	4, 49, 112, 275		P40874	N-methyl-L-tryptophan oxidase (EC 1.5.3.-)	b1059	AAM	0.22
1120178	REC04753	<i>yceP</i>	N	84	31		P75927	Hypothetical protein yceP	b1060	UNC	0.00
1120710	REC04754	<i>dinI</i>	N	81	64		Q47143	DNA-damage-inducible protein I	b1061	NAM	0.00
1121830	REC04755	<i>pyrC</i>	N	348	77, 206, 253, 328		P05020	Dihydroorotase (EC 3.5.2.3)	b1062	NCM	0.31
1122496	REC04756	<i>yceB</i>	N	186	12		P09995	Putative lipoprotein yceB precursor	b1063	UNC	0.00
1123277	REC04757	<i>grxB</i>	N	215	142		P39811	Glutaredoxin 2	b1064	AAM	0.06
1124579	REC04758	<i>yceL</i>	N	412	281		P77042	Hypothetical transport protein yceL	b1065	UNC	0.06
1124785	REC01028	<i>rimJ</i>	N	194	40, 45, 143		P09454	Ribosomal-protein-alanine acetyltransferase (EC 2.3.1.128)	b1066	PMS	0.41
1125380	REC01029	<i>yceH</i>	N	215	60, 177, 197		P29217	Hypothetical protein yceH	b1067	UNC	0.13
1126029	REC01030	<i>mviM</i>	N	307	17, 111, 166, 182		P75931	Virulence factor mviM homolog	b1068	UNC	0.13
1127062	REC01031	<i>mviN</i>	E	511	-	< 0.01	P75932	Virulence factor mviN homolog	b1069	UNC	0.81
1129053	REC04759	<i>flgN</i>	N	138	81		P43533	Flagella synthesis protein flgN	b1070	UNC	0.00
1129351	REC04760	<i>flgM</i>	N	97	32, 61		P43532	Negative regulator of flagellin synthesis	b1071	RCD	0.00
1130086	REC04761	<i>flgA</i>	N	219	114		P75933	Flagella basal body P-ring formation protein flgA precursor	b1072	SMC	0.13
1130241	REC01035	<i>flgB</i>	N	138	9, 112		P75934	Flagellar basal-body rod protein flgB	b1073	SMC	0.34
1130661	REC01036	<i>flgC</i>	N	134	26		P75935	Flagellar basal-body rod protein flgC	b1074	SMC	0.56
1131077	REC01037	<i>flgD</i>	N	231	10, 179		P75936	Basal-body rod modification protein flgD	b1075	SMC	0.28
1131797	REC01038	<i>flgE</i>	N	402	46, 161, 356, 372		P75937	Flagellar hook protein flgE	b1076	SMC	0.53
1133025	REC01039	<i>flgF</i>	N	251	18, 53, 163		P75938	Flagellar basal-body rod protein flgF	b1077	SMC	0.47
1133952	REC01040	<i>flgG</i>	N	260	9, 136, 217		P75939	Flagellar basal-body rod protein flgG	b1078	SMC	0.56
1134787	REC01041	<i>flgH</i>	N	232	50, 63		P75940	Flagellar L-ring protein precursor	b1079	SMC	0.38
1135497	REC01042	<i>flgI</i>	N	365	97, 219, 332, 358		P75941	Flagellar P-ring protein precursor	b1080	SMC	0.41
1136594	REC01043	<i>flgJ</i>	N	313	3, 39, 173		P75942	Peptidoglycan hydrolase flgJ (EC 3.2.1.-)	b1081	SMC	0.22
1137601	REC01044	<i>flgK</i>	N	547	390, 485, 489		P33235	Flagellar hook-associated protein 1	b1082	SMC	0.56
1139256	REC01045	<i>flgL</i>	X	317	-		P29744	Flagellar hook-associated protein 3	b1083	SMC	0.28
1143590	REC04762	<i>rne</i>	E	1061	-	< 0.001	P21513	Ribonuclease E (EC 3.1.4.-)	b1084	NAM	0.56
1143671	REC01047	?	E	124	-	< 0.3	P75943	FROM BASES 1137539 TO 1147976 (SECTION 99 OF 400) OF T	b1085	UNC	0.00
1144163	REC01048	<i>rluC</i>	N	319	180, 220, 269, 282		P23851	Ribosomal large subunit pseudouridine synthase C (EC 4.2.1.70)	b1086	NAM	0.72
1145857	REC04763	<i>yceF</i>	N	207	142, 160		P27244	Maf-like protein yceF	b1087	UNC	0.75
1146017	REC01050	<i>yceD</i>	N	173	92, 158		P14189	Hypothetical protein yceD	b1088	UNC	0.19
1146590	REC01051	<i>xpmX</i>	?	57	-		P02435	50S ribosomal protein L32	b1089	PMS	0.69
1146874	REC01052	<i>plsX</i>	N	346	15, 124, 162, 233, 307		P72940	Fatty acid/phospholipid synthesis protein plsX	b1090	UNC	0.72
1147982	REC01053	<i>fabH</i>	E	317	-	< 0.05	P24249	3-oxoacyl-[acyl-carrier-protein] synthase III (EC 2.3.1.41)	b1091	LPC	0.84
1148951	REC01054	<i>fabD</i>	E	309	-	< 0.05	P25715	Malonyl CoA-acyl carrier protein transacylase (EC 2.3.1.39)	b1092	LPC	0.84
1149893	REC01055	<i>fabG</i>	E	244	-	< 0.05	P25716	3-oxoacyl-[acyl-carrier-protein] reductase (EC 1.1.1.100)	b1093	LPC	0.91
1150838	REC01056	<i>acpP</i>	?	78	-		P02901	Acyl carrier protein	b1094	LPC	0.88
1151162	REC01057	<i>fabF</i>	N	413	10, 51, 161, 187, 315, 332		P39435	3-oxoacyl-[acyl-carrier-protein] synthase II (EC 2.3.1.41)	b1095	LPC	0.91
1152523	REC01058	<i>pabC</i>	N	269	131, 143, 167, 258		P28305	4-amino-4-deoxychorismate lyase (EC 4.-.-.-)	b1096	NCM	0.09
1153335	REC01059	<i>yceG</i>	N	340	42, 282		P28306	Hypothetical protein yceG	b1097	UNC	0.78
1154347	REC01060	<i>tmk</i>	E	213	-	< 0.2	P37345	Thymidylate kinase (EC 2.7.4.9)	b1098	NCM	0.88
1154985	REC01061	<i>hoIB</i>	E	334	-	< 0.05	P28631	DNA polymerase III, delta' subunit (EC 2.7.7.7)	b1099	NAM	0.75
1156000	REC01062	<i>yceH</i>	N	265	205, 259		P37346	Putative deoxyribonuclease yceH (EC 3.1.21.-)	b1100	UNC	1.00
1157092	REC01063	<i>ptsG</i>	N	477	117, 168, 281, 337		P05053	PTS system, glucose-specific IIBC component (EC 2.7.1.69)	b1101	MTR	0.47
1160774	REC04764	<i>fluE</i>	N	729	98, 166, 290, 479, 583, 716		P16869	FhuE receptor precursor	b1102	MTR	0.13
1161108	REC01065	<i>yceF</i>	N	119	66		P36950	HIT-like protein yceF	b1103	UNC	0.94
1161470	REC01066	<i>yceL</i>	N	125	7, 33		P75946	Hypothetical protein yceL	b1104	UNC	0.03
1161861	REC01067	<i>yceM</i>	N	213	3, 117		P75947	Hypothetical protein yceM	b1105	UNC	0.03
1162483	REC01068	<i>yceN</i>	N	274	13		P75948	Hypothetical protein yceN	b1106	UNC	0.00
1163318	REC01069	<i>nagZ</i>	N	341	186, 227		P75949	Beta-hexosaminidase (EC 3.2.1.52)	b1107	LPC	0.66
1164309	REC01070	<i>yceP</i>	E	199	-	< 0.3	P75950	Hypothetical protein yceP	b1108	UNC	0.03
1165308	REC01071	<i>ndh</i>	N	434	188		P00393	NADH dehydrogenase (EC 1.6.99.3)	b1109	BEN	0.69
1166822	REC01072	<i>yceJ</i>	N	179	135		P37796	Hypothetical protein yceJ	b1110	UNC	0.06
1168133	REC04765	<i>yceQ</i>	N	236	191		P75952	Hypothetical transcriptional regulator yceQ	b1111	UNC	0.22
1168296	REC01074	<i>yceR</i>	N	85	22		P75953	Hypothetical protein yceR precursor	b1112	UNC	0.00
1169597	REC04766	<i>yceS</i>	N	320	233, 282, 299		P75954	Hypothetical protein yceS precursor	b1113	UNC	0.16
1173187	REC04767	<i>mfd</i>	N	1148	36, 164, 305, 498, 571, 578, 687, 746, 960		P30958	Transcription-repair coupling factor	b1114	NAM	0.94
1174388	REC04768	<i>yceT</i>	N	357	88, 99, 176, 209, 266		P75955	Hypothetical protein yceT	b1115	UNC	0.00
1174650	REC01078	<i>loIC</i>	E	399	-	< 0.05	P75956	Lipoprotein releasing system transmembrane protein loIC	b1116	LPC	0.31
1175857	REC01079	<i>loID</i>	E	228	-	< 0.1	P75957	Lipoprotein releasing system ATP-binding protein loID	b1117	MTR	0.84
1176543	REC01080	<i>loIE</i>	E	414	-	< 0.01	P75958	Lipoprotein releasing system transmembrane protein loIE	b1118	LPC	0.66
1177816	REC01081	<i>yceX</i>	N	303	233		P75959	Hypothetical protein yceX	b1119	UNC	0.53
1178743	REC01082	<i>cobB</i>	N	279	148		P75960	CobB protein	b1120	UNC	0.50
1180490	REC04769	<i>yceZ</i>	N	262	1, 47, 91, 171, 234		P75961	Hypothetical protein yceZ	b1121	UNC	0.00
1180957	REC04770	<i>ymlA</i>	N	156	10, 118		P75962	Hypothetical protein ymlA	b1122	UNC	0.00
1182052	REC04771	<i>potD</i>	E	348	326	< 0.05	P23861	Spermidine/putrescine-binding periplasmic protein precursor	b1123	MTR	0.69
1182843	REC04772	<i>potC</i>	E	264	-	< 0.05	P23859	Spermidine/putrescine transport system permease protein potC	b1124	MTR	0.69
1183667	REC04773	<i>potB</i>	N	275	28		P23860	Spermidine/putrescine transport system permease protein potB	b1125	MTR	0.66
1184817	REC04774	<i>potA</i>	N	378	132, 199, 232, 288, 369		P23858	Spermidine/putrescine transport ATP-binding protein potA	b1126	MTR	0.34
1185067	REC01089	<i>pepT</i>	N	408	16, 51, 66, 233		P29745	Peptidase T (EC 3.4.11.14)	b1127	PMS	0.28
1187472	REC04775	<i>yceD</i>	E	376	-	< 0.05	P27431	Hypothetical protein yceD	b1128	UNC	0.13
1188999	REC04776	<i>phoQ</i>	N	486	22, 117, 195, 237, 338, 373, 435, 439		P23837	Sensor protein phoQ (EC 2.7.3.-)	b1129	SMC	0.25
1189670	REC04777	<i>phoP</i>	N	223	48, 176		P23836	Transcriptional regulatory protein phoP	b1130	SMC	0.81
1191209	REC04778	<i>purB</i>	N	456	172, 188		P25739	Adenylosuccinate lyase (EC 4.3.2.2)</			

1191854	REC04779	ycfC	N	213	103, 124					P25746	Hypothetical protein ycfC	b1132	UNC	0.16
1193041	REC04780	trmU	E	383	333	< 0.05				P25745	tRNA (5-methylaminomethyl-2-thiouridylyl)-methyltransferase (E	b1133	NAM	0.97
1193511	REC04781	ymfB	N	153	40					P75965	Putative Nudix hydrolase ymfB (EC 3.6.-.-)	b1134	UNC	0.09
1194144	REC04782	ymfC	N	207	4, 14, 66, 76, 175					P75966	Hypothetical protein ymfC	b1135	UNC	0.97
1194346	REC01098	icd	N	416	24, 71, 280, 385					P08200	Isocitrate dehydrogenase [NADP] (EC 1.1.1.42)	b1136	CHM	0.38
1196755	REC04783	ymfD	N	221	180, 221					P75967	Hypothetical protein ymfD	b1137	UNC	0.00
1197460	REC04784	ymfE	X	234	-					P75968	Hypothetical protein ymfE	b1138	UNC	0.00
1197918	REC01101	lit	X	297	-					P11072	Bacteriophage T4 late gene expression blocking protein	b1139	RCD	0.00
1200029	REC04785	intE	N	375	-					P75969	Prophage lambda integrase	b1140	PHT	0.00
1200255	REC04786	ymfG	N	81	-					P75970	Excisionase-like protein from lambdoid prophage 14	b1141	UNC	0.00
1200603	REC04787		N	103	-					P75971	Very hypothetical 11.0 kDa protein in intE-pin intergenic region	b1142	UNC	0.00
1200675	REC01105	ymfI	E	128	-	0.40				P75972	Hypothetical protein ymfI	b1143	UNC	0.00
1201283	REC04788	ymfJ	E	94	-	0.53				P75973	Hypothetical protein ymfJ	b1144	UNC	0.00
1201944	REC01108		E	167	-	< 0.3				P75975	FROM BASES 1195814 TO 1209543 (SECTION 104 OF 400) OF	b1146	UNC	0.00
1202156	REC04789	ymfK	E	224	-	< 0.2				P75974	Putative lambdoid prophage e14 repressor protein C2	b1145	UNC	0.00
1202479	REC01109	ymfL	N	189	114, 159					P75976	Hypothetical protein ymfL	b1147	UNC	0.00
1203045	REC01110	ymfM	N	112	47, 80					P75977	Hypothetical protein ymfM	b1148	UNC	0.00
1203393	REC01111	ymfN	N	455	99, 131, 326, 424					P75978	Hypothetical protein ymfN	b1149	UNC	0.13
1204772	REC01112	ymfR	?	60	-					P75979	Hypothetical protein ymfR	b1150	UNC	0.00
1204954	REC01113	ymfO	N	157	13					P75980	Hypothetical protein ymfO	b1151	UNC	0.03
1205354	REC01114	ymfP	N	263	64, 96, 147, 163					P75981	Hypothetical protein ymfP in lambdoid prophage e14 region	b1152	UNC	0.06
1206136	REC01115	ymfQ	N	194	106, 115					P75982	Hypothetical protein ymfQ in lambdoid prophage e14 region precu	b1153	UNC	0.00
1206724	REC01116	ycfK	N	209	23, 46, 105					P45581	Hypothetical protein ycfK	b1154	UNC	0.00
1207355	REC01117	ymfS	N	137	67					P09154	Hypothetical protein ymfS	b1155	UNC	0.00
1208342	REC04790	tfaE	N	200	22, 41, 51, 98, 121, 130, 156, 170					P09153	Tail fiber assembly protein homolog from lambdoid prophage e14	b1156	UNC	0.03
1208881	REC04791	stfE	N	179	36, 71, 86, 119					P33227	Side tail fiber protein homolog from lambdoid prophage e14	b1157	UNC	0.03
1208908	REC01120	pinE	N	184	22, 32, 176					P03014	DNA-invertase from lambdoid prophage e14	b1158	PHT	0.44
1209569	REC01121	mcrA	N	277	96, 260					P24200	5-methylcytosine-specific restriction enzyme A (EC 3.1.2.1-)	b1159	NAM	0.00
1211226	REC04792	eIba	E	107	-	< 0.3				P75987	Enhancing lycopene biosynthesis protein 1	b1160	UNC	0.00
1212330	REC04793	ycgX	E	134	-	< 0.2				P75988	Hypothetical protein ycgX	b1161	UNC	0.00
1213282	REC04794	ycgE	N	243	18, 129, 132					P75989	Hypothetical transcriptional regulator ycgE	b1162	UNC	0.09
1214698	REC04795	ycgF	N	403	38, 158, 318, 390					P75990	Hypothetical protein ycgF	b1163	UNC	0.06
1215012	REC01126	ycgZ	N	78	44, 61					P75991	Hypothetical protein ycgZ	b1164	UNC	0.00
1215291	REC01127	ymgA	N	90	2, 36, 57					P75992	Hypothetical protein ymgA	b1165	UNC	0.00
1215592	REC01128	ymgB	N	88	72					P75993	Hypothetical protein ymgB	b1166	UNC	0.00
1215971	REC01129	ymgC	N	82	44					P75994	Hypothetical protein ymgC	b1167	UNC	0.00
1216509	REC01130	ycgG	N	521	24, 60, 133, 264, 403, 432, 464, 497					P75995	Hypothetical protein ycgG	b1168	UNC	0.31
1218170	REC06761	ymgF	N	84	36, 61					P58034	Hypothetical protein ymgF	b1169	UNC	0.00
1218824	REC01131		N	506	34, 45, 77, 130, 146, 191, 241, 354					P75996	O506 WAS O411 AND O104	b1169	UNC	0.00
1220429	REC01132		N	338	59, 237, 327, 333					P75997	FROM BASES 1220357 TO 1232354 (SECTION 106 OF 400) OF	b1170	UNC	0.16
1221863	REC04796	ymgD	N	111	47, 71					P75998	Hypothetical protein ymgD precursor	b1171	UNC	0.00
1222151	REC04797		N	94	80					P75999	ORF O243#4	b1172	UNC	0.00
1222918	REC01135		X	70	-					P76000	FROM BASES 1220357 TO 1232354 (SECTION 106 OF 400) OF	b1173	UNC	0.00
1223768	REC04798	minE	X	88	-					P18198	Cell division topological specificity factor	b1174	RCD	0.50
1224584	REC04799	minD	E	270	-	< 0.01				P18197	Septum site-determining protein minD	b1175	UNC	0.72
1225303	REC04800	minC	N	231	34, 118, 127					P18196	Septum site-determining protein minC	b1176	RCD	0.31
1225823	REC01139	ycgJ	N	122	28, 37, 76					P76001	Hypothetical protein ycgJ precursor	b1177	UNC	0.00
1226695	REC04801	ycgK	N	133	68					P76002	Protein ycgK precursor	b1178	UNC	0.00
1226904	REC01141	ycgL	X	108	-					P76003	Protein ycgL	b1179	UNC	0.09
1227302	REC01142	ycgM	E	219	186	< 0.05				P76004	Protein ycgM	b1180	UNC	0.56
1228023	REC01143	ycgN	N	158	27, 130, 139					P76005	Hypothetical protein ycgN	b1181	UNC	0.25
1229623	REC04802	hlyE	N	305	189, 206, 239, 294					P77335	Hemolysin E, chromosomal	b1182	UNC	0.00
1229990	REC01145	umuD	N	139	46, 127					P04153	UmuD protein (EC 3.4.2.1-)	b1183	UNC	0.00
1230409	REC01146	umuC	N	422	322, 365					P04152	UmuC protein	b1184	UNC	0.06
1232253	REC04803	dsbB	N	176	59, 89					P30018	Disulfide bond formation protein B	b1185	PMS	0.16
1233940	REC04804	nhaB	N	513	75, 98, 375, 452, 472					P27377	Na(+)/H(+) antiporter 2	b1186	MTR	0.09
1234161	REC01149	fadR	N	239	10					P09371	Fatty acid metabolism regulator protein	b1187	RCD	0.06
1236464	REC04805	ycgB	N	510	32, 61, 222, 292, 322, 372					P29013	Hypothetical protein ycgB	b1188	UNC	0.19
1236794	REC01151	dadA	E	432	273	< 0.05				P29011	D-amino acid dehydrogenase small subunit (EC 1.4.99.1)	b1189	AAM	0.44
1238102	REC01152	dadX	N	356	18, 106, 243					P29012	Alanine racemase, catabolic (EC 5.1.1.1)	b1190	AAM	0.88
1241168	REC04806	ycgO	N	536	79, 205, 506, 508					P76007	Putative Na(+)/H(+) exchanger ycgO	b1191	UNC	0.25
1242289	REC01155	mltE	N	241	11, 29, 108					P76009	Membrane-bound lytic murein transglycosylase E (EC 3.2.1.-)	b1193	LPC	0.03
1242303	REC04807	ldcA	N	304	113					P76008	Muramoyltetrapeptide carboxypeptidase (EC 3.4.17.13)	b1192	LPC	0.34
1243750	REC04808	ycgR	N	244	113					P76010	Hypothetical protein ycgR	b1194	UNC	0.03
1243951	REC01157	ymgE	N	84	5, 32					P76011	Transglycosylase associated protein	b1195	UNC	0.13
1244383	REC01158	ycgY	N	146	107, 136					P76012	Hypothetical protein ycgY	b1196	UNC	0.00
1246599	REC04809	treA	N	565	51, 67, 146, 194, 256, 339					P13482	Periplasmic trehalase precursor (EC 3.2.1.28)	b1197	CHM	0.09
1248340	REC04810	ycgC	N	473	185, 200, 455					P37349	Hypothetical protein ycgC	b1198	UNC	0.06
1248980	REC04811	ycgS	E	210	-	< 0.2				P76014	Protein ycgS	b1199	UNC	0.28
1250091	REC04812	ycgT	N	366	113, 145, 170, 195, 334					P76015	Hypothetical protein ycgT	b1200	UNC	0.28
1250280	REC01163	dhaR	N	642	81, 237, 260, 335, 617					P76016	Glycerol metabolism operon regulatory protein	b1201	RCD	0.00
1255175	REC04813	ycgV	N	955	29, 170, 715, 915					P76017	Hypothetical protein ycgV	b1202	UNC	0.03
1257035	REC04814	ychF	E	363	358	< 0.05				P31216	Probable GTP-binding protein ychF	b1203	UNC	1.00
1257736	REC04815	pth	E	194	-	< 0.2				P23932	Peptidyl-tRNA hydrolase (EC 3.1.1.29)	b1204	NAM	1.00
1258014	REC01167	ychH	E	92	-	0.46				P31807	Hypothetical protein ychH	b1205	UNC	0.00
1259999	REC04816	ychM	N	550	53, 93, 237, 296					P40877	Putative sulfate transporter ychM	b1206	UNC	0.47
1261098	REC04817	prsA	E	315	-	< 0.05				P08330	Ribose-phosphate pyrophosphokinase (EC 2.7.6.1)	b1207	CHM	0.91
1262100	REC04818	ispE	E	283	-	< 0.1				P24209	4-diphosphocytidyl-2-C-methyl-D-erythritol kinase (EC 2.7.1.148)	b1208	LPC	0.81
1262723	REC04819	loIB	X	207	-					P24208	Outer-membrane lipoprotein loIB precursor	b1209	LPC	0.09
1262937	REC01172	hemA	X	418	-					P13580	Glutamyl-tRNA reductase (EC 1.2.1.-)	b1210	NCM	0.59
1264235	REC01173	prfA	X	360	-					P07011	Peptide chain release factor 1	b1211	PMS	1.00
1265317	REC01174	hemK	E	277	-	< 0.05				P37186	Protein methyltransferase hemK (EC 2.1.1.-)	b1212	NCM	0.97
1266147	REC01175	ychQ	E	130	-	< 0.2				Q46755	Hypothetical protein ychQ	b1213	UNC	0.09
1266543	REC01176	ychA	N	269	152, 259					P20101	Hypothetical protein ychA	b1214	UNC	0.22
1267388	REC01177	kdsA	N*	284	221					P17579	2-dehydro-3-deoxyphosphooctonate aldolase (EC 4.1.2.16)	b1215	CHM	0.59
1271072	REC04820	chaA	N	366	119, 142, 282, 344					P31801	Calcium/proton antiporter	b1216	MTR	0.28
1271342	REC01179	chaB	X	76	-					P39162	Cation transport regulator chaB	b1217	RCD	0.00
1271709	REC01180	chaC	N	238	162, 210					P39163	Cation transport protein chaC	b1218	MTR	0.16
1272822	REC04821	ychN	N	117	26					P39164	Hypothetical protein ychN	b1219	UNC	0.00
1273148	REC01182	ychO	N	417	102, 232, 364, 382					P39165	Hypothetical protein ychO	b1220	UNC	0.00
1275052	REC04822	narL	N	216	14					P10957	Nitrate/nitrite response regulator protein narL	b1221	SMC	0.34
1276841	REC04823	narX	N	598	155					P10956	Nitrate/nitrite sensor protein narX (EC 2.7.3.-)	b1222	SMC	0.50
1277180	REC01185	narK	N	463	355, 378					P10903	Nitrite extrusion protein 1	b1223	SMC	0.06

1279087	REC01186	<i>narG</i>	N	1247	19, 27, 53, 86, 96, 236, 307, 332, 543, 648, 753, 761, 1142, 1208	P09152	Respiratory nitrate reductase 1 alpha chain (EC 1.7.99.4)	b1224	SMC	0.22
1282827	REC01187	<i>narH</i>	N	512	4, 215, 433	P11349	Respiratory nitrate reductase 1 beta chain (EC 1.7.99.4)	b1225	SMC	0.22
1284362	REC01188	<i>narJ</i>	N	236	178	P11351	Respiratory nitrate reductase 1 delta chain (EC 1.7.99.4)	b1226	SMC	0.13
1285072	REC01189	<i>narI</i>	N	225	20, 205	P11350	Respiratory nitrate reductase 1 gamma chain (EC 1.7.99.4)	b1227	SMC	0.22
1285932	REC01190		E	91	-	P76023	FROM BASES 1278800 TO 1289447 (SECTION 111 OF 400) OF	b1228	UNC	0.00
1286411	REC04824	<i>tpx</i>	?	33	-	P02338	Protamine-like protein	b1229	UNC	0.00
1287847	REC04825	<i>pruU</i>	E	280	-	P37051	Formyltetrahydrofolate deformylase (EC 3.5.1.10)	b1232	NCM	0.56
1288355	REC04826	<i>yehJ</i>	N	152	60, 97, 98	P37052	Hypothetical protein yehJ	b1233	UNC	0.22
1288429	REC01194	<i>yehK</i>	N	314	218	P37053	Hypothetical protein yehK	b1234	UNC	0.56
1289465	REC01195	<i>hnr</i>	E	337	-	P37055	Hnr protein	b1235	UNC	0.16
1290680	REC01196	<i>galU</i>	E	302	-	P25520	UTP--glucose-1-phosphate uridylyltransferase (EC 2.7.7.9)	b1236	CHM	0.78
1292145	REC04827	<i>hns</i>	E	137	-	P08936	DNA-binding protein H-NS	b1237	UNC	0.09
1292750	REC01198	<i>tdk</i>	E	205	-	P23331	Thymidine kinase (EC 2.7.1.21)	b1238	NCM	0.41
1294239	REC04828	<i>yehG</i>	N	196	84	P30192	Hypothetical protein yehG	b1239	UNC	0.00
1297344	REC04830	<i>adhE</i>	N	891	10, 55, 123, 232, 280, 848	P17547	Aldehyde-alcohol dehydrogenase	b1241	MSM	0.50
1297821	REC01202	<i>yehE</i>	N	215	76, 121, 164	P25743	Hypothetical protein yehE	b1242	UNC	0.56
1299206	REC01203	<i>oppA</i>	N	543	9, 184, 221, 244, 276, 310, 453, 500, 525	P23843	Periplasmic oligopeptide-binding protein precursor	b1243	MTR	0.72
1300923	REC01204	<i>oppB</i>	N	306	122, 147, 222	P31132	Oligopeptide transport system permease protein oppB	b1244	MTR	0.72
1301858	REC01205	<i>oppC</i>	E	302	79	P77664	Oligopeptide transport system permease protein oppC	b1245	MTR	0.81
1302778	REC01206	<i>oppD</i>	E	337	-	P76027	Oligopeptide transport ATP-binding protein oppD	b1246	MTR	0.75
1303788	REC01207	<i>oppF</i>	N	334	17, 233, 301	P77737	Oligopeptide transport ATP-binding protein oppF	b1247	MTR	0.47
1305252	REC04831	<i>yciU</i>	N	135	42	P76028	Hypothetical protein yciU	b1248	UNC	0.06
1306669	REC04832	<i>cis</i>	N	486	281	P31071	Cardiolipin synthetase (EC 2.7.8.-)	b1249	LPC	0.63
1308293	REC04833	<i>kch</i>	N	417	118, 139, 209, 254, 317, 327, 412	P31069	Putative potassium channel protein	b1250	UNC	0.34
1308985	REC04834	<i>yciI</i>	N	130	73	P31070	Protein yciI	b1251	UNC	0.22
1309113	REC01212	<i>tonB</i>	E	239	-	P02929	TonB protein	b1252	MTR	0.06
1310270	REC04835	<i>yciA</i>	E	132	-	P04379	Putative acyl-CoA thioester hydrolase yciA (EC 3.1.2.-)	b1253	UNC	0.59
1310914	REC04836	<i>ispZ</i>	E	179	168	P21366	Probable intracellular septation protein	b1254	UNC	0.38
1311687	REC04837	<i>yciC</i>	N	247	61, 183	P21365	Hypothetical protein yciC	b1255	UNC	0.03
1312044	REC01216	<i>ompW</i>	N	212	81	P21364	Outer membrane protein W precursor	b1256	SMC	0.25
1313248	REC04838	<i>yciE</i>	N	168	13, 27, 146	P21363	Protein yciE	b1257	UNC	0.07
1313794	REC04839	<i>yciF</i>	N	166	20, 39, 63, 64, 97, 134	P21362	Protein yciF	b1258	UNC	0.09
1314116	REC04840	<i>yciG</i>	N	78	40, 45	P21361	Hypothetical protein yciG	b1259	UNC	0.03
1315246	REC04841	<i>trpA</i>	N	268	37, 161, 206, 250, 265	P00928	Tryptophan synthase alpha chain (EC 4.2.1.20)	b1260	AAM	0.84
1316439	REC04842	<i>trpB</i>	N	397	262, 306, 365, 391	P00932	Tryptophan synthase beta chain (EC 4.2.1.20)	b1261	AAM	0.88
1317812	REC04843	<i>trpC</i>	N	453	231, 236, 271, 314, 344, 388	P00909	Tryptophan biosynthesis protein trpC	b1262	AAM	0.84
1319408	REC04844	<i>trpD</i>	N	531	117, 171, 181, 314, 365, 497	P00904	Anthranilate synthase component II (EC 4.1.3.27)	b1263	AAM	0.84
1320970	REC04845	<i>trpE</i>	N	520	29, 377	P00895	Anthranilate synthase component I (EC 4.1.3.27)	b1264	AAM	0.81
1321244	REC01226	<i>trpH</i>	N	293	17, 48, 101	P77666	Protein trpH	b1266	UNC	0.19
1322086	REC01227	<i>yciO</i>	N	218	28, 159	P45847	Protein yciO	b1267	UNC	0.31
1322770	REC01228	<i>yciQ</i>	N	631	28, 75, 172, 200, 240, 277, 288, 344, 369, 391, 413, 418, 474, 483, 546, 5	P45848	Hypothetical protein yciQ	b1268	UNC	0.06
1324876	REC01229	<i>yciL</i>	E	291	237	P37765	Hypothetical protein yciL	b1269	UNC	0.97
1326381	REC04847	<i>btuR</i>	E	196	107	P13040	COB(l)alamin adenosyltransferase (EC 2.5.1.17)	b1270	NCM	0.41
1327136	REC04848	<i>yciK</i>	E	252	125	P31808	Hypothetical oxidoreductase yciK (EC 1.-.-.-)	b1271	UNC	0.78
1327356	REC01232	<i>sohB</i>	N	349	43, 55, 201, 213, 231, 252, 302	P24213	Possible protease sohB (EC 3.4.21.-)	b1272	UNC	0.78
1328692	REC04849	<i>yciN</i>	N	83	29	P46132	Protein yciN	b1273	UNC	0.03
1329072	REC01234	<i>topA</i>	E	865	-	P06612	DNA topoisomerase I (EC 5.9.9.1.2)	b1274	NAM	0.97
1331879	REC01235	<i>cysB</i>	N	324	18, 89, 95, 249, 315	P06613	Cys regulon transcriptional activator	b1275	RCD	0.19
1333148	REC06676	<i>yciX</i>	N	54	18	P58094	Hypothetical protein yciX		UNC	0.00
1333855	REC01236	<i>acnA</i>	N	891	126, 231, 277, 778	P25516	Aconitate hydratase 1 (EC 4.2.1.3)	b1276	CHM	0.56
1337184	REC04850	<i>ribA</i>	E	196	-	P25523	GTP cyclohydrolase II (EC 3.5.4.25)	b1277	NCM	0.84
1337354	REC01238	<i>pppB</i>	N	254	32, 96, 221	P18201	Phosphatidylglycerophosphatase B (EC 3.1.3.27)	b1278	LPC	0.06
1338267	REC01239	<i>yciS</i>	E	102	-	P77614	Hypothetical protein yciS	b1279	UNC	0.06
1338582	REC06490	<i>yciM</i>	N	389	260, 347, 379	P45576	Hypothetical protein yciM precursor	b1280	UNC	0.16
1339945	REC01241	<i>pyrF</i>	E	245	170	P08244	Orotidine 5'-phosphate decarboxylase (EC 4.1.1.23)	b1281	NCM	0.66
1340679	REC01242	<i>yciH</i>	N	109	43, 91	P08245	Protein yciH	b1282	UNC	0.16
1341352	REC04851	<i>osmB</i>	N	72	29, 31, 58	P17873	Osmotically inducible lipoprotein B precursor	b1283	LPC	0.00
1342370	REC04852	<i>yciT</i>	N	249	7, 62, 208	P76034	Hypothetical transcriptional regulator yciT	b1284	UNC	0.09
1344766	REC04853	<i>yciR</i>	N	661	11, 63, 132, 325, 603	P77334	Hypothetical protein yciR	b1285	UNC	0.53
1346936	REC04854	<i>rnb</i>	N	644	422, 425, 527, 572, 582	P30850	Exoribonuclease II (EC 3.1.13.1)	b1286	NAM	0.28
1348209	REC04855	<i>yciW</i>	?	401	30	P76035	Hypothetical protein yciW	b1287	UNC	0.00
1349063	REC04856	<i>fabI</i>	E	262	-	P29132	Enoyl-[acyl-carrier-protein] reductase [NADH] (EC 1.3.1.9)	b1288	LPC	0.69
1349784	REC04857	<i>ycjD</i>	N	117	57, 64, 113	P45736	Hypothetical protein ycjD	b1289	UNC	0.22
1350658	REC04858	<i>sapF</i>	N	268	148, 165	P36637	Peptide transport system ATP-binding protein sapF	b1290	MTR	0.06
1351652	REC04859	<i>sapD</i>	N	330	105, 129	P36635	Peptide transport system ATP-binding protein sapD	b1291	MTR	0.06
1352542	REC04860	<i>sapC</i>	N	296	19, 125, 148, 203	Q47624	Peptide transport system permease protein sapC	b1292	MTR	0.06
1353494	REC04861	<i>sapB</i>	N	321	160, 248, 266	Q47623	Peptide transport system permease protein sapB	b1293	MTR	0.06
1355134	REC04862	<i>sapA</i>	N	547	169, 203, 310	Q47622	Peptide transport periplasmic protein sapA precursor	b1294	MTR	0.06
1355692	REC04863	<i>ymjA</i>	N	81	37	P76036	Hypothetical protein ymjA	b1295	UNC	0.00
1357265	REC04864	<i>ycjJ</i>	N	479	100, 179, 291, 305, 422	P76037	Hypothetical transport protein ycjJ	b1296	UNC	0.44
1359010	REC04865	<i>ycjK</i>	N	498	37, 64, 171, 172	P78061	Putative glutamine synthetase (EC 6.3.1.2)	b1297	UNC	0.78
1359132	REC01258	<i>ycjL</i>	N	258	81, 144, 153	P76038	Hypothetical protein ycjL	b1298	UNC	0.38
1359935	REC01259	<i>ycjC</i>	N	185	93, 110	P38522	Hypothetical protein ycjC	b1299	UNC	0.41
1360767	REC01260	<i>aldH</i>	N	495	19, 46, 92, 177, 253, 410, 473	P23883	Putative aldehyde dehydrogenase (EC 1.2.1.3)	b1300	UNC	0.41
1362256	REC01261	<i>ordL</i>	N	426	151, 368	P37906	Probable oxidoreductase ordL (EC 1.-.-.-)	b1301	UNC	0.31
1363574	REC01262	<i>goaG</i>	N	421	5, 239, 275	P50457	4-aminobutyrate aminotransferase (EC 2.6.1.19)	b1302	AAM	0.50
1365951	REC04866	<i>pspF</i>	N	330	28, 107, 277, 289	P37344	Psp operon transcriptional activator	b1303	RCD	0.03
1366103	REC06492	<i>pspA</i>	N	222	143	P23853	Phage shock protein A	b1304	UNC	0.19
1366825	REC01265	<i>pspB</i>	?	74	-	P23854	Phage shock protein B	b1305	UNC	0.03
1367049	REC01266	<i>pspC</i>	E	119	-	P23855	Phage shock protein C	b1306	UNC	0.03
1367417	REC01267	<i>pspD</i>	N	73	21	P23856	Phage shock protein D	b1307	UNC	0.00
1367713	REC01268	<i>pspE</i>	E	104	104	P23857	Phage shock protein E precursor	b1308	UNC	0.06
1368213	REC01269	<i>ycjM</i>	N	568	59, 97, 107, 186, 221, 229, 296, 424	P76041	Putative sucrose phosphorylase (EC 2.4.1.7)	b1309	UNC	0.16
1369933	REC01270	<i>ycjN</i>	N	430	133	P76042	Putative ABC transporter periplasmic binding protein ycjN precursor	b1310	UNC	0.22
1371246	REC01271	<i>ycjO</i>	N	293	84	P77653	Hypothetical ABC transporter permease protein ycjO	b1311	UNC	0.41
1372114	REC01272	<i>ycjP</i>	N	280	81, 132, 251	P77716	Hypothetical ABC transporter permease protein ycjP	b1312	UNC	0.47
1372987	REC01273	<i>ycjQ</i>	N	350	59, 253	P76043	Hypothetical zinc-type alcohol dehydrogenase-like protein ycjQ	b1313	UNC	0.03
1374049	REC01274	<i>ycjR</i>	?	265	246	P76044	Hypothetical protein ycjR	b1314	UNC	0.16
1374856	REC01275	<i>ycjS</i>	N	351	194	P77503	Hypothetical oxidoreductase ycjS (EC 1.-.-.-)	b1315	UNC	0.50
1375908	REC01276	<i>ycjT</i>	N	755	93, 232, 358, 412, 471, 524, 687, 737, 754	P77154	Hypothetical transport protein ycjT	b1316	UNC	0.19
1378172	REC01277	<i>ycjU</i>	N	219	40, 140, 219	P77366	Putative beta-phosphoglucosylase (EC 5.4.2.6)	b1317	UNC	0.16
1378845	REC01278	<i>ycjV</i>	N	322	170, 282	P77481	Hypothetical ABC transporter ATP-binding protein ycjV	b1318	UNC	0.28
1379971	REC01279	<i>ompG</i>	N	301	63	P76045	Outer membrane protein G precursor	b1319	SMC	0.00

1381985	REC04867	<i>ycjW</i>	N	332	50, 64, 88, 129, 166	P77615	Hypothetical transcriptional regulator ycjW	b1320	UNC	0.03
1382141	REC01281	<i>ycjX</i>	N	465	24, 401	P76046	Hypothetical protein ycjX	b1321	UNC	0.19
1383535	REC01282	<i>ycjF</i>	E	353	-	P45525	Hypothetical protein ycjF	b1322	UNC	0.16
1384744	REC01283	<i>tyzR</i>	N	513	265, 391, 465	P07604	Transcriptional regulatory protein tyrR	b1323	RCD	0.59
1386835	REC04868	<i>tpx</i>	N	168	67	P37901	Thiol peroxidase (EC 1.11.1.-)	b1324	MSM	0.44
1386912	REC01285	<i>ycjG</i>	N	335	65, 78, 137, 317	P51981	Hypothetical protein ycjG	b1325	UNC	0.31
1388682	REC04869	<i>ycjI</i>	E	262	-	P51983	Hypothetical protein ycjI	b1326	UNC	0.00
1389889	REC04870	<i>ycjY</i>	N	310	102, 173, 219, 291	P76049	Hypothetical protein ycjY	b1327	UNC	0.13
1390015	REC01288	<i>ycjZ</i>	N	299	127, 136, 244, 298	P77333	Hypothetical transcriptional regulator ycjZ	b1328	UNC	0.72
1391230	REC01289	<i>mppA</i>	N	544	126, 206, 256, 265, 397, 406, 431, 476, 477, 507	P77348	Periplasmic murein peptide-binding protein precursor	b1329	MTR	0.06
1393946	REC04871	<i>ynaI</i>	N	343	95, 203, 330	P77253	Hypothetical protein ynaI	b1330	UNC	0.13
1394100	REC06520		X	338	-	P03837	Transposase insH for insertion sequence element IS5	b1331	PHT	0.34
1395389	REC01292	<i>ynaJ</i>	E	85	-	P76050	Hypothetical protein ynaJ	b1332	UNC	0.00
1396646	REC04872	<i>ydaA</i>	N	316	-	P03807	Protein ydaA	b1333	UNC	0.47
1397550	REC04873	<i>fnr</i>	N	250	-	P03019	Fumarate and nitrate reductase regulatory protein	b1334	RCD	0.50
1398260	REC04874	<i>ogt</i>	X	171	-	P09168	Methylated-DNA-protein-cysteine methyltransferase (EC 2.1.1.63)	b1335	NAM	0.78
1399803	REC04875	<i>abgT</i>	N	510	37, 191	P46133	Aminobenzoyl-glutamate transport protein	b1336	MTR	0.19
1401279	REC04876	<i>abgB</i>	N	481	83, 293, 466	P76052	Aminobenzoyl-glutamate utilization protein B	b1337	UNC	0.31
1402604	REC04877	<i>abgA</i>	N	441	239, 378	P77357	Aminobenzoyl-glutamate utilization protein A	b1338	UNC	0.66
1402765	REC01299	<i>abgR</i>	N	302	43, 108, 155, 218	P77744	Putative transcriptional regulator abgR	b1339	UNC	0.06
1404003	REC01300	<i>ydaL</i>	E	187	-	P76053	Hypothetical protein ydaL	b1340	UNC	0.28
1405879	REC04878	<i>ydaM</i>	N	430	7, 29, 40, 59, 155, 374	P77302	Hypothetical protein ydaM	b1341	UNC	0.13
1406074	REC01302	<i>ydaN</i>	N	327	57, 71, 99, 141, 262, 280	P76054	Hypothetical protein ydaN	b1342	UNC	0.78
1407535	REC01303	<i>dbpA</i>	N	457	32, 157, 327, 453	P21693	ATP-independent RNA helicase dbpA	b1343	SMC	0.28
1409972	REC04879	<i>ydaO</i>	N	311	35, 167, 250, 278	P76055	Hypothetical protein ydaO	b1344	UNC	0.50
1411259	REC04880	<i>intR</i>	N	411	104, 127, 208, 259, 302, 345	P76056	Putative lambdaoid prophage Rac integrase	b1345	UNC	0.00
1411500	REC04881	<i>ydaQ</i>	N	79	54	P76057	Hypothetical protein ydaQ	b1346	UNC	0.00
1411764	REC04882	<i>ydaC</i>	X	69	-	P33230	Hypothetical protein ydaC	b1347	UNC	0.00
1411951	REC04883	<i>lar</i>	X	64	-	P33229	Restriction alleviation and modification enhancement protein	b1348	UNC	0.00
1412817	REC04884	<i>recT</i>	N	269	79, 113, 144	P33228	RecT protein	b1349	NAM	0.06
1415410	REC04885	<i>recE</i>	N	866	91, 141, 471, 524, 539, 662, 676, 784, 844	P15032	Exodeoxyribonuclease VIII (EC 3.1.11.-)	b1350	NAM	0.00
1415787	REC04886	<i>racC</i>	N	91	11, 44	P15033	RacC protein	b1351	UNC	0.00
1416265	REC04887	<i>kiI</i>	?	77	-	P38393	Kil protein	b1352	RCD	0.00
1416572	REC01313	<i>sieB</i>	N	203	33, 54, 117, 188	P38392	Superinfection exclusion protein B	b1353	UNC	0.00
1417192	REC01314		N	58	28	P76060	FROM BASES 1415432 TO 1425731 (SECTION 123 OF 400) OF	b1354	UNC	0.00
1418265	REC04889	<i>racR</i>	E	158	140	P76062	Rac prophage repressor	b1356	RCD	0.06
1418389	REC01317	<i>ydaS</i>	E	98	86, 95	P76063	Hypothetical protein ydaS precursor	b1357	UNC	0.06
1418708	REC01318	<i>ydaT</i>	E	140	-	P76064	Hypothetical protein ydaT	b1358	UNC	0.00
1419143	REC01319	<i>ydaU</i>	E	285	249	P76065	Hypothetical protein ydaU	b1359	UNC	0.06
1420007	REC01320	<i>ydaV</i>	N	248	50, 140, 165	P77546	Hypothetical protein ydaV	b1360	UNC	0.09
1420725	REC01321	<i>ydaW</i>	N	203	36, 155, 195	P76066	Hypothetical protein ydaW	b1361	UNC	0.00
1421363	REC01322	<i>rspR</i>	N	101	96	P77551	Putative Rz endopeptidase from lambdaoid prophage Rac (EC 3.4.-)	b1362	UNC	0.00
1421806	REC01323	<i>trkG</i>	N	485	89, 258, 287, 299, 327, 331, 375, 411, 444	P23849	Trk system potassium uptake protein trkG	b1363	MTR	0.16
1423202	REC01324		N	93	27, 87	P76067	FROM BASES 1415432 TO 1425731 (SECTION 123 OF 400) OF	b1364	UNC	0.00
1423401	REC01325	<i>ynaK</i>	N	87	20, 41, 65	P76068	Hypothetical protein ynaK	b1365	UNC	0.03
1423645	REC01326	<i>ydaY</i>	N	119	11, 36, 69	P76069	Hypothetical protein ydaY	b1366	UNC	0.00
1424079	REC01327		N	77	49	P76070	FROM BASES 1415432 TO 1425731 (SECTION 123 OF 400) OF	b1367	UNC	0.00
1424478	REC01328	<i>ynaA</i>	N	342	22, 77, 161	P77658	Hypothetical protein ynaA	b1368	UNC	0.00
1426547	REC01331		N	153	83	P77184	FROM BASES 1425674 TO 1439104 (SECTION 124 OF 400) OF	b1371	UNC	0.00
1426750	REC04890	<i>insH5</i>	E	326	-	P76071	Transposase insH for insertion sequence element IS5Y	b1370	PHT	0.34
1427067	REC01332	<i>stfR</i>	N	1122	24, 128, 165, 329, 598, 708, 814, 1029, 1038, 1110	P76072	Side tail fiber protein homolog from lambdaoid prophage Rac	b1372	UNC	0.00
1430435	REC01333	<i>tfaR</i>	N	191	16, 62, 86, 121, 146, 179	P77163	Tail fiber assembly protein homolog from lambdaoid prophage Rac	b1373	UNC	0.03
1431698	REC04891	<i>pinR</i>	N	196	5, 44, 75, 142, 173	P77574	Putative DNA-invertase from lambdaoid prophage Rac	b1374	UNC	0.03
1432281	REC04892	<i>ynaE</i>	N	88	27	P76073	Hypothetical protein ynaE	b1375	UNC	0.00
1433715	REC04893	<i>ynaF</i>	N	168	14, 27, 45, 54, 94, 145	P73903	Unknown protein 2D_000B3L from 2D-page	b1376	UNC	0.13
1434917	REC04894	<i>ompN</i>	N	377	74, 114, 126, 180, 199, 228, 300, 345	P77747	Outer membrane protein N precursor	b1377	UNC	0.06
1438808	REC04895	<i>ydbK</i>	N	1174	36, 222, 299, 624, 861, 1092, 1138	P52647	Probable pyruvate-flavodoxin oxidoreductase (EC 1.2.7.-)	b1378	UNC	0.34
1439082	REC06678	<i>ydbJ</i>	?	88	-	P52646	Hypothetical protein ydbJ precursor	b1379	UNC	0.00
1439767	REC04896	<i>hsIJ</i>	E	140	-	P52644	Heat shock protein hsIJ	b1379	UNC	0.03
1440867	REC04897	<i>ldhA</i>	N	329	121, 224, 280, 325	P52643	D-lactate dehydrogenase (EC 1.1.1.28)	b1380	CHM	0.47
1441075	REC01341	<i>ydbH</i>	N	879	10, 105, 249, 321, 770, 838, 853, 872	P52645	Hypothetical protein ydbH	b1381	UNC	0.03
1443711	REC01342	<i>ynbE</i>	N	61	12, 36	P76075	Hypothetical protein ynaE	b1382	UNC	0.03
1443898	REC01343	<i>ydbL</i>	N	110	47	P76076	Hypothetical protein ydbL precursor	b1383	UNC	0.03
1445307	REC04898	<i>feaR</i>	N	301	183, 188, 230	Q47129	Transcriptional activator feaR	b1384	RCD	0.22
1445540	REC01345	<i>feaB</i>	N	500	32, 347, 357, 424	P80668	Phenylacetaldehyde dehydrogenase (EC 1.2.1.39)	b1385	AAM	0.19
1449373	REC04899	<i>tnyA</i>	N	757	33, 197, 417, 545, 719	P46883	Copper amine oxidase precursor (EC 1.4.3.6)	b1386	AAM	0.06
1451666	REC04900	<i>maoC</i>	N	681	16, 188	P77455	MaoC protein	b1387	UNC	0.19
1451951	REC01348	<i>paaA</i>	N	309	140, 245, 249	P76077	Phenylacetic acid degradation protein paaA	b1388	MSM	0.09
1452892	REC01349	<i>paaB</i>	X	95	-	P76078	Phenylacetic acid degradation protein paaB	b1389	MSM	0.09
1453188	REC01350	<i>paaC</i>	E	248	-	P76079	Phenylacetic acid degradation protein paaC	b1390	MSM	0.09
1453943	REC01351	<i>paaD</i>	N	167	36, 78	P76080	Phenylacetic acid degradation protein paaD	b1391	MSM	0.09
1454454	REC01352	<i>paaE</i>	N	356	23, 48, 78, 98	P76081	Probable phenylacetic acid degradation NADH oxidoreductase par	b1392	UNC	0.38
1455521	REC01353	<i>paaF</i>	N	255	32, 59, 146, 186, 250	P76082	Probable enoyl-CoA hydratase paaF (EC 4.2.1.17)	b1393	UNC	0.28
1456288	REC01354	<i>paaG</i>	N	262	222	P77467	Probable enoyl-CoA hydratase paaG (EC 4.2.1.17)	b1394	UNC	0.44
1457078	REC01355	<i>paaH</i>	N	475	294, 337	P76083	Probable 3-hydroxybutyryl-CoA dehydrogenase (EC 1.1.1.157)	b1395	UNC	0.41
1458495	REC01356	<i>paaI</i>	N	140	79, 105	P76084	Phenylacetic acid degradation protein paaI	b1396	UNC	0.13
1458917	REC01357	<i>paaJ</i>	N	401	60	P77525	Probable beta-ketoacyl-CoA thiolase (EC 2.3.1.-)	b1397	UNC	0.28
1460149	REC01358	<i>paaK</i>	N	437	284	P76085	Phenylacetyl-coenzyme A ligase (EC 6.2.1.30)	b1398	MSM	0.13
1461563	REC01359	<i>paaX</i>	E	316	-	P76086	Phenylacetic acid degradation operon negative regulatory protein	b1399	RCD	0.00
1462495	REC01360	<i>paaY</i>	E	196	167	P77181	Phenylacetic acid degradation protein paaY	b1400	UNC	0.16
1463416	REC01361	<i>ydbA</i>	N	852	48, 138, 180, 419, 759, 795	P76858	RtoA protein	b1401	UNC	0.03
1466850	REC06523	<i>insD2</i>	X	301	-	P19777	Transposase insD for insertion element IS2A/D/F/H/I/K	b1402	PHT	0.56
1467218	REC06524	<i>insC2</i>	X	136	-	P19776	Transposase insC for insertion element IS2A/D/F/H/I/K	b1403	PHT	0.56
1467382	REC06526	<i>insI3</i>	X	383	-	P37246	Transposase insI for insertion sequence element IS30B/C/D	b4284	PHT	0.22
1468714	REC01365	<i>ydbA</i>	N	1107	647, 805	P33666	Hypothetical protein ydbA	b1404	UNC	0.06
1472245	REC01366	<i>ydbC</i>	N	286	176	P25906	Hypothetical oxidoreductase ydbC (EC 1.-.-.-)	b1406	UNC	0.25
1473162	REC01367	<i>ydbD</i>	N	770	37, 60, 310, 360, 376, 414, 435, 450, 472, 529, 531, 579, 607, 675, 688, 7	P25907	Hypothetical protein ydbD	b1407	UNC	0.00
1475639	REC01368	<i>ynbA</i>	N	203	72	P76090	Hypothetical protein ynbA	b1408	UNC	0.06
1476250	REC01369	<i>ynbB</i>	X	298	-	P76091	Hypothetical protein ynbB	b1409	UNC	0.94
1477162	REC01370	<i>ynbC</i>	N	585	233, 248, 292, 299, 388, 467, 544	P76092	Hypothetical protein ynbC	b1410	UNC	0.25
1478933	REC01371	<i>ynbD</i>	N	430	36, 136, 218	P76093	Hypothetical protein ynbD	b1411	UNC	0.09
1480884	REC04903	<i>acpD</i>	E	201	-	P41407	Acyl carrier protein phosphodiesterase (EC 3.1.4.14)	b1412	LPC	0.34
1481142	REC01373	<i>hrpA</i>	N	1281	17, 114, 169, 228, 265, 397, 420, 890, 1022, 1103	P43329	ATP-dependent helicase hrpA	b1413	UNC	0.28

1485259	REC01374	ycdF	N	266	94, 207	P34209	Protein ycdF	b1414	UNC	0.00
1486256	REC01375	aJdA	N	479	312, 464	P25553	Aldehyde dehydrogenase A (EC 1.2.1.22)	b1415	CHM	0.13
1487988	REC04904	gapC	?	83	-	P33898	Glyceraldehyde 3-phosphate dehydrogenase C (EC 1.2.1.12)	b1416	CHM	0.97
1488389	REC04905	gapC	N	134	94	P33898	Glyceraldehyde 3-phosphate dehydrogenase C (EC 1.2.1.12)	b1418	BEN	0.31
1488890	REC01378	cybB	N	188	83, 181	P08732	Cytochrome b561	b1419	UNC	0.03
1489701	REC01379	ycdA	N	57	34	P23864	Hypothetical protein ycdA precursor	b1419	UNC	0.00
1489940	REC06875	ycdB	N	76	36	P77193	SIMILAR TO	b1421	SMC	0.63
1490494	REC01381	trg	E	546	-	P05704	Methyl-accepting chemotaxis protein III	b1422	UNC	0.22
1493236	REC04907	ycdI	N	354	89, 287	P77171	Hypothetical transcriptional regulator ydci	b1423	UNC	0.09
1493312	REC01383	ycdJ	N	447	29, 441	P76097	Hypothetical protein ydcJ	b1424	UNC	0.06
1494880	REC01384	ycdG	N	551	17, 246, 376, 432	P40120	Protein ydcG precursor	b1426	UNC	0.00
1496732	REC01386	ycdH	?	55	-	P46135	Hypothetical protein ydcH	b1427	PMS	0.19
1496962	REC01387	rimL	E	179	-	P13857	Ribosomal-protein-serine acetyltransferase (EC 2.3.1.-)	b1428	UNC	0.00
1498473	REC04909	ycdK	N	326	105, 157, 310	P76100	Hypothetical protein ydcK	b1429	UNC	0.13
1498597	REC01389	tehA	N	330	181, 301, 326	P25396	Tellurite resistance protein tehA	b1430	UNC	0.09
1499586	REC01390	tehB	N	197	158	P25397	Tellurite resistance protein tehB	b1431	UNC	0.00
1500481	REC01391	ycdL	N	222	57	P76101	Hypothetical lipoprotein ydcL precursor	b1432	UNC	0.31
1501681	REC01392	ycdM	N	402	26, 105, 170	P76102	Hypothetical protein ydcM	b1434	UNC	0.09
1504196	REC01394	ycdN	E	178	171	P77626	Hypothetical protein ydcN	b1433	UNC	0.25
1504365	REC04910	ycdO	N	478	100, 267, 311, 446, 453	P76103	Hypothetical protein ydcO	b1435	UNC	0.16
1504763	REC01395	ycdP	N	667	135, 363, 458, 583, 659	P76104	Putative protease ydcP precursor (EC 3.4.-.-)	b1436	UNC	0.00
1507088	REC04911	yncJ	N	76	45	P76105	Hypothetical protein yncJ precursor	b1437	UNC	0.00
1507471	REC04912	yncK	N	65	22	P76106	FROM BASES 1506783 TO 1516942 (SECTION 131 OF 400) OF	b1438	UNC	0.00
1507511	REC01398	ycdQ	E	145	44	P76107	Hypothetical protein ycdQ	b1439	UNC	0.31
1508027	REC01399	ycdR	N	468	114, 171, 467	P77730	Hypothetical protein ycdR	b1440	UNC	0.06
1508678	REC01400	ycdS	N	381	10, 53, 90, 165	P76108	Putative ABC transporter periplasmic binding protein ydcS precursor	b1441	UNC	0.09
1510841	REC01401	ycdT	E	337	-	P77795	Hypothetical ABC transporter ATP-binding protein ycdT	b1442	UNC	0.06
1511855	REC01402	ycdU	E	313	-	P77156	Hypothetical ABC transporter permease protein ycdU	b1443	UNC	0.06
1512786	REC01403	ycdV	E	264	207	P77505	Hypothetical ABC transporter permease protein ycdV	b1444	UNC	0.25
1513602	REC01404	ycdW	N	474	208	P77674	Putative betaine aldehyde dehydrogenase (EC 1.2.1.8)	b1445	UNC	0.00
1515338	REC01405	ycdX	?	82	-	P76109	Hypothetical protein ycdX	b1446	UNC	0.00
1515672	REC01406	ycdY	N	77	34	P76110	Hypothetical protein ycdY	b1447	UNC	0.03
1516355	REC04913	ycdZ	E	149	-	P76111	Hypothetical protein ycdZ	b1448	UNC	0.50
1516870	REC04914	yncA	E	172	172	P76112	Hypothetical acetyltransferase yncA (EC 2.3.1.-)	b1449	UNC	0.44
1516958	REC01409	yncB	N	376	10, 54, 114, 312, 325	P76113	Putative NADP-dependent oxidoreductase yncB (EC 1.-.-.-)	b1450	UNC	0.16
1518229	REC01410	yncC	N	240	98, 175, 198, 215, 216, 236	P76114	Hypothetical transcriptional regulator yncC	b1451	UNC	0.28
1521089	REC04915	yncD	N	700	258, 320, 377, 415, 481, 556, 573, 587, 614, 642, 672	P76115	Probable tonB-dependent receptor yncD precursor	b1452	UNC	0.00
1521331	REC01412	yncE	E	353	-	P76116	Hypothetical protein yncE precursor	b1453	MTR	0.22
1524055	REC04916	ansP	N	516	151, 379	P77610	L-asparagine permease	b1454	UNC	0.13
1524271	REC01414	yncG	N	205	151	P76117	Hypothetical GST-like protein yncG	b1455	UNC	0.00
1524964	REC01415	yncH	N	70	-	P76118	Hypothetical protein yncH	b1456	UNC	0.00
1525914	REC01416	rhsE	N	682	-	P24211	RhsE protein	b1457	UNC	0.00
1527946	REC01417	ycdD	?	160	-	P31991	Hypothetical protein ycdD	b1458	UNC	0.00
1528610	REC01418	yncI	N	248	-	P76119	FROM BASES 1528490 TO 1540683 (SECTION 133 OF 400) OF	b1459	UNC	0.00
1529400	REC01419	yncJ	?	66	-	P76120	FROM BASES 1528490 TO 1540683 (SECTION 133 OF 400) OF	b1460	UNC	0.03
1529840	REC01420	ycdC	N	378	-	P28917	H repeat-associated protein ydcC	b1461	UNC	0.00
1531076	REC01421	ycdE	N	77	-	P31992	Hypothetical protein ycdE	b1462	UNC	0.06
1531923	REC04917	ydhH	N	205	13, 57	P76121	Hypothetical protein ydhH	b1463	MSM	0.19
1532048	REC01423	nhoA	E	281	-	P77567	N-hydroxyarylamine O-acetyltransferase (EC 2.3.1.118)	b1464	UNC	0.47
1533882	REC04918	yddE	E	297	-	P37757	Hypothetical protein yddE	b1465	SMC	0.22
1534641	REC04919	narV	N	226	101	P19316	Respiratory nitrate reductase 2 gamma chain (EC 1.7.99.4)	b1466	SMC	0.09
1535333	REC04920	narW	N	231	18, 94	P19317	Respiratory nitrate reductase 2 delta chain (EC 1.7.99.4)	b1467	SMC	0.22
1536877	REC04921	narY	N	514	69, 160, 199, 249, 356, 376, 423, 497	P19318	Respiratory nitrate reductase 2 beta chain (EC 1.7.99.4)	b1468	SMC	0.25
1540614	REC04922	narZ	N	1246	6, 115, 132, 277, 305, 350, 351, 497, 609, 1118	P19319	Respiratory nitrate reductase 2 alpha chain (EC 1.7.99.4)	b1469	SMC	0.22
1542084	REC04923	narU	N	462	2, 72, 95	P37758	Nitrite extrusion protein 2	b1470	UNC	0.00
1542743	REC04924	yddJ	N	111	73, 100	P76122	Hypothetical protein yddJ	b1471	UNC	0.03
1543738	REC04925	yddK	E	318	306	P76123	Hypothetical protein yddK	b1472	UNC	0.00
1544052	REC04926	yncL	E	96	-	P77519	FROM BASES 1540626 TO 1550846 (SECTION 134 OF 400) OF	b1473	UNC	0.13
1545193	REC04927	yddG	N	293	19, 177, 230, 252	P46136	Hypothetical protein yddG	b1474	SMC	0.09
1545425	REC01434	fdnG	N	1015	73, 322, 383, 426, 543, 669, 678, 787, 787	P24183	Formate dehydrogenase, nitrate-inducible, major subunit (EC 1.2.-.-)	b1475	BEN	0.06
1548485	REC01435	fdnH	N	294	67, 176, 229	P24184	Formate dehydrogenase, nitrate-inducible, iron-sulfur subunit	b1476	SMC	0.13
1549362	REC01436	fdnI	N	217	88	P24185	Formate dehydrogenase, nitrate-inducible, cytochrome b556(FDN)	b1477	UNC	0.00
1550784	REC04928	yddM	E	120	-	P76125	Hypothetical protein yddM	b1478	CHM	0.75
1551892	REC04929	adhP	N	346	72, 154, 189, 289	P39451	Alcohol dehydrogenase, propanol-preferring (EC 1.1.1.1)	b1479	BEN	0.22
1553720	REC04930	sfcA	N	574	45, 187	P26616	NAD-dependent malic enzyme (EC 1.1.1.38)	b1480	PMS	0.00
1553987	REC04931	xpsV	N	45	10	P28690	30S ribosomal protein S22	b1481	Bdm	protein
1554367	REC04932	bdm	N	92	6, 18	P76127	Bdm protein	b1482	UNC	0.22
1554649	REC01442	osmC	N	143	32, 46	P23929	Osmotically inducible protein C	b1483	UNC	0.28
1556062	REC04933	yddO	N	308	47, 107	P77622	Hypothetical ABC transporter ATP-binding protein yddO	b1484	UNC	0.03
1557041	REC04934	yddP	N	328	86, 242, 279	P77268	Hypothetical ABC transporter ATP-binding protein yddP	b1485	UNC	0.06
1557934	REC04935	yddQ	E	298	-	P77463	Hypothetical ABC transporter permease protein yddQ	b1486	UNC	0.03
1558953	REC04936	yddR	N	340	37, 185, 242	P77308	Hypothetical ABC transporter permease protein yddR	b1487	UNC	0.09
1560505	REC04937	ydds	N	516	45, 62, 102, 141, 152, 207, 281, 299, 312, 339, 368, 398, 444, 464, 465	P76128	Putative ABC transporter periplasmic binding protein ydds precursor	b1488	SMC	0.16
1561100	REC04938	ddpX	N	193	157, 182	P77790	D-alanyl-D-alanine dipeptidase (EC 3.4.13.-)	b1489	UNC	0.25
1563781	REC04939	yddU	N	807	36, 87, 129, 228, 673	P76129	Hypothetical protein yddU	b1490	UNC	0.34
1565164	REC04940	yddV	N	460	81, 175, 276, 288, 351, 362	P77793	Hypothetical protein yddV	b1491	UNC	0.19
1566847	REC04941	yddW	N	439	29, 368, 379	P76130	Hypothetical lipoprotein yddW precursor	b1492	UNC	0.13
1568513	REC04942	xasA	N	511	70	P39183	Amino acid antipporter	b1493	AAM	0.19
1570069	REC04943	gadB	N	466	8, 42, 66, 103, 110, 185, 252, 271, 286, 310	P28302	Glutamate decarboxylase beta (EC 4.1.1.15)	b1494	UNC	0.84
1573226	REC04944	pqqL	N	931	55, 153, 185, 211, 596, 752, 803, 831, 921, 924	P31828	Probable zinc protease pqqL (EC 3.4.99.-)	b1495	UNC	0.31
1575643	REC04945	yddB	N	790	24, 116, 163, 282, 298, 349, 399, 438, 462, 565, 581, 601, 612, 634, 661,	P31827	Hypothetical protein yddB	b1496	UNC	0.06
1577366	REC04946	yddA	N	561	98, 131, 193, 193, 224, 251, 282, 290, 328, 347, 382, 413, 417, 447, 487,	P31826	Hypothetical ABC transporter ATP-binding protein yddA	b1497	UNC	0.06
1578829	REC04947	ydeM	N	390	60, 128, 280, 361, 369	P76134	Hypothetical protein ydeM	b1498	UNC	0.06
1580581	REC04948	ydeN	N	571	47, 88, 158, 169, 197, 246, 274, 285, 310, 341, 362, 380, 409, 412, 435	P77318	Putative sulfatase ydeN precursor (EC 3.1.6.-)	b1499	UNC	0.00
1581711	REC04949	ydeO	N	253	14, 141, 152, 212, 230	P76135	Hypothetical transcriptional regulator ydeO	b1500	UNC	0.00
1581983	REC04950	ydeP	?	65	-	P76136	FROM BASES 1577448 TO 1588149 (SECTION 137 OF 400) OF	b1501	UNC	0.50
1584510	REC04951	ydeQ	N	759	12, 35, 48, 197, 481, 688, 757	P77561	Hypothetical protein ydeP	b1502	UNC	0.00
1585758	REC04952	ydeQ	N	304	62	P75588	Hypothetical fimbrial-like protein ydeQ precursor	b1503	UNC	0.00
1586320	REC04953	ydeR	N	167	33, 131	P77294	Hypothetical fimbrial-like protein ydeR precursor	b1504	UNC	0.00
1586863	REC04954	ydeS	N	176	27, 74, 117, 120	P77789	Hypothetical fimbrial-like protein ydeS precursor	b1505	UNC	0.09
1588025	REC04955	ydeT	N	382	107, 165, 197, 215, 279, 301, 350, 372	P76137	FROM BASES 1577448 TO 1588149 (SECTION 137 OF 400) OF	b1506	UNC	0.00
1588580	REC04956	ydeU	X	59	-	P76138	FROM BASES 1588092 TO 1598300 (SECTION 138 OF 400) OF	b1507	UNC	0.19
1590200	REC04957	hipA	N	440	178, 179	P23874	Protein hipA	b1507	UNC	0.19

1590466	REC04958	<i>hipB</i>	?	88	-		P23873	Protein hipB	b1508	RCD	0.00
1592089	REC04959	<i>ydeU</i>	N	466	70, 236, 351		P77286	Hypothetical protein ydeU	b1509	UNC	0.16
1596110	REC04960	<i>ydeK</i>	N	1325	200, 235, 254, 309, 311, 399, 432, 479, 507, 555, 571, 582, 615, 779, 111		P32051	Hypothetical lipoprotein ydeK precursor	b1510	UNC	0.19
1598233	REC04961	<i>ydeV</i>	N	530	97, 822		P77432	Hypothetical sugar kinase ydeV	b1511	UNC	0.41
1599265	REC04962	<i>ydeW</i>	N	317	226, 232		P76141	Hypothetical transcriptional regulator ydeW	b1512	UNC	0.16
1599514	REC01473	<i>ego</i>	N	511	242, 396, 497		P77257	Putative ABC transporter ATP-binding protein ego	b1513	UNC	0.06
1601043	REC01474	<i>ydeY</i>	N	342	77, 312		P77672	Hypothetical ABC transporter permease protein ydeY	b1514	UNC	0.03
1602071	REC01475	<i>ydeZ</i>	N	330	187		P77651	Hypothetical ABC transporter permease protein ydeZ	b1515	UNC	0.38
1603075	REC01476	<i>yneA</i>	N	340	76, 135, 171, 187		P76142	Hypothetical protein yneA precursor	b1516	UNC	0.09
1604124	REC01477	<i>yneB</i>	N	291	21, 44, 51, 118, 120, 177, 178, 237, 239, 254		P76143	Putative aldolase yneB (EC 4.2.1.-)	b1517	UNC	0.19
1605023	REC01478	<i>yneC</i>	N	96	79		P76144	Hypothetical protein yneC	b1518	UNC	0.09
1605370	REC01479	<i>tam</i>	N	252	204		P76145	Trans-aconitate methyltransferase (EC 2.1.1.-)	b1519	CHM	0.28
1607097	REC04963	<i>yneE</i>	N	321	62		P76146	Hypothetical protein yneE	b1520	UNC	0.13
1608704	REC04964	<i>uxaB</i>	N	483	239		P24214	Altronate oxidoreductase (EC 1.1.1.58)	b1521	CHM	0.13
1609878	REC04965	<i>yneF</i>	N	315	186, 308		P76147	Hypothetical protein yneF	b1522	UNC	0.44
1610349	REC04966	<i>yneG</i>	E	119	-	0.41	P76148	Hypothetical protein yneG	b1523	UNC	0.00
1611275	REC04967	<i>yneH</i>	N	308	113, 208		P77470	Probable glutaminase yneH (EC 3.5.1.2)	b1524	UNC	0.41
1612751	REC04968	<i>yneI</i>	N	470	69, 130		P76149	Aldehyde-dehydrogenase like protein yneI (EC 1.2.1.-)	b1525	UNC	0.63
1612828	REC01486	<i>yneJ</i>	N	293	28, 77, 209, 269		P77309	Hypothetical transcriptional regulator yneJ	b1526	UNC	0.72
1613787	REC01487	<i>yneK</i>	N	371	3, 13, 33, 137, 310, 352, 370		P76150	Hypothetical protein yneK	b1527	UNC	0.00
1615052	REC01488	<i>sotB</i>	N	396	100, 269, 331		P31122	Sugar efflux transporter	b1528	MTR	0.34
1616932	REC04969	<i>marC</i>	N	221	171		P31123	Multiple antibiotic resistance protein marC	b1529	MTR	0.56
1617201	REC01490	<i>marR</i>	N	125	14, 28, 41, 49, 71, 73, 102		P27245	Multiple antibiotic resistance protein marR	b1530	NAM	0.09
1617592	REC01491	<i>marA</i>	E	129	-	< 0.1	P72746	Multiple antibiotic resistance protein marA	b1531	RCD	0.06
1618013	REC01492	<i>marB</i>	?	72	51		P31121	Multiple antibiotic resistance protein marB	b1532	MSM	0.00
1619062	REC04970	<i>eama</i>	N	266	54, 206, 251		P31125	Probable amino acid metabolite efflux pump	b1533	UNC	0.25
1619356	REC01494	<i>ydeE</i>	E	395	323, 370	< 0.001	P31126	Hypothetical protein ydeE	b1534	UNC	0.81
1621874	REC04971	<i>ydeH</i>	N	296	27, 39, 64, 81, 121, 170, 185, 219, 249, 296		P31129	Hypothetical protein ydeH	b1535	UNC	0.00
1622521	REC04972	<i>ydeI</i>	N	130	49, 126		P31130	Hypothetical protein ydeI precursor	b1536	UNC	0.06
1622797	REC01497	<i>ydeJ</i>	X	172	-		P31131	Hypothetical protein ydeJ	b1537	UNC	0.03
1625404	REC04973	<i>dcp</i>	N	681	33, 41, 203, 301, 429		P24171	Peptidyl-dipeptidase dcp (EC 3.4.15.5)	b1538	PMS	0.22
1625541	REC01499	<i>ydfG</i>	N	248	1, 186		P39831	Probable oxidoreductase ydfG (EC 1.-.-.-)	b1539	UNC	0.78
1626376	REC01500	<i>ydfH</i>	N	228	35, 87		P77577	Hypothetical transcriptional regulator ydfH	b1540	UNC	0.53
1627239	REC01501	<i>ydfZ</i>	?	67	-		P76153	Hypothetical protein ydfZ	b1541	UNC	0.00
1628937	REC04974	<i>ydfI</i>	N	486	23, 33, 80, 196, 241, 261		P77260	Hypothetical oxidoreductase ydfI (EC 1.-.-.-)	b1542	UNC	0.03
1630309	REC04975	<i>ydfJ</i>	N	427	49, 188, 254, 306, 398, 412		P77228	Hypothetical metabolite transport protein ydfJ	b1543	UNC	0.41
1631063	REC01504	<i>ydfK</i>	N	88	10, 51, 58		P76154	Hypothetical protein ydfK	b1544	UNC	0.00
1631646	REC01505	<i>pinQ</i>	N	196	7, 59, 74, 103, 118, 180, 192		P77170	Putative DNA-invertase from lambdoid prophage Qin	b1545	UNC	0.00
1632909	REC06567	<i>tfaQ</i>	N	191	25, 77, 112, 166, 180		P76155	Tail fiber assembly protein homolog from lambdoid prophage Qin	b1546	UNC	0.03
1633871	REC04977	<i>stfQ</i>	?	320	287		P77515	Side tail fiber protein homolog from lambdoid prophage Qin	b1547	UNC	0.00
1634391	REC04978	<i>nohA</i>	?	189	165		P31061	Prophage Qin DNA packaging protein NU1 homolog	b1548	UNC	0.00
1635056	REC01509	<i>ydfO</i>	N	141	7, 66		P76156	Hypothetical protein ydfO	b1549	UNC	0.00
1635809	REC04979	<i>gnsB</i>	?	58	-		P77695	GnsB protein	b1550	UNC	0.00
1636169	REC04980	<i>ynfN</i>	?	63	4		P76157	Hypothetical protein ynfN	b1551	UNC	0.00
1636691	REC04981	<i>cspI</i>	?	70	56		P77605	Cold shock-like protein cspI	b1552	UNC	0.72
1637551	REC04982	<i>ydfP</i>	X	165	-		P76158	Hypothetical protein ydfP precursor	b1553	UNC	0.00
1638081	REC04983	<i>ydfQ</i>	N	177	46, 74, 85, 158		P76159	Probable lysozyme from lambdoid prophage Qin (EC 3.2.1.17)	b1554	UNC	0.00
1638389	REC04984	<i>ydfR</i>	E	103	-	< 0.3	P76160	Hypothetical protein ydfR	b1555	UNC	0.00
1638684	REC04985	<i>essQ</i>	E	96	82, 88	< 0.3	P77237	Lysis protein S homolog from lambdoid prophage Qin	b1556	UNC	0.00
1639578	REC04986	<i>cspB</i>	N	71	53		P36995	Cold shock-like protein cspB	b1557	UNC	0.72
1639879	REC01518	<i>cspF</i>	N	70	9, 30		P39819	Cold shock-like protein cspF	b1558	UNC	0.00
1641295	REC04987	<i>ydfT</i>	N	260	11, 57, 98, 108, 177		P76161	Antitermination protein Q homolog from lambdoid prophage Qin	b1559	UNC	0.00
1642367	REC04988	<i>ydfU</i>	N	362	114, 312		P76162	Hypothetical protein ydfU	b1560	UNC	0.00
1642926	REC04989	<i>rem</i>	?	83	-		P07010	Hypothetical rem protein	b1561	UNC	0.00
1643298	REC04990	<i>hokD</i>	?	51	-		P70709	HokD protein	b1562	UNC	0.00
1643657	REC04991	<i>relE</i>	E	95	-	< 0.2	P07008	Hypothetical relE protein	b1563	UNC	0.06
1643896	REC04992	<i>relB</i>	?	79	-		P70707	RelB protein	b1564	UNC	0.00
1643921	REC01525	<i>ydfV</i>	E	101	-	< 0.2	P76163	Hypothetical protein ydfV	b1565	UNC	0.00
1644429	REC01526	<i>flxA</i>	N	110	13, 44, 70, 88		P77609	Protein flxA	b1566	UNC	0.00
1645660	REC04994	<i>ydfX</i>	N	96	36		P76165	Hypothetical protein ydfX	b1568	UNC	0.00
1645874	REC04995	<i>dicC</i>	?	76	-		P06965	Repressor protein of division inhibition gene dicB	b1569	RCD	0.00
1645958	REC01530	<i>dica</i>	E	135	-	< 0.1	P06966	Repressor protein of division inhibition gene dicB	b1570	RCD	0.00
1646532	REC01531	<i>ydfA</i>	?	51	-		P29008	Hypothetical protein ydfA	b1571	UNC	0.00
1646847	REC01533	<i>ydfC</i>	N	72	10, 26		P21418	Hypothetical protein ydfC	b1573	UNC	0.00
1647633	REC01534	<i>dicB</i>	?	62	47		P09557	Division inhibition protein dicB	b1575	RCD	0.00
1647818	REC01535	<i>ydfD</i>	N	63	25, 44, 55		P29010	Hypothetical protein ydfD	b1576	UNC	0.00
1648102	REC01536	<i>ydfE</i>	N	306	6, 52, 63, 182		Q47138	Hypothetical protein ydfE	b1577	UNC	0.00
1648905	REC06568		E	218	-	< 0.05	P19777	Transposase insD for insertion element IS2A/D/F/H/I/K	b1578	PHT	0.56
1649536	REC01538	<i>intQ</i>	N	398	50, 92, 129, 152, 171, 243, 273, 366		P76168	Putative lambdoid prophage Qin defective integrase	b1579	UNC	0.00
1651939	REC04996	<i>rspB</i>	N	339	49, 191, 212		P38105	Starvation sensing protein rspB (EC 1.1.1.-)	b1580	UNC	0.22
1653165	REC04997	<i>rspA</i>	N	404	118, 119, 319, 383, 402		P38104	Starvation sensing protein rspA	b1581	UNC	0.13
1653697	REC04998	<i>ynfA</i>	E	108	-	< 0.3	P76169	Hypothetical protein ynfA	b1582	UNC	0.31
1653832	REC01542	<i>ynfB</i>	N	113	42		P76170	Hypothetical protein ynfB precursor	b1583	UNC	0.00
1654208	REC01543	<i>speG</i>	N	186	55, 68, 110, 112, 133, 173		P37354	Spermidine N(1)-acetyltransferase (EC 2.3.1.57)	b1584	AAM	0.16
1655517	REC04999	<i>ynfC</i>	N	248	1, 113, 199, 221, 223, 247		P76171	Hypothetical protein ynfC	b1585	UNC	0.00
1655547	REC01545	<i>ynfD</i>	E	115	97	< 0.3	P76172	Hypothetical protein ynfD precursor	b1586	UNC	0.03
1656093	REC01546	<i>ynfE</i>	N	808	215, 400, 488, 764, 785		P77374	Putative dimethyl sulfoxide reductase chain ynfE precursor (EC 1.1.1.587)	b1587	UNC	0.09
1658577	REC01547	<i>ynfF</i>	N	808	25, 63, 202, 206, 269, 403, 500, 605, 806		P77783	Probable dimethyl sulfoxide reductase chain ynfF precursor (EC 1.1.1.588)	b1588	UNC	0.03
1661014	REC01548	<i>ynfG</i>	E	205	-	< 0.2	P77313	Probable anaerobic dimethyl sulfoxide reductase chain ynfG	b1589	BEN	0.13
1661633	REC01549	<i>ynfH</i>	N	284	172, 259, 259, 283		P76173	Anaerobic dimethyl sulfoxide reductase chain ynfH	b1590	BEN	0.03
1662521	REC01550	<i>ynfI</i>	N	207	153		P76174	Hypothetical protein ynfI precursor	b1591	UNC	0.03
1663279	REC01551	<i>ynfJ</i>	N	438	64, 155, 182, 290, 373		P76175	Putative chloride channel protein erC-like	b1592	UNC	0.47
1665255	REC05000	<i>ynfK</i>	N	235	45, 162		P77201	Putative dethiobiotin synthetase (EC 6.3.3.3)	b1593	UNC	0.69
1666588	REC05001	<i>mlc</i>	N	406	21, 233, 283		P50456	Mlc protein	b1594	UNC	0.25
1667616	REC05002	<i>ynfL</i>	N	297	20		P77559	Hypothetical transcriptional regulator ynfL	b1595	UNC	0.34
1667723	REC01555	<i>ynfM</i>	N	417	119, 366, 375, 409		P43531	Hypothetical transport protein ynfM	b1596	UNC	0.81
1669373	REC01556	<i>asr</i>	N	111	30, 46		P36560		b1597	UNC	0.00
1669984	REC01557	<i>ydgD</i>	N	273	66		P76176	Putative protease ydgD precursor (EC 3.4.21.-)	b1598	UNC	0.03
1671173	REC05003	<i>ydgE</i>	E	109	-	0.32	P77670	Hypothetical protein ydgE	b1599	UNC	0.44
1671525	REC05004	<i>ydgF</i>	N	121	37, 61, 70, 102, 112		P77412	Hypothetical protein ydgF	b1600	UNC	0.44
1671937	REC01560	<i>ydgG</i>	N	344	54, 63, 80, 119, 169		P77535	Hypothetical protein ydgG	b1601	UNC	0.31
1674384	REC05005	<i>pntB</i>	N	462	76, 276, 402		P07002	NAD(P) transhydrogenase subunit beta (EC 1.6.1.2)	b1602	BEN	0.44
1675927	REC05006	<i>pntA</i>	N	510	83, 505		P70701	NAD(P) transhydrogenase subunit alpha (EC 1.6.1.2)	b1603	BEN	0.63

1676451	REC01563	<i>ydgH</i>	N	314	79, 89, 168, 235	P76177	Protein ydgH precursor	b1604	UNC	0.00
1677581	REC01564	<i>ydGI</i>	N	460	88, 365	P77429	Putative arginine/ornithine antiporter	b1605	UNC	0.25
1679000	REC01565	<i>ydGB</i>	N	240	86, 106	P52109	Hypothetical oxidoreductase ydgB (EC 1.-.-.-)	b1606	UNC	0.06
1680054	REC05007	<i>ydGC</i>	N	111	57	P52110	Hypothetical regulatory ydgC	b1607	UNC	0.06
1680174	REC01567	<i>rstA</i>	N	242	85, 86, 126, 219	P52108	Transcriptional regulatory protein rstA	b1608	RCD	0.81
1680906	REC01568	<i>rstB</i>	E	433	347	P18392	Sensor protein rstB (EC 2.7.3.-)	b1609	SMC	0.16
1682283	REC01569	<i>tus</i>	E	309	43	P16525	DNA replication terminus site-binding protein	b1610	NAM	0.00
1684612	REC05008	<i>fumC</i>	N	467	55, 403	P05042	Fumarate hydratase class II (EC 4.2.1.2)	b1611	CHM	0.69
1686401	REC05009	<i>fumA</i>	N	548	17, 74, 191, 216, 219, 292, 294, 313, 364	P00923	Fumarate hydratase class I, aerobic (EC 4.2.1.2)	b1612	CHM	0.31
1686600	REC01572	<i>manA</i>	N	391	56, 205, 271	P00946	Mannose-6-phosphate isomerase (EC 5.3.1.8)	b1613	CHM	0.34
1687876	REC01573	<i>ydGA</i>	E	502	-	P77804	Hypothetical protein ydGA	b1614	UNC	0.03
1690863	REC05010	<i>uidC</i>	N	417	63, 149, 337	Q47706	Membrane-associated protein uidC precursor	b1615	LPC	0.00
1692287	REC05011	<i>uidB</i>	N	457	45, 149, 435	P30868	Glucuronide carrier protein	b1616	CHM	0.06
1694095	REC05012	<i>uidA</i>	N	603	215, 359, 410	P05804	Beta-glucuronidase (EC 3.2.1.31)	b1617	CHM	0.06
1695076	REC05013	<i>uidR</i>	E	196	-	Q59431	Uid operon repressor	b1618	RCD	0.09
1696064	REC05014	<i>hdhA</i>	N	255	18, 38, 64, 102, 247	P25529	7-alpha-hydroxysteroid dehydrogenase (EC 1.1.1.159)	b1619	LPC	0.19
1697204	REC05015	<i>maII</i>	N	342	320, 342	P18811	Maltose regulon regulatory protein mail	b1620	RCD	0.00
1697379	REC01580	<i>maIX</i>	N	530	45, 149, 528	P19642	PTS system, maltose and glucose-specific IIBC component (EC	b1621	MTR	0.16
1698981	REC01581	<i>maLY</i>	N	390	185, 187, 206, 222	P23256	MalY protein	b1622	CHM	0.31
1700257	REC01582	<i>add</i>	N	333	45	P22333	Adenosine deaminase (EC 3.5.4.4)	b1623	NCM	0.34
1702371	REC05016	<i>ydjJ</i>	N	359	4, 41, 71, 89, 146, 154	P77376	Hypothetical oxidoreductase ydjJ (EC 1.-.-.-)	b1624	UNC	0.38
1702500	REC06681	<i>blr</i>	N	66	23, 52	P56976	Beta-lactam resistance protein	b1625	MSM	0.00
1702973	REC01584	<i>ydjT</i>	N	71	57	P76179	Hypothetical protein ydjT	b1626	UNC	0.00
1703250	REC01585	<i>ydjK</i>	N	154	26, 38, 78, 141, 151	P76180	Hypothetical protein ydjK	b1627	BEN	0.25
1703791	REC01586	<i>rnfA</i>	N	193	10, 108, 170, 182	P77223	Electron transport complex protein rnfA	b1628	BEN	0.28
1704372	REC01587	<i>rnfB</i>	X	192	-	P77611	Electron transport complex protein rnfC	b1629	BEN	0.25
1704943	REC01588	<i>rnfC</i>	N	740	139, 293, 334, 556, 644	P76182	Electron transport complex protein rnfD	b1630	BEN	0.22
1707166	REC01589	<i>rnfD</i>	N	352	44, 151, 250, 299	P77285	Electron transport complex protein rnfG	b1631	BEN	0.13
1708228	REC01590	<i>rnfG</i>	N	206	73	P77179	Electron transport complex protein rnfE	b1632	BEN	0.25
1708852	REC01591	<i>rnfE</i>	N	231	52, 81, 124	P20625	Endonuclease III (EC 4.2.99.18)	b1633	NAM	0.97
1709547	REC01592	<i>nth</i>	N	211	88, 164, 187	P77304	Hypothetical transporter ydGR	b1634	UNC	0.31
1710793	REC01593	<i>ydGR</i>	E	500	-	P39100	Glutathione S-transferase (EC 2.5.1.18)	b1635	BEN	0.44
1712401	REC01594	<i>gst</i>	N	201	102, 191	P77150	Pyridoxamine kinase (EC 2.7.1.35)	b1636	NCM	0.34
1713913	REC05017	<i>pdxY</i>	N	287	38, 153, 180, 197, 242	P00951	Tyrosyl-tRNA synthetase (EC 6.1.1.1)	b1637	PMS	1.00
1715246	REC05018	<i>tyrS</i>	E	424	160	P28225	Pyridoxamine 5'-phosphate oxidase (EC 1.4.3.5)	b1638	NCM	0.47
1716031	REC05019	<i>pdxH</i>	N	218	67, 171	P28224	Hypothetical protein ydHA	b1639	UNC	0.03
1716338	REC05020	<i>ydHA</i>	?	82	-	P77570	Hypothetical protein ydHH	b1640	UNC	0.41
1717626	REC05021	<i>ydHH</i>	N	369	70, 145, 212, 300	P55741	Outer membrane lipoprotein slyB precursor	b1641	RCD	0.06
1717900	REC01600	<i>slyB</i>	N	155	64, 102, 133	P55740	Transcriptional regulator slyA	b1642	RCD	0.19
1718854	REC05022	<i>slyA</i>	N	146	7	P76184	Hypothetical protein ydHI	b1643	UNC	0.00
1719049	REC01602	<i>ydHI</i>	?	78	-	P76185	Hypothetical protein ydHJ	b1644	UNC	0.06
1719246	REC01603	<i>ydHJ</i>	N	299	188, 294	P76186	Hypothetical protein ydHK	b1645	UNC	0.13
1720145	REC01604	<i>ydHK</i>	N	670	21, 122, 184, 272, 379, 465, 492, 586	P53635	Superoxide dismutase [Cu-Zn] precursor (EC 1.15.1.1)	b1646	MSM	0.28
1722679	REC05023	<i>sodC</i>	N	173	127, 163	P76187	Hypothetical oxidoreductase ydHF (EC 1.-.-.-)	b1647	UNC	0.34
1723656	REC05024	<i>ydHF</i>	N	298	141	P76189	Hypothetical transcriptional regulator ydHM	b1648	UNC	0.13
1724047	REC01608	<i>ydHM</i>	N	199	105	P76188	Hypothetical protein ydHL precursor	b1649	UNC	0.25
1724082	REC05025	<i>ydHL</i>	E	125	-	P77258	N-ethylmaleimide reductase (EC 1.-.-.-)	b1650	BEN	0.50
1724683	REC01609	<i>nema</i>	N	365	86, 219, 301	Q59384	Lactoylglutathione lyase (EC 4.4.1.5)	b1651	CHM	0.53
1725861	REC01610	<i>gloA</i>	?	135	76	P30014	Ribonuclease T (EC 3.1.13.-)	b1652	NAM	0.16
1726371	REC01611	<i>rnt</i>	E	215	-	P30015	Probable ATP-dependent helicase lhr (EC 3.6.1.-)	b1653	UNC	0.38
1727111	REC01612	<i>lhr</i>	N	1538	54, 191, 320, 454, 654, 710, 871, 989, 1046, 1130, 1377, 1432, 1480	P37010	Protein ydHD	b1654	UNC	0.47
1732125	REC05026	<i>ydHD</i>	E	115	-	P76190	Hypothetical protein ydHO precursor	b1655	UNC	0.38
1732459	REC01614	<i>ydHO</i>	N	271	99, 204, 217	P09157	Superoxide dismutase [Fe] (EC 1.15.1.1)	b1656	MSM	0.47
1733402	REC01615	<i>sodB</i>	N	193	11, 170	P77389	Hypothetical transport protein ydHP	b1657	UNC	0.38
1735314	REC05027	<i>ydHP</i>	N	389	75, 256, 335, 367	P15039	Purine nucleotide synthesis repressor	b1658	RCD	0.22
1735868	REC01617	<i>purR</i>	N	341	19, 289	P37598	Hypothetical transcriptional regulator ydHB	b1659	UNC	0.06
1737822	REC05028	<i>ydHB</i>	N	310	99	P37597	Hypothetical transport protein ydHC	b1660	UNC	0.59
1737935	REC01619	<i>ydHC</i>	N	403	147, 203, 306	P30010	Cyclopropane-fatty-acyl-phospholipid synthase (EC 2.1.1.79)	b1661	LPC	0.47
1739437	REC01620	<i>cfa</i>	N	382	127, 263, 302	P29015	Riboflavin synthase alpha chain (EC 2.5.1.9)	b1662	NCM	0.84
1741266	REC05029	<i>ribE</i>	E	213	-	P37340	Multidrug resistance protein norM	b1663	MTR	0.88
1741481	REC01622	<i>norM</i>	N	457	133, 335, 456	P77552	Hypothetical protein ydHQ	b1664	UNC	0.00
1744151	REC05030	<i>ydHQ</i>	N	418	260, 309, 310, 352, 405	P77225	Protein ydHR precursor	b1667	UNC	0.00
1744724	REC01624	<i>ydHR</i>	E	101	-	P77148	Hypothetical protein ydHS	b1668	UNC	0.00
1745155	REC01625	<i>ydHS</i>	N	534	27, 109, 189, 381, 382, 400	P77147	Hypothetical protein ydHT	b1669	UNC	0.00
1747583	REC05031	<i>ydHT</i>	N	270	78	P77409	PhsC protein homolog	b1670	UNC	0.00
1748372	REC05032	<i>ydHU</i>	N	261	77, 82, 194, 207	P77375	Putative ferredoxin-like protein ydHX	b1671	UNC	0.00
1749088	REC05033	<i>ydHX</i>	E	239	222	P77564	Hypothetical protein ydHW	b1672	UNC	0.00
1749748	REC05034	<i>ydHW</i>	?	215	15	P76192	Hypothetical protein ydHV	b1673	UNC	0.03
1751854	REC05035	<i>ydHV</i>	N	700	31, 173, 424, 665	P77186	Putative ferredoxin-like protein ydHY	b1674	UNC	0.00
1752501	REC05036	<i>ydHY</i>	N	208	36, 85, 186	P77274	Hypothetical protein ydHZ	b1675	UNC	0.00
1753165	REC05037	<i>ydHZ</i>	N	69	10, 29, 45, 64	P14178	Pyruvate kinase I (EC 2.7.1.40)	b1676	CHM	0.88
1753722	REC01633	<i>pykF</i>	N	470	139, 405	P02937	Major outer membrane lipoprotein precursor	b1677	LPC	0.00
1755445	REC01634	<i>lpp</i>	X	78	-	P76193	Hypothetical protein ynhG precursor	b1678	UNC	0.19
1756749	REC05038	<i>ynhG</i>	N	334	182	P76194	SufE protein	b1679	UNC	0.31
1757314	REC05039	<i>sufE</i>	N	138	105	P77444	Selenocysteine lyase (EC 4.4.1.16)	b1680	NCM	0.94
1758547	REC05040	<i>csdB</i>	N	406	103, 286, 300, 337, 345, 391	P77689	SufD protein	b1681	UNC	0.59
1759815	REC05041	<i>sufD</i>	N	423	64, 379	P77499	Probable ATP-dependent transporter sufC	b1682	UNC	0.59
1760536	REC05042	<i>sufC</i>	N	248	88, 118	P77522	SufB protein	b1683	UNC	0.59
1762072	REC05043	<i>sufB</i>	N	508	9, 88, 247	P77667	SufA protein	b1684	UNC	0.66
1762410	REC05044	<i>sufA</i>	E	122	122	P76195	Hypothetical protein ydIH	b1685	UNC	0.00
1763227	REC05045	<i>ydIH</i>	?	89	-	P77781	Hypothetical protein ydII	b1686	UNC	0.28
1763656	REC05046	<i>ydII</i>	E	136	-	P77748	Hypothetical protein ydIJ	b1687	UNC	0.16
1766709	REC05047	<i>ydIJ</i>	N	1018	19, 38, 59, 76, 273, 321, 361, 496	P77175	Hypothetical protein ydIK	b1688	UNC	0.69
1767098	REC01645	<i>ydIK</i>	N	370	127, 298	P76196	Hypothetical protein ydIL	b1689	UNC	0.00
1768612	REC01646	<i>ydIL</i>	N	127	60, 68	P76197	Hypothetical transport protein ydIM	b1690	UNC	0.06
1769095	REC01647	<i>ydIM</i>	N	404	55, 330, 365	P76198	Hypothetical transport protein ydIN	b1691	UNC	0.06
1770530	REC01648	<i>ydIN</i>	N	423	118, 151, 169, 195, 231, 262, 301, 322, 391	P28244	Hypothetical shikimate 5-dehydrogenase-like protein ydIB	b1692	UNC	0.88
1771813	REC01649	<i>ydIB</i>	N	288	131	P05194	3-dehydroquininate dehydratase (EC 4.2.1.10)	b1693	AAM	0.19
1772710	REC01650	<i>aroD</i>	N	252	14, 190, 223, 227	P37766	Hypothetical protein ydIF	b1694	UNC	0.22
1773611	REC01651	<i>ydIF</i>	N	531	14, 19, 82, 112, 132, 173, 210, 224, 255, 287, 289, 321, 330, 393, 508	P76200	Hypothetical protein ydIO	b1695	UNC	0.44
1775166	REC01652	<i>ydIO</i>	E	401	55	P77402	Hypothetical transcriptional regulator ydIP	b1696	UNC	0.31
1777325	REC05048	<i>ydIP</i>	N	303	54, 80, 84, 128, 174, 219	P76201	Putative electron transfer flavoprotein subunit ydIQ	b1697	UNC	0.09
1777641	REC01654	<i>ydIQ</i>	N	254	32, 128, 208					

1778425	REC01655	<i>ydiR</i>	E	312	19	< 0.05	P77378	Putative electron transfer flavoprotein subunit ydiR	b1698	UNC	0.31
1779419	REC01656	<i>ydiS</i>	N	429	10, 161		P77337	Probable electron transfer flavoprotein-quinone oxidoreductase yd	b1699	UNC	0.22
1780705	REC01657	<i>ydiT</i>	E	97	-	0.37	P77714	Ferredoxin-like protein ydiT	b1700	UNC	0.13
1781001	REC01658	<i>ydiD</i>	N	566	192, 198, 283, 427, 466, 510		P38135	Hypothetical protein ydiD	b1701	UNC	0.81
1785136	REC05049	<i>ppsA</i>	?	792	27, 51, 719, 778		P23538	Phosphoenolpyruvate synthase (EC 2.7.9.2)	b1702	CHM	0.53
1785469	REC01660	<i>ydiA</i>	N	277	34, 77, 104, 191		P03822	Hypothetical protein ydiA	b1703	UNC	0.47
1786459	REC01661	<i>aroH</i>	E	348	-	< 0.01	P00887	Phospho-2-dehydro-3-deoxyheptonate aldolase, Trp-sensitive (EC	b1704	AAM	0.41
1787637	REC01662	<i>ydiE</i>	?	63	-		P40721	Hypothetical protein ydiE	b1705	UNC	0.00
1789268	REC05050	<i>ydiU</i>	N	478	14, 162, 209, 359		P77649	Hypothetical protein ydiU	b1706	UNC	0.31
1790044	REC05051	<i>ydiV</i>	N	237	120, 163, 199		P76204	Hypothetical protein ydiV	b1707	UNC	0.00
1790755	REC05052	<i>nlpC</i>	N	154	6, 44, 66, 72, 91, 134		P23898	Probable lipoprotein nlpC precursor	b1708	UNC	0.19
1791582	REC05053	<i>btuD</i>	N	249	34, 128, 170, 181, 217, 223		P06611	Vitamin B12 transport ATP-binding protein btuD (EC 3.6.3.33)	b1709	NCM	0.03
1792133	REC05054	<i>btuE</i>	E	183	-	< 0.1	P06610	Vitamin B12 transport periplasmic protein btuE	b1710	UNC	0.38
1793176	REC05055	<i>btuC</i>	N	326	4, 95		P06609	Vitamin B12 transport system permease protein btuC	b1711	MTR	0.44
1793576	REC05056	<i>ihfA</i>	X	99	-		P06984	Integration host factor alpha-subunit	b1712	NAM	0.44
1795968	REC05057	<i>pheT</i>	?	795	480		P07395	Phenylalanyl-tRNA synthetase beta chain (EC 6.1.1.20)	b1713	PMS	1.00
1796966	REC05058	<i>pheS</i>	?	327	149		P08312	Phenylalanyl-tRNA synthetase alpha chain (EC 6.1.1.20)	b1714	PMS	1.00
1797773	REC05060	<i>rpmI</i>	E	118	-	< 0.2	P02421	50S ribosomal protein L20	b1716	PMS	1.00
1798023	REC05061	<i>rpmI</i>	?	65	56		P07085	50S ribosomal protein L35	b1717	PMS	0.28
1798662	REC05062	<i>infC</i>	E	180	-	< 0.05	P02999	Translation initiation factor IF-3	b1718	PMS	1.00
1800594	REC05063	<i>thrS</i>	E	642	-	< 0.001	P00955	Threonyl-tRNA synthetase (EC 6.1.1.3)	b1719	PMS	1.00
1801118	REC01677		N	157	13, 36, 44, 73, 110		P76205	Ankyrin-repeat protein B	b1720	UNC	0.00
1801602	REC01678	<i>arpB</i>	N	471	50, 124, 139, 163, 217, 385, 446		P76205	Ankyrin-repeat protein B	b1721	UNC	0.00
1804107	REC05064	<i>ydiY</i>	E	252	3	< 0.05	P76206	Hypothetical protein ydiY precursor	b1722	UNC	0.06
1804394	REC01680	<i>pkfB</i>	N	309	7, 29, 129, 197, 308		P06999	6-phosphofructokinase isozyme 2 (EC 2.7.1.11)	b1723	SMC	0.16
1805424	REC01681	<i>ydiZ</i>	E	96	-	< 0.3	P76207	Hypothetical protein ydiZ	b1724	UNC	0.00
1805820	REC01682	<i>yniA</i>	X	286	247		P77739	Hypothetical protein yniA	b1725	UNC	0.16
1807257	REC05065	<i>yniB</i>	N	178	126		P76208	Hypothetical protein yniB	b1726	UNC	0.00
1807404	REC01684	<i>yniC</i>	N	222	36, 147, 169, 189		P77247	Hypothetical protein yniC	b1727	UNC	0.16
1808223	REC01685	<i>ydiM</i>	N	200	57		P76209	Hypothetical protein ydiM precursor	b1728	UNC	0.06
1808958	REC01686	<i>ydiN</i>	N	463	12, 263, 377, 396		P77529	Hypothetical symporter ydiN	b1729	UNC	0.53
1811168	REC05066	<i>ydiO</i>	N	271	107, 218, 227		P76210	Hypothetical protein ydiO	b1730	UNC	0.00
1811708	REC05067	<i>cedA</i>	N	87	6, 44, 69		P76211	Cell division activator cedA	b1731	RCD	0.00
1811891	REC01689	<i>katE</i>	N	753	145, 230, 371, 460, 671, 679		P21179	Catalase HPii (EC 1.11.1.6)	b1732	MSM	0.50
1815159	REC05068	<i>ydjC</i>	N	249	55		P37794	Hypothetical protein ydjC	b1733	UNC	0.13
1816524	REC05069	<i>celF</i>	N	450	175, 228, 238, 318, 320, 366, 370, 397		P17411	6-phospho-beta-glucosidase (EC 3.2.1.86)	b1741	CHM	0.16
1817471	REC05070	<i>celD</i>	N	280	130		P17410	Cel operon repressor	b1735	RCD	0.06
1817829	REC05071	<i>celC</i>	E	116	94	< 0.3	P17335	PTS system, cellobiose-specific IIA component (EC 2.7.1.69)	b1736	MTR	0.22
1819238	REC05072	<i>celB</i>	N	452	11, 36, 115, 129, 170, 191		P17334	PTS system, cellobiose-specific IIC component	b1737	MTR	0.22
1819643	REC05073	<i>celA</i>	E	106	-	< 0.3	P17409	PTS system, cellobiose-specific IIB component (EC 2.7.1.69)	b1738	MTR	0.19
1820280	REC05074	<i>osmE</i>	X	112	-		P23933	Osmotically inducible lipoprotein E precursor	b1739	UNC	0.03
1820482	REC01697	<i>nadE</i>	E	275	-	< 0.05	P18843	NH(3)-dependent NAD(+) synthetase (EC 6.3.5.1)	b1740	NCM	0.91
1821539	REC01698	<i>ydjQ</i>	E	295	-	< 0.05	P76213	Hypothetical protein ydjQ	b1741	UNC	0.00
1823024	REC05075	<i>ydjR</i>	E	212	-	< 0.1	P76214	Hypothetical protein ydjR	b1742	UNC	0.19
1823649	REC05076	<i>spy</i>	N	161	13		P77754	Spheroplast protein Y precursor	b1743	UNC	0.03
1824947	REC05077	<i>astE</i>	?	322	250, 256, 294		P76215	Succinylglutamate desuccinylase (EC 3.1.-.-)	b1744	AAM	0.06
1826283	REC05078	<i>astB</i>	E	447	19	< 0.01	P76216	Succinylarginine dihydrolase (EC 3.-.-.-)	b1745	AAM	0.06
1827758	REC05079	<i>astD</i>	N	492	5, 121, 174, 309, 440		P76217	Succinylglutamic semialdehyde dehydrogenase (EC 1.2.1.-)	b1746	CHM	0.13
1828789	REC05080	<i>astA</i>	E	344	317	< 0.05	P76218	Arginine N-succinyltransferase (EC 2.3.1.109)	b1747	AAM	0.09
1830006	REC05081	<i>argM</i>	N	406	30, 100, 221, 228, 348		P77581	Succinylornithine transaminase (EC 2.6.1.-)	b1748	AAM	0.34
1830452	REC01706	<i>xthA</i>	N	268	90, 94, 214		P09030	Exodeoxyribonuclease III (EC 3.1.11.2)	b1749	NAM	0.81
1831377	REC01707	<i>ydjX</i>	N	252	41, 210, 224		P76219	Hypothetical protein ydjX	b1750	UNC	0.03
1831978	REC01708	<i>ydjY</i>	N	279	10, 24, 105		P76220	Hypothetical protein ydjY precursor	b1751	UNC	0.00
1832832	REC01709	<i>ydjZ</i>	N	235	4, 52		P76221	Hypothetical protein ydjZ	b1752	UNC	0.28
1833539	REC01710	<i>ynjA</i>	E	182	-	< 0.3	P76222	Hypothetical protein ynjA	b1753	UNC	0.09
1834094	REC01711	<i>ynjB</i>	N	389	249		P76223	Protein ynjB	b1754	UNC	0.09
1835281	REC01712	<i>ynjC</i>	N	496	3, 15, 395		P76224	Hypothetical ABC transporter permease protein ynjC	b1755	UNC	0.06
1836771	REC01713	<i>ynjD</i>	E	217	-	< 0.2	P76909	Hypothetical ABC transporter ATP-binding protein ynjD	b1756	UNC	0.06
1837476	REC01714	<i>ynjE</i>	N	440	195		P78067	Putative thiosulfate sulfurtransferase ynjE precursor (EC 2.8.1.1)	b1757	UNC	0.72
1839433	REC05082	<i>ynjF</i>	N	208	65		P76226	Hypothetical protein ynjF	b1758	UNC	0.09
1839514	REC01716	<i>nudG</i>	N	135	96		P77788	CTP pyrophosphorylase (EC 3.6.1.-)	b1759	NAM	0.38
1840159	REC05083	<i>ynjH</i>	N	90	62		P76227	Hypothetical protein ynjH precursor	b1760	UNC	0.00
1840395	REC01718	<i>gdhA</i>	N	447	46, 149, 278, 335		P00370	NADP-specific glutamate dehydrogenase (EC 1.4.1.4)	b1761	MSM	0.56
1843018	REC05084	<i>ynjI</i>	N	387	45, 121, 145, 195, 233, 243, 267, 278, 341, 356		P76228	Hypothetical protein ynjI	b1762	UNC	0.00
1844984	REC05085	<i>topB</i>	N	653	33, 120, 596		P14294	DNA topoisomerase III (EC 5.99.1.2)	b1763	NAM	0.25
1846032	REC05086	<i>seLD</i>	E	347	-	< 0.05	P16456	Selenide, water dikinase (EC 2.7.9.3)	b1764	MSM	0.16
1846700	REC05087	<i>ydjA</i>	E	183	-	< 0.1	P24250	Protein ydjA	b1765	UNC	0.31
1846861	REC01723	<i>sppA</i>	N	618	38, 239, 245, 271		P08395	Protease IV (EC 3.4.21.-)	b1766	PMS	0.78
1848884	REC01724	<i>ansA</i>	N	338	22, 37, 90, 173, 289, 298		P18840	L-asparaginase I (EC 3.5.5.1)	b1767	AAM	0.56
1848993	REC01725	<i>pncA</i>	N	219	112, 208		P21369	Pyrazinamidase/nicotinamidase	b1768	NCM	0.59
1852003	REC05088	<i>ydjE</i>	N	452	28, 84, 84, 137, 141, 165, 174, 217, 243, 281, 324, 338, 381, 444		P38055	Hypothetical metabolite transport protein ydjE	b1769	UNC	0.53
1852878	REC05089	<i>ydjF</i>	N	252	59, 120, 196, 242		P77721	Hypothetical transcriptional regulator ydjF	b1770	UNC	0.19
1853995	REC05090	<i>ydjG</i>	X	326	-		P77256	Hypothetical oxidoreductase ydjG (EC 1.-.-.-)	b1771	UNC	0.22
1854973	REC05091	<i>ydjH</i>	N	322	54, 83		P77493	Hypothetical sugar kinase ydjH	b1772	UNC	0.47
1855793	REC05092	<i>ydjI</i>	N	278	14, 116, 141, 202, 244		P77704	Hypothetical protein ydjI	b1773	UNC	0.00
1856857	REC05093	<i>ydjJ</i>	N	347	75, 265, 283, 298		P77280	Hypothetical zinc-type alcohol dehydrogenase-like protein ydjJ	b1774	UNC	0.56
1858253	REC05094	<i>ydjK</i>	N	459	397		P76230	Hypothetical metabolite transport protein ydjK	b1775	UNC	0.53
1859356	REC05095	<i>ydjL</i>	X	358	-		P77539	Hypothetical zinc-type alcohol dehydrogenase-like protein ydjL	b1776	UNC	0.09
1860043	REC05096	<i>yeaC</i>	X	105	-		P76231	Hypothetical protein yeaC	b1777	UNC	0.06
1860453	REC05097	<i>msrB</i>	X	137	-		P39903	Peptide methionine sulfoxide reductase msrB (EC 1.8.4.6)	b1778	PMS	0.78
1860795	REC01736	<i>gapA</i>	E	331	-	< 0.1	P06977	Glyceraldehyde 3-phosphate dehydrogenase A (EC 1.2.1.12)	b1779	CHM	0.97
1861853	REC01737	<i>yeaD</i>	N	301	209		P39173	Unknown protein from 2D-page	b1780	UNC	0.19
1863660	REC05098	<i>yeaE</i>	N	284	177, 212, 267		P76234	Hypothetical protein yeaE	b1781	UNC	0.19
1864496	REC05099	<i>miPA</i>	N	248	139, 188		P77486	MitA-interacting protein precursor	b1782	UNC	0.09
1864932	REC01740	<i>yeaG</i>	N	644	32, 296, 352, 422, 500		P77391	Hypothetical protein yeaG	b1783	UNC	0.19
1866979	REC01741	<i>yeaH</i>	N	427	278, 332, 339, 353, 367, 416		P76235	Hypothetical protein yeaH	b1784	UNC	0.59
1868409	REC01742	<i>yeaI</i>	N	491	142, 277, 295, 298, 343, 362, 368, 413, 487		P76236	Hypothetical protein yeaI	b1785	UNC	0.59
1869885	REC01743	<i>yeaJ</i>	N	556	48, 77, 185, 203, 242, 316, 554		P76237	Hypothetical protein yeaJ	b1786	UNC	0.59
1871598	REC01744	<i>yeaK</i>	N	167	9, 14, 37, 105, 162		P76238	Hypothetical protein yeaK	b1787	UNC	0.00
1872254	REC05100		?	50	-		P76239	FROM BASES 1860594 TO 1872342 (SECTION 163 OF 400) OF	b1788	UNC	0.00
1872376	REC01746	<i>yeaL</i>	N	148	15, 30, 56, 97, 129		P76240	Hypothetical protein yeaL	b1789	UNC	0.16
1873600	REC05101	<i>yeaM</i>	N	273	157, 239		P76241	Hypothetical transcriptional regulator yeaM	b1790	UNC	0.28
1873697	REC01748	<i>yeaN</i>	E	393	-	< 0.001	P76242	Hypothetical transport protein yeaN	b1791	UNC	0.53

1874912	REC01749	<i>yeaO</i>	E	122	-	< 0.2	P76243	Hypothetical protein yeaO	b1792	UNC	0.25
1875556	REC05102	<i>yoaF</i>	?	84	-		P76244	Hypothetical protein yoaF	b1793	UNC	0.00
1875610	REC01751	<i>yeaP</i>	N	384	193, 232, 286, 299, 336, 378		P76245	Hypothetical protein yeaP	b1794	UNC	0.00
1877279	REC05103	<i>yeaQ</i>	N	82	6, 14, 67, 79		P76246	Hypothetical protein yeaQ	b1795	UNC	0.00
1877609	REC05104	<i>yoaG</i>	?	60	-		P76247	Hypothetical protein yoaG	b1796	UNC	0.09
1877972	REC05105	<i>yeaR</i>	X	119	-		P76248	Hypothetical protein yeaR	b1797	UNC	0.00
1878783	REC05106	<i>yeaS</i>	X	212	-		P76249	Hypothetical protein yeaS	b1798	UNC	0.41
1879854	REC05107	<i>yeaT</i>	X	314	-		P76250	Hypothetical transcriptional regulator yeaT	b1799	UNC	0.72
1879936	REC01757	<i>yeaU</i>	X	361	-		P76251	Probable tartrate dehydrogenase (EC 1.1.1.93)	b1800	UNC	0.28
1881212	REC01758	<i>yeaV</i>	X	481	-		P76252	Probable transport protein yeaV	b1801	UNC	0.19
1882689	REC01759	<i>yeaW</i>	X	374	-		P76253	Putative dioxygenase alpha subunit yeaW (EC 1.14.1.-)	b1802	UNC	0.31
1883869	REC01760	<i>yeaX</i>	X	321	-		P76254	Putative dioxygenase beta subunit yeaX (EC 1.-.-.-)	b1803	UNC	0.25
1886015	REC05108	<i>rnd</i>	N	375	76		P09155	Ribonuclease D (EC 3.1.26.3)	b1804	NAM	0.47
1887770	REC05109	<i>fadD</i>	N	561	178, 399, 451, 533		P29212	Long-chain-fatty-acid-CoA ligase (EC 6.2.1.3)	b1805	LPC	0.84
1888556	REC05110	<i>yeaY</i>	N	193	144		P76255	Hypothetical lipoprotein yeaY precursor	b1806	UNC	0.09
1889291	REC05111	<i>yeaZ</i>	E	231	-	< 0.2	P76256	Hypothetical protease yeaZ (EC 3.4.--)	b1807	UNC	1.00
1891259	REC05112	<i>yoaA</i>	N	636	2, 134, 284, 474, 566		P76257	Probable ATP-dependent helicase yoaA	b1808	UNC	0.47
1891343	REC01766	<i>yoaB</i>	E	130	-	0.34	P76258	Hypothetical protein yoaB	b1809	UNC	0.81
1892097	REC01767	<i>yoaC</i>	N	119	3, 31, 55, 89, 107		P76259	Hypothetical protein yoaC	b1810	UNC	0.00
1892755	REC05113	<i>yoaH</i>	N	59	27, 50		P76260	Hypothetical protein yoaH	b1811	UNC	0.06
1892829	REC01769	<i>pabB</i>	N	453	41, 125		P05041	Para-aminobenzoate synthase component I (EC 4.1.3.-)	b1812	NCM	0.72
1894194	REC01770	<i>yeaB</i>	X	192	-		P43337	Hypothetical protein yeaB	b1813	UNC	0.38
1894956	REC01771	<i>sdaA</i>	N	454	311		P16095	L-serine dehydratase 1 (EC 4.2.1.13)	b1814	AAM	0.66
1896421	REC01772	<i>yoaD</i>	N	542	220, 310		P76261	Hypothetical protein yoaD	b1815	UNC	0.31
1896909	REC05114	<i>yoaE</i>	N	518	71, 260, 390, 446		P76262	Hypothetical protein yoaE	b1816	UNC	0.84
1900072	REC01774	<i>manX</i>	N	323	173, 182		P08186	PTS system, mannose-specific IIAB component (EC 2.7.1.69)	b1817	CHM	0.31
1901106	REC01775	<i>manY</i>	N	266	208		P08187	PTS system, mannose-specific IIC component	b1818	MTR	0.16
1901910	REC01776	<i>manZ</i>	N	286	74, 78, 147, 219, 252		P08188	PTS system, mannose-specific IID component	b1819	MTR	0.16
1902825	REC01777	<i>yobD</i>	N	152	42, 67, 72, 115		P76263	Hypothetical protein yobD	b1820	UNC	0.03
1903658	REC01778	<i>yebN</i>	N	206	139		P76264	Hypothetical protein yebN	b1821	UNC	0.25
1905084	REC05115	<i>rxmA</i>	X	269	-		P36999	Ribosomal RNA large subunit methyltransferase A (EC 2.1.1.51)	b1822	NAM	0.22
1905459	REC05116	<i>cspC</i>	X	69	-		P36996	Cold shock-like protein cspC	b1823	UNC	0.72
1905615	REC05117	<i>yobF</i>	?	47	-		P76265	Hypothetical protein yobF	b1824	UNC	0.00
1906572	REC05118	<i>yebO</i>	N	95	65		P76266	Hypothetical protein yebO	b1825	UNC	0.00
1906790	REC05119	<i>yobG</i>	?	47	-		P76267	Hypothetical protein yobG	b1826	UNC	0.00
1908123	REC05120	<i>kdgR</i>	N	263	229, 236		P76268	Transcriptional regulator kdgR	b1827	RCD	0.41
1908189	REC01785	<i>yebQ</i>	N	494	443, 474		P76269	Hypothetical transport protein yebQ	b1828	UNC	0.31
1910600	REC05121	<i>htpX</i>	N	293	133, 157, 175, 178		P23894	Probable protease htpX (EC 3.4.24.-)	b1829	UNC	0.63
1912840	REC05122	<i>prc</i>	N	682	21, 51, 238, 482, 682		P23865	Tail-specific protease precursor (EC 3.4.21.-)	b1830	MSM	0.84
1912979	REC05123	<i>proQ</i>	?	39	-		P45571	ProP effector	b1831	UNC	0.09
1914206	REC05124	<i>yebR</i>	N	183	77		P76270	Protein yebR	b1832	UNC	0.38
1914282	REC01790	<i>yebS</i>	N	427	75, 194, 389		P76271	Hypothetical protein yebS	b1833	UNC	0.13
1915528	REC01791	<i>yebT</i>	N	879	265, 293, 316, 404, 433, 531, 608, 690, 777		P76272	Hypothetical protein yebT	b1834	UNC	0.16
1918241	REC01792	<i>yebU</i>	N	481	77, 132, 240, 415, 429		P76273	Hypothetical protein yebU	b1835	UNC	0.09
1919789	REC01793	<i>yebV</i>	?	83	69		P76274	Hypothetical protein yebV	b1836	UNC	0.00
1920061	REC01794	<i>yebW</i>	N	91	20		P76275	Hypothetical protein yebW	b1837	UNC	0.00
1920996	REC05125	<i>ppha</i>	N	219	124		P55798	Serine/threonine protein phosphatase 1 (EC 3.1.3.16)	b1838	PMS	0.16
1921730	REC05126	<i>yebY</i>	E	113	-	0.37	P76277	Hypothetical protein yebY precursor	b1839	UNC	0.00
1922615	REC05127	<i>yebZ</i>	N	290	57, 180, 198		P76278	Hypothetical protein yebZ	b1840	UNC	0.06
1922993	REC05128	<i>yobA</i>	N	124	42		P76279	Protein yobA precursor	b1841	UNC	0.00
1923132	REC01799	<i>hoLE</i>	?	76	-		P28689	DNA polymerase III, theta subunit (EC 2.7.7.7)	b1842	NAM	0.00
1923464	REC01800	<i>yobB</i>	N	218	33, 68		P76280	Hypothetical protein yobB	b1843	UNC	0.00
1924144	REC01801	<i>exoX</i>	N	220	42		P76281	Exodeoxyribonuclease X (EC 3.1.11.-)	b1844	NAM	0.00
1926863	REC05129	<i>ptrB</i>	N	686	403, 578, 604, 654		P24555	Protease II (EC 3.4.21.83)	b1845	PMS	0.47
1927731	REC05130	<i>yebE</i>	E	219	-	< 0.2	P33218	Hypothetical protein yebE	b1846	UNC	0.22
1928426	REC05131	<i>yebF</i>	N	122	72, 107, 115		P33219	Hypothetical lipoprotein yebF precursor	b1847	UNC	0.00
1928771	REC05132	<i>yebG</i>	E	96	-	0.46	P33220	Hypothetical protein yebG	b1848	UNC	0.06
1928905	REC01806	<i>purT</i>	N	392	66, 116		P33221	Phosphoribosylglycinamide formyltransferase 2 (EC 2.1.2.-)	b1849	NCM	0.22
1930780	REC05133	<i>eda</i>	N	213	70, 109, 186		P10177	KHG/KDPG aldolase	b1850	CHM	0.63
1932628	REC05134	<i>edd</i>	N	603	163, 250, 341, 410, 426, 568		P25530	Phosphogluconate dehydratase (EC 4.2.1.12)	b1851	CHM	0.34
1934338	REC05135	<i>zwf</i>	E	491	-	< 0.01	P22992	Glucose-6-phosphate 1-dehydrogenase (EC 1.1.1.49)	b1852	CHM	0.84
1934676	REC01810	<i>hexR</i>	N	289	68, 87, 172, 268		P46118	Hex regulon repressor	b1853	RCD	0.34
1935673	REC01811	<i>pykA</i>	N	480	254, 286, 408, 477		P21599	Pyruvate kinase II (EC 2.7.1.40)	b1854	CHM	0.88
1938217	REC05136	<i>msbB</i>	N	323	201, 260		P24205	Lipid A biosynthesis (KDO)2-(lauroyl)-lipid IVA acyltransferase (EC b1855)	b1855	LPC	0.22
1939596	REC05137	<i>yebA</i>	N	419	110, 223, 302		P24204	Hypothetical protein yebA precursor	b1856	UNC	0.72
1940661	REC05138	<i>znuA</i>	N	328	31, 49, 68		P39172	High-affinity zinc uptake system protein znuA precursor	b1857	MTR	0.56
1940686	REC01815	<i>znuC</i>	N	251	154		P52648	High-affinity zinc uptake system ATP-binding protein znuC	b1858	MTR	0.91
1941438	REC01816	<i>znuB</i>	N	261	24, 84, 207		P39832	High-affinity zinc uptake system membrane protein znuB	b1859	MTR	0.69
1943380	REC05139	<i>ruvB</i>	N	336	22, 332		P08577	Holliday junction DNA helicase ruvB	b1860	NAM	0.94
1944000	REC05140	<i>ruvA</i>	N	203	2, 24, 141, 152		P08576	Holliday junction DNA helicase ruvA	b1861	NAM	0.94
1944176	REC01819	<i>yebB</i>	N	233	55, 112, 155, 205		P24238	Hypothetical protein yebB	b1862	UNC	0.00
1945400	REC05141	<i>ruvC</i>	E	173	-	< 0.2	P24239	Crossover junction endodeoxyribonuclease ruvC (EC 3.1.22.4)	b1863	NAM	0.72
1946175	REC05142	<i>yebC</i>	E	246	-	< 0.05	P24237	Protein yebC	b1864	UNC	0.88
1946656	REC05143	<i>nudB</i>	E	150	-	< 0.2	P24236	dATP pyrophosphohydrolase (EC 3.6.1.-)	b1865	NCM	0.09
1948546	REC05144	<i>aspS</i>	E	590	-	< 0.001	P21889	Aspartyl-tRNA synthetase (EC 6.1.1.12)	b1866	PMS	1.00
1948823	REC01824	<i>yecD</i>	N	199	22, 67		P37347	Hypothetical isochorismatase family protein yecD	b1867	UNC	0.38
1949419	REC01825	<i>yecE</i>	N	272	24, 211, 213		P37348	Hypothetical protein yecE	b1868	UNC	0.31
1950260	REC01826	<i>yecN</i>	N	141	35, 40, 71		P76289	Hypothetical protein yecN	b1869	UNC	0.06
1950726	REC01827	<i>yecO</i>	N	247	112		P76290	Protein yecO	b1870	UNC	0.16
1951466	REC01828	<i>yecP</i>	E	323	282	< 0.1	P76291	Hypothetical protein yecP	b1871	UNC	0.19
1955049	REC05145	<i>torZ</i>	N	815	127, 158, 300, 353		P46923	Trimethylamine-N-oxide reductase 2 precursor (EC 1.6.6.9)	b1872	SMC	0.09
1956156	REC05146	<i>torY</i>	N	366	2, 45, 115, 337		P52005	Cytochrome c-type protein torY	b1873	SMC	0.06
1956984	REC05147	<i>cutC</i>	E	146	-	0.39	P46719	Copper homeostasis protein cutC	b1874	UNC	0.28
1957876	REC05148	<i>yecM</i>	N	190	65		P52007	Protein yecM	b1875	UNC	0.06
1958086	REC01833	<i>args</i>	E	577	-	< 0.05	P11875	Arginyl-tRNA synthetase (EC 6.1.1.19)	b1876	PMS	1.00
1959975	REC01834	<i>yecT</i>	N	169	24, 32		P76296	Hypothetical protein yecT	b1877	UNC	0.00
1960996	REC05149	<i>flhE</i>	N	130	-		P76297	Flagellar protein flhE precursor	b1878	UNC	0.00
1963074	REC05150	<i>flhA</i>	N	692	-		P76298	Flagellar biosynthesis protein flhA	b1879	SMC	0.59
1964215	REC05151	<i>flhB</i>	N	382	129, 154, 266		P76299	Flagellar biosynthesis protein flhB	b1880	SMC	0.59
1965061	REC05152	<i>cheZ</i>	N	214	114		P07366	Chemotaxis protein cheZ	b1881	SMC	0.09
1965461	REC05153	<i>cheY</i>	N	129	62		P06143	Chemotaxis protein cheY	b1882	SMC	0.50
1966525	REC05154	<i>cheB</i>	?	349	25		P07330	Protein-glutamate methyltransferase (EC 3.1.1.61)	b1883	SMC	0.44
1967388	REC05155	<i>cheR</i>	E	286	-	< 0.05	P				

1969008	REC05156	tap	N	533	54, 161, 205, 213, 320, 349, 481		P07018	Methyl-accepting chemotaxis protein IV	b1885	SMC	0.63
1970715	REC05157	tar	N	553	10, 40, 58, 82, 115, 145, 190, 220, 229, 351, 436, 446, 488		P07017	Methyl-accepting chemotaxis protein II	b1886	SMC	0.63
1971363	REC05158	cheW	E	167	166	< 0.1	P07365	Chemotaxis protein cheW	b1887	SMC	0.41
1973348	REC05159	cheA	N	654	90, 186, 233, 319, 322, 515, 527		P07363	Chemotaxis protein cheA (EC 2.7.3.-)	b1888	MSM	0.56
1974279	REC05160	motB	N	308	168, 283		P09349	Chemotaxis motB protein	b1889	SMC	0.50
1975163	REC05161	motA	E	295	-	< 0.05	P09348	Chemotaxis motA protein	b1890	SMC	0.53
1975868	REC05162	flhC	N	192	108		P11165	Flagellar transcriptional activator flhC	b1891	RCD	0.03
1976230	REC05163	flhD	N	119	14, 20, 67		P11164	Flagellar transcriptional activator flhD	b1892	RCD	0.03
1977045	REC06654	insB6	N	167	67, 158		P03830	Insertion element IS1 1/5/6 protein insB	b3445	PHT	0.00
1977239	REC06655	insA6	X	91	-		P03827	Insertion element IS1 1/2/3/5/6 protein insA	b3444	PHT	0.00
1977777	REC01852	yecG	E	142	-	0.33	P46888	Hypothetical protein yecG	b1895	UNC	0.06
1979636	REC05166	otsA	N	474	-		P31677	Alpha, alpha-trehalose-phosphatase [UDP-forming] (EC 2.4.1.3)	b1896	CHM	0.19
1980411	REC05167	otsB	N	266	-		P31678	Trehalose-phosphatase (EC 3.1.3.12)	b1897	CHM	0.13
1980838	REC05168	araH	N	86	-		P08532	L-arabinose transport system permease protein araH	b1898	MTR	0.00
1981566	REC05169	araG	N	234	14, 74, 205, 214		P08531	L-arabinose transport system permease protein araG	b1900	MTR	0.13
1983092	REC05170	araF	E	504	-	< 0.01	P08531	L-arabinose transport ATP-binding protein araG	b1900	MTR	0.06
1984151	REC05171	araF	E	329	174, 308	< 0.05	P02924	L-arabinose-binding periplasmic protein precursor	b1901	MTR	0.09
1984948	REC01859	ftnB	N	167	18, 47, 70, 124		P52091	Ferritin-like protein 2	b1902	UNC	0.00
1985467	REC01860	ftnA	N	112	65		P67307	FROM BASES 1975196 TO 1986052 (SECTION 173 OF 400) OF	b1903	UNC	0.00
1986245	REC01861	yecR	N	107	66		P76308	Hypothetical protein yecR	b1904	UNC	0.00
1986739	REC01862	ftnA	N	165	51, 76, 153		P23887	Ferritin 1	b1905	NCM	0.00
1987513	REC05172	yecH	?	79	-		P46887	Hypothetical protein yecH	b1906	UNC	0.00
1987704	REC01864	tyrP	N	403	10, 34, 56, 223, 244, 334, 335, 360		P18199	Tyrosine-specific transport protein	b1907	MTR	0.16
1988642	REC05173	yecA	N	221	166		P06979	Hypothetical protein yecA	b1908	UNC	0.09
1990840	REC05174	pgsA	E	182	-	< 0.1	P06978	CDP-diaclylglycerol-glycerol-3-phosphate 3-phosphatidyltransferase	b1912	LPC	0.94
1992663	REC05175	uvrC	N	588	94, 145, 163, 257, 297, 442		P70728	Excinuclease ABC subunit C	b1913	NAM	0.97
1993382	REC05176	uvrY	N	218	8, 38, 96, 147, 173		P07027	UvrY protein	b1914	UNC	0.31
1993841	REC01869	yecF	N	74	1, 13, 69		P46120	Hypothetical protein yecF	b1915	UNC	0.00
1994855	REC05177	sdiA	N	240	51, 55, 74, 80, 97, 106, 118, 204		P07026	Regulatory protein sdiA	b1916	RCD	0.19
1995837	REC05178	yecC	N	250	27, 106, 194		P37774	Hypothetical amino-acid ABC transporter ATP-binding protein yecC	b1917	UNC	0.34
1996502	REC05179	yecS	N	222	47, 170, 207		P76315	Hypothetical amino-acid ABC transporter permease protein yecS	b1918	UNC	0.66
1997599	REC05180	yedO	X	360	-		P76316	Putative 1-aminocyclopropane-1-carboxylate deaminase (EC 4.1.1.5)	b1919	UNC	0.19
1998408	REC05181	fliY	?	266	17		P39174	Cystine-binding periplasmic protein precursor	b1920	MTR	0.53
1999083	REC05182	fliZ	N	195	24, 165, 190		P52627	Fliz protein	b1921	UNC	0.00
1999812	REC05183	fliA	N	239	50, 84, 127, 154		P31804	RNA polymerase sigma factor for flagellar operon	b1922	RCD	0.44
2001629	REC05184	fliC	N	498	17, 21, 43, 114, 130, 166, 212, 297, 414		P04949	Flagellin	b1923	SMC	0.53
2001895	REC01878	fliD	N	468	24, 62, 139, 166, 208, 278, 325, 465		P24216	Flagellar hook-associated protein 2	b1924	SMC	0.28
2003326	REC01879	fliS	N	136	61		P26608	Flagellar protein flis	b1925	UNC	0.31
2003736	REC01880	fliT	N	121	73		P26610	Flagellar protein flit	b1926	UNC	0.00
2004179	REC01881	amyA	N	495	68, 115, 154, 165, 173, 200, 233, 240, 283, 335, 358, 391, 405, 425		P26612	Cytoplasmic alpha-amylase (EC 3.2.1.1)	b1927	CHM	0.09
2006113	REC05185	yedD	N	137	94		P31063	Hypothetical lipoprotein yedD precursor	b1928	UNC	0.00
2006300	REC01883	yedE	E	401	249	< 0.001	P31064	Hypothetical protein yedE	b1929	UNC	0.06
2007502	REC01884	yedF	N	77	50		P31065	Hypothetical protein yedF	b1930	UNC	0.09
2007844	REC01885	yedK	?	217	152		P76318	Hypothetical protein yedK	b1931	UNC	0.22
2008622	REC01886	yedL	N	159	18, 34, 77, 110, 142		P76319	Hypothetical acetyltransferase yedL (EC 2.3.1.-)	b1932	UNC	0.19
2009561	REC05186	yedN	?	63	-		P76321	Hypothetical protein yedN	b1933	UNC	0.00
2009891	REC05187	yedM	N	106	20		P76321	Hypothetical protein yedM	b1935	UNC	0.00
2010373	REC05188	yedM	N	116	56		P76322	FROM BASES 2008529 TO 2019581 (SECTION 176 OF 400) OF	b1936	UNC	0.00
2010524	REC01890	fliE	X	104	-		P25797	Flagellar hook-basal body complex protein flie	b1937	SMC	0.28
2011036	REC05189	fliE	X	104	-		P25798	Flagellar M-ring protein	b1938	SMC	0.56
2011251	REC01892	fliF	N	552	183, 226, 452		P31067	Flagellar motor switch protein flig	b1939	SMC	0.56
2012902	REC01893	fliG	N	331	92, 211, 261		P31068	Flagellar assembly protein flih	b1940	SMC	0.13
2013869	REC01894	fliH	N	235	106, 167		P52612	Flagellum-specific ATP synthase (EC 3.6.3.14)	b1941	SMC	1.00
2014576	REC01895	fliI	N	457	195, 269, 408		P52613	Flagellar flj protein	b1942	SMC	0.09
2015968	REC01896	fliJ	E	147	146	< 0.3	P52614	Flagellar hook-length control protein	b1943	SMC	0.13
2016408	REC01897	fliK	N	375	62, 136, 221, 244, 328, 338		P06973	Flagellar flil protein	b1944	SMC	0.28
2017640	REC01898	fliL	E	154	-	< 0.2	P06974	Flagellar motor switch protein flim	b1945	SMC	0.53
2018109	REC01899	fliM	N	334	27, 195, 245		P15070	Flagellar motor switch protein flin	b1946	SMC	0.56
2019110	REC01900	fliN	E	137	-	< 0.2	P22586	Flagellar protein flio	b1947	SMC	0.06
2019586	REC01901	fliO	N	101	42		P33133	Flagellar biosynthetic protein flip precursor	b1948	UNC	0.59
2019891	REC01902	fliP	N	245	10, 32, 217		P33134	Flagellar biosynthetic protein fliq	b1949	SMC	0.41
2020638	REC01903	fliQ	N	89	48		P33135	Flagellar biosynthetic protein flir	b1950	SMC	0.53
2020915	REC01904	fliR	N	261	184, 233		P24210	Colanic acid capsular biosynthesis activation protein A	b1951	SMC	0.00
2021990	REC01905	rcaS	N	207	12, 83, 142		P76328	Hypothetical protein yodD	b1953	UNC	0.00
2022993	REC01907	yodD	?	80	-		P76329	Hypothetical protein yodP	b1955	UNC	0.00
2023533	REC01908	yedP	N	271	53, 55, 153		P76330	Hypothetical protein yodQ	b1956	UNC	0.22
2026054	REC05191	yedQ	N	569	74, 87		P76331	Hypothetical protein yodC	b1957	UNC	0.00
2026392	REC05192	yodC	?	60	-		P46125	Hypothetical protein yodI	b1958	UNC	0.25
2027388	REC05193	yedI	N	305	74, 211, 239, 298		P09185	Hypothetical transport protein yedA	b1959	UNC	0.16
2027561	REC01912	yedA	N	306	125		P09184	Very short patch repair protein (EC 3.1.-.-)	b1960	UNC	0.09
2028940	REC05194	vsr	N	156	90		P11876	DNA-cytosine methyltransferase (EC 2.1.1.73)	b1961	NAM	0.16
2030339	REC05195	dcm	E	472	452	< 0.01	P46144	Hypothetical protein yedJ	b1962	UNC	0.19
2031101	REC05196	yedJ	N	231	3, 26, 170		P76334	Hypothetical protein yedR	b1963	UNC	0.00
2031524	REC05197	yedR	?	127	5		P76335	Potential outer membrane protein yedS precursor	b1964	UNC	0.00
2032043	REC01917	yedS	N	171	79, 85, 106, 118		P76335	Potential outer membrane protein yedS precursor	b1965	UNC	0.00
2032568	REC01918	yedT	?	69	-		P76335	DE: POTENTIAL OUTER MEMBRANE PROTEIN YEDS PRECURSOR	b1966	UNC	0.00
2032861	REC01919	yedU	N	134	79, 129		P31658	Protein yedU	b1967	UNC	0.16
2033857	REC01920	yedU	N	283	3, 22, 44, 67, 98, 162, 228, 279		P76339	Putative sensor-like histidine kinase yedV (EC 2.7.3.-)	b1968	UNC	0.03
2036174	REC05198	yedV	N	452	397, 438		P76340	Probable transcriptional regulatory protein yedW	b1969	UNC	0.81
2036893	REC05199	yedW	N	239	-		P76341	Transthyretin-like protein precursor	b1970	UNC	0.31
2036978	REC01923	yedX	N	137	-		P76342	Hypothetical protein yedY	b1971	UNC	0.31
2037500	REC01924	yedY	N	334	-		P76343	Hypothetical protein yedZ	b1972	UNC	0.25
2038505	REC01925	yedZ	N	211	135, 173, 189		P76344	Hypothetical protein yodA	b1973	UNC	0.13
2039397	REC01926	yodA	N	216	54, 61, 127, 208		P76345	Cytochrome b561 homolog 1	b1974	UNC	0.31
2040360	REC01927	yodB	N	186	37, 104, 115, 154		P76346	Hypothetical protein yee	b1976	UNC	0.13
2041634	REC01928	yeeI	E	278	259	< 0.05	P76347	Hypothetical protein yeeJ	b1978	UNC	0.00
2042885	REC01929	yeeJ	N	2383	69, 219, 370, 463, 595, 645, 758, 963, 1084, 1198, 1243, 1381, 1419, 1611		P76349	Hypothetical protein yeeL	b1979	UNC	0.00
2050624	REC05200	yeeK	?	108	80		P76349	Hypothetical protein yeeL	b1980	UNC	0.00
2051350	REC05201	yeeL	X	234	-		P76350	Shikimate transporter	b1981	MTR	0.41
2051665	REC01932	shIA	N	438	315, 360, 378		P15272	AMP nucleosidase (EC 3.2.2.4)	b1982	NCM	0.28
2053083	REC01933	amn	N	484	24, 60, 82, 117, 285, 293, 406, 424		P76351	Hypothetical protein yeeN	b1983	UNC	0.16
2054880	REC01934	yeeN	N	238	79		P76352	Hypothetical protein yeeO	b1985	UNC	0.22
2057868	REC06488	yeeO	?	547	-						

2058936	REC05203	cbI	X	316	-		Q47083	Transcriptional regulator cbI	b1987	UNC	0.72
2059955	REC05204	nac	N	305	188, 265		Q47005	Nitrogen assimilation regulatory protein nac	b1988	RCD	0.16
2061345	REC05205	erfK	N	310	94, 251		P39176	Protein erfK/srfK precursor	b1990	UNC	0.19
2062489	REC05206	cobT	N	359	97, 117, 271, 323		P36562	Nicotinate-nucleotide-dimethylbenzimidazole phosphoribosyltrans	b1991	NCM	0.41
2063244	REC05207	cobS	N	247	194		P36561	Cobalamin [5'-phosphate] synthase (EC 2.-.-.)	b1992	NCM	0.38
2063786	REC05208	cobU	N	181	13, 61		P46886	Bifunctional cobalamin biosynthesis protein cobU	b1993	NCM	0.47
2065343	REC05209		N	338	247		P03837	Transposase insH for insertion sequence element IS5	b1994	PHT	0.34
2066630	REC01943		X	139	-		P76356	O139	b1995	UNC	0.00
2067879	REC00345	insD3	X	301	-		P19777	Transposase insD for insertion element IS2A/D/F/H/I/K	b1996	PHT	0.56
2068247	REC05211	insC3	X	136	-		P19776	Transposase insC for insertion element IS2A/D/F/H/I/K	b1997	PHT	0.56
2068266	REC01946		X	86	-		P76358	FROM BASES 2060088 TO 2072764 (SECTION 181 OF 400) OF	b1998	UNC	0.00
2068523	REC01947	yeeP	N	236	106, 136		P76359	Hypothetical protein yeeP	b1999	UNC	0.00
2069405	REC01948	flu	N	1091	74, 169, 201, 287, 359, 679, 811, 1003, 1077		P39180	Antigen 43 precursor	b2000	UNC	0.00
2072795	REC01949	yeeR	N	512	162, 477		P76361	Hypothetical protein yeeR	b2001	UNC	0.00
2074330	REC01950	yeeS	N	148	42, 97		P76362	Putative radC-like protein yeeS	b2002	UNC	0.00
2074839	REC01951	yeeT	N	73	45		P76363	Hypothetical protein yeeT	b2003	UNC	0.00
2075134	REC01952	yeeU	N	122	89, 103		P76364	Hypothetical protein yeeU	b2004	UNC	0.00
2075591	REC01953	yeeV	E	124	110	< 0.3	P76365	Hypothetical protein yeeV	b2005	UNC	0.00
2075962	REC01954	yeeW	?	64	61		P76366	Hypothetical protein yeeW	b2006	UNC	0.00
2077449	REC05212	yeeX	N	131	15, 49, 81, 96		P76367	Hypothetical protein yeeX	b2007	UNC	0.13
2078613	REC05213	yeeA	N	352	140, 146, 290		P33011	Hypothetical protein yeeA	b2008	UNC	0.06
2079284	REC05214	gyrI	E	157	-	< 0.2	P33012	DNA gyrase inhibitory protein	b2009	RCD	0.00
2080575	REC05215	dacD	N	390	66, 108, 309		P33013	Penicillin-binding protein 6B precursor (EC 3.4.16.4)	b2010	LPC	0.72
2080778	REC01959	sbcB	N	475	52, 145, 151, 227, 266		P04995	Exodeoxyribonuclease I (EC 3.1.11.1)	b2011	NAM	0.19
2082475	REC05216	yeeD	?	75	-		P33014	Hypothetical protein yeeD	b2012	UNC	0.09
2083547	REC05217	yeeE	N	352	291		P33015	Hypothetical protein yeeE	b2013	UNC	0.09
2085090	REC05218	yeeF	X	454	-		P33016	Hypothetical transport protein yeeF	b2014	UNC	0.34
2086301	REC05219	yeeY	X	316	-		P76369	Hypothetical transcriptional regulator yeeY	b2015	UNC	0.72
2087150	REC05220	yeeZ	N	274	12, 52, 109, 137, 191, 221		P76370	Protein yeeZ precursor	b2016	UNC	0.25
2087487	REC06686	yoeB	?	84	-		P56605	Hypothetical protein yoeB	UNC	0.19	
2087762	REC05221	yefM	X	92	69		P46147	Hypothetical protein yefM	b2017	UNC	0.16
2088214	REC01967	hisG	X	299	-		P10366	ATP phosphoribosyltransferase (EC 2.4.2.17)	b2019	AAM	0.75
2089119	REC01968	hisD	N	434	132, 171, 237, 335		P06988	Histidinol dehydrogenase (EC 1.1.1.23)	b2020	AAM	0.75
2090420	REC01969	hisC	N	356	7, 141, 201		P06986	Histidinol-phosphate aminotransferase (EC 2.6.1.9)	b2021	AAM	0.78
2091487	REC01970	hisB	N	356	94, 177, 272		P06987	Histidine biosynthesis bifunctional protein hisB	b2022	AAM	0.75
2092557	REC01971	hisH	N	196	42		P10375	Imidazole glycerol phosphate synthase subunit hisH (EC 2.4.2.-)	b10373	AAM	0.75
2093144	REC01972	hisA	N	246	123, 146, 216		P10371	1-(5-phosphoribosyl)-5-[(5-phosphoribosylamino)methylideneamino]	b2024	AAM	0.75
2093866	REC01973	hisF	N	258	102, 146, 161, 207		P10373	Imidazole glycerol phosphate synthase subunit hisF (EC 4.1.3.-)	b2025	AAM	0.75
2094636	REC06489	hisI	N	203	40, 106, 133, 193		P06989	Histidine biosynthesis bifunctional protein hisI	b2026	AAM	0.75
2096359	REC05222	wzzB	N	338	44, 143		P76372	Chain length determinant protein	b2027	UNC	0.03
2097635	REC05223	ugd	N	388	31, 83, 83, 119, 147, 180, 210, 217, 254, 268, 289, 311, 328, 349		P76373	UDP-glucose 6-dehydrogenase (EC 1.1.1.22)	b2028	SMC	0.59
2099290	REC05224	gnd	N	468	103, 374, 401		P00350	6-phosphogluconate dehydrogenase, decarboxylating (EC 1.1.1.4)	b2029	CHM	0.69
2100933	REC04395		?	338	284		P03837	Transposase insH for insertion sequence element IS5	b2030	PHT	0.34
2101411	REC05226	wbbL	N	157	26, 40, 109, 132		P66667	Putative lipopolysaccharide biosynthesis glycosyl transferase wbbL	b2031	UNC	0.00
2102531	REC05227	yefI	N	372	32, 294		P37751	Hypothetical protein yefI	b2032	UNC	0.00
2103106	REC05228	wbbJ	N	196	84, 169		P37750	Putative lipopolysaccharide biosynthesis O-acetyl transferase wbb	b2033	UNC	0.00
2104079	REC05229	yefG	N	330	-		P37749	Hypothetical protein yefG	b2034	UNC	0.03
2105248	REC05230	rfc	N	388	-		P37748	O-antigen polymerase	b2035	UNC	0.00
2106351	REC05231	glf	X	367	-		P37747	UDP-galactopyranose mutase (EC 5.4.99.9)	b2036	CHM	0.22
2107606	REC05232	rfbX	N	415	34, 74, 111, 186, 207, 281, 283, 306, 325, 328, 348, 375, 397		P37746	Putative O-antigen transporter	b2037	UNC	0.09
2108160	REC05233	rfbC	N	185	43, 89, 171		P37745	dTDP-4-dehydrohamnose 3,5-epimerase (EC 5.1.3.13)	b2038	CHM	0.50
2109041	REC05234	rfbA	N	293	27, 126, 186, 222		P37744	Glucose-1-phosphate thymidyltransferase (EC 2.7.7.24)	b2039	MSM	0.59
2109998	REC05235	rfbD	N	299	4, 20, 45, 80, 85, 105, 121, 154, 216		P37760	dTDP-4-dehydrohamnose reductase (EC 1.1.1.133)	b2040	CHM	0.56
2111083	REC05236	rfbB	N	361	48, 82, 89, 139, 184, 209, 234, 254, 295, 317, 345		P37759	dTDP-glucose 4,6-dehydratase (EC 4.2.1.46)	b2041	MSM	0.75
2112349	REC05237	galF	E	297	297	< 0.01	P78083	UTP-glucose-1-phosphate uridylyltransferase (EC 2.7.7.9)	b2042	CHM	0.78
2113918	REC05238	wcaM	N	464	47, 168, 192, 193, 235, 259, 303, 325, 439		P71244	Colanic acid biosynthesis protein wcaM	b2043	UNC	0.00
2115149	REC05239	wcaL	N	406	81, 200, 342		P71243	Putative colanic acid biosynthesis glycosyl transferase wcaL (EC 2	b2044	UNC	0.47
2116426	REC05240	wcaK	N	426	48, 148		P71242	Colanic acid biosynthesis protein wcaK	b2045	UNC	0.03
2118180	REC05241	wzxC	N	492	66, 165, 278, 406, 425, 450		P77377	Lipopolysaccharide biosynthesis protein wzxC	b2046	LPC	0.25
2119576	REC05242	wcaJ	N	464	63, 244, 327		P71241	Putative colanic biosynthesis UDP-glucose lipid carrier transferase	b2047	UNC	0.69
2121001	REC05243	manB	N	456	153, 222, 278, 338		P24175	Phosphomannomutase (EC 5.4.2.8)	b2048	CHM	0.88
2122542	REC05244	manC	N	478	122, 168, 407, 425, 475		P24174	Mannose-1-phosphate guananylyltransferase (EC 2.7.7.22)	b2049	CHM	0.47
2123768	REC05245	wcaI	N	407	13, 92, 396		P32057	Putative colanic acid biosynthesis glycosyl transferase wcaI	b2050	UNC	0.22
2124247	REC05246	nudD	N	160	81		P32056	GDP-mannose mannose hydrolyase (EC 3.6.1.-)	b2051	CHM	0.03
2125212	REC05247	fcI	N	321	100, 171		P32055	GDP-fucose synthetase	b2052	CHM	0.31
2126336	REC05248	gmd	N	373	132, 142, 301, 353, 372		P32054	GDP-mannose 4,6-dehydratase (EC 4.2.1.47)	b2053	CHM	0.44
2126910	REC05249	wcaF	N	182	8, 33, 74, 78, 92, 106, 126, 128, 175		P71240	Putative colanic acid biosynthesis acetyltransferase wcaF (EC 2.3.	b2054	UNC	0.13
2127672	REC05250	wcaE	N	248	11, 36, 84, 143, 228		P71239	Putative colanic acid biosynthesis glycosyl transferase wcaE	b2055	UNC	0.06
2128900	REC05251	wcaD	N	405	16, 91, 123, 305		P71238	Putative colanic acid polymerase	b2056	UNC	0.00
2130092	REC05252	wcaC	N	405	78		P71237	Putative colanic acid biosynthesis glycosyl transferase wcaC	b2057	UNC	0.03
2130577	REC05253	wcaB	N	162	12, 31		P77558	Putative colanic acid biosynthesis acetyltransferase wcaB (EC 2.3	b2058	UNC	0.00
2131419	REC05254	wcaA	N	279	35, 89, 124, 260, 276		P77414	Putative colanic acid biosynthesis glycosyl transferase wcaA	b2059	UNC	0.31
2133710	REC05255	wzc	N	732	1, 169, 338, 428, 496, 605, 648, 726		P76387	Tyrosine-protein kinase wzc (EC 2.7.1.112)	b2060	LPC	0.13
2134120	REC05256	wzb	E	147	120, 138	< 0.3	P77153	Low molecular weight protein-tyrosine-phosphatase wzb (EC 3.1.3	b2061	CHM	0.59
2135265	REC05257	wza	N	379	27, 29, 77, 102, 141, 211		P76388	Putative polysaccharide export protein wza precursor	b2062	UNC	0.16
2135858	REC02011	yegH	N	549	34, 351, 399, 444		P76389	Hypothetical protein yegH	b2063	UNC	0.84
2139634	REC05258	asmA	N	617	70, 144, 226, 269, 313		P28249	Protein asmA precursor	b2064	UNC	0.22
2140237	REC05259	dcd	N	193	38, 39		P28248	Deoxycytidine triphosphate deaminase (EC 3.5.4.13)	b2065	NCM	0.56
2141024	REC05260	udk	N	231	29, 70		P31218	Uridine kinase (EC 2.7.1.48)	b2066	NCM	0.34
2141288	REC02015	yegE	N	1105	34, 222, 286, 362, 380, 671, 758, 905, 1053		P38097	Hypothetical protein yegE	b2067	UNC	0.22
2145562	REC05261	a.lkA	N	282	7, 18, 212, 265		P04395	DNA-3-methyladenine glycosylase II (EC 3.2.2.21)	b2068	NAM	0.68
2145633	REC02017	yegD	N	471	16, 22, 98, 112, 156, 208, 354, 396		P69282	Hypothetical chaperone protein yegD	b2069	UNC	1.00
2149007	REC05262	yegI	N	648	156, 299, 343, 399, 450		P76393	Hypothetical protein yegI	b2070	UNC	0.06
2149207	REC02019	yegJ	N	153	69, 91, 97		P76394	Hypothetical protein yegJ	b2071	UNC	0.06
2150494	REC05263	yegK	N	253	10, 42, 172, 233		P76395	Hypothetical protein yegK	b2072	UNC	0.03
2151150	REC05264	yegL	E	219	-	< 0.1	P76396	Hypothetical protein yegL	b2073	UNC	0.03
2151891	REC02022	yegM	N	464	181		P76397	Hypothetical protein yegM precursor	b2074	UNC	0.34
2153285	REC02023	yegN	N	1040	211, 328, 472, 696, 771, 877, 961		P76398	Hypothetical protein yegN	b2075	UNC	0.75
2156408	REC02024	yegO	N	1025	79, 280, 324, 339, 458, 618, 802, 1016		P76399	Hypothetical protein yegO	b2076	UNC	0.75
2159486	REC02025	yegB	N	471	31, 67, 138, 366		P36554	Hypothetical transport protein yegB	b2077	UNC	0.34
2160898	REC02026	baeS	N	467	75, 115, 219, 292, 294, 396, 441		P30847	Sensor protein baeS (EC 2.7.3.-)	b2078	SMC	0.31
2162298	REC02027	baeR	N	240	34		P30846	Transcriptional regulatory protein baeR	b2079	SMC	0.59

2163172	REC02028	yegP	E	123	-	< 0.3	P76402	Hypothetical protein yegP	b2080	UNC	0.06
2163690	REC02029	yegQ	N	453	118, 289, 336, 420, 443		P76403	Putative protease yegQ (EC 3.4.-.-)	b2081	UNC	0.38
2165542	REC05265	ogrK	N	72	62		P37057	Prophage P2 OGR protein	b2082	UNC	0.00
2165770	REC05266		?	48	-		P76404	FROM BASES 2163066 TO 2175408 (SECTION 188 OF 400) OF	b2083	UNC	0.00
2166023	REC05267		N	88	53, 68		P76405	FROM BASES 2163066 TO 2175408 (SECTION 188 OF 400) OF	b2084	UNC	0.00
2166388	REC05268	yegR	N	125	47, 119		P76406	Hypothetical protein yegR	b2085	UNC	0.00
2166734	REC02034	yegS	N	299	129, 212, 216, 237, 276		P76407	Hypothetical protein yegS	b2086	UNC	0.34
2168161	REC05269	gatR	N	148	23, 51, 71, 133		P36930	Galactitol utilization operon repressor		RCD	0.00
2168249	REC06521		N	102	1		P77681	Transposase insE for insertion sequence IS3A/B/C/D/E/FA/IB	b2088	PHT	0.56
2168554	REC06522		N	288	129, 157, 194		P05822	Transposase insF for insertion sequence IS3A/B/C/D/E/FA	b2089	PHT	0.56
2169755	REC05270	gatR	N	112	66		O07943	GALACTITOL UTILIZATION OPERON REPRESSOR		RCD	0.00
2170895	REC05271	gatD	E	346	9	< 0.01	P37190	Galactitol-1-phosphate 5-dehydrogenase (EC 1.1.1.251)	b2091	CHM	0.13
2172298	REC05272	gatC	N	451	45, 68, 117, 401, 421		P37189	PTS system, galactitol-specific IIC component	b2092	MTR	0.03
2172586	REC05273	gatB	N	94	4, 53, 72		P37188	PTS system, galactitol-specific IIB component (EC 2.7.1.69)	b2093	MTR	0.06
2173069	REC05274	gatA	N	150	3, 13, 124		P37187	PTS system, galactitol-specific IIA component (EC 2.7.1.69)	b2094	MTR	0.13
2174341	REC05275	gatZ	N	420	70		P37191	Putative tagatose 6-phosphate kinase gatZ (EC 2.7.1.144)	b2095	UNC	0.13
2175230	REC05276	gatY	N	286	37, 257		P37192	Tagatose-bisphosphate aldolase gatY (EC 4.1.2.-)	b2096	CHM	0.63
2176656	REC05277	fbAB	N	374	32, 165, 370		P71295	Fructose-bisphosphate aldolase class I (EC 4.1.2.13)	b2097	CHM	0.09
2176841	REC02046	yegT	N	425	44, 49, 95, 152, 260, 424		P76417	Putative nucleoside transporter yegT	b2098	UNC	0.03
2178115	REC02047	yegU	N	334	35, 70, 73, 153, 324		P76418	Hypothetical protein yegU	b2099	UNC	0.06
2179116	REC02048	yegV	N	321	34, 89, 136		P76419	Hypothetical sugar kinase yegV	b2100	UNC	0.59
2180801	REC05278	yegW	N	248	156, 167, 206		P76420	Hypothetical transcriptional regulator yegW	b2101	UNC	0.53
2181680	REC05279	yegX	N	275	19, 50, 51, 96, 127, 255, 263		P76421	Hypothetical protein yegX	b2102	UNC	0.19
2182536	REC05280	thiD	N	266	18, 60, 78, 105, 122, 188, 244		P76422	Phosphomethylpyrimidine kinase (EC 2.7.4.7)	b2103	NCM	0.81
2183321	REC05281	thiM	N	262	86, 215		P76423	Hydroxyethylthiazole kinase (EC 2.7.1.50)	b2104	NCM	0.28
2183816	REC05282	yohL	E	90	-	< 0.2	P76424	Hypothetical protein yohL	b2105	UNC	0.19
2183937	REC02054	yohM	N	274	62, 130, 198, 216, 260, 273		P76425	Hypothetical protein yohM	b2106	UNC	0.06
2184800	REC02055	yohN	N	172	29, 74, 100, 137, 140, 164		P76426	Hypothetical protein yohN precursor	b2107	UNC	0.00
2186434	REC05283	yehA	N	344	301, 338		P33340	Hypothetical protein yehA precursor	b2108	UNC	0.00
2188930	REC05284	yehB	N	826	61, 96, 122, 154, 159, 177, 213, 230, 254, 259, 277, 279, 301, 320, 335, 5		P33341	Hypothetical outer membrane usher protein yehB precursor	b2109	UNC	0.13
2189665	REC05285	yehC	E	239	-	< 0.05	P33342	Hypothetical fibrial chaperone yehC precursor	b2110	UNC	0.00
2190242	REC05286	yehD	E	180	-	< 0.05	P33343	Hypothetical protein yehD precursor	b2111	UNC	0.00
2190816	REC05287	yehE	N	93	9		P33344	Hypothetical protein yehE precursor	b2112	UNC	0.00
2192218	REC05288	mrp	N	379	52, 74, 79, 105, 160, 212		P21590	Mrp protein	b2113	UNC	0.81
2192320	REC02062	metG	E	677	-	< 0.001	P00959	Methionyl-tRNA synthetase (EC 6.1.1.10)	b2114	PMS	1.00
2194494	REC02063		N	274	35, 57, 98, 112, 147, 152, 179, 191, 195, 201, 210, 216, 230, 246, 251		P33345	Molybdate metabolism regulator	b2115	RCD	0.06
2195430	REC02064	moIR	N	645	34, 55, 68, 103, 104, 164, 204, 206, 253, 264, 327, 612		P33346	Molybdate metabolism regulator	b2116	RCD	0.06
2197288	REC02065		N	333	86		P33345	Molybdate metabolism regulator	b2117	RCD	0.06
2198299	REC02066	yehI	N	1210	102, 155, 235, 235, 282, 383, 422, 425, 468, 545, 555, 761, 785, 857, 113		P33346	Hypothetical protein yehI	b2118	UNC	0.06
2201992	REC06809	yehK	N	105	12, 15, 40, 45, 70		P33347	Hypothetical protein yehK	b2119	UNC	0.00
2202550	REC02067	yehL	N	384	21, 45, 58, 74, 129, 153, 190, 214, 263		P33348	Hypothetical protein yehL	b2119	UNC	0.00
2203715	REC02068	yehM	N	759	272, 478, 566, 734, 751		P33349	Hypothetical protein yehM	b2120	UNC	0.03
2205987	REC02069	yehP	N	378	6, 70, 74, 130, 132, 182, 242		P33352	Hypothetical protein yehP	b2121	UNC	0.03
2207096	REC02070	yehQ	N	622	469, 606, 607		P33353	Hypothetical protein yehQ	b2122	UNC	0.00
2209233	REC02071	yehR	N	157	2, 45, 103		P33354	Hypothetical lipoprotein yehR precursor	b2123	UNC	0.06
2210216	REC05289	yehS	N	156	13, 72, 117		P33355	Hypothetical protein yehS	b2124	UNC	0.06
2210997	REC05290	yehT	N	244	25, 138		P33356	Hypothetical protein yehT	b2125	UNC	0.16
2212664	REC05292	yehU	N	561	64, 102, 107, 235, 268, 295, 442, 507		P33357	Hypothetical protein yehU precursor	b2126	UNC	0.28
2212886	REC02076	mlrA	N	243	113, 213		P33358	MerR-like regulator A	b2127	RCD	0.09
2214496	REC05293	yehW	N	243	204		P33359	Hypothetical ABC transporter permease protein yehW	b2128	UNC	0.22
2215427	REC05294	yehX	N	308	112, 148, 255		P33360	Hypothetical ABC transporter ATP-binding protein yehX	b2129	UNC	0.53
2216577	REC05295	yehY	N	385	59, 140		P33361	Hypothetical ABC transporter permease protein yehY	b2130	UNC	0.31
2217501	REC05296	yehZ	N	305	161, 259		P33362	Hypothetical protein yehZ precursor	b2131	UNC	0.53
2220009	REC05297	bgIX	N	765	21, 70, 74, 142, 181, 221, 252, 281, 327, 392		P33363	Periplasmic beta-glucosidase precursor (EC 3.2.1.21)	b2132	CHM	0.25
2220205	REC02082	dId	N	571	65, 90, 213, 275, 281, 327, 403		P06149	D-lactate dehydrogenase (EC 1.1.1.28)	b2133	CHM	0.13
2222899	REC05298	pbpG	N	313	69		P33364	Penicillin-binding protein 7 precursor (EC 3.4.99.-)	b2134	LPC	0.16
2223675	REC05299	yohC	N	203	21, 146		P33365	Hypothetical protein yohC	b2135	UNC	0.03
2223785	REC02085	yohD	N	204	38, 169		P33366	Hypothetical protein yohD	b2136	UNC	0.13
2225290	REC05300	yohF	N	253	139		P33368	Hypothetical oxidoreductase yohF (EC 1.-.-.-)	b2137	UNC	0.25
2226539	REC05301	yohG	N	398	19, 47, 102, 183, 210, 368		P33369	Hypothetical outer-membrane lipoprotein yohG precursor		UNC	0.00
2226859	REC05302	yohH	N	96	2, 31, 74		P33370		b2139	UNC	0.00
2228405	REC05303	yohI	N	315	84, 163, 188, 298, 301		P33371	Hypothetical protein yohI	b2140	UNC	0.91
2228644	REC02090	yohJ	X	132	-		P33372	Hypothetical protein yohJ	b2141	UNC	0.13
2229039	REC02091	yohK	N	231	136, 151, 218		P33373	Hypothetical protein yohK	b2142	UNC	0.34
2229864	REC02092	cdd	N	294	164, 215, 253		P13652	Cytidine deaminase (EC 3.5.4.5)	b2143	NCM	0.06
2230898	REC02093	sana	N	239	61, 67, 149, 150, 207, 209		P33017	SanA protein	b2144	UNC	0.06
2231620	REC02094	yehS	N	79	27		P76439	Hypothetical protein yehS	b2145	UNC	0.00
2232053	REC02095	yehT	N	412	2, 78, 152, 217, 407		P76440	Hypothetical oxidoreductase yehT	b2146	UNC	0.66
2233279	REC02096	yehA	N	413	69, 229, 301, 310, 407, 412		P25889	Hypothetical protein yehA	b2147	UNC	0.31
2235773	REC05304	mgIC	?	336	13, 32		P32300	Galactoside transport system permease protein mgIC	b2148	MTR	0.19
2237309	REC05305	mgIA	N	506	20, 90, 109, 149, 176, 178, 207, 237, 249, 296, 296, 322, 322, 345, 364, 3		P23199	Galactoside transport ATP-binding protein mgIA	b2149	MTR	0.59
2238368	REC05306	mgIB	E	332	-	< 0.01	P02927	D-galactose-binding periplasmic protein precursor	b2150	MTR	0.19
2239688	REC05307	gals	N	346	4, 24, 56, 63, 150, 170		P25748	Mgl repressor and galactose ultrinduction factor	b2151	RCD	0.03
2240987	REC05308	yehB	N	385	201, 225, 240, 260, 318, 362		P25747	Hypothetical protein yehB	b2152	UNC	0.16
2241672	REC05309	foIE	E	222	-	< 0.1	P27511	GTP cyclohydrolase I (EC 3.5.4.16)	b2153	NCM	0.75
2241930	REC02103	yehG	N	278	143		P33018	Hypothetical protein yehG	b2154	UNC	0.28
2244789	REC05310	cirA	N	663	-		P17315	Colicin I receptor precursor	b2155	UNC	0.34
2246552	REC05311	lysP	N	489	-		P25737	Lysine-specific permease	b2156	MTR	0.34
2247638	REC05312	yehE	N	293	-		P32484	Hypothetical transcriptional regulator yehE	b2157	UNC	0.72
2247737	REC02107	yehH	N	349	-		P33019	Hypothetical protein yehH	b2158	UNC	0.44
2248860	REC02108	nfo	N	285	-		P12638	Endonuclease IV (EC 3.1.21.2)	b2159	NAM	0.31
2249720	REC02109	yehI	N	362	-		P33020	Hypothetical sugar kinase yehI	b2160	UNC	0.59
2252165	REC05313	yehJ	E	416	-	< 0.05	P33021	Hypothetical transport protein yehJ	b2161	UNC	0.22
2253206	REC05314	yehK	N	313	-		P33022	Hypothetical protein yehK	b2162	UNC	0.41
2253375	REC02112	yehL	E	219	-	< 0.05	P33023	Hypothetical protein yehL	b2163	UNC	0.00
2255355	REC05315	yehM	E	416	-	< 0.01	P33024	Hypothetical transport protein yehM	b2164	UNC	0.22
2256387	REC05316	yehN	?	312	136, 213, 216, 275		P33025	Hypothetical protein yehN	b2165	UNC	0.22
2257316	REC05317	yehC	N	313	32, 47, 71, 92, 97, 131, 175, 179, 203, 211, 224, 225, 242, 250, 262, 270		P02035	Hypothetical sugar kinase yehC	b2166	UNC	0.59
2259430	REC05318	fruA	N	563	144, 184, 235, 287, 302, 383, 411, 455, 549		P20966	PTS system, fructose-specific IIB component (EC 2.7.1.69)	b2167	MTR	0.47
2260385	REC05319	fruK	N	95	311		P23539	1-phosphofructokinase (EC 2.7.1.56)	b2168	CHM	0.50
2261515	REC05320	fruB	N	376	41, 107, 164, 172		P24217	PTS system, fructose-specific IIA/FPr component (EC 2.7.1.69)	b2169	MTR	0.09
2261883	REC02119	setB	N	393	80, 157, 200		P33026	Sugar efflux transporter B	b2170	MTR	0.00
2263215	REC02120	yehP	N	275	55, 190, 217, 243, 250, 265		P33028	Protein yehP	b2171	UNC	1.00

2264265	REC02121	yeiQ	N	488	57, 176, 248, 328, 483	P33029	Hypothetical oxidoreductase yeiQ (EC 1.--.-)	b2172	UNC	0.28
2265849	REC02122	yeiR	N	328	25, 83, 312	P33030	Hypothetical protein yeiR	b2173	UNC	0.56
2266838	REC02123	yeiU	N	249	36, 70, 90, 92, 204, 224	P76445	Hypothetical protein yeiU	b2174	UNC	0.03
2267999	REC02124	spr	N	188	30, 38, 66, 80, 139	P77685	Lipoprotein spr precursor	b2175	LPC	0.16
2268746	REC02125	rtn	N	518	107, 213, 402, 492	P76446	Rtn protein	b2176	UNC	0.31
2270378	REC02126	yejA	N	606	87, 170, 301, 302, 404, 497, 499	P33913	Hypothetical protein yejA precursor	b2177	UNC	0.25
2272199	REC02127	yejB	N	364	89, 210, 313, 344, 345	P33914	Hypothetical ABC transporter permease protein yejB	b2178	UNC	0.28
2273293	REC02128	yejE	E	341	295	P33915	Hypothetical ABC transporter permease protein yejE	b2179	UNC	0.81
2274320	REC02129	yejF	N	529	23, 43, 80, 363, 479	P33916	Hypothetical ABC transporter ATP-binding protein yejF	b2180	UNC	0.31
2276257	REC05321	yejG	N	114	26	P33917	Hypothetical protein yejG	b2181	UNC	0.00
2277780	REC05322	bcr	N	396	66, 221, 244, 272	P28246	Bicyclomycin resistance protein	b2182	MTR	0.59
2278503	REC05323	rsuA	N	231	85, 142	P33918	Ribosomal small subunit pseudouridine synthase A (EC 4.2.1.70)	b2183	NAM	0.97
2278652	REC02133	yejH	N	586	128, 178, 248, 378, 552, 574	P33919	Hypothetical protein yejH	b2184	UNC	0.16
2280537	REC02134	xp1Y	E	94	64, 103, 184	P02426	50S ribosomal protein L25	b2185	PMS	0.81
2281967	REC05324	yejK	N	335	87, 132, 156, 203, 217, 249, 285	P33920	37 kDa nucleoid-associated protein	b2186	UNC	0.13
2282149	REC02136	yejL	?	75	-	P33921	Hypothetical protein yejL	b2187	UNC	0.06
2282396	REC02137	yejM	N	586	328, 470, 514, 539	P33922	Hypothetical protein yejM	b2188	UNC	0.09
2286920	REC05325	yejO	N	836	12, 195, 249, 251, 267, 299, 338, 406, 477, 577, 610, 660, 688, 708, 784	P33924	Hypothetical outer membrane protein yejO	b2190	UNC	0.00
2286925	REC02139		N	40	2, 2, 31	P76451	FROM BASES 2276392 TO 2288352 (SECTION 198 OF 400) OF	b2191	UNC	0.00
2288101	REC06543		N	338	27, 294, 295	P03837	Transposase insH for insertion sequence element IS5	b2192	PHT	0.34
2288520	REC02142	narP	N	215	64, 103, 184	P31802	Nitrate/nitrite response regulator protein narP	b2193	SMC	0.63
2290430	REC05327	ccmH	N	350	43, 212, 276, 324	P33925	Cytochrome c-type biogenesis protein ccmH precursor	b2194	UNC	0.25
2290984	REC05328	dsbE	N	185	90	P33926	Thiol:disulfide interchange protein dsbE	b2195	UNC	0.59
2292924	REC05329	ccmF	N	647	242, 291, 384, 430, 608, 609	P33927	Cytochrome c-type biogenesis protein ccmF	b2196	UNC	0.41
2293400	REC05330	ccmE	E	159	-	P33928	Cytochrome c-type biogenesis protein ccmE	b2197	UNC	0.31
2293606	REC05331	ccmD	N	69	24	P36770	Heme exporter protein D	b2198	MTR	0.06
2294340	REC05332	ccmC	N	245	49, 194	P33929	Heme exporter protein C	b2199	MTR	0.34
2295044	REC05333	ccmB	N	220	22, 135	P33930	Heme exporter protein B	b2200	MTR	0.25
2295658	REC05334	ccmA	N	205	44, 169	P33931	Heme exporter protein A	b2201	MTR	0.31
2296279	REC05335	napC	N	200	139, 165	P33932	Cytochrome c-type protein napC	b2202	BEN	0.19
2296759	REC05336	napB	N	156	95, 133	P33933	Diheme cytochrome c napB precursor	b2203	BEN	0.19
2297598	REC05337	napH	N	287	74, 86, 107	P33934	Ferredoxin-type protein napH	b2204	UNC	0.06
2298280	REC05338	napG	N	231	43, 173, 173, 200	P33936	Ferredoxin-type protein napG	b2205	UNC	0.06
2300773	REC05339	napA	N	828	344, 641, 701, 826	P33937	Periplasmic nitrate reductase precursor (EC 1.7.99.4)	b2206	SMC	0.34
2301033	REC05340	napD	N	87	55	P33938	NapD protein	b2207	UNC	0.16
2301517	REC05341	napF	N	164	101, 127, 135	P33939	Ferredoxin-type protein napF	b2208	UNC	0.16
2301925	REC02158	eco	N	162	7, 49, 61	P23827	Ecotin precursor	b2209	MSM	0.03
2304774	REC05342	mgo	N	548	20, 57, 258	P33940	Malate:quinone oxidoreductase (EC 1.1.99.16)	b2210	CHM	0.25
2306635	REC05343	yojI	N	547	45, 138, 195, 328, 490	P33941	Hypothetical ABC transporter ATP-binding protein yojI	b2211	UNC	0.09
2307361	REC05344	alkB	N	216	151	P05050	Alkylated DNA repair protein alkB	b2212	NAM	0.19
2308425	REC05345	ada	N	354	66, 91, 278	P06134	ADA regulatory protein	b2213	NAM	0.78
2309554	REC05346	apbE	N	351	10, 105, 197, 251	P33944	Thiamine biosynthesis lipoprotein apbE precursor	b2214	NCM	0.56
2310769	REC05347	ompC	N	367	6, 249, 296	P06996	Outer membrane protein C precursor	b2215	SMC	0.00
2311508	REC02165	yojN	N	890	18, 62, 88, 126, 246, 302, 588, 618, 707	P39838	Putative sensor-like histidine kinase yojN (EC 2.7.3.-)	b2216	UNC	0.00
2314197	REC02166	rscB	N	216	146, 199	P14374	Capsular synthesis regulator component B	b2217	SMC	0.06
2317848	REC05348	rscC	N	933	60, 356, 611, 644, 648, 762, 900	P14376	Sensor protein rscC (EC 2.7.3.-)	b2218	SMC	0.06
2318063	REC02168	atoS	N	608	6, 10, 31, 59, 79, 87, 105, 130, 139, 203, 221, 280, 318, 336, 363, 440, 50	Q06067	Sensor protein atoS (EC 2.7.3.-)	b2219	SMC	0.63
2319886	REC02169	atoC	N	461	425, 455	Q06065	Acetoacetate metabolism regulatory protein atoC	b2220	SMC	0.75
2321467	REC02170	atoD	N	220	42, 80	P76458	Acetate CoA-transferase alpha subunit (EC 2.8.3.8)	b2221	LPC	0.41
2322129	REC02171	atoA	N	216	10, 40, 184	P76459	Acetate CoA-transferase beta subunit (EC 2.8.3.8)	b2222	LPC	0.41
2322776	REC02172	atoE	N	440	107, 177, 212, 282	P76460	Short-chain fatty acids transporter	b2223	MTR	0.16
2324129	REC02173	atoB	N	394	147, 290, 365	P76461	Acetyl-CoA acetyltransferase (EC 2.3.1.9)	b2224	LPC	0.66
2326163	REC05349	yfaP	N	258	94, 157, 205, 255	P76462	Hypothetical protein yfaP precursor	b2225	UNC	0.06
2327817	REC05350	yfaQ	N	549	215, 226, 505, 530, 542	P76463	Hypothetical protein yfaQ precursor	b2226	UNC	0.06
2328303	REC05351		N	161	5, 38	P76464	Hypothetical protein yfaS precursor	b2227	UNC	0.00
2332332	REC05352	yfaS	N	1337	6, 139, 181, 188, 220, 376, 455, 546, 712, 812, 846, 904, 957, 1015, 1029	P76464	Hypothetical protein yfaS precursor	b2229	UNC	0.13
2333006	REC05353	yfaT	N	216	25, 41	P76466	Hypothetical protein yfaT precursor	b2229	UNC	0.09
2334712	REC05354	yfaA	N	578	234, 284, 469, 497, 523, 560	P17994	Hypothetical protein yfaA	b2230	UNC	0.06
2337440	REC05355	gyrA	E	875	-	P09097	DNA gyrase subunit A (EC 5.99.1.3)	b2231	NAM	1.00
2337587	REC02181	ubiG	E	240	-	P17993	3-demethylubiquinone-9-3-methyltransferase (EC 2.1.1.64)	b2232	NCM	0.44
2342189	REC05356	yfaL	N	1250	12, 34, 34, 55, 125, 128, 143, 200, 225, 337, 404, 436, 524, 565, 661, 725	P45508	Hypothetical protein yfaL precursor	b2233	UNC	0.16
2342885	REC06544	nrda	E	761	-	P00452	Ribonucleoside-diphosphate reductase 1 alpha chain (EC 1.17.4.1b)2234	b2234	NCM	0.88
2345404	REC02184	nrdb	E	376	-	P00453	Ribonucleoside-diphosphate reductase 1 beta chain (EC 1.17.4.1)	b2235	NCM	0.75
2346534	REC02185	yfaE	N	84	49, 78	P37910	Hypothetical ferredoxin-like protein yfaE	b2236	UNC	0.13
2347492	REC05357	inaA	N	216	159, 206, 209	P27294	Protein inaA	b2237	UNC	0.03
2347707	REC02187	yfaH	?	68	-	P45505	Hypothetical protein yfaH	b2238	UNC	0.00
2349031	REC05358	glpQ	N	358	45, 283, 349	P09394	Glycero-phosphoryl diester phosphodiesterase, periplasmic precu	b2239	LPC	0.41
2350394	REC05359	glpT	N	452	39, 121, 154, 182	P08194	Glycerol-3-phosphate transporter	b2240	MTR	0.22
2350667	REC02190	glpA	N	542	244, 320	P13032	Anaerobic glycerol-3-phosphate dehydrogenase subunit A (EC 1.1b)2241	b2241	CHM	0.09
2352285	REC02191	glpB	N	419	106, 136	P13033	Anaerobic glycerol-3-phosphate dehydrogenase subunit B (EC 1.1b)2242	b2242	CHM	0.06
2353541	REC02192	glpC	N	396	96, 121, 206, 252, 316, 334, 385	P13034	Anaerobic glycerol-3-phosphate dehydrogenase subunit C	b2243	BEN	0.09
2354924	REC02193	yfaD	E	299	280	P37014	Hypothetical protein yfaD	b2244	UNC	0.00
2356865	REC05360	yfaU	N	267	42, 84, 201, 257	P76469	Hypothetical protein yfaU	b2245	UNC	0.09
2358211	REC05361	yfaV	E	442	432	P76470	Hypothetical transport protein yfaV	b2246	UNC	0.34
2359446	REC05362	yfaW	N	405	108, 158, 237	P77215	Hypothetical protein yfaW	b2247	UNC	0.03
2360231	REC05363	yfaX	N	260	227	P77732	Hypothetical transcriptional regulator yfaX	b2248	UNC	0.00
2361653	REC05364	cinA	N	400	17, 68, 126, 307	P77808	CinA-like protein	b2249	UNC	0.81
2362316	REC05365	yfaZ	N	187	93	P76471	Hypothetical protein yfaZ precursor	b2250	UNC	0.00
2362574	REC02200	yfaO	N	141	87	P52006	Putative Nudix hydrolase yfaO (EC 3.6.-.-)	b2251	UNC	0.00
2363640	REC05366	ais	X	200	-	P45565	Ais protein	b2252	UNC	0.00
2363915	REC02202	yfbE	X	390	-	P77690	Hypothetical protein yfbE	b2253	UNC	0.63
2365091	REC02203	yfbF	N	322	289, 301	P77757	Putative glycosyl transferase yfbF (EC 2.-.-.-)	b2254	UNC	0.56
2366059	REC02204	yfbG	N	660	13, 26, 57, 111, 112, 169, 213, 287, 424, 493, 495, 609, 615	P77398	Hypothetical protein yfbG	b2255	UNC	0.13
2368038	REC02205	yfbH	N	296	36	P76472	Hypothetical protein yfbH	b2256	UNC	0.06
2368928	REC02206	yfbI	N	550	249, 287, 295, 309, 444, 486	P76473	Hypothetical protein yfbI	b2257	UNC	0.28
2370577	REC06734	yfbW	N	111	46, 71	Q47377	Hypothetical protein yfbW	b2258	UNC	0.00
2370630	REC02207	yfbJ	N	222	28, 53, 143, 172, 212	P76474	Hypothetical protein yfbJ	b2258	UNC	0.00
2371588	REC05367	pmrD	N	98	56, 78	P37590	Polymyxin B resistance protein pmrD	b2259	UNC	0.00
2373023	REC05368	menE	E	451	-	P37353	O-succinylbenzoic acid--CoA ligase (EC 6.2.1.26)	b2260	NCM	0.41
2373982	REC05369	menC	X	320	293	P29208	O-succinylbenzoate-CoA synthase (EC 4.2.1.-)	b2261	NCM	0.13
2374839	REC05370	menB	X	285	-	P27290	Naphthoate synthase (EC 4.1.3.36)	b2262	NCM	0.50
2375612	REC05371	yfbB	X	252	-	P37355	Hypothetical protein yfbB	b2263	UNC	0.25
2377279	REC05372	menD	?	556	-	P71109	Menaquinone biosynthesis protein menD	b2264	NCM	0.28

2378438	REC05373	menF	N	356	21, 57, 232, 245, 280		P38051	Menaquinone-specific isochorismate synthase (EC 5.4.99.6)	b2265	NCM	0.34
2379047	REC05374	e1aB	N	101	2, 25, 100		P52084	ElaB protein	b2266	UNC	0.06
2379563	REC05375	e1aA	E	153	-	< 0.1	P52077	Protein elaA	b2267	UNC	0.38
2379610	REC02217	e1aC	N	311	89, 111, 159, 170, 222, 232, 284		Q47012	Protein elaC	b2268	UNC	0.31
2380733	REC02218	e1aD	N	403	5, 26, 186		Q47013	ElaD protein	b2269	UNC	0.00
2383742	REC05376	yfbK	N	575	17, 73, 74, 94, 107, 167, 386, 540		P76481	Hypothetical protein yfbK	b2270	UNC	0.09
2383874	REC02220	yfbL	N	325	29, 68, 84, 110, 130, 186, 188, 223, 240		P76482	Hypothetical protein yfbL	b2271	UNC	0.06
2384954	REC02221	yfbM	N	167	20, 111		P76483	Hypothetical protein yfbM	b2272	UNC	0.03
2386446	REC05377	yfbN	X	238	-		P76484	Hypothetical protein yfbN	b2273	UNC	0.00
2386601	REC02223	yfbO	N	158	41, 56, 84, 105, 107, 146		P76485	Hypothetical protein yfbO	b2274	UNC	0.00
2387133	REC02224	yfbP	N	283	9, 56, 57, 101, 162, 253		P76486	Hypothetical protein yfbP	b2275	UNC	0.00
2389345	REC05378	nuoN	N	425	152, 315, 389		P33608	NADH dehydrogenase I chain N (EC 1.6.5.3)	b2276	BEN	0.59
2391061	REC05379	nuoM	N	509	12, 200, 294, 301		P31978	NADH dehydrogenase I chain M (EC 1.6.5.3)	b2277	BEN	0.66
2393066	REC05380	nuoL	N	613	101, 118, 236, 280, 413, 461, 529, 577		P33607	NADH dehydrogenase I chain L (EC 1.6.5.3)	b2278	BEN	0.72
2393365	REC05381	nuoK	?	100	-		P33606	NADH dehydrogenase I chain K (EC 1.6.5.3)	b2279	BEN	0.56
2393916	REC05382	nuoJ	N	184	31, 73		P33605	NADH dehydrogenase I chain J (EC 1.6.5.3)	b2280	BEN	0.56
2394470	REC05383	nuoI	N	180	51		P33604	NADH dehydrogenase I chain I (EC 1.6.5.3)	b2281	BEN	0.56
2395462	REC05384	nuoH	N	325	35, 201, 313		P33603	NADH dehydrogenase I chain H (EC 1.6.5.3)	b2282	BEN	0.56
2398191	REC05385	nuoG	N	910	419, 563, 715		P33602	NADH dehydrogenase I chain G (EC 1.6.5.3)	b2283	BEN	0.63
2399575	REC05386	nuoF	N	445	66, 199, 218, 262, 357		P31979	NADH dehydrogenase I chain F (EC 1.6.5.3)	b2284	BEN	0.53
2400072	REC05387	nuoE	X	166	-		P33601	NADH dehydrogenase I chain E (EC 1.6.5.3)	b2285	BEN	0.53
2401877	REC05388	nuoC	N	600	45, 211, 219, 288, 377, 500		P33599	NADH dehydrogenase I chain C/D (EC 1.6.5.3)	b2286	BEN	0.59
2402633	REC05389	nuoB	N	220	64, 134, 220		P33598	NADH dehydrogenase I chain B (EC 1.6.5.3)	b2287	BEN	0.59
2403092	REC05390	nuoA	N	147	60, 61		P33597	NADH dehydrogenase I chain A (EC 1.6.5.3)	b2288	BEN	0.56
2404661	REC05391	lrhA	N	312	20, 27, 50, 213, 248, 274		P36771	Probable transcriptional regulator LrhA	b2289	UNC	0.72
2405581	REC02239	yfbQ	X	405	-		P77227	Probable aminotransferase yfbQ (EC 2.6.1.-)	b2290	UNC	0.41
2406882	REC02240	yfbR	N	199	34		P76491	Hypothetical protein yfbR	b2291	UNC	0.09
2409372	REC05392	yfbS	N	610	4, 242, 320, 509		P77741	Hypothetical protein yfbS	b2292	UNC	0.28
2410127	REC05393	yfbT	N	222	177		P77625	Protein yfbT	b2293	UNC	0.19
2410632	REC05394	yfbU	N	170	2, 20, 123		P76492	Protein yfbU	b2294	UNC	0.03
2411152	REC05395	yfbV	N	151	46, 72, 97, 119		P77496	Hypothetical protein yfbV	b2295	UNC	0.06
2411490	REC02245	ackA	E	400	-	< 0.01	P15046	Acetate kinase (EC 2.7.2.1)	b2296	MSM	0.81
2412767	REC02246	pta	N	714	424, 439, 516, 674, 692, 708		P39184	Phosphate acetyltransferase (EC 2.3.1.8)	b2297	MSM	0.94
2415080	REC02247	yfcC	N	513	38, 100, 215, 348, 473, 495		P39263	Hypothetical protein yfcC	b2298	UNC	0.22
2417196	REC05396	yfcD	N	180	118, 137		P76494	Hypothetical protein yfcD	b2299	UNC	0.03
2417808	REC05397	yfcE	N	184	6, 25, 30, 58, 64, 78, 102, 126, 151		P76495	Hypothetical protein yfcE	b2300	UNC	0.09
2418505	REC05398	yfcF	N	214	35, 169, 181, 206		P77544	Hypothetical GST-like protein yfcF	b2301	UNC	0.13
2418641	REC02251	yfcG	N	215	31		P77526	Hypothetical GST-like protein yfcG	b7302	UNC	0.44
2419345	REC02252	foiX	N	120	9, 15, 65, 111		P80449	D-erythro-7,8-dihydropyridoxin triphosphate epimerase (EC 5.-.-.-)	b2303	NCM	0.03
2419728	REC02253	yfcH	E	297	-	< 0.01	P77775	Hypothetical protein yfcH	b2304	UNC	0.38
2421559	REC05399	yfcI	N	296	23, 49, 64, 88, 103, 116, 158, 160, 183, 224		P77768	Hypothetical protein yfcI	b2305	UNC	0.00
2422529	REC05400	hisP	N	257	11, 200		P07109	Histidine transport ATP-binding protein hisP	b2306	MTR	0.78
2423253	REC05401	hisM	N	238	57, 79		P20091	Histidine transport system permease protein hisM	b2307	MTR	0.69
2423936	REC05402	hisQ	N	228	176		P52094	Histidine transport system permease protein hisQ	b2308	MTR	0.16
2424808	REC05403	hisJ	N	260	4, 60		P39182	Histidine-binding periplasmic protein precursor	b2309	MTR	0.22
2425811	REC05404	argT	N	260	23, 165, 196, 211		P09551	Lysine-arginine-ornithine-binding periplasmic protein precursor	b2310	MTR	0.22
2426646	REC05405	ubiX	E	189	-	< 0.1	P09550	3-octaprenyl-4-hydroxybenzoate carboxy-lyase (EC 4.1.1.-)	b2311	NCM	0.53
2428258	REC05406	purF	N	505	4, 5, 32, 48, 72, 177		P00496	Amidophosphoribosyltransferase (EC 2.4.2.14)	b2312	NCM	0.78
2428783	REC05407	cvpA	E	162	144		P08550	Colicin V production protein	b2313	UNC	0.41
2429677	REC05408	dedD	N	211	19, 57, 63, 126, 166	< 0.2	P09549	DedD protein	b2314	UNC	0.03
2430962	REC05409	foiC	X	422	-		P08192	FoIC bifunctional protein	b2315	MSM	0.91
2431946	REC05410	accD	N*	304	49		P08193	Acetyl-coenzyme A carboxylase carboxyl transferase subunit beta	b2316	LPC	0.84
2432761	REC05411	dedA	N	219	86, 124, 152		P09548	DedA protein	b2317	UNC	0.44
2433656	REC05412	truA	N	270	42, 147, 185, 268, 269		P07649	IRNA pseudouridine synthase A (EC 4.2.1.70)	b2318	NAM	1.00
2434669	REC05413	usg	N*	337	82		P08390	USG-1 protein	b2319	UNC	0.88
2435871	REC05414	pdxB	N	378	6, 160, 259, 289		P05459	Erythronate-4-phosphate dehydrogenase (EC 1.1.1.-)	b2320	NCM	0.06
2435970	REC02270	div	N	331	170, 222, 283		P15286	DIV protein	b2321	UNC	0.00
2438140	REC05415	yfcJ	N	392	41, 96, 320, 378		P77549	Hypothetical protein yfcJ	b2322	UNC	0.19
2439625	REC05416	fabb	E	406	-	< 0.01	P14926	3-oxoacyl-[acyl-carrier-protein] synthase I (EC 2.3.1.41)	b2323	LPC	0.75
2439724	REC02273	yfcK	N	688	28, 72, 82, 221, 285, 507, 600, 653		P77182	Hypothetical protein yfcK	b2324	UNC	0.44
2442189	REC05417	yfcL	N	92	39		P76496	Hypothetical protein yfcL	b2325	UNC	0.03
2442771	REC05418	yfcM	N	182	131		P76938	Hypothetical protein yfcM	b2326	UNC	0.06
2443580	REC05419	yfcA	N	269	172, 175, 206, 219, 265		P14008	Hypothetical protein yfcA	b2327	UNC	0.53
2444404	REC05420	mepA	N	274	35, 61, 157, 192		P14007	Penicillin-insensitive murein endopeptidase precursor (EC 3.4.99.-)	b2328	LPC	0.16
2445493	REC05421	aroC	N	361	6, 59, 89, 143, 232		P12008	Chorismate synthase (EC 4.6.1.4)	b2329	AAM	0.88
2446626	REC02280	yfcN	N	183	52, 190		P77458	Hypothetical protein yfcN	b2331	UNC	0.22
2446793	REC05422	yfcB	N	421	5, 178, 244, 296, 306, 410		P39199	Hypothetical adenine-specific methylase yfcB (EC 2.1.1.72)	b2330	NAM	0.97
2448084	REC05423	yfcO	N	278	27, 77, 172, 258, 273		P76498	Hypothetical protein yfcO precursor	b2332	UNC	0.00
2448610	REC05424	yfcP	N	179	6, 60, 68, 93, 162		P76499	Hypothetical fimbrial-like protein yfcP precursor	b2333	UNC	0.00
2449095	REC05425	yfcQ	N	162	15, 20, 60, 66, 88, 92, 114, 156		P76500	Hypothetical fimbrial-like protein yfcQ precursor	b2334	UNC	0.00
2449604	REC05426	yfcR	N	170	29, 40, 73, 92, 128		P76501	Hypothetical protein yfcR precursor	b2335	UNC	0.00
2450356	REC05427	yfcS	N	250	2, 12		P77599	Hypothetical fimbrial chaperone yfcS precursor	b2336	UNC	0.00
2451272	REC05428	yfcU	N	298	144		P77196	Hypothetical outer membrane usher protein yfcU precursor	b2337	UNC	0.00
2453021	REC05429	yfcV	N	578	111, 25, 69, 126, 149, 171, 250, 283, 304, 336, 441, 558		P77196	Hypothetical outer membrane usher protein yfcU precursor	b2337	UNC	0.06
2453666	REC05430	yfcV	N	187	111, 132, 186		P77288	Hypothetical fimbrial-like protein yfcV precursor	b2339	UNC	0.00
2454832	REC05431	sixa	X	161	-		P76502	Phosphohistidine phosphatase sixA (EC 3.1.3.-)	b2340	SMC	0.09
2457179	REC05432	yfcX	N	714	72, 154, 211, 283, 447, 488, 518, 541, 617, 634		P77399	Putative fatty oxidation complex alpha subunit	b2341	UNC	0.38
2458489	REC05433	yfcY	N	436	332, 380		P76503	Probable 3-ketoacyl-CoA thiolase (EC 2.3.1.16)	b2342	UNC	0.38
2458978	REC05434	yfcZ	N	102	18		P76504	Hypothetical protein yfcZ	b2343	UNC	0.03
2459320	REC02293	fadL	N	448	32, 49, 104, 128, 159, 172, 216, 266, 433		P10384	Long-chain fatty acid transport protein precursor	b2344	UNC	0.22
2461032	REC02294	yfdF	N	352	280, 314		P76505	Hypothetical protein yfdF	b2345	UNC	0.00
2463027	REC05435	vacJ	N	251	68, 141, 185, 194, 211		P76506	VacJ lipoprotein precursor	b2346	UNC	0.31
2463321	REC02296	yfdC	N	310	20, 101, 186, 248, 297		P37327	Hypothetical protein yfdC	b2347	UNC	0.03
2464565	REC02297	intS	X	385	-		P37326	Putative prophage CPS-53 integrase	b2349	UNC	0.00
2465875	REC02298	yfdG	X	120	-		P77682	Bactoprenol-linked glucose translocase homolog from prophage C b2350	b2350	UNC	0.00
2466234	REC02299	yfdH	X	306	-		P77293	Bactoprenol glucosyl transferase homolog from prophage CPS-53	b2351	UNC	0.41
2467151	REC02300	yfdI	N	443	-		P76507	Hypothetical protein yfdI	b2352	UNC	0.00
2468781	REC02301	tfaS	N	114	-		P77326	Tail fiber assembly protein homolog from prophage CPS-53	b2353	UNC	0.03
2469537	REC05436	yfdK	N	146	-		P77656	Hypothetical protein yfdK	b2354	UNC	0.00
2470082	REC05437	yfdL	X	172	-		P76508	Hypothetical protein yfdL	b2355	UNC	0.00
2470440	REC05438	yfdM	X	102	-		P76509	Hypothetical protein yfdM	b2356	UNC	0.00
2470901	REC05439	yfdN	X	164	-		P76510	Hypothetical protein yfdN	b2357	UNC	0.00
2471266	REC05440	yfdO	X	122	-		P76511	Hypothetical protein yfdO	b2358	UNC	0.00

2471540	REC02307	yfdP	N	148	82		P76512	Hypothetical protein yfdP	b2359	UNC	0.03
2472052	REC02308	yfdQ	N	274	37, 43, 89, 94, 134, 142, 195, 214, 238		P76513	Hypothetical protein yfdQ	b2360	UNC	0.03
2472977	REC02309	yfdR	N	187	4, 19, 61, 87, 168		P76514	Hypothetical protein yfdR	b2361	UNC	0.03
2473531	REC02310	yfdS	X	120	-		P76515	Hypothetical protein yfdS	b2362	UNC	0.00
2473893	REC02311	yfdT	X	101	-		P76516	Hypothetical protein yfdT	b2363	UNC	0.00
2475649	REC05441	dsdC	N	311	12, 80		P46068	D-serine deaminase activator	b2364	RCD	0.06
2475867	REC02313	dsdX	N	445	12, 74, 126, 178, 209, 240, 287, 309, 385		P08555	DsdX permease	b2365	UNC	0.09
2477222	REC02314	dsdA	X	442	-		P00926	D-serine dehydratase (EC 4.2.1.14)	b2366	AAM	0.13
2480196	REC05442	emrY	X	512	-		P52600	Multidrug resistance protein Y	b2367	MSM	0.00
2481359	REC05443	emrK	X	387	-		P52599	Multidrug resistance protein K	b2368	MTR	0.50
2481775	REC02317	evgA	N	204	-		P30854	Positive transcription regulator evgA	b2369	SMC	0.00
2482394	REC02318	evgS	N	1197	-		P30855	Sensor protein evgS precursor (EC 2.7.3.-)	b2370	SMC	0.09
2487227	REC05444	yfdE	X	394	-		P76518	Hypothetical protein yfdE	b2371	UNC	0.25
2488206	REC05445	yfdV	X	314	-		P76519	Hypothetical protein yfdV	b2372	UNC	0.13
2489970	REC05446	yfdU	N	564	17, 137, 161, 282, 306		P78093	Probable oxalyl-CoA decarboxylase (EC 4.1.1.8)	b2373	UNC	0.03
2491274	REC05447	yfdW	N	416	274, 325		P77407	Hypothetical protein yfdW	b2374	UNC	0.00
2492422	REC05448	yfdX	E	211	5	< 0.1	P76520	YfdX protein precursor	b2375	UNC	0.00
2492718	REC06604	ypdI	N	91	12, 29, 61, 71		O32528	Hypothetical lipoprotein ypdI precursor	b2376	UNC	0.00
2493312	REC05449	yfdY	N	80	17, 77		P76521	Hypothetical protein yfdY	b2377	UNC	0.00
2493599	REC02325	ddg	N	328	289		P76522	DDG protein	b2378	UNC	0.00
2496315	REC05450	yfdZ	N	412	4, 296, 381		P77434	Hypothetical aminotransferase yfdZ (EC 2.6.1.-)	b2379	UNC	0.63
2496691	REC02327	ypdA	N	565	15, 48, 115, 179, 250, 429		P76523	Hypothetical protein ypdA	b2380	UNC	0.16
2498403	REC02328	ypdB	N	244	4, 60, 152, 209		P77742	Hypothetical protein ypdB	b2381	UNC	0.31
2499150	REC02329	ypdC	N	285	154, 217, 236, 241		P77396	Hypothetical transcriptional regulator ypdC	b2382	UNC	0.13
2502505	REC05451	ypdD	N	831	563, 564, 598, 629, 682, 798, 819		P77439	Putative phosphoenolpyruvate-protein phosphotransferase ypdD (b2383	UNC	0.75
2503567	REC05452	ypdE	N	345	39, 49, 157, 194		P77585	Hypothetical protein ypdE	b2384	UNC	0.00
2504652	REC05453	ypdF	N	361	8, 85		P76524	Putative peptidase ypdF (EC 3.4.-.-)	b2385	UNC	0.84
2505914	REC05454	ypdG	N	415	178, 370		P77579	Putative PTS system IIC component ypdG (EC 2.7.1.69)	b2386	UNC	0.47
2506262	REC05455	ypdH	E	108	-	0.39	P76525	Putative PTS system IIB component ypdH (EC 2.7.1.69)	b2387	UNC	0.09
2507446	REC05456	g1k	N	321	16, 25, 53, 109, 113, 225, 272		P46880	Glucokinase (EC 2.7.1.2)	b2388	CHM	0.38
2507650	REC02336	yfeO	N	418	90, 180		P76526	Hypothetical protein yfeO	b2389	UNC	0.00
2509021	REC02337	ypeC	?	108	-		P76527	Hypothetical protein ypeC precursor	b2390	UNC	0.00
2510726	REC05457	mntH	N	412	48, 88, 207, 283, 295		P77145	Manganese transport protein mntH	b2392	MTR	0.50
2511062	REC02340	nupC	N	400	36, 137		P33031	Nucleoside permease nupC	b2393	MTR	0.22
2512345	REC06606	insL3	N	372	201, 218, 225, 246, 252, 286, 299, 330, 332		P08409	Putative transposase insL for insertion sequence element IS186A/	b2394	UNC	0.00
2515969	REC05458	yfeA	N	768	134, 220, 238, 290, 308, 424, 458, 549, 567, 604, 611, 642, 651, 691, 695		P23842	Hypothetical protein yfeA	b2395	UNC	0.06
2516472	REC02343	yfeC	N	119	15, 32, 107		P27239	Hypothetical protein yfeC	b2398	UNC	0.00
2516833	REC02344	yfeD	N	130	18, 26, 51, 56, 101		P27238	Hypothetical protein yfeD	b2399	UNC	0.00
2518692	REC05459	g1tX	E	471	449	< 0.0001	P04805	Glutamyl-tRNA synthetase (EC 6.1.1.17)	b2400	PMS	1.00
2520497	REC05460	xapR	N	294	6, 13, 14, 19, 42, 67, 100, 219, 290		P23841	Xanthosine operon regulatory protein	b2405	RCD	0.06
2522005	REC05461	xapB	N	418	48, 50, 155, 276, 311, 337, 353, 379, 415		P45562	Xanthosine permease	b2406	MTR	0.00
2522898	REC05462	xapA	N	277	40, 158, 236, 262		P45563	Xanthosine phosphorylase (EC 2.4.2.-)	b2407	NCM	0.38
2523147	REC02349	yfeN	N	254	72, 89, 102, 119, 139, 147, 168, 198, 216, 240		P45564	Hypothetical protein yfeN	b2408	UNC	0.00
2524876	REC05463	yfeR	N	308	38, 73, 82		P77500	Hypothetical transcriptional regulator yfeR	b2409	UNC	0.19
2524966	REC02351	yfeH	N	332	128, 155, 216, 238, 331		P39836	Hypothetical protein yfeH	b2410	UNC	0.25
2526188	REC06690	ypeB	N	75	27		P56604	Hypothetical protein ypeB	b2411	UNC	0.09
2528196	REC05464	ligA	E	671	-	< 0.0001	P15042	DNA ligase (EC 6.5.1.2)	b2411	NAM	1.00
2529253	REC05465	zipA	E	328	-	< 0.01	P77173	Cell division protein zipA	b2412	RCD	0.13
2529483	REC02354	cysZ	N	253	102, 151, 232		P12610	CysZ protein	b2413	UNC	0.89
2530429	REC02355	cysK	N	323	96, 170, 182, 206, 264, 281		P11096	Cysteine synthase A (EC 4.2.99.8)	b2414	AAM	0.04
2531784	REC02356	ptsH	N	85	15, 58		P70706	Phosphocarrier protein HPr	b2415	MTR	0.66
2532086	REC02357	ptsI	N	575	76, 329, 451, 478		P08839	Phosphoenolpyruvate-protein phosphotransferase (EC 2.7.3.9)	b2416	MTR	0.81
2533854	REC02358	crr	N	169	28		P08837	PTS system, glucose-specific IIA component (EC 2.7.1.69)	b2417	MTR	0.47
2535257	REC05466	pdxK	N	283	5, 92		P40191	Pyridoxine kinase (EC 2.7.1.35)	b2418	NCM	0.34
2535362	REC02360	yfeK	N	124	78, 121		Q47702	Hypothetical protein yfeK precursor	b2419	UNC	0.31
2535769	REC02361	yfeS	N	244	61, 172		P78271	Hypothetical protein yfeS	b2420	UNC	0.06
2537603	REC06608	cysM	N	303	126, 240		P16703	Cysteine synthase B (EC 4.2.99.8)	b2421	AAM	0.84
2538834	REC05467	cysA	N	365	128, 169, 253, 283, 280, 342		P16676	Sulfate transport ATP-binding protein cysA	b2422	MTR	0.91
2539273	REC05468	cysW	E	149	-	< 0.3	P16702	Sulfate transport system permease protein cysW	b2423	MTR	0.44
2540532	REC05469	cysU	N	277	88, 209		P16701	Sulfate transport system permease protein cysT	b2424	MTR	0.66
2541548	REC05470	cysP	N	338	32, 143, 186		P16700	Thiosulfate-binding protein precursor	b2425	MTR	0.41
2542709	REC05471	ucpA	N	285	9, 228		P37440	Oxidoreductase ucpA (EC 1.-.-.-)	b2426	UNC	0.31
2543629	REC05472	yfeT	N	285	72, 114		P77245	Hypothetical protein yfeT	b2427	UNC	0.16
2543793	REC02368	yfeU	N	298	56, 74, 77, 134, 152, 173		P76535	Protein yfeU	b2428	UNC	0.31
2544693	REC02369	yfeV	N	474	34, 84, 125, 154, 196, 302, 389		P77272	Putative PTS system IIBC component yfeV (EC 2.7.1.69)	b2429	UNC	0.47
2546035	REC02370	yfeW	N	463	62, 235, 395, 412, 446		P77619	Hypothetical protein yfeW precursor	b2430	UNC	0.31
2548592	REC05473	yfeX	N	308	32, 66, 109, 191		P76536	Hypothetical protein yfeX	b2431	UNC	0.16
2549236	REC05474	yfeY	N	191	42, 126		P76537	Hypothetical protein yfeY precursor	b2432	UNC	0.00
2549752	REC05475	yfeZ	N	151	40, 46, 108, 113		P76538	Hypothetical protein yfeZ	b2433	UNC	0.03
2550269	REC05476	ypeA	N	178	122		P76539	Hypothetical protein ypeA	b2434	UNC	0.84
2550372	REC02375	amiA	N	289	113, 163, 202		P36548	Probable N-acetylmuramoyl-L-alanine amidase amiA precursor (E	b2435	UNC	0.06
2551245	REC02376	hemF	N	299	36, 60, 115, 238, 294		P36553	Coproporphyrinogen III oxidase, aerobic (EC 1.3.3.3)	b2436	NCM	0.38
2553202	REC05477	eutR	N	350	180		P36547	Ethanolamine operon regulatory protein	b2437	RCD	0.09
2553754	REC05478	eutK	N	168	103		P76540	Ethanolamine utilization protein eutK precursor	b2438	UNC	0.00
2554420	REC05479	eutL	E	219	-	< 0.1	P76541	Ethanolamine utilization protein eutL	b2439	UNC	0.06
2555317	REC05480	eutC	N	295	51, 246, 276		P19636	Ethanolamine ammonia-lyase light chain (EC 4.3.1.7)	b2440	AAM	0.16
2556741	REC05481	eutB	N	467	91, 378, 417, 433		P19635	Ethanolamine ammonia-lyase heavy chain (EC 4.3.1.7)	b2441	AAM	0.16
2556791	REC02382	intZ	N	431	48, 82, 188, 321, 372, 396		P76542	Putative prophage CPZ-55 integrase	b2442	UNC	0.16
2558277	REC02383	yffL	N	213	114, 208		P76543	Hypothetical protein yffL	b2443	UNC	0.00
2559388	REC02384	yffM	E	81	-	0.52	P76544	Hypothetical protein yffM	b2444	UNC	0.00
2559630	REC02385	yffN	N	127	9, 68		P76545	Hypothetical protein yffN	b2445	UNC	0.00
2560131	REC02386	yffO	E	138	-	< 0.3	P76546	Hypothetical protein yffO	b2446	UNC	0.00
2560544	REC02387	yffP	N	197	29		P76547	Hypothetical protein yffP	b2447	UNC	0.00
2561597	REC02388	yffQ	N	130	77		P76548	Hypothetical protein yffQ	b2448	UNC	0.00
2562000	REC02389	yffR	?	130	18		P76549	Hypothetical protein yffR precursor	b2449	UNC	0.00
2562513	REC02390	yffS	E	279	-	< 0.1	P76550	Hypothetical protein yffS	b2450	UNC	0.00
2564904	REC05482	eutA	N	467	74, 88, 333		P76551	Ethanolamine utilization protein eutA	b2451	UNC	0.06
2566127	REC05483	eutH	N	408	79, 302, 338		P76552	Ethanolamine utilization protein eutH	b2452	UNC	0.13
2567558	REC05484	eutG	N	404	217		P76553	Ethanolamine utilization protein eutG	b2453	UNC	0.50
2568357	REC05485	eutJ	N	278	114, 146, 162, 198, 201		P77277	Ethanolamine utilization protein eutJ	b2454	UNC	0.06
2569771	REC05486	eutE	N	467	201, 297		P77445	Ethanolamine utilization protein eutE	b2455	UNC	0.03
2570070	REC05487	eutN	E	95	76	0.43	P77633	Ethanolamine utilization protein eutN	b2456	UNC	0.09
2570512	REC05488	eutM	N	111	57		P77606	Ethanolamine utilization protein eutM precursor	b2457	UNC	0.13

2571525	REC05489	<i>eutD</i>	N	338	43	P77218	Ethanolamine utilization protein eutD	b2458	UNC	0.91
2572325	REC05490	<i>eutT</i>	N	267	51, 125	P76554	Ethanolamine utilization cobalamin adenosyltransferase (EC 2.5.1	b2459	MTR	0.03
2573023	REC05491	<i>eutQ</i>	N	233	143, 148, 171	P76555	Ethanolamine utilization protein eutQ	b2460	UNC	0.06
2573477	REC05492	<i>eutP</i>	N	159	80	P76556	Ethanolamine utilization protein eutP	b2461	UNC	0.06
2573897	REC05493	<i>eutS</i>	N	135	18, 34, 104, 119	P76557	Ethanolamine utilization protein eutS	b2462	UNC	0.06
2576397	REC05494	<i>maeB</i>	N	759	1, 213, 366, 520, 581, 619, 751	P76558	NADP-dependent malic enzyme (EC 1.1.1.40)	b2463	BEN	0.59
2576686	REC02404	<i>talA</i>	N	316	26, 148	P78258	Transaldolase A (EC 2.2.1.2)	b2464	CHM	0.78
2577656	REC02405	<i>tktB</i>	N	667	8, 160, 380, 423, 447, 483, 494	P33570	Transketolase 2 (EC 2.2.1.1)	b2465	CHM	0.94
2580797	REC05495	<i>ypfG</i>	N	347	223, 232, 336	P76559	Hypothetical protein ypfG precursor	b2466	UNC	0.00
2581498	REC05496	<i>ypfH</i>	N	191	152	P37128	Hypothetical protein ypfH	b2467	UNC	0.34
2583545	REC05497	<i>aegA</i>	N	659	36, 265, 278, 315, 430, 456, 467, 606, 628	P37127	AegA protein	b2468	UNC	0.66
2583751	REC02409	<i>narQ</i>	N	566	96, 103	P27896	Nitrate/nitrite sensor protein narQ (EC 2.7.3.-)	b2469	SMC	0.09
2585615	REC02410	<i>acrD</i>	N	1037	102, 135, 164, 210, 229, 250, 256, 307, 318, 478, 642, 953, 1004	P24177	Probable aminoglycoside efflux pump	b2470	UNC	0.75
2589267	REC02411	<i>yffB</i>	E	118	-	P24178	Protein yffB	b2471	UNC	0.38
2589627	REC02412	<i>dapE</i>	E	375	-	P24176	Succinyl-diaminopimelate desuccinylase (EC 3.5.1.18)	b2472	AAM	0.75
2590758	REC06691	?	?	74	-	P77259	SIMILAR TO	UNC	0.00	
2591814	REC05498	<i>ypfH</i>	N	240	151, 224	P76561	Hypothetical protein ypfH	b2473	UNC	0.38
2593879	REC05499	<i>ypfI</i>	N	671	220, 223, 251, 291, 301, 352, 484, 519, 630	P76562	Hypothetical protein ypfI	b2474	UNC	0.06
2594757	REC05500	<i>ypfJ</i>	N	287	117	P76563	Hypothetical protein ypfJ	b2475	UNC	0.28
2595638	REC05501	<i>purC</i>	N	237	23, 43, 44, 77, 150, 177, 180	P21155	Phosphoribosylaminoimidazole-succinocarboxamide synthase (EC	b2476	NCM	0.59
2596888	REC05502	<i>njPB</i>	N	345	4, 52, 91, 134, 172, 200, 291, 314, 343	P21167	Lipoprotein-34 precursor	b2477	UNC	0.00
2597780	REC05503	<i>dapA</i>	E	292	-	P05640	Dihydrodipicolinate synthase (EC 4.2.1.52)	b2478	AAM	0.84
2597860	REC02419	<i>gcvR</i>	E	212	-	P23483	Glycine cleavage system transcriptional repressor	b2479	RCD	0.09
2598498	REC02420	<i>bcp</i>	N	156	46, 63, 84, 101, 116, 143	P23480	Bacterioferritin comigratory protein	b2480	UNC	0.72
2599182	REC02421	<i>hyfA</i>	N	218	12, 45, 109	P23481	Hydrogenase-4 component A (EC 1.-.-.-)	b2481	BEN	0.00
2599838	REC02422	<i>hyfB</i>	N	672	467, 561	P23482	Hydrogenase-4 component B (EC 1.-.-.-)	b2482	BEN	0.06
2601846	REC02423	<i>hyfC</i>	N	322	87, 95, 114, 185, 254	P77858	Hydrogenase-4 component C (EC 1.-.-.-)	b2483	BEN	0.00
2602831	REC02424	<i>hyfD</i>	N	479	1, 448	P77416	Hydrogenase-4 component D (EC 1.-.-.-)	b2484	BEN	0.22
2604282	REC02425	<i>hyfE</i>	N	216	120	P77524	Hydrogenase-4 component E (EC 1.-.-.-)	b2485	LPC	0.03
2604937	REC02426	<i>hyfF</i>	N	526	197, 315, 369, 481, 499	P77437	Hydrogenase-4 component F (EC 1.-.-.-)	b2486	BEN	0.03
2606507	REC02427	<i>hyfG</i>	N	555	122, 147, 499	P77329	Hydrogenase-4 component G (EC 1.-.-.-)	b2487	BEN	0.00
2608184	REC02428	<i>hyfH</i>	X	181	-	P77423	Hydrogenase-4 component H	b2488	BEN	0.03
2608726	REC02429	<i>hyfI</i>	N	252	55, 244	P77668	Hydrogenase-4 component I (EC 1.-.-.-)	b2489	BEN	0.00
2609414	REC02430	<i>hyfJ</i>	N	158	15, 33, 108	P77453	Hydrogenase-4 component J (EC 1.-.-.-)	b2490	LPC	0.00
2609941	REC02431	<i>hyfR</i>	N	663	18, 139, 285, 321, 429, 446, 557, 661	P71229	Hydrogenase-4 transcriptional activator	b2491	RCD	0.03
2611954	REC02432	<i>focB</i>	N	282	6, 119, 122, 152, 195, 204, 229, 252	P77733	Probable formate transporter 2	b2492	UNC	0.16
2613901	REC05504	<i>perM</i>	N	353	54, 84, 130, 198, 331	P77406	Putative permease perM	b2493	UNC	0.34
2614114	REC02434	<i>yfgC</i>	?	47	92	P76568	Hypothetical protein yfgC precursor	b2494	UNC	0.38
2615598	REC02435	<i>yfgD</i>	N	119	42	P76569	Protein yfgD	b2495	UNC	0.19
2616841	REC05505	<i>yfgE</i>	E	248	-	P76570	Hypothetical protein yfgE	b2496	UNC	0.16
2618180	REC05506	<i>uraA</i>	N	429	20, 107, 279, 423	P33780	Uracil permease	b2497	MTR	0.47
2618919	REC05507	<i>upp</i>	N	217	176	P25532	Uracil phosphoribosyltransferase (EC 2.4.2.9)	b2498	NCM	0.81
2619217	REC02439	<i>purX</i>	N	345	51, 107, 235	P08179	Phosphoribosylformylglycinamide cyclo-ligase (EC 6.3.3.1)	b2499	NCM	0.78
2620254	REC02440	<i>purN</i>	N	612	8, 94, 135, 182	P08179	Phosphoribosylglycinamide formyltransferase (EC 2.1.2.2)	b2500	NCM	0.78
2621064	REC02441	<i>ppk</i>	N	288	15, 484, 520, 533, 640, 655	P28688	Polyphosphate kinase (EC 2.7.4.1)	b2501	MSM	0.50
2623135	REC02442	<i>ppx</i>	N	513	42, 125, 322, 339, 478	P29014	Exopolyposphatase (EC 3.6.1.11)	b2502	MSM	0.69
2626958	REC05508	<i>yfgF</i>	N	747	9, 74, 87, 120, 134, 135, 161, 170, 213, 282, 318, 328, 561, 622	P77172	Hypothetical protein yfgF	b2503	UNC	0.53
2627812	REC02445	<i>yfgH</i>	?	172	7, 166	P76572	Hypothetical lipoprotein yfgH precursor	b2505	UNC	0.00
2628346	REC02446	<i>yfgI</i>	X	179	-	P76573	Hypothetical protein yfgI	b2506	UNC	0.00
2630555	REC05509	<i>guaA</i>	N	525	60, 76, 365	P04079	GMP synthase [glutamine-hydrolyzing] (EC 6.3.5.2)	b2507	NCM	0.84
2632090	REC05510	<i>guaB</i>	N	488	14, 321, 373, 440, 456	P06981	Inosine-5'-monophosphate dehydrogenase (EC 1.1.1.205)	b2508	NCM	0.78
2632252	REC02449	<i>xseA</i>	N	456	174, 412	P04994	Exodeoxyribonuclease VII large subunit (EC 3.1.11.6)	b2509	NAM	0.81
2633870	REC05511	<i>yfgJ</i>	N	83	45	P76575	Hypothetical protein yfgJ	b2510	UNC	0.03
2635415	REC05512	<i>engA</i>	E	503	-	P77254	Probable GTP-binding protein engA	b2511	UNC	1.00
2636672	REC05513	<i>yfgL</i>	N	392	25, 74, 118, 160, 192, 201, 227, 243, 364	P77774	Hypothetical protein yfgL	b2512	UNC	0.19
2637303	REC05514	<i>yfgM</i>	N	206	22, 72, 115, 181	P76576	Hypothetical protein yfgM	b2513	UNC	0.16
2638595	REC05515	<i>hisS</i>	E	424	-	P04804	Histidyl-tRNA synthetase (EC 6.1.1.21)	b2514	PMS	1.00
2639824	REC05516	<i>ispG*</i>	E	372	-	P27433	1-hydroxy-2-methyl-2-(E)-butenyl 4-diphosphate synthase (<i>gcpE</i>)	b2515	LPC	0.84
2640864	REC05517	<i>yfgA</i>	N	337	156, 182, 216, 280	P27434	Hypothetical protein yfgA	b2516	UNC	0.09
2642303	REC05518	<i>yfgB</i>	N	384	53, 112, 194, 198	P36979	Hypothetical protein yfgB	b2517	UNC	0.88
2642884	REC05519	<i>ndk</i>	E	143	-	P24233	Nucleoside diphosphate kinase 1C (EC 2.7.4.6)	b2518	MSM	0.84
2645345	REC05520	<i>pbpC</i>	N	770	126, 127, 184, 356, 731, 757	P76577	Penicillin-binding protein 1C	b2519	LPC	0.28
2650307	REC05521	<i>yfhM</i>	N	1653	309, 534, 788, 791, 823, 886, 908, 913, 923, 1024, 1084, 1344, 1471, 1558	P76578	Hypothetical lipoprotein yfhM precursor	b2520	UNC	0.22
2650355	REC02461	<i>sseA</i>	N	334	49, 85, 101, 239, 260, 319, 321	P31142	3-mercaptopyruvate sulfuryltransferase (EC 2.8.1.2)	b2521	MSM	0.41
2652962	REC05522	<i>sseB</i>	N	261	204, 245	P31143	Protein sseB	b2522	UNC	0.00
2654465	REC05523	<i>pepB</i>	N	456	71, 122, 144, 151, 171, 197, 267, 339, 369	P37095	Peptidase B (EC 3.4.11.-)	b2523	AAM	0.09
2654756	REC05524	<i>yfhJ</i>	N	66	40	P37096	Hypothetical protein yfhJ	b2524	UNC	0.16
2655103	REC05525	<i>fdx</i>	E	111	-	P25528	Ferredoxin, 2Fe-2S	b2525	BEN	0.44
2656955	REC05526	<i>hscA</i>	E	616	-	P36541	Chaperone protein hscA	b2526	UNC	0.25
2657487	REC05527	<i>hscB</i>	E	171	-	P36540	Chaperone protein hscB	b2527	PMS	0.19
2657906	REC05528	<i>yfhF</i>	?	107	14	P36539	Protein yfhF	b2528	UNC	0.66
2658309	REC05529	<i>nifU</i>	E	128	-	P77310	NifU-like protein	b2529	UNC	0.69
2659575	REC05530	<i>iscS</i>	E	412	-	P39171	Cysteine desulfurase (EC 4.4.1.-)	b2530	NCM	0.94
2660151	REC05531	<i>yfhP</i>	N	162	99	P77484	Hypothetical protein yfhP	b2531	UNC	0.50
2661343	REC05532	<i>yfhQ</i>	N	246	30, 39, 102, 120, 131, 154, 170, 179, 209, 242	P77438	Hypothetical tRNA/rRNA methyltransferase yfhQ (EC 2.1.1.-)	b2532	UNC	0.44
2661462	REC02473	<i>subB</i>	E	267	-	P22783	Inositol-1-monophosphatase (EC 3.1.3.25)	b2533	LPC	0.78
2662383	REC02474	<i>yfhR</i>	N	293	199	P77538	Hypothetical protein yfhR	b2534	UNC	0.09
2663434	REC02475	<i>csiE</i>	N	433	56, 78, 276, 311, 401	P54901	Stationary phase inducible protein csiE	b2535	UNC	0.00
2665866	REC05533	<i>hcaT</i>	N	379	55, 125, 191, 261, 320	Q47142	Probable 3-phenylpropionic acid transporter	b2536	UNC	0.22
2666916	REC05534	<i>hcaR</i>	?	296	-	Q47141	Hca operon transcriptional activator	b2537	RCD	0.09
2667052	REC02478	<i>hcaE</i>	N	453	170, 279, 305, 310, 385	Q47139	3-phenylpropionate dioxxygenase alpha subunit (EC 1.14.1.-)	b2538	MSM	0.16
2668410	REC02479	<i>hcaF</i>	E	172	-	Q47140	3-phenylpropionate dioxxygenase beta subunit (EC 1.14.1.-)	b2539	MSM	0.03
2668928	REC02480	<i>hcaC</i>	E	106	-	P77266	3-phenylpropionate dioxxygenase ferredoxin subunit	b2540	BEN	0.13
2669245	REC02481	<i>hcaB</i>	N	270	70, 80, 183	P77646	2,3-dihydroxy-2,3-dihydro-phenylpropionate dehydrogenase (EC 1	b2541	MSM	0.00
2670067	REC02482	<i>hcaD</i>	N	400	147, 180, 348, 369	P77650	3-phenylpropionate dioxxygenase ferredoxin-NAD(+) reductase co	b2542	MSM	0.28
2671294	REC02483	<i>yphA</i>	N	164	7, 55, 57, 78, 84, 98, 153	P77751	Hypothetical protein yphA	b2543	UNC	0.19
2672708	REC05535	<i>yphB</i>	N	290	26, 34, 166, 221, 268	P76584	Hypothetical protein yphB	b2544	UNC	0.53
2673814	REC05536	<i>yphC</i>	N	364	47, 243, 200, 331	P77360	Hypothetical zinc-type alcohol dehydrogenase-like protein yphC	b2545	UNC	0.53
2674845	REC05537	<i>yphD</i>	N	332	84, 121, 196, 219, 253, 286, 288, 308	P77315	Hypothetical ABC transporter permease protein yphD	b2546	UNC	0.00
2676381	REC05538	<i>yphE</i>	N	503	258, 319, 348, 366, 419	P77509	Hypothetical ABC transporter ATP-binding protein yphE	b2547	UNC	0.03
2677387	REC05539	<i>yphF</i>	N	327	18, 19, 28, 162, 191, 318	P77269	ABC transporter periplasmic binding protein yphF precursor	b2548	UNC	0.03
2680858	REC05540	<i>yphG</i>	N	1124	143, 195, 263, 327, 432, 476, 578, 591, 640, 781, 805, 960, 1050, 1101	P76585	Hypothetical protein yphG	b2549	UNC	0.00
2680877	REC02490	<i>yphH</i>	N	399	347	P76586	Hypothetical protein yphH	b2550	UNC	0.03

2683527	REC05541	<i>glyA</i>	E	417	-	< 0.01	P00477	Serine hydroxymethyltransferase (EC 2.1.2.1)	b2551	AAM	0.97
2683855	REC02492	<i>hmp</i>	N	396	66, 279, 292, 298, 334		P24232	Flavohemoprotein (EC 1.6.99.7) (EC 1.14.12.17)	b2552	NCM	0.53
2685428	REC05542	<i>glnB</i>	N	112	37, 90		P05826	Nitrogen regulatory protein P-II 1	b2553	SMC	0.66
2686823	REC05543	<i>yfhA</i>	N	444	42, 136, 225, 244, 344, 412		P21712	Hypothetical protein yfhA	b2554	UNC	0.09
2687526	REC05544	<i>yfhG</i>	?	237	2		P37328	Hypothetical protein yfhG	b2555	UNC	0.00
2689181	REC05545	<i>yfhK</i>	N	496	21, 54, 125, 180, 373, 397, 427, 485		P52101	Putative sensor-like histidine kinase yfhK (EC 2.7.3.-)	b2556	UNC	0.03
2693563	REC05546	<i>purL</i>	N	1295	89, 368, 543, 589, 593, 639, 1007, 1045, 1128, 1198		P15254	Phosphoribosylformylglycinamide synthase (EC 6.3.5.3)	b2557	NCM	0.78
2693959	REC02498	<i>yfhD</i>	N	472	61, 211, 230, 248, 250, 408, 417, 449		P30135	Hypothetical protein yfhD	b2558	UNC	0.13
2695910	REC05547	<i>yfhC</i>	E	178	-	< 0.1	P30134	Hypothetical protein yfhC	b2559	UNC	0.78
2696507	REC05548	<i>yfhB</i>	N	190	2, 91, 177		P30133	Hypothetical protein yfhB	b2560	UNC	0.00
2696707	REC02501	<i>yfhH</i>	?	306	46		P37767	Hypothetical protein yfhH	b2561	UNC	0.53
2697683	REC02502	<i>yfhL</i>	N	86	52, 54, 66		P52102	Putative ferredoxin-like protein yfhL	b2562	UNC	0.38
2699018	REC05549	<i>acpS</i>	E	126	109	< 0.2	P24224	Holo-[acyl-carrier protein] synthase (EC 2.7.8.7)	b2563	NCM	0.75
2699749	REC05550	<i>pdxJ</i>	E	243	-	< 0.05	P24223	Pyridoxal phosphate biosynthetic protein pdxJ	b2564	NCM	0.47
2700489	REC06647	<i>recO</i>	N	242	46, 100		P15027	DNA repair protein recO	b2565	NAM	0.50
2701406	REC05552	<i>era</i>	E	301	-	< 0.01	P06616	GTP-binding protein era	b2566	UNC	0.97
2702083	REC05553	<i>rnc</i>	E	226	-	< 0.05	P05797	Ribonuclease III (EC 3.1.26.3)	b2567	NAM	0.97
2703329	REC05554	<i>lepB</i>	E	324	314	< 0.01	P00803	Signal peptidase I (EC 3.4.21.89)	b2568	PMS	0.97
2705144	REC05555	<i>lepA</i>	N	599	175, 331, 454		P07682	GTP-binding protein lepA	b2569	UNC	1.00
2705821	REC05556	<i>rseC</i>	N	159	7, 54, 156		P46187	Sigma-E factor regulatory protein rseC	b2570	RCD	0.09
2706774	REC05557	<i>rseB</i>	N	318	25, 108, 159, 251, 296, 303		P46186	Sigma-E factor regulatory protein rseB precursor	b2571	RCD	0.13
2707424	REC05558	<i>rseA</i>	N	216	88, 96, 144, 197		P38106	Sigma-E factor negative regulatory protein	b2572	RCD	0.06
2708032	REC05559	<i>rpoE</i>	?	191	-		P34086	RNA polymerase sigma-E factor	b2573	RCD	0.50
2708440	REC02514	<i>nadB</i>	N	540	60, 70, 77, 155, 239, 359, 448, 505, 527		P10902	L-aspartate oxidase (EC 1.4.3.16)	b2574	NCM	0.53
2710904	REC05560	<i>yfiC</i>	N	285	29, 43		P31825	Hypothetical protein yfiC	b2575	UNC	0.50
2710916	REC02516	<i>srmB</i>	?	444	-		P21507	ATP-dependent RNA helicase srmB	b2576	SMC	0.16
2713385	REC05561	<i>yfiE</i>	N	308	168, 255		P33634	Hypothetical transcriptional regulator yfiE	b2577	UNC	0.72
2713443	REC02518	<i>yfiK</i>	N	195	73, 120		P38101	Hypothetical protein yfiK	b2578	UNC	0.31
2714469	REC05562	<i>yfiD</i>	E	127	-	< 0.3	P33633	Protein yfiD	b2579	UNC	0.06
2714774	REC02520	<i>ung</i>	N	229	144, 162		P12295	Uracyl-DNA glycosylase (EC 3.2.2.-)	b2580	NAM	0.69
2716548	REC05563	<i>yfiF</i>	N	345	78, 150, 172, 205, 206		P33635	Hypothetical tRNA/rRNA methyltransferase yfiF (EC 2.1.1.-)	b2581	UNC	0.97
2716755	REC02522	<i>trxC</i>	E	139	-	< 0.3	P33636	Thioredoxin 2	b2582	MSM	0.97
2717219	REC02523	<i>yfiP</i>	N	240	107, 110, 212		Q47319	Hypothetical protein yfiP	b2583	UNC	0.06
2717973	REC02524	<i>yfiQ</i>	N	886	58, 61, 104, 104, 297, 416, 453, 481, 792, 838		P76594	Hypothetical protein yfiQ	b2584	UNC	0.25
2720744	REC02525	<i>pssA</i>	E	452	-	< 0.05	P23830	CDP-diacylglycerol-serine O-phosphatidyltransferase (EC 2.7.8.8)	b2585	LPC	0.06
2722199	REC02526	<i>yfiM</i>	N	90	7, 20		P46126	Hypothetical protein yfiM	b2586	UNC	0.03
2723766	REC05564	<i>kgtP</i>	N	432	110, 227, 331, 372		P17448	Alpha-ketoglutarate permease	b2587	MTR	0.31
2732193	REC05565	<i>clpB</i>	N	857	88, 802		P03815	ClpB protein	b2592	UNC	0.94
2733054	REC05566	<i>yfiH</i>	N	243	11, 21, 147		P33644	Hypothetical protein yfiH	b2593	UNC	0.69
2734031	REC05567	<i>rJdU</i>	E	326	312	< 0.1	P33643	Ribosomal large subunit pseudouridine synthase D (EC 4.2.1.70)	b2594	NAM	1.00
2734166	REC02531	<i>yfiO</i>	N	245	4, 43		P77146	Hypothetical lipoprotein yfiO precursor	b2595	UNC	0.38
2734933	REC02532	?	?	68	-		P76595	FROM BASES 2732002 TO 2744130 (SECTION 236 OF 400) OF	b2596	UNC	0.00
2735174	REC02533	<i>yfiA</i>	N	113	51, 111		P11285	Protein yfiA	b2597	UNC	0.06
2735765	REC02535	<i>pheA</i>	N	386	6, 70, 100, 139, 267, 349		P07022	P-protein	b2599	AAM	0.78
2738089	REC05568	<i>tyrA</i>	N	373	65, 188		P07023	T-protein	b2600	AAM	0.13
2739170	REC05569	<i>aroF</i>	N	356	7, 15, 34, 58, 63, 121, 270		P00888	Phospho-2-dehydro-3-deoxyheptonate aldolase, Tyr-sensitive (EC 4.1.1.2)	b2601	AAM	0.41
2739341	REC02538	<i>yfiL</i>	N	134	50, 63, 88		P11289	Hypothetical protein yfiL	b2602	UNC	0.03
2739895	REC02539	<i>yfiR</i>	N	172	4, 58, 89, 170, 172		P76597	Hypothetical protein yfiR precursor	b2603	UNC	0.03
2740403	REC02540	<i>yfiN</i>	N	408	1, 2, 326		P46139	Hypothetical protein yfiN	b2604	UNC	0.19
2741645	REC02541	<i>yfiB</i>	N	160	87, 117, 119		P07021	Putative lipoprotein yfiB precursor	b2605	UNC	0.03
2742550	REC05570	<i>rpL5</i>	E	115	-	< 0.3	P02420	50S ribosomal protein L19	b2606	PMS	1.00
2743359	REC05571	<i>trmD</i>	E	255	-	< 0.05	P07020	tRNA (Guanine-N(1)-)methyltransferase (EC 2.1.1.31)	b2607	NAM	1.00
2743947	REC05572	<i>rimM</i>	E	185	-	< 0.1	P21504	16S rRNA processing protein rimM	b2608	NAM	0.88
2744205	REC05573	<i>xpsP</i>	E	82	-	< 0.3	P02372	30S ribosomal protein S16	b2609	PMS	0.97
2745815	REC05574	<i>fth</i>	E	453	-	< 0.001	P07019	Signal recognition particle protein	b2610	PMS	1.00
2745907	REC02547	<i>ypjD</i>	N	288	80, 208		P76599	Hypothetical protein ypjD	b2611	UNC	0.16
2746818	REC02548	<i>ypjE</i>	E	196	194	< 0.1	P37908	Hypothetical protein ypjE	b2612	UNC	0.03
2747398	REC02549	<i>yfjD</i>	N	227	1, 103, 145, 197		P37908	Hypothetical protein yfjD	b2613	UNC	0.91
2748729	REC05575	<i>grpE</i>	E	197	-	< 0.1	P09372	GrpE protein	b2614	PMS	1.00
2748852	REC02551	<i>ppnK</i>	E	292	-	< 0.05	P37768	Probable inorganic polyphosphate/ATP-NAD kinase (EC 2.7.1.23)	b2615	MSM	0.94
2749816	REC02552	<i>recN</i>	N	553	46, 76, 89, 103, 276, 432, 464, 530, 534		P05824	DNA repair protein recN	b2616	NAM	0.84
2751815	REC02553	<i>smpA</i>	?	50	-		P23089	Small protein A precursor	b2617	UNC	0.06
2752337	REC05576	<i>yfjF</i>	E	102	-	0.30	P52119	Protein yfjF	b2618	UNC	0.16
2752785	REC05577	<i>yfjG</i>	E	158	-	< 0.2	P52121	Hypothetical protein yfjG	b2619	UNC	0.34
2752917	REC02556	<i>smpB</i>	N	160	83, 114		P32052	SsrA-binding protein	b2620	NAM	1.00
2754180	REC02557	<i>intA</i>	N	413	31, 139, 143		P32053	Prophage CP4-57 integrase	b2622	PHT	0.22
2756621	REC05578	<i>yfjH</i>	X	318	-		P52123	Hypothetical protein yfjH	b2623	UNC	0.00
2756665	REC02559	<i>alpA</i>	X	70	-		P33997	Prophage CP4-57 regulatory protein alpA	b2624	RCD	0.06
2757006	REC02560	<i>yfjI</i>	X	469	-		P52124	Hypothetical protein yfjI	b2625	UNC	0.00
2758568	REC02561	<i>yfjJ</i>	X	208	-		P52125	Hypothetical protein yfjJ	b2626	UNC	0.03
2761561	REC05579	<i>yfjK</i>	N	729	-		P52126	Hypothetical protein yfjK	b2627	UNC	0.00
2763174	REC05580	<i>yfjL</i>	N	538	16, 119, 194, 248		P52127	Hypothetical protein yfjL	b2628	UNC	0.00
2763797	REC05581	<i>yfjM</i>	N	87	13, 38, 46		P52128	Hypothetical protein yfjM	b2629	UNC	0.00
2763939	REC02565	<i>yfjN</i>	N	357	81, 135, 172, 249		P52129	Hypothetical protein yfjN	b2630	UNC	0.00
2765056	REC02566	<i>yfjO</i>	?	106	-		P52130	Hypothetical protein yfjO	b2631	UNC	0.00
2765725	REC02567	<i>yfjP</i>	N	289	116, 155, 156, 192		P52131	Hypothetical protein yfjP	b2632	UNC	0.00
2766686	REC02568	<i>yfjQ</i>	N	273	96, 153, 226, 229		P52132	Hypothetical protein yfjQ	b2633	UNC	0.00
2767724	REC02569	<i>yfjR</i>	N	233	131, 154		P52133	Hypothetical transcriptional regulator yfjR	b2634	UNC	0.03
2768310	REC06651	<i>ypjK</i>	N	130	84, 104		P52134	Hypothetical protein ypjK precursor	b2635	UNC	0.03
2768453	REC06652	<i>yfjS</i>	?	230	37, 56		O52982	Hypothetical lipoprotein yfjS precursor	b2636	UNC	0.03
2769169	REC02571	<i>yfjT</i>	N	155	123		P52135	Hypothetical protein yfjT precursor	b2637	UNC	0.00
2770175	REC05582	<i>yfjU</i>	N	104	62		P52136	Putative arsenate reductase (EC 1.97.1.5)	b2638	UNC	0.00
2770706	REC05583	<i>yfjV</i>	N	172	27, 64, 65, 105, 144, 170		P52137	Putative arsenical pump membrane protein	b2639	UNC	0.31
2771057	REC05584	<i>yfjW</i>	?	66	49		P77014	PUTATIVE ARSENICAL PUMP MEMBRANE PROTEIN	b2640	UNC	0.31
2771339	REC06653	<i>yfjX</i>	N	567	1, 3, 333		P52138	Hypothetical protein yfjW	b2642	UNC	0.00
2773940	REC02577	<i>yfjY</i>	X	152	-		P52139	Hypothetical protein yfjX	b2643	UNC	0.03
2774407	REC02578	<i>yfjZ</i>	X	160	-		P52140	Putative radC-like protein yfjY	b2644	UNC	0.03
2774886	REC06877	<i>ypjJ</i>	X	70	-		P58033	Hypothetical protein ypjJ	b2645	UNC	0.00
2775136	REC02579	<i>yfjZ</i>	X	105	-		P52141	Hypothetical protein yfjZ	b2646	UNC	0.00
2775474	REC02580	<i>ypjF</i>	E	109	-	0.34	Q46953	Hypothetical protein ypjF	b2646	UNC	0.00
2780876	REC05586	<i>ypjA</i>	N	1569	412, 559, 669, 741, 817, 919, 1045, 1170, 1262, 1274, 1407, 1467, 1524		P52143	Hypothetical outer membrane protein ypjA	b2647	UNC	0.03
2781228	REC05587	<i>pinH</i>	X	47	-		P76611	Putative DNA-invertase from prophage CP4-44	b2648	UNC	0.00
2782449	REC05588	<i>ypjB</i>	X	263	-		P76612	Hypothetical protein ypjB	b2649	UNC	0.00

2783031	REC05589	<i>ypjC</i>	E	160	-	0.39	P76613	Hypothetical protein ypjC	b2650	UNC	0.00
2783241	REC06656		N	43	-		P76614	Hypothetical protein b2651	b2651	UNC	0.00
2784417	REC02587	<i>ygaQ</i>	X	110	-		P76616	Hypothetical protein ygaQ	b2654	UNC	0.00
2784768	REC02588		X	164	-		Q9ZAZ7	Subunit 1 of the gab-activator protein		RCD	0.00
2785267	REC02589		X	62	-		P76618	FROM BASES 2775730 TO 2786129 (SECTION 240 OF 400) OF	b2656	UNC	0.00
2785627	REC02590		X	210	-		Q9R7D4	Subunit 2 of the gab-activator protein		RCD	0.00
2786398	REC02591	<i>ygaD</i>	N	90	-		P76620	Hypothetical protein ygaD	b2658	UNC	0.00
2786901	REC02592	<i>ygaT</i>	N	360	-		P76621	Hypothetical protein ygaT	b2659	UNC	0.00
2787937	REC02593	<i>gabC</i>	X	444	-		Q9ZAZ8	GAB DTP GENE CLUSTER REPRESSOR		AAM	0.41
2789294	REC02594	<i>gabD</i>	N	482	147, 311, 395		P25526	Succinate-semialdehyde dehydrogenase [NADP+] (EC 1.2.1.16)	b2661	MSM	0.66
2790756	REC02595	<i>gabT</i>	N	426	64, 161, 256		P22256	4-aminobutyrate aminotransferase (EC 2.6.1.19)	b2662	AAM	0.47
2792274	REC02596	<i>gabP</i>	N	466	203, 281, 302, 314, 332, 339, 340, 367, 377, 378, 404, 432, 434		P25527	GABA permease	b2663	MTR	0.19
2793677	REC02597	<i>ygaE</i>	N	226	36, 107, 112, 162		P37338	Hypothetical transcriptional regulator ygaE	b2664	UNC	0.50
2794807	REC05591	<i>ygaU</i>	E	149	-	< 0.1	P39169	Unknown protein from 2D-page	b2665	UNC	0.13
2795049	REC05592	<i>ygaE</i>	?	52	-		P77240	Hypothetical protein ygaE	b2666	UNC	0.13
2795232	REC02600	<i>ygaV</i>	N	99	78, 97		P77295	Hypothetical transcriptional regulator ygaV	b2667	UNC	0.28
2795541	REC02601	<i>ygaP</i>	E	174	-	< 0.05	P55734	Hypothetical protein ygaP	b2668	UNC	0.31
2796516	REC05593	<i>stpA</i>	N	134	28, 89, 106		P30017	DNA-binding protein stpA	b2669	UNC	0.09
2797185	REC02603	<i>ygaW</i>	N	149	8, 136		P76626	Hypothetical protein ygaW	b2670	UNC	0.03
2798015	REC05594	<i>ygaC</i>	N	114	23, 87, 100		P36931	Hypothetical protein ygaC	b2671	UNC	0.00
2798155	REC02605	<i>ygaM</i>	?	113	71		Q47413	Hypothetical protein ygaM	b2672	UNC	0.06
2798744	REC02606	<i>nrhH</i>	E	81	-	< 0.3	Q47414	Glutaredoxin-like protein nrhH	b2673	AAM	0.19
2798986	REC02607	<i>nrhI</i>	E	136	-	< 0.1	Q47415	NrdI protein	b2674	UNC	0.28
2799369	REC02608	<i>nrhE</i>	N	714	15, 67, 113, 386, 440, 488, 493, 545, 565, 575		P39452	Ribonucleoside-diphosphate reductase 2 alpha chain (EC 1.17.4.1)	b2675	NCM	0.47
2801523	REC02609	<i>nrhF</i>	N	319	41, 51, 160, 171, 230, 255		P37146	Ribonucleoside-diphosphate reductase 2 beta chain (EC 1.17.4.1)	b2676	NCM	0.88
2802836	REC02610	<i>proV</i>	N	400	195, 185, 229, 251, 252, 282, 319, 365		P14175	Glycine betaine/L-proline transport ATP-binding protein proV	b2677	MTR	0.34
2804031	REC02611	<i>proW</i>	N	354	9, 17, 133, 140		P14176	Glycine betaine/L-proline transport system permease protein proW	b2678	MTR	0.34
2805153	REC02612	<i>proX</i>	N	330	1, 92, 103, 181, 257		P14177	Glycine betaine-binding periplasmic protein precursor	b2679	MTR	0.13
2806337	REC02613		X	88	-		P76628	Hypothetical protein ygaY	b2680	UNC	0.59
2806597	REC02614	<i>ygaY</i>	N	305	255		P76628	Hypothetical protein ygaY	b2681	UNC	0.59
2807638	REC02615	<i>ygaZ</i>	N	245	56, 77, 128, 177, 209, 221		P76630	Hypothetical protein ygaZ	b2682	UNC	0.53
2808365	REC02616	<i>ygaH</i>	N	111	19, 73		P43667	Hypothetical protein ygaH	b2683	UNC	0.00
2808791	REC02617	<i>mprA</i>	N	176	18, 135, 142		P24201	Transcriptional repressor mprA	b2684	RCD	0.13
2809448	REC02618	<i>emrA</i>	N	390	173, 340, 361		P27303	Multidrug resistance protein A	b2685	MTR	0.50
2810637	REC02619	<i>emrB</i>	N	512	6, 38, 101, 137, 191, 309, 441		P27304	Multidrug resistance protein B	b2686	MTR	0.81
2812754	REC05595	<i>luxS</i>	?	171	62		P45578	Autoinducer-2 production protein luxS	b2687	RCD	0.38
2814461	REC05596	<i>gshA</i>	N	518	56, 85, 118, 194, 282		P06980	Glutamate--cysteine ligase (EC 6.3.2.2)	b2688	AAM	0.16
2814962	REC05597	<i>ygaA</i>	N	142	56, 141		P76631	Hypothetical protein ygaA	b2689	UNC	0.25
2815525	REC05598	<i>ygaB</i>	N	188	10, 136, 144, 163, 174		P77475	Hypothetical protein ygaB	b2690	UNC	0.81
2817168	REC05599	<i>csrA</i>	X	61	-		P31803	Carbon storage regulator	b2696	RCD	0.28
2820033	REC05600	<i>alaS</i>	E	876	-	< 0.0001	P00957	Alanyl-tRNA synthetase (EC 6.1.1.7)	b2697	PMS	1.00
2820662	REC05601	<i>oraA</i>	N	166	77		P33596	Regulatory protein recX	b2698	UNC	0.16
2821792	REC05602	<i>recA</i>	N	353	215		P03017	RecA protein	b2699	NAM	0.97
2822369	REC05603	<i>ygaD</i>	N	165	64, 154		P41053	Protein ygaD	b2700	UNC	0.56
2823599	REC05604	<i>mltB</i>	N	361	29, 137		P41052	Membrane-bound lytic murein transglycosylase B precursor (EC 3	b2701	LPC	0.31
2823855	REC02630	<i>srhA</i>	N	187	27, 122, 139, 144, 152		P56579	PTS system, glucitol/sorbitol-specific IIC2 component	b2702	MTR	0.06
2824415	REC02631	<i>srhE</i>	N	319	47, 143, 229, 260		P56580	PTS system, glucitol/sorbitol-specific IIB component (EC 2.7.1.6)	b2703	MTR	0.06
2825385	REC02632	<i>srhB</i>	?	123	111		P05706	PTS system, glucitol/sorbitol-specific IIA component (EC 2.7.1.69)	b2704	MTR	0.06
2825760	REC02633	<i>srhD</i>	N	259	23, 246		P05707	Sorbitol-6-phosphate 2-dehydrogenase (EC 1.1.1.140)	b2705	CHM	0.13
2826644	REC02634	<i>gutM</i>	N	119	87		P15081	Glucitol operon activator protein	b2706	RCD	0.03
2827070	REC02635	<i>srhR</i>	N	257	19, 195		P15082	Glucitol operon repressor	b2707	RCD	0.09
2827875	REC02636	<i>gutQ</i>	N	308	8, 12, 38, 56, 94, 98, 169		P17115	GutQ protein	b2708	UNC	0.00
2830387	REC05605	<i>ygaA</i>	N	529	62, 225, 264, 405, 466		P37013	Hypothetical sigma-54-dependent transcriptional regulator ygaA	b2709	UNC	0.59
2830499	REC02639	<i>f1rD</i>	N	479	145, 154, 382, 401, 450, 456		Q46877	Flavorubredoxin	b2710	BEN	0.34
2831935	REC02640	<i>f1rR</i>	N	377	50, 97, 99		P73596	F1rD-NAD(+) reductase (EC 1.18.1.-)	b2711	BEN	0.69
2835448	REC06486	<i>hypF</i>	N	750	22, 86, 98, 148, 202, 215, 265, 266, 298, 332, 365, 497, 568, 694		P30131	Hydrogenase maturation protein hypF	b2712	UNC	0.19
2836128	REC05608	<i>hydN</i>	N	175	108		P30132	Electron transport protein hydN	b2713	BEN	0.00
2837290	REC05609	<i>ascG</i>	N	337	13, 46, 83, 273		P24242	Cryptic asc operon repressor	b2714	RCD	0.06
2837547	REC02644	<i>ascF</i>	N	485	203		P24241	PTS system, arbutin-, cellobiose-, and salicin-specific IIABC comp	b2715	MTR	0.47
2839013	REC02645	<i>ascB</i>	N	474	48, 381		P24240	6-phospho-beta-glucosidase ascB (EC 3.2.1.86)	b2716	CHM	0.22
2841066	REC05610	<i>hycI</i>	E	156	-	0.34	Q57451	Hydrogenase 3 maturation protease (EC 3.4.-.-)	b2717	BEN	0.00
2841469	REC05611	<i>hycH</i>	N	136	105		P16434	Formate hydrogenlyase maturation protein hycH	b2718	BEN	0.00
2842233	REC05612	<i>hycG</i>	N	255	27		P16433	Formate hydrogenlyase subunit 7	b2719	BEN	0.00
2842775	REC05613	<i>hycF</i>	E	180	-	< 0.3	P16432	Formate hydrogenlyase subunit 6	b2720	BEN	0.06
2844494	REC05614	<i>hycE</i>	N	569	114, 447		P16431	Formate hydrogenlyase subunit 5 precursor	b2721	BEN	0.03
2845435	REC05615	<i>hycD</i>	N	307	72, 94, 115, 231, 242		P16430	Formate hydrogenlyase subunit 4	b2722	BEN	0.06
2847264	REC06487	<i>hycC</i>	N	608	26, 36, 69, 347, 370, 451, 453, 506		P16429	Formate hydrogenlyase subunit 3	b2723	BEN	0.00
2847872	REC05617	<i>hycB</i>	X	203	-		P16428	Formate hydrogenlyase subunit 2	b2724	BEN	0.00
2848458	REC05618	<i>hycA</i>	N	153	110, 146		P16427	Formate hydrogenlyase regulatory protein hycA	b2725	RCD	0.00
2848670	REC02655	<i>hypA</i>	?	116	99		P24189	HypA protein	b2726	UNC	0.06
2849024	REC02656	<i>hypB</i>	N	290	32, 78, 122, 143, 186, 286		P24190	Hydrogenase isoenzymes nickel incorporation protein hypB	b2727	BEN	0.22
2849887	REC02657	<i>hypC</i>	?	90	-		P24191	Hydrogenase isoenzymes formation protein hypC	b2728	BEN	0.03
2850159	REC02658	<i>hypD</i>	N	373	91, 152, 201, 286		P24192	Hydrogenase isoenzymes formation protein hypD	b2729	UNC	0.19
2851319	REC02659	<i>hypE</i>	N	322	42, 129, 143, 165, 168, 187		P24193	Hydrogenase isoenzymes formation protein hypE	b2730	UNC	0.22
2852361	REC02660	<i>fh1A</i>	N	692	88, 134, 281, 366, 434, 583		P19323	Formate hydrogenlyase transcriptional activator	b2731	RCD	0.06
2854829	REC05619	<i>ygaA</i>	E	117	-	< 0.3	P25728	Hypothetical protein ygaA	b2732	UNC	0.00
2855116	REC02662	<i>mutS</i>	N	853	125, 170, 176, 255, 307, 472, 489, 566, 694, 792, 852		P23908	DNA mismatch repair protein mutS	b2733	NAM	0.91
2857783	REC02663	<i>pphB</i>	N	218	23, 76, 104, 180, 200		P55799	Serine/threonine protein phosphatase 2 (EC 3.1.3.16)	b2730A	PMS	0.16
2859287	REC05620	<i>ygbI</i>	N	265	108, 246, 260, 262		P52598	Hypothetical transcriptional regulator ygbI	b2735	UNC	0.25
2859453	REC02665	<i>ygbJ</i>	N	302	46, 89		Q46888	Hypothetical oxidoreductase ygbJ (EC 1.1.-.-)	b2736	UNC	0.09
2860358	REC02666	<i>ygbK</i>	E	388	-	< 0.01	Q46889	Hypothetical protein ygbK	b2737	UNC	0.09
2861616	REC02667	<i>ygbL</i>	N	212	169, 173		Q46890	Hypothetical aldolase class II protein ygbL	b2738	UNC	0.47
2862259	REC02668	<i>ygbM</i>	N	258	11, 64, 147, 169		Q46891	Hypothetical protein ygbM	b2739	UNC	0.22
2863124	REC02669	<i>ygbN</i>	N	454	43, 96, 347, 388, 445		Q46892	Hypothetical permease ygbN	b2740	UNC	0.31
2865574	REC05621	<i>rpoS</i>	N	330	128, 143, 171, 199		P13445	RNA polymerase sigma factor rpoS	b2741	RCD	0.13
2866776	REC05622	<i>nlpD</i>	N	379	25, 84, 148, 156, 178, 220, 315, 364, 372		P33648	Lipoprotein nlpD precursor	b2742	LPC	0.38
2867542	REC05623	<i>pcm</i>	N	208	160		P24206	Protein-L-isoaspartate O-methyltransferase (EC 2.1.1.77)	b2743	PMS	0.41
2868297	REC05624	<i>surE</i>	N	253	29, 156		P36664	Acid phosphatase surE (EC 3.1.3.2)	b2744	MSM	0.63
2869327	REC05625	<i>ygbO</i>	N	349	99, 121, 314		Q57261	Protein ygbO	b2745	UNC	0.22
2869803	REC05626	<i>ispF</i>	E	159	-	< 0.2	P36663				

2872015	REC05630	<i>cysC</i>	?	201	177	P23846	Adenylylsulfate kinase (EC 2.7.1.25)	b2750	MSM	0.56
2873442	REC05631	<i>cysN</i>	N	475	58, 94, 118, 140, 165, 247, 292, 322, 370, 420, 455	P23845	Sulfate adenylyltransferase subunit 1 (EC 2.7.7.4)	b2751	MSM	0.44
2874352	REC05632	<i>cysD</i>	N	302	225	P21156	Sulfate adenylyltransferase subunit 2 (EC 2.7.7.4)	b2752	MSM	0.41
2874604	REC02682	<i>iap</i>	N	345	33, 41, 168, 171, 335, 340	P10423	Alkaline phosphatase isozyme conversion protein precursor (EC 3.1.3.1)	b2753	MSM	0.03
2876942	REC05633	<i>ygbF</i>	N	116	37, 89	P45956	Hypothetical protein ygbF	b2754	UNC	0.00
2877795	REC05634	<i>ygbT</i>	N	305	72, 275	Q46896	Hypothetical protein ygbT	b2755	UNC	0.00
2878410	REC05635	<i>ygcH</i>	N	199	98, 120, 140, 192	Q46897	Hypothetical protein ygcH	b2756	UNC	0.00
2879077	REC05636	<i>ygcJ</i>	N	226	181, 188	Q46898	Hypothetical protein ygcJ precursor	b2757	UNC	0.00
2880165	REC05637	<i>ygcI</i>	N	363	30, 202, 236, 240, 255, 313, 343	Q46899	Hypothetical protein ygcI	b2758	UNC	0.00
2880660	REC05638	<i>ygcK</i>	N	160	5, 87, 127, 160	P76632	Hypothetical protein ygcK	b2759	UNC	0.00
2882161	REC05639	<i>ygcL</i>	N	502	86, 183, 196, 249, 326, 345, 399, 451, 482	Q46901	Hypothetical protein ygcL	b2760	UNC	0.00
2885242	REC05640	<i>ygcB</i>	X	888	848	P38036	Hypothetical protein ygcB	b2761	UNC	0.03
2886335	REC05641	<i>cysH</i>	N	244	132, 147	P17854	Phosphoadenosine phosphosulfate reductase (EC 1.8.99.4)	b2762	MSM	0.50
2888122	REC05642	<i>cysI</i>	N	570	251, 269, 277, 339, 537	P17846	Sulfite reductase [NADPH] hemoprotein beta-component (EC 1.8.1.1)	b2763	MSM	0.38
2889921	REC05643	<i>cysJ</i>	N	599	9, 137, 184, 212, 456	P38038	Sulfite reductase [NADPH] flavoprotein alpha-component (EC 1.8.1.1)	b2764	MSM	0.38
2890237	REC02694	<i>ygcM</i>	N	121	57, 105	Q46903	Putative 6-pyruvoyl tetrahydropterin synthase (EC 4.6.1.10)	b2765	UNC	0.41
2890650	REC02695	<i>ygcN</i>	N	433	57, 87, 137, 214, 261, 391, 416	Q46904	Probable electron transfer flavoprotein-quinone oxidoreductase yg	b2766	UNC	0.00
2891906	REC02696	<i>ygcO</i>	N	98	69, 95	Q46905	Ferredoxin-like protein ygcO	b2767	UNC	0.13
2892219	REC02697	<i>ygcP</i>	?	191	37	Q46906	Hypothetical protein ygcP	b2768	UNC	0.19
2893835	REC05644	<i>ygcQ</i>	N	297	97, 155, 175, 232	Q46907	Putative electron transfer flavoprotein subunit ygcQ	b2769	UNC	0.00
2894584	REC05650	<i>ygcR</i>	N	261	56, 173	Q46908	Putative electron transfer flavoprotein subunit ygcR	b2770	UNC	0.50
2895965	REC05646	<i>ygcS</i>	N	469	189, 380, 444	Q46909	Hypothetical metabolite transport protein ygcS	b2771	UNC	0.00
2896781	REC05647	<i>ygcU</i>	N	264	39, 102, 111, 177, 192	Q46911	Hypothetical flavoprotein ygcU	b2772	UNC	0.00
2897440	REC05648	<i>ygcV</i>	N	218	31, 94, 172	Q46911	Hypothetical flavoprotein ygcV	b2773	UNC	0.06
2898370	REC05650	<i>ygcW</i>	N	286	5, 55, 165, 183, 232	P76633	Hypothetical oxidoreductase ygcW (EC 1.-.-.-)	b2774	UNC	0.03
2898614	REC06504	<i>ygcE</i>	N	425	98, 118, 333, 374	P77031	Hypothetical protein ygcE	b2775	UNC	0.00
2899918	REC02707	<i>ygcE</i>	N	492	196, 291, 334, 419, 433	P55138	Hypothetical sugar kinase ygcE	b2776	UNC	0.41
2903440	REC05651	<i>ygcF</i>	N	223	7, 30, 38	P55139	Hypothetical protein ygcF	b2777	UNC	0.19
2903664	REC02709	<i>ygcG</i>	X	313	143, 245, 302	P55140	Hypothetical protein ygcG	b2778	UNC	0.22
2905963	REC05652	<i>eno</i>	X	432	-	P08324	Enolase (EC 4.2.1.11)	b2779	CHM	0.97
2907688	REC05653	<i>pyrG</i>	E	545	-	P08398	CTP synthase (EC 6.3.4.2)	b2780	NCM	0.94
2908707	REC05654	<i>mazG</i>	N	263	10, 21, 46	P33646	MazG protein	b2781	UNC	0.63
2909113	REC05655	<i>chpA</i>	N	111	9, 68, 73	P33645	PemK-like protein 1	b2782	UNC	0.09
2909361	REC05656	<i>chpR</i>	N	82	60	P18534	PemL-like protein 1	b2783	UNC	0.06
2911673	REC05657	<i>reLA</i>	N	744	326, 368, 412, 415	P11585	GTP pyrophosphokinase (EC 2.7.6.5)	b2784	MSM	0.25
2913022	REC05658	<i>rumA</i>	N	433	321	P55135	23S rRNA (Uracil-5-)-methyltransferase rumA (EC 2.1.1.-)	b2785	NAM	0.72
2913079	REC02717	<i>barA</i>	N	918	67, 95, 176, 337	P26607	Sensor protein barA (EC 2.7.3.-)	b2786	UNC	0.31
2917407	REC05659	<i>gudD</i>	N	446	76, 191, 204	P76637	Glucarate dehydratase (EC 4.2.1.40)	b2787	CHM	0.13
2918768	REC05660	<i>gudX</i>	N	446	31, 123, 315, 319	Q46915	Glucarate dehydratase related protein (EC 4.2.1.-)	b2788	UNC	0.03
2920122	REC05661	<i>gudP</i>	N	450	190, 324, 422	Q46916	Probable glucarate transporter	b2789	UNC	0.34
2921006	REC05662	<i>yqcA</i>	N	149	73, 108, 109	Q46917	Hypothetical protein yqcA	b2790	UNC	0.34
2921806	REC05663	<i>yqcB</i>	N	260	41, 64, 160, 180, 184, 233	Q46918	Hypothetical protein yqcB	b2791	UNC	1.00
2922135	REC05664	<i>yqcC</i>	N	109	19, 45	Q46919	Hypothetical protein yqcC	b2792	UNC	0.06
2923302	REC05665	<i>syd</i>	N	181	49	P43526	Syd protein	b2793	UNC	0.03
2923370	REC02725	<i>yqcD</i>	N	282	43, 71, 226	Q46920	Hypothetical protein yqcD	b2794	UNC	0.59
2924330	REC02726	<i>ygdH</i>	N	454	13, 167, 256, 266, 432	P37350	Hypothetical protein ygdH	b2795	UNC	0.09
2926251	REC02727	<i>sdac</i>	N	429	201, 206, 255, 348, 353, 385, 391, 411	P36559	Serine transporter	b2796	MTR	0.13
2927598	REC02728	<i>sdaB</i>	N	455	43, 48, 69, 118, 125, 153, 167, 207, 380	P30744	L-serine dehydratase 2 (EC 4.2.1.13)	b2797	AAM	0.66
2928987	REC02729	<i>xni</i>	N	281	39, 147	P38506	Exodeoxyribonuclease IX (EC 3.1.11.-)	b2798	NAM	0.03
2931038	REC05666	<i>fucO</i>	N	383	40, 160, 182, 196, 211, 341	P11549	Lactaldehyde reductase (EC 1.1.1.77)	b2799	CHM	0.16
2931710	REC05667	<i>fucA</i>	N	215	15, 34, 56, 96, 113, 194	P11550	L-fucose phosphate aldolase (EC 4.1.2.17)	b2800	CHM	0.27
2932257	REC02732	<i>fucP</i>	N	438	41, 173, 211	P11551	L-fucose permease	b2801	MTR	0.42
2933606	REC02733	<i>fucI</i>	N	591	366, 490, 523, 525	P11552	L-fucose isomerase (EC 5.3.1.25)	b2802	CHM	0.16
2935460	REC02734	<i>fucK</i>	N	482	5, 38, 194, 219, 316, 396	P11553	L-fuculokinase (EC 2.7.1.51)	b2803	CHM	0.03
2936910	REC02735	<i>fucU</i>	?	140	106	P11555	Fucose operon fucU protein	b2804	UNC	0.19
2937390	REC02736	<i>fucR</i>	N	243	4, 170	P11554	L-fucose operon activator	b2805	RCD	0.06
2939265	REC05668	<i>ygdE</i>	N	366	69, 115, 310	P32066	Hypothetical protein ygdE	b2806	UNC	0.09
2939653	REC05669	<i>ygdD</i>	N	131	92	P32065	Hypothetical protein ygdD	b2807	UNC	0.16
2940589	REC05670	<i>gcvA</i>	N	305	171, 219	P32064	Glycine cleavage system transcriptional activator	b2808	RCD	0.28
2941170	REC05671	<i>ygdI</i>	?	76	68	Q46924	Hypothetical lipoprotein ygdI precursor	b2809	UNC	0.00
2941359	REC02741	<i>csdA</i>	N	401	11, 23, 172, 236, 244, 357	Q46925	Cysteine sulfinate desulfinase (EC 4.4.1.-)	b2810	NCM	0.94
2942564	REC02742	<i>ygdK</i>	E	147	-	Q46926	Hypothetical protein ygdK	b2811	UNC	0.19
2943864	REC05672	<i>ygdL</i>	N	268	96, 251	Q46927	Hypothetical protein ygdL	b2812	UNC	0.75
2945200	REC05673	<i>mJtA</i>	N	365	44, 129, 129, 289	P46885	Membrane-bound lytic murein transglycosylase A precursor (EC 3.1.1.1)	b2813	LPC	0.41
2947122	REC05674	<i>amiC</i>	N	447	67, 119, 216, 331, 372	Q46929	N-acetylmuramoyl-L-alanine amidase amiC precursor (EC 3.5.1.2)	b2817	LPC	0.84
2947264	REC02746	<i>argA</i>	N	443	71, 86, 107, 109, 133, 154, 197, 222, 223, 255, 433	P08295	Amino-acid acetyltransferase (EC 2.3.1.1)	b2818	AAM	0.47
2950483	REC05675	<i>recD</i>	N	608	46, 117, 205, 335, 469, 483, 572, 573, 602	P04993	Exodeoxyribonuclease V alpha chain (EC 3.1.11.5)	b2819	NAM	0.63
2954025	REC05676	<i>recB</i>	N	1180	405, 560, 599, 601, 763, 881, 903, 910, 967	P08394	Exodeoxyribonuclease V beta chain (EC 3.1.11.5)	b2820	NAM	0.31
2956906	REC06513	<i>ptrA</i>	N	962	270, 361, 437, 536, 577, 614, 728, 744, 762, 783, 794, 801, 861, 914, 943	P05458	Protease III precursor (EC 3.4.24.55)	b2821	PMS	0.19
2960450	REC05678	<i>recC</i>	N	1122	194, 358, 398, 551, 743, 823, 850	P07648	Exodeoxyribonuclease V gamma chain (EC 3.1.11.5)	b2822	NAM	0.25
2960786	REC05679	<i>ppdC</i>	?	107	-	P08372	Prepilin peptidase dependent protein C precursor	b2823	UNC	0.00
2961136	REC05680	<i>ygdB</i>	N	121	1, 18, 114	P08370	Hypothetical protein ygdB precursor	b2824	UNC	0.00
2961738	REC05681	<i>ppdB</i>	N	187	31, 42, 58, 73, 78, 97, 139, 170, 183	P08371	Prepilin peptidase dependent protein B precursor	b2825	UNC	0.00
2962199	REC05682	<i>ppdA</i>	N	156	20	P33554	Prepilin peptidase dependent protein A precursor	b2826	UNC	0.00
2963177	REC05683	<i>thyA</i>	E	264	-	P00470	Thymidylate synthase (EC 2.1.1.45)	b2827	NCM	0.81
2964059	REC05684	<i>lgt</i>	E	291	-	P37149	Prolipoprotein diacylglycerol transferase (EC 2.4.99.-)	b2828	PMS	0.97
2964656	REC05685	<i>ptsP</i>	N	748	29, 158, 194, 355, 399, 405, 453, 456, 482, 580, 663	P37177	Phosphoenolpyruvate-protein phosphotransferase ptsP (EC 2.7.3.1)	b2829	CHM	0.75
2966999	REC05686	<i>nudH</i>	N	176	116	Q46930	Probable (di)nucleoside polyphosphate hydrolase (EC 3.6.1.-)	b2830	UNC	0.44
2967684	REC02759	<i>mutH</i>	N	229	52, 110, 162	P06722	DNA mismatch repair protein mutH	b2831	NAM	0.06
2968442	REC02760	<i>ygdQ</i>	N	237	26, 76, 158	Q46931	Hypothetical protein ygdQ	b2832	UNC	0.03
2969293	REC02761	<i>ygdR</i>	N	72	46, 70	Q46932	Hypothetical lipoprotein ygdR precursor	b2833	UNC	0.03
2969619	REC02762	<i>tas</i>	N	346	52, 56, 119, 295	Q46933	Tas protein	b2834	UNC	0.19
2971884	REC05687	<i>ygeD</i>	N	397	57, 94, 99, 107, 152	P39196	Hypothetical protein ygeD	b2835	UNC	0.09
2974036	REC05688	<i>as</i>	N	719	237, 339, 357, 449, 516, 617, 632	P31119	AAS bifunctional protein	b2836	LPC	0.19
2974621	REC02765	<i>galR</i>	N	343	111, 133, 181, 221, 254, 277, 312, 325	P03024	Galactose operon repressor	b2837	RCD	0.13
2976921	REC05689	<i>lysA</i>	N	420	153, 216, 381	P00861	Diaminopimelate decarboxylase (EC 4.1.1.20)	b2838	AAM	0.81
2977043	REC02767	<i>lysR</i>	X	311	-	P03030	Transcriptional activator protein lysR	b2839	RCD	0.19
2978657	REC05690	<i>ygeA</i>	N	230	43, 99, 105	P03813	Hypothetical protein ygeA	b2840	UNC	0.19
2980204	REC05691	<i>araE</i>	N	472	413	P09830	Arabinose-proton symporter	b2841	MTR	0.00
2981280	REC05692	<i>kduD</i>	X	253	-	P37769	2-deoxy-D-gluconate 3-dehydrogenase (EC 1.1.1.125)	b2842	LPC	0.31
2982146	REC05693	<i>kduI</i>	X	278	-	Q46938	4-deoxy-L-threo-5-hexosulose-uronate ketol-isomerase (EC 5.3.1.1)	b2843	BEN	0.13
2983617	REC05694	<i>ygeF</i>	X	394	-	Q46939	Probable acetyl-CoA acetyltransferase (EC 2.3.1.9)	b2844	UNC	0.66
2983869	REC02773	<i>ygeG</i>	X	409	-	Q46940	Hypothetical trans-protein ygeG	b2845	UNC	0.13

2985498	REC02774	<i>yqeH</i>	X	230	-	Q46941	Hypothetical protein yqeH	b2846	UNC	0.00
2986524	REC02775	<i>yqeI</i>	X	269	-	Q46942	Hypothetical protein yqeI	b2847	UNC	0.00
2987314	REC06515	<i>yqeJ</i>	X	164	-	Q46943	Hypothetical protein yqeJ	b2848	UNC	0.00
2988394	REC06516	<i>yqeK</i>	X	145	-	P77136	Hypothetical protein yqeK	b2849	UNC	0.00
2988576	REC06517	<i>yqeF</i>	X	148	-	Q46786	Hypothetical protein yqeF	b2850	UNC	0.00
2989290	REC02776	<i>yqeG</i>	X	163	-	Q46787	Hypothetical protein yqeG	b2851	UNC	0.00
2990116	REC02777	<i>yqeH</i>	X	458	-	P76639	Hypothetical protein yqeH	b2852	UNC	0.00
2991660	REC02778	<i>yqeI</i>	X	72	-	Q46789	Hypothetical protein yqeI	b2853	UNC	0.00
2992021	REC02779		E	138	-	Q46790	ORF_O138	b2854	UNC	0.03
2992928	REC05695	<i>yqeK</i>	N	148	-	Q46791	Hypothetical transcriptional regulator yqeK	b2856	UNC	0.00
2993114	REC05696		N	51	-			b2857	UNC	0.00
2993767	REC05697		N	143	-	Q46793	ORF_F143	b2857	UNC	0.00
2993991	REC05698		N	73	-	P76640	FROM BASES 2988059 TO 2997958 (SECTION 259 OF 400) OF	b2858	UNC	0.00
2994409	REC05699		N	141	-	Q46795	ORF_F141	b2859	UNC	0.00
2995299	REC06518	<i>insD4</i>	N	301	-	P19777	Transposase insD for insertion element IS2A/D/F/H/I/K	b2860	PHT	0.56
2995622	REC06519	<i>insC4</i>	X	121	-	P19776	Transposase insC for insertion element IS2A/D/F/H/I/K	b2861	PHT	0.56
2996010	REC05702	<i>yqeP</i>	X	99	-	Q46796	Hypothetical protein yqeP	b2862	UNC	0.00
2996892	REC05703	<i>yqeQ</i>	X	278	-	Q46797	Hypothetical protein yqeQ	b2863	UNC	0.00
2997937	REC05704	<i>yqeR</i>	X	259	-	Q46798	Hypothetical lipoprotein yqeR precursor	b2865	UNC	0.66
2998367	REC02790	<i>xdhA</i>	N	752	310, 347, 396, 595, 632, 697, 707	Q46799	Xanthine dehydrogenase, molybdenum binding subunit (EC 1.1.1.-)	b2866	BEN	0.31
3000636	REC02791	<i>xdhB</i>	N	292	54, 76, 131	Q46800	Xanthine dehydrogenase, FAD binding subunit (EC 1.1.1.204)	b2867	BEN	0.34
3001511	REC02792	<i>xdhC</i>	N	159	72, 111	Q46801	Xanthine dehydrogenase iron-sulfur binding subunit	b2868	BEN	0.25
3003808	REC05705	<i>yqeV</i>	N	592	1, 41, 61, 77, 95, 143, 215, 270, 328, 329, 357, 380, 387, 410, 438, 460	Q46802	Hypothetical sigma-54-dependent transcriptional regulator yqeV	b2869	UNC	0.19
3004356	REC02794	<i>yqeW</i>	N	363	15, 74	Q46803	Hypothetical protein yqeW	b2870	UNC	0.84
3005531	REC02795	<i>yqeX</i>	N	398	181, 270, 296, 328, 336	Q46804	Putative diaminopropionate ammonia-lyase (EC 4.3.1.15)	b2871	UNC	0.03
3006785	REC02796	<i>yqeY</i>	N	403	13, 107, 114, 144, 225, 348	Q46805	Hypothetical protein yqeY	b2872	UNC	0.38
3008037	REC02797	<i>yqeZ</i>	N	465	448, 450	Q46806	Hypothetical hydrolase yqeZ (EC 3.-.-.-)	b2873	UNC	0.16
3009482	REC02798	<i>yqeA</i>	N	310	14, 61, 61, 100, 126, 148, 172, 215	Q46807	Carbamate kinase-like protein yqeA	b2874	UNC	0.25
3012260	REC05706	<i>yqeB</i>	N	541	5, 94, 208, 277, 426, 457	Q46808	Hypothetical protein yqeB	b2875	UNC	0.22
3013015	REC05707	<i>yqeC</i>	?	235	15	Q46809	Hypothetical protein yqeC	b2876	UNC	0.00
3013181	REC02801	<i>ygfJ</i>	N	192	46, 87, 107, 154, 159	Q46810	Hypothetical protein ygfJ	b2877	UNC	0.22
3014081	REC02802	<i>ygfK</i>	N	1032	5, 528, 712, 721, 726, 740, 754, 805, 1028	Q46811	Hypothetical protein ygfK	b2878	UNC	0.00
3017116	REC02803	<i>ssnA</i>	N	464	16, 72, 145, 278	Q46812	SsnA protein	b2879	UNC	0.03
3018561	REC02804	<i>ygfM</i>	E	259	-	Q46813	Hypothetical protein ygfM	b2880	UNC	0.00
3019337	REC02805	<i>xhdH</i>	N	956	104, 195, 443, 457, 510, 587, 697, 864	Q46814	Possible hypoxanthine oxidase xhdH (EC 1.-.-.-)	b2881	UNC	0.19
3022315	REC02806	<i>ygfO</i>	N	485	18, 71, 430, 453, 477	Q46815	Putative purine permease ygfO	b2882	UNC	0.38
3023787	REC02807	<i>guaD</i>	N	439	62, 87, 107, 121, 356	P76641	Guanine deaminase (EC 3.5.4.3)	b2883	NCM	0.47
3025142	REC02808	<i>ygfQ</i>	N	189	55	Q46817	Hypothetical protein ygfQ	b2884	UNC	0.66
3025678	REC02809	<i>ygfR</i>	N	276	25, 226	Q46818	Hypothetical protein ygfR	b2885	UNC	0.66
3027035	REC05708	<i>ygfS</i>	N	163	20, 100, 132, 134	Q46819	Putative electron transport protein ygfS	b2886	UNC	0.00
3028966	REC05709	<i>ygfT</i>	N	644	128, 142, 203, 225, 260, 331, 336	Q46820	Hypothetical protein ygfT	b2887	UNC	0.66
3029318	REC02812	<i>ygfU</i>	N	505	309, 329, 358, 372, 410, 469, 501	Q46821	Putative purine permease ygfU	b2888	UNC	0.38
3031085	REC02813	<i>idi</i>	N	182	27, 55, 75, 119, 139	Q46822	Isopentenyl-diphosphate delta-isomerase (EC 5.3.3.2)	b2889	LPC	0.09
3033194	REC05710	<i>lysS</i>	X	505	-	P13030	Lysyl-tRNA synthetase (EC 6.1.1.6)	b2890	NAM	0.91
3034302	REC06534	<i>prfB</i>	?	365	-	P07012	Peptide chain release factor 2	b2891	PMS	0.88
3036126	REC05712	<i>recJ</i>	N	577	26, 140, 209, 246, 437, 465, 491	P21893	Single-stranded-DNA-specific exonuclease recJ (EC 3.1.-.-)	b2892	NAM	0.91
3036842	REC05713	<i>dsbC</i>	N	236	192	P21892	Thiol:disulfide interchange protein dsbC precursor	b2893	PMS	0.22
3037763	REC05714	<i>xerD</i>	?	298	253	P21891	Integrase/recombinase xerD	b2894	NAM	0.81
3037875	REC02819	<i>fldB</i>	N	173	8, 90, 132, 143	P41050	Flavodoxin 2	b2895	CHM	0.25
3038843	REC05715	<i>ygfX</i>	N	135	20, 89	Q46824	Hypothetical protein ygfX	b2896	UNC	0.00
3039090	REC05716	<i>ygfY</i>	E	88	-	Q46825	Hypothetical protein ygfY	b2897	UNC	0.13
3039333	REC02822	<i>ygfZ</i>	X	326	-	P39179	Unknown protein from 2D-page	b2898	UNC	0.72
3041168	REC05717	<i>yqfA</i>	N	219	6, 136, 188	Q46827	Hypothetical protein yqfA	b2899	UNC	0.63
3041643	REC05718	<i>yqfB</i>	E	103	-	Q46828	Hypothetical protein yqfB	b2900	UNC	0.06
3041682	REC06535	<i>bgIA</i>	N	479	15, 60, 100, 122, 307, 376, 447	Q46829	6-phospho-beta-glucosidase bgIA (EC 3.2.1.86)	b2901	CHM	0.22
3043921	REC06536	<i>ygfF</i>	X	247	-	P52037	Hypothetical oxidoreductase ygfF (EC 1.-.-.-)	b2902	UNC	0.28
3047061	REC05719	<i>gcvP</i>	N	957	95, 313, 430, 558, 578, 684, 703, 737, 777, 806, 847, 913, 930, 934	P33195	Glycine dehydrogenase [decarboxylating] (EC 1.4.4.2)	b2903	AAM	0.56
3047569	REC05720	<i>gcvH</i>	N	129	60	P23884	Glycine cleavage system H protein	b2904	MSM	0.63
3048687	REC05721	<i>gcvT</i>	N	364	21, 125, 195, 204, 231, 273	P27248	Aminomethyltransferase (EC 2.1.2.10)	b2905	AAM	0.72
3050337	REC05722	<i>visC</i>	N	400	182	P25535	Protein visC (EC 1.-.-.-)	b2906	UNC	0.41
3051538	REC05723	<i>ubiH</i>	E	392	371	P25534	2-octaprenyl-6-methoxyphenol hydroxylase (EC 1.14.13.-)	b2907	NCM	0.19
3052860	REC05724	<i>pepP</i>	N	441	152, 206, 224, 301, 365	P15034	Xaa-Pro aminopeptidase (EC 3.4.11.9)	b2908	PMS	0.31
3053470	REC05725	<i>ygfB</i>	E	194	-	P25533	Hypothetical protein ygfB	b2909	UNC	0.13
3053632	REC02833	<i>ygfE</i>	N	109	53, 65	P45580	Hypothetical protein ygfE	b2910	UNC	0.16
3054261	REC02834	<i>yqfA</i>	N	182	10, 42, 45, 81, 152	P09160	Hypothetical protein yqfA	b2912	UNC	0.78
3056430	REC05726	<i>serA</i>	N	410	101, 210, 247, 370, 406	P08328	D-3-phosphoglycerate dehydrogenase (EC 1.1.1.95)	b2913	AAM	0.75
3057345	REC05727	<i>rpiA</i>	X	219	-	P27252	Ribose 5-phosphate isomerase A (EC 5.3.1.6)	b2914	CHM	0.69
3057631	REC05728	<i>yqfE</i>	N	76	29	P52038	Hypothetical protein yqfE	b2915	UNC	0.00
3057773	REC02838	<i>icia</i>	N	297	18, 81, 180, 192	P24194	Chromosome initiation inhibitor	b2916	RCD	0.16
3058870	REC02839	<i>sbm</i>	N	714	67, 98, 153, 286, 576, 703	P27253	Sbm protein	b2917	UNC	0.28
3061007	REC02840	<i>argK</i>	N	331	7, 40, 62, 99, 127, 158	P27254	LAO/AO transport system kinase (EC 2.7.-.-)	b2918	MTR	0.13
3061971	REC02841	<i>yqfG</i>	N	275	22, 67	P52045	Hypothetical protein yqfG	b2919	UNC	0.03
3062822	REC02842	<i>yqfH</i>	N	492	69, 321	P52043	Hypothetical protein yqfH	b2920	UNC	0.22
3065208	REC05729	<i>ygfI</i>	N	303	12, 28, 86, 92, 124, 148, 195, 235, 257, 259, 265, 279, 291	P52044	Hypothetical transcriptional regulator ygfI	b2921	UNC	0.00
3066100	REC05730	<i>yggE</i>	N	246	2, 162, 191, 213	P11668	Hypothetical protein yggE	b2922	UNC	0.16
3066828	REC05731	<i>yggA</i>	E	211	187	P11667	Hypothetical protein yggA	b2923	UNC	0.38
3067827	REC05732	<i>yggB</i>	?	286	21	P11666	Hypothetical protein yggB	b2924	UNC	0.88
3069264	REC05733	<i>fbaA</i>	E	359	352	P11604	Fructose-bisphosphate aldolase class II (EC 4.1.2.13)	b2925	CHM	0.22
3070642	REC05734	<i>pgk</i>	E	387	-	P11665	Phosphoglycerate kinase (EC 2.7.2.3)	b2926	CHM	0.97
3071711	REC05735	<i>epd</i>	N	339	38, 45, 73, 141, 247	P11603	D-erythrose 4-phosphate dehydrogenase (EC 1.2.1.-)	b2927	NCM	0.38
3072709	REC05736	<i>yggC</i>	N	237	27, 35	P11664	Hypothetical protein yggC	b2928	UNC	0.13
3073215	REC05737	<i>yggD</i>	N	169	98	P11663	Hypothetical protein yggD	b2929	UNC	0.00
3074202	REC05738	<i>yggF</i>	N	321	54, 317	P21437	Hypothetical protein yggF	b2930	UNC	0.00
3075188	REC05739	<i>yggP</i>	N	329	32, 60, 67, 151, 192	P52048	Hypothetical protein yggP	b2932	UNC	0.00
3075475	REC05740		N	118	24, 45, 76, 93			b2932	UNC	0.00
3076878	REC05741	<i>cmtA</i>	N	462	209, 352, 395, 419	P32059	PTS system, mannitol (Cryptic)-specific IIBC component (EC 2.7.1.6)	b2933	MTR	0.25
3077349	REC05742	<i>cmtB</i>	N	147	46	P32058	PTS system, mannitol (Cryptic)-specific IIA component (EC 2.7.1.6)	b2934	MTR	0.03
3079654	REC06542	<i>tktA</i>	E	663	-	P27302	Transketolase 1 (EC 2.2.1.1)	b2935	CHM	0.94
3079806	REC02858	<i>yggG</i>	N	294	101, 141, 194, 249, 290	P25894	Putative metalloprotease yggG (EC 3.4.24.-)	b2936	UNC	0.00
3081816	REC05744	<i>speB</i>	N	306	129, 249	P16936	Agmatinase (EC 3.5.3.11)	b2937	AAM	0.38
3083930	REC05745	<i>speA</i>	N	658	139, 243, 309, 361	P21170	Biosynthetic arginine decarboxylase (EC 4.1.1.19)	b2938	AAM	0.28
3084085	REC05746	<i>yggB</i>	?	48	-	P46877	Hypothetical protein yggB	b2939	UNC	0.00
3084206	REC02862	<i>yggC</i>	?	71	-	P46878	Hypothetical protein yggC	b2940	UNC	0.00

3084669	REC05747	yggD	?	83	80			P46879	Hypothetical protein yggD		b2941	UNC	0.00
3084725	REC02864	metK	E	384	-		< 0.01	P04384	S-adenosylmethionine synthetase (EC 2.5.1.6)		b2942	MSM	0.97
3086303	REC02865	galP	N	464	356, 361			P37021	Galactose-proton symporter		b2943	MTR	0.16
3087774	REC02866	sprt	N	165	12, 103			P39902	Protein sprT		b2944	UNC	0.09
3088366	REC02867	enda	N	235	17, 40, 42, 55, 69, 101			P25736	Endonuclease I precursor (EC 3.1.21.1)		b2945	NAM	0.09
3089126	REC02868	yggJ	N	252	96, 151, 174			P37912	Hypothetical protein yggJ		b2946	UNC	0.78
3089897	REC02869	gshB	E	316	-		< 0.01	P04425	Glutathione synthetase (EC 6.3.2.3)		b2947	AAM	0.41
3090884	REC02870	yggE	E	211	-		< 0.05	P52049	Protein yggE		b2948	UNC	0.50
3091519	REC02871	yggF	E	138	-		< 0.2	P52050	Hypothetical protein yggF		b2949	UNC	0.81
3093117	REC02873	yggS	N	234	29, 180, 234			P52054	Hypothetical protein yggS		b2951	UNC	0.81
3093144	REC05748	yggR	N	341	20, 114, 188, 203, 285, 310, 325			P52052	Hypothetical protein yggR		b2950	UNC	0.59
3093839	REC02874	yggT	N	188	153, 181			P52058	Hypothetical protein yggT		b2952	UNC	0.13
3094390	REC02875	yggU	X	100	-			P52060	Hypothetical protein yggU		b2953	UNC	0.06
3094700	REC02876	yggV	X	197	-			P52061	Hypothetical protein yggV		b2954	UNC	0.84
3095286	REC02877	yggW	N	378	17, 56, 90, 116, 162, 320			P52062	Hypothetical protein yggW		b2955	UNC	0.97
3097584	REC05749	yggM	N	335	3, 93, 229			P46142	Hypothetical protein yggM		b2956	UNC	0.00
3098747	REC05750	ansB	E	348	-		< 0.01	P00805	L-asparaginase II precursor (EC 3.5.1.1)		b2957	AAM	0.56
3099642	REC05751	yggN	N	239	71, 93, 110, 135, 149, 155			P46143	Hypothetical protein yggN		b2958	UNC	0.00
3100181	REC05752	yggL	E	118	-		< 0.2	P38521	Hypothetical protein yggL		b2959	UNC	0.06
3100870	REC05753	yggH	N	239	154, 180			P32049	Hypothetical methyltransferase yggH (EC 2.1.1.-)		b2960	UNC	0.88
3101031	REC02883	mutY	N	350	30, 89, 112			P17802	A/G-specific adenine glycosylase (EC 3.2.2.-)		b2961	NAM	0.75
3102111	REC02884	yggX	?	91	80			P52065	Protein yggX		b2962	UNC	0.22
3102448	REC02886	mltC	N	360	28, 70, 184, 199, 279, 304, 359			P52066	Membrane-bound lytic murein transglycosylase C precursor (EC 3	b2963	LPC	0.09	
3103684	REC02887	nupG	N	434	63, 160, 184, 254, 372, 400			P09452	Nucleoside permease nupG		b2964	MTR	0.03
3107233	REC05754	speC	N	731	82, 119, 183, 332, 462, 541, 690			P21169	Ornithine decarboxylase, constitutive (EC 4.1.1.17)		b2965	AAM	0.16
3107570	REC02889	yggA	N	235	8, 71, 130			Q46831	Hypothetical protein yggA		b2966	UNC	0.19
3109143	REC05755	yghD	N	178	40, 93			Q46832	Putative general secretion pathway protein M-type yghD		b2968	UNC	0.03
3110005	REC05756	yghE	N	286	20, 202, 232, 252			Q46833	Putative general secretion pathway protein L-type yghE		b2969	UNC	0.06
3110937	REC05757	yghF	N	288	30, 107, 193, 205			Q46834	Putative general secretion pathway protein C-type yghF precursor	b2970	UNC	0.03	
3111494	REC05758	yghG	N	136	20, 68, 120			Q46835	Hypothetical lipoprotein yghG precursor	b2971	UNC	0.00	
3112492	REC05759	pppA	?	310	232			Q46836	Leader peptidase pppA	b2972	PMS	0.00	
3115113	REC05760	yghJ	N	848	107, 200, 412, 415, 457, 464, 649, 669, 721, 775, 795			Q46837	Putative lipoprotein acfD homolog precursor		b2974	UNC	0.03
3117128	REC05761		N	675	31, 39, 261, 291, 321, 334, 645, 660						b2975	UNC	0.00
3119295	REC05762	glcA	N	560	462, 520, 525			Q46839	Glycolate permease glcA		b2975	MTR	0.25
3121821	REC05763	glcB	X	723	-			P37330	Malate synthase G (EC 4.1.3.2)		b2976	CHM	0.25
3122247	REC05764	glcG	X	134	-			P45504	Protein glcG		b2977	UNC	0.09
3124537	REC05765	glcF	N	761	93, 151, 198, 220, 285, 321, 410, 435, 573, 611, 634			P52074	Glycolate oxidase iron-sulfur subunit		b2978	CHM	0.47
3126036	REC05766	glcD	N	499	293, 402			P52075	Glycolate oxidase subunit glcD		b2979	CHM	0.69
3126287	REC02902	glcC	N	254	84, 153, 245			P52072	Glc operon transcriptional activator		b2980	RCD	0.06
3128193	REC06552		N	338	42			P03837	Transposase insH for insertion sequence element IS5		b2982	PHT	0.34
3128230	REC05767	yghO	N	390	58, 81, 109, 218, 300, 361			Q46840	Hypothetical protein yghO		b2981	UNC	0.06
3130333	REC05768	yghQ	N	325	14, 144, 197			Q46841	Hypothetical protein yghQ		b2983	UNC	0.06
3131227	REC05769	yghR	N	252	41, 91, 180, 252			Q46842	Hypothetical ATP-binding protein yghR		b2984	UNC	0.00
3131972	REC05770	yghS	N	237	26, 141, 233			Q46843	Hypothetical ATP-binding protein yghS		b2985	UNC	0.00
3132146	REC02908	yghT	N	230	49, 76, 181			Q46844	Hypothetical ATP-binding protein yghT		b2986	UNC	0.00
3134386	REC05771	pi tB	N	499	2, 41, 54, 79, 228, 242, 302, 314, 347, 455			P43676	Probable low-affinity inorganic phosphate transporter 2		b2987	UNC	0.66
3136537	REC05772	gsp	N	619	284, 570			P43675	Bifunctional glutathionylspermidine synthetase/amidase		b2988	AAM	0.00
3136694	REC02911	yghU	N	304	26, 34, 173, 258			Q46845	Hypothetical GST-like protein yghU		b2989	UNC	0.44
3137979	REC05773	hybG	E	82	71		0.36	P37185	Hydrogenase-2 operon protein hybG		b2990	UNC	0.13
3138333	REC05774	hybF	N	113	60, 60			P37184	Probable hydrogenase nickel incorporation protein hybF		b2991	UNC	0.06
3138814	REC05775	hybE	N	162	7, 111			P37183	Hydrogenase-2 operon protein hybE		b2992	UNC	0.00
3139301	REC05776	hybD	E	164	-		< 0.2	P37182	Hydrogenase-2 maturation protease (EC 3.4.24.-)		b2993	BEN	0.13
3141004	REC05777	hybC	N	567	37, 62, 97, 122, 237, 324, 350, 354, 385, 399, 459, 505			P37181	Hydrogenase-2 large chain precursor (EC 1.18.99.1)		b2994	BEN	0.19
3142179	REC06554	hybB	N	392	177, 263, 342			P37180	Probable Ni/Fe-hydrogenase 2 B-type cytochrome subunit		b2995	UNC	0.00
3143155	REC05779	hybA	N	328	138, 278			P37179	Hydrogenase-2 operon protein hybA precursor		b2996	UNC	0.00
3144276	REC05780	hybO	N	372	95, 224, 235, 259, 266, 309, 342			Q46847	Hydrogenase-2 small chain precursor (EC 1.18.99.1)		b2997	BEN	0.06
3144752	REC05781	yghW	N	95	24, 54			Q46848	Hypothetical protein yghW		b2998	UNC	0.00
3145281	REC05782		N	136	54, 123, 124			Q46849	ORF_F136		b2999	UNC	0.25
3145706	REC05783		X	141	-			Q46850	ORF_F141		b3000	UNC	0.00
3145912	REC02923	yghZ	N	346	231, 265			Q46851	Hypothetical protein yghZ		b3001	UNC	0.25
3147486	REC05784	yghA	E	164	-		< 0.2	P52082	Hypothetical protein yghA		b3002	UNC	0.28
3147677	REC02925	yghA	N	294	22, 38, 57, 107, 202			P25887	Hypothetical oxidoreductase yghA (EC 1.-.-.-)		b3003	UNC	0.44
3148737	REC02926		?	81	-			Q46853	ORF_O81		b3004	UNC	0.00
3149258	REC05785	exbD	N	141	82			P18784	Biopolymer transport exbD protein		b3005	MTR	0.44
3149999	REC05786	exbB	N	244	22			P18783	Biopolymer transport exbB protein		b3006	MTR	0.31
3150147	REC05787		?	51	-			Q46854	ORF_F51		b3007	UNC	0.00
3150251	REC02930	metC	N	395	79, 104, 147, 207, 309, 371, 375			P06721	Cystathionine beta-lyase (EC 4.4.1.8)		b3008	AAM	0.66
3151578	REC02931	yghB	N	219	9, 28			P33196	Hypothetical protein yghB		b3009	UNC	0.00
3153369	REC02933	yqhD	N	387	173, 224, 225, 260, 331			Q46856	Hypothetical oxidoreductase yqhD (EC 1.1.-.-)		b3011	UNC	0.50
3153403	REC05788	yqhC	N	375	83, 293			Q46855	Hypothetical transcriptional regulator yqhC		b3010	UNC	0.31
3154754	REC02934	dkgA	N	236	17, 21, 80			Q46857	2,5-diketeto-D-gluconic acid reductase A (EC 1.1.1.-)		b3012	CHM	0.53
3155664	REC02936	yqhG	N	309	10, 148, 171			Q46858	Hypothetical protein yqhG precursor		b3013	UNC	0.00
3156644	REC02937	yqhH	?	85	-			Q46860	Hypothetical lipoprotein yqhH precursor		b3014	UNC	0.00
3158185	REC05789	ygiQ	N	413	80, 152, 268, 303, 351, 360, 408			Q46861	Hypothetical protein ygiQ		b3015	UNC	0.13
3159162	REC05790	ygiR	N	325	228, 293, 322			Q46862			b3016	UNC	0.13
3160685	REC05791	sufI	N	470	21, 53			P26648	Protein sufI precursor		b3017	UNC	0.03
3161497	REC05792	pIsC	E	245	-		< 0.05	P26647	1-acyl-sn-glycerol-3-phosphate acyltransferase (EC 2.3.1.51)		b3018	NAM	0.91
3163989	REC05793	parC	E	752	-		< 0.001	P20082	Topoisomerase IV subunit A (EC 5.99.1.-)		b3019	NAM	0.59
3165734	REC05794	ygiS	N	535	78, 96, 338, 344, 376, 478, 510, 514, 529			Q46863	Putative binding protein ygiS precursor		b3020	UNC	0.72
3166262	REC05795	ygiT	E	131	107		< 0.2	Q46864	Hypothetical protein ygiT		b3021	UNC	0.03
3166560	REC05796	ygiU	N	98	35, 74			Q46865	Hypothetical protein ygiU		b3022	UNC	0.03
3167247	REC05797	ygiV	?	160	-			Q46866	Hypothetical protein ygiV		b3023	UNC	0.09
3167692	REC05798	ygiW	N	130	10, 25, 65, 67, 86			P52083	Protein ygiW precursor		b32024	UNC	0.06
3167844	REC02948	ygiX	N	219	59, 205, 216			P52076	Probable transcriptional regulatory protein ygiX		b3025	UNC	0.81
3168500	REC02949	ygiY	N	449	14			P40719	Probable sensor protein ygiY (EC 2.7.3.-)		b3026	UNC	0.72
3170227	REC05799	ygiZ	E	110	99		< 0.3	Q46867	Hypothetical protein ygiZ		b3027	UNC	0.00
3170546	REC02951	mdaB	N	193	88, 91, 111, 144, 173			P40717	Modulator of drug activity B		b3028	UNC	0.19
3171158	REC02952	ygiN	N	104	20, 29, 102			P40718	Protein ygiN		b3029	UNC	0.00
3173412	REC05800	parE	E	630	-		< 0.0001	P20083	Topoisomerase IV subunit B (EC 5.99.1.-)		b3030	NAM	0.56
3174022	REC05801	yqiA	N	193	99, 184			P36653	Hypothetical protein yqiA		b3031	UNC	0.09
3174849	REC05802	icc	N	275	128, 242			P36650	Icc protein		b3032	RCD	0.28
3175296	REC05803	yqiB	E	140	134		< 0.2	P36652	Hypothetical protein yqiB		b3033	UNC	0.06
3175926	REC05804	nudF	N	209	92, 170, 174			P36651	ADP-ribose pyrophosphatase (EC 3.6.1.13)		b3034	NCM	0.13

3176125	REC02958	toIC	N	495	196	P02930	Outer membrane protein toIC precursor	b3035	PMS	0.28
3177612	REC02959	ygiA	N	86	61	Q92363	Hypothetical protein YGIA	b3036	UNC	0.00
3177727	REC02960	ygiB	N	234	22, 72, 133, 165, 210	P24195	Hypothetical protein ygiB	b3037	UNC	0.03
3178437	REC02961	ygiC	N	386	24, 47, 55, 197, 230, 264, 290, 369	P24196	Hypothetical protein ygiC	b3038	UNC	0.19
3180450	REC05805	ygiD	N	271	123, 127, 219	P24197	Hypothetical protein ygiD	b3039	UNC	0.13
3180566	REC02963	zupT	N	257	85, 201, 243	P24198	Zinc transporter zupT	b3040	MTR	0.31
3182482	REC05806	ribB	E	217	-	P24199	3,4-dihydroxy-2-butanone 4-phosphate synthase	b3041	NCM	0.53
3182796	REC02965	yqiC	N	116	14	Q46868	Hypothetical protein yqiC	b3042	UNC	0.16
3183430	REC02966	ygiL	N	183	142	P39834	Hypothetical fimbrial-like protein ygiL precursor	b3043	UNC	0.00
3184203	REC06560	insC5	X	121	-	P19776	Transposase insC for insertion element IS2A/D/F/H/I/K	b3044	PHT	0.56
3184526	REC06561	insD5	X	301	-	P19777	Transposase insD for insertion element IS2A/D/F/H/I/K	b3045	PHT	0.56
3185416	REC06562	yqiG	X	821	-	P76655	Hypothetical outer membrane usher protein yqiG precursor	b3046	UNC	0.09
3187888	REC02970	yqiH	N	252	66, 83, 112, 234	P77616	Hypothetical fimbrial chaperone yqiH precursor	b3047	UNC	0.00
3188648	REC02971	yqiI	N	354	52, 59, 168, 169, 195, 289, 307	P76656	Hypothetical protein yqiI precursor	b3048	UNC	0.00
3189955	REC05807	glgS	N	66	34, 62	P26649	Glycogen synthesis protein glgS	b3049	UNC	0.00
3190224	REC02973	yqiJ	X	209	-	P76657	Hypothetical protein yqiJ	b3050	UNC	0.00
3190880	REC02974	yqiK	N	553	237, 282, 305, 485, 501, 546	P77306	Hypothetical protein yqiK	b3051	UNC	0.09
3194394	REC05808	rfaE	N	477	325, 352	P76658	ADP-heptose synthase (EC 2.7.7.-)	b3052	LPC	0.44
3197282	REC05809	glnE	N	946	271, 393, 487, 764, 777	P30870	Glutamate-ammonia-ligase adenyllyltransferase (EC 2.7.7.42)	b3053	SMC	0.41
3198606	REC05810	ygiF	N	433	14, 25, 30, 295, 309, 427	P30871	Hypothetical protein ygiF	b3054	UNC	0.22
3198848	REC02978	ygiM	N	206	63, 89, 196	P39202	Hypothetical protein ygiM precursor	b3055	UNC	0.09
3199532	REC02979	cca	E	412	-	P06961	tRNA nucleotidyltransferase (EC 2.7.7.25)	b3056	NAM	0.56
3201772	REC05811	upk	N	273	3, 28, 159, 211	P31054	Putative undecaprenol kinase (EC 2.7.1.66)	b3057	UNC	0.78
3202233	REC05812	foiB	N	123	53	P31055	Dihydroneopterin aldolase (EC 4.1.2.25)	b3058	NCM	0.16
3202335	REC02982	ygiH	N	205	20, 165, 181	P31056	Hypothetical protein ygiH	b3059	UNC	0.72
3203897	REC05813	ygiP	N	310	33, 68, 92, 115, 182, 240, 290	P45463	Hypothetical transcriptional regulator ygiP	b3060	UNC	0.72
3204104	REC02984	ttdA	X	303	-	P05847	L(+)-tartrate dehydratase alpha subunit (EC 4.2.1.32)	b3061	CHM	0.09
3205012	REC02985	ttdB	N	201	14, 43, 145	P05851	L(+)-tartrate dehydratase beta subunit (EC 4.2.1.32)	b3062	CHM	0.00
3205665	REC02986	yjgE	N	487	29, 30, 168, 214, 313, 402, 432	P39414	Putative tartrate carrier	b3063	UNC	0.00
3208184	REC05814	gcp	X	337	-	P05852	Probable O-sialoglycoprotein endopeptidase (EC 3.4.24.57)	b3064	UNC	1.00
3208422	REC02988	rpsU	X	71	-	P02379	30S ribosomal protein S21	b3065	PMS	0.63
3208748	REC02989	dnaG	E	581	-	P02923	DNA primase (EC 2.7.7.-)	b3066	NAM	0.97
3210688	REC02990	rpoD	E	613	-	P00579	RNA polymerase sigma factor rpoD	b3067	RCD	0.97
3213114	REC05815	mug	N	168	62, 145	P43342	G/U mismatch-specific DNA glycosylase (EC 3.2.2.-)	b3068	MSM	0.03
3214132	REC05816	yqjH	N	254	11, 87, 89, 182	Q46871	Hypothetical protein yqjH	b3070	UNC	0.16
3214420	REC02993	yqjI	N	207	33, 172, 175	Q46872	Hypothetical protein yqjI	b3071	UNC	0.19
3216717	REC05817	aer	N	506	75, 112, 186, 243, 436, 447, 460	P50466	Aerotaxis receptor	b3072	SMC	0.25
3217024	REC02995	yjgG	N	496	14, 102, 127, 197, 249, 382, 443	P42588	Probable ornithine aminotransferase (EC 2.6.1.13)	b3073	UNC	0.16
3218888	REC05818	yqjH	N	110	45	P42589	Hypothetical protein yqjH	b3074	UNC	0.06
3219107	REC02997	ebgR	N	327	6, 53, 83, 96, 226, 263, 277, 290, 306, 317	P06846	Ebg operon repressor	b3075	RCD	0.22
3220238	REC02998	ebgA	N	1042	159, 223, 316, 392, 773, 808, 860, 905, 975	P06864	Evolved beta-galactosidase alpha-subunit (EC 3.2.1.23)	b3076	CHM	0.06
3223363	REC02999	ebgC	N	149	8, 60, 71	P24225	Evolved beta-galactosidase beta-subunit	b3077	CHM	0.00
3223875	REC03000	yjgI	N	477	1, 171	P42590	Hypothetical transporter yjgI	b3078	UNC	0.00
3225442	REC03001	yjgJ	N	356	43, 66, 94, 96, 185, 241, 248, 321	P42591	Hypothetical protein yjgJ precursor	b3079	UNC	0.00
3226529	REC03002	yjgK	N	783	47, 57, 93, 159, 206, 261, 441, 442	P42592	Hypothetical protein yjgK precursor	b3080	UNC	0.00
3229306	REC03003	fadh	N	672	294, 508, 579	P42593	2,4-dienoyl-CoA reductase [NADPH] (EC 1.3.1.34)	b3081	LPC	0.31
3231785	REC05819	yjgM	X	138	-	P42594	Hypothetical protein yjgM	b3082	UNC	0.00
3232096	REC05820	yjgN	X	104	-	P42595	Hypothetical protein yjgN	b3083	UNC	0.13
3233546	REC05821	yjgO	N	388	112, 134, 204, 223, 244, 252, 276, 324, 369	P42596	Putative ribosomal RNA small subunit methyltransferase D (EC 2.2.1.22)	b3084	UNC	0.09
3233565	REC03007	yjgP	N	179	46, 132	P42597	Hypothetical protein yjgP	b3085	UNC	0.06
3234181	REC03008	yjgQ	E	230	-	P42598	Hypothetical protein yjgQ	b3086	UNC	0.06
3234934	REC03010	yjgR	N	334	158, 258, 299	P42599	Hypothetical oxidoreductase yjgR (EC 1.-.-.-)	b3087	UNC	0.56
3236222	REC03011	yjgT	N	321	88, 182, 245, 284, 319	P42601	Hypothetical protein yjgT	b3088	UNC	0.31
3237584	REC03012	yjgU	N	414	53, 87, 252, 280	P42602	Hypothetical symporter yjgU	b3089	UNC	0.28
3239384	REC05822	yjgV	N	183	15	P42603	Hypothetical protein yjgV	b3090	UNC	0.00
3240954	REC05823	uxaA	N	495	7, 106, 136, 222, 225, 327, 387, 392, 431, 487	P42604	Altronate hydrolase (EC 4.2.1.7)	b3091	CHM	0.13
3242381	REC05824	uxaC	X	470	-	P42607	Uronate isomerase (EC 5.3.1.12)	b3092	CHM	0.23
3242744	REC06601	exuT	N	472	77, 100, 143, 159, 186, 197, 261, 287, 348, 376, 384, 423	P42609	Hexuronate transporter	b3093	MTR	0.34
3244277	REC03019	exuR	N	263	122, 242	P42608	Exu regulon transcriptional regulator	b3094	RCD	0.09
3245413	REC03020	yqjA	E	220	-	P42614	Hypothetical protein yqjA	b3095	UNC	0.50
3246079	REC03021	yqjB	E	127	-	P42615	Hypothetical protein yqjB	b3096	UNC	0.00
3246594	REC06602	yqjC	N	127	32, 59	P42616	Protein yqjC precursor	b3097	UNC	0.06
3247015	REC03023	yqjD	N	101	16, 71, 92	P42617	Hypothetical protein yqjD	b3098	UNC	0.06
3247323	REC03024	yqjE	N	134	19, 24	P42618	Hypothetical protein yqjE	b3099	UNC	0.06
3247717	REC03025	yqjK	E	99	-	Q47710	Hypothetical protein yqjK	b3100	UNC	0.00
3248112	REC03026	yqjF	N	160	8, 156	P42619	Hypothetical protein yqjF	b3101	UNC	0.19
3248664	REC03027	yqjG	N	328	232, 252, 327	P42620	Hypothetical protein yqjG	b3102	UNC	0.28
3249944	REC06603	yhaH	N	121	23, 46, 76, 87, 119	P42621	Hypothetical protein yhaH	b3103	UNC	0.19
3250551	REC03029	yhaI	N	118	35, 53, 81, 106	P42622	Hypothetical protein yhaI	b3104	UNC	0.19
3251854	REC05827	yhaJ	N	298	201, 264	P42623	Hypothetical transcriptional regulator yhaJ	b3105	UNC	0.06
3251959	REC03031	yhaK	X	233	-	P42624	Hypothetical protein yhaK	b3106	UNC	0.41
3252677	REC03032	yhaL	?	56	-	P42625	Hypothetical protein yhaL	b3107	UNC	0.00
3253547	REC05828	yhaM	N	188	1, 80, 111	P42626	Hypothetical protein yhaM	b3108	UNC	0.06
3254292	REC05829	yhaN	N	187	18, 130	P42627	Hypothetical protein yhaN	b3109	UNC	0.03
3255597	REC05830	yhaO	N	425	109, 286	P42628	Hypothetical transport protein yhaO	b3110	UNC	0.13
3256755	REC05831	tdcG	N	275	6, 121, 125, 159, 196	P42630	L-serine dehydratase tdcG (EC 4.2.1.13)	b3111	AAM	0.66
3257297	REC05832	tdcG	E	140	138	P42630	L-serine dehydratase tdcG (EC 4.2.1.13)	b3112	AAM	0.66
3257815	REC05833	tdcF	N	150	29	P42631	TdcF protein	b3113	UNC	0.81
3260059	REC05834	tdcE	N	746	18, 92, 417, 605, 673	P42632	Keto-acid formate acetyltransferase (EC 2.3.1.-)	b3114	CHM	0.00
3261313	REC05835	tdcD	N	406	41, 166, 223, 334, 403	P11868	Propionate kinase (EC 2.7.2.-)	b3115	CHM	0.03
3262658	REC05836	tdcC	X	443	-	P11867	Threonine/serine transporter	b3116	MTR	0.13
3263669	REC05837	tdcB	N	329	36, 64, 98, 135, 170, 213, 239	P05792	Threonine dehydratase catabolic (EC 4.2.1.16)	b3117	AAM	0.75
3264706	REC05838	tdcA	N	312	98, 185	P11036	Tdc operon transcriptional activator	b3118	RCD	0.03
3264895	REC03044	tdcR	E	114	-	P11866	Threonine dehydratase operon activator protein	b3119	RCD	0.00
3265474	REC03045	yhaB	N	186	60	P11865	Hypothetical protein yhaB	b3120	UNC	0.00
3266056	REC03046	yhaC	N	395	-	P11864	Hypothetical protein yhaC	b3121	UNC	0.00
3267304	REC03047		N	54	-	Q47711	ORF_054	b3122	UNC	0.00
3269492	REC05839	garK	X	408	-	P23524	Glycerate kinase 2 (EC 2.7.1.31)	b3124	CHM	0.38
3270407	REC05840	garL	N	299	36, 53, 72, 116, 167, 185, 207, 222	P23523	2-hydroxy-3-oxopropionate reductase (EC 1.1.1.60)	b3125	CHM	0.47
3271198	REC05841	garD	N	256	51, 184	P23522	2-dehydro-3-deoxyglucarate aldolase (EC 4.1.2.20)	b3126	CHM	0.19
3272548	REC05842	garP	N	444	14, 161, 348	P42613	Probable galactarate transporter	b3127	UNC	0.34
3272923	REC03052	garD	N	523	100, 143, 172, 194, 231, 256	P39829	D-galactarate dehydratase (EC 4.2.1.42)	b3128	CHM	0.19
3274643	REC03053	soha	N	111	50, 53	P15373	HtrA suppressor protein	b3129	NAM	0.03

3274978	REC03054	yhaV	N	154	46, 154	P42901	Hypothetical protein yhaV	b3130	UNC	0.03
3276306	REC05843	agaR	N	269	198	P42902	Putative aga operon transcriptional repressor	b3131	UNC	0.16
3276555	REC03056	agaZ	N	426	87, 312, 396	P42903	Putative tagatose 6-phosphate kinase agaZ (EC 2.7.1.144)	b3132	UNC	0.13
3277822	REC03057	agaY	E	169	-	P42904	PTS system, N-acetylgalactosamine-specific IIB component 2 (EC 2.7.1.14)	b3133	CHM	0.03
3278342	REC03058	agaW	E	133	121	P42905	PTS system, N-acetylgalactosamine-specific IIC component 2	b3134	MTR	0.00
3278763	REC06605	agaA	N	167	37	P42906	Putative N-acetylgalactosamine-6-phosphate deacetylase (EC 3.5.1.31)	b3135	UNC	0.00
3279617	REC03060	agaS	N	384	142, 189, 230, 247, 280, 383	P42907	Putative tagatose-6-phosphate ketose/aldose isomerase (EC 5.-.-.b3136)	b3136	UNC	0.03
3280784	REC03061	agaY	N	286	189, 231, 233	P42908	Tagatose-bisphosphate aldolase agaY (EC 4.1.2.-)	b3137	CHM	0.63
3281811	REC03062	agaB	?	158	10	P42909	PTS system, N-acetylgalactosamine-specific IIB component 1 (EC 2.7.1.14)	b3138	MTR	0.03
3282326	REC03063	agaC	N	267	79, 102	P42910	PTS system, N-acetylgalactosamine-specific IIC component 1	b3139	MTR	0.16
3283119	REC03064	agaD	N	263	182, 220, 239, 258	P42911	PTS system, N-acetylgalactosamine-specific IID component	b3140	MTR	0.16
3283911	REC03065	agaI	N	251	16, 56, 73, 89, 187, 221, 232	P42912	Putative galactosamine-6-phosphate isomerase (EC 5.3.1.-)	b3141	UNC	0.03
3285067	REC03066	yraH	N	194	2, 66	P42913	Hypothetical fimbrial-like protein yraH precursor	b3142	UNC	0.00
3285731	REC03067	yraI	N	231	25, 127	P42914	Hypothetical fimbrial chaperone yraI precursor	b3143	UNC	0.00
3286455	REC03068	yraJ	N	838	260, 378, 407, 439, 467, 532, 593, 682, 707	P42915	Hypothetical outer membrane usher protein yraJ precursor	b3144	UNC	0.06
3288982	REC03069	yraK	N	363	124	P43319	Hypothetical protein yraK precursor	b3145	UNC	0.00
3290976	REC05844	yraL	N	286	97, 162, 195, 200, 242, 284	P45528	Hypothetical protein yraL	b3146	UNC	1.00
3291041	REC03071	yraM	N	678	30, 98, 307, 407, 537	P45464	Hypothetical protein yraM	b3147	UNC	0.13
3293035	REC03072	yraN	X	131	-	P45465	Hypothetical protein yraN	b3148	UNC	0.59
3293450	REC03073	yraO	N	196	14, 72, 140, 145	P45466	Hypothetical protein yraO	b3149	UNC	0.16
3294050	REC03074	yraP	N	191	33, 89	P45467	Hypothetical protein yraP precursor	b3150	UNC	0.19
3295779	REC05845	yraQ	N	346	47, 201, 247, 271	P45468	Hypothetical protein yraQ	b3151	UNC	0.00
3296532	REC05846	yraR	E	226	-	P45469	Hypothetical protein yraR	b3152	UNC	0.06
3296573	REC03077	yhbO	?	186	11	P45470	Hypothetical protein yhbO	b3153	UNC	0.41
3297556	REC05847	yhbP	E	147	-	P45471	Hypothetical protein yhbP	b3154	UNC	0.03
3297607	REC03079	yhbQ	E	100	-	P45472	Hypothetical protein yhbQ	b3155	UNC	0.16
3298399	REC05848	yhbS	E	167	154	P45473	Hypothetical acetyltransferase yhbS (EC 2.3.1.-)	b3156	UNC	0.34
3298917	REC05849	yhbT	N	174	82	P45474	Hypothetical protein yhbT	b3157	UNC	0.09
3299126	REC03082	yhbU	N	331	2, 132, 265	P45527	Putative protease yhbU precursor (EC 3.4.-.-)	b3158	UNC	0.19
3300112	REC03083	yhbV	N	298	130, 200, 248	P45475	Hypothetical protein yhbV	b3159	UNC	0.59
3301089	REC03084	yhbW	N	335	87, 106, 132, 155, 189, 294	P45529	Hypothetical protein yhbW	b3160	UNC	0.47
3303458	REC05850	mtr	X	414	406	P22306	Tryptophan-specific transport protein	b3161	MTR	0.13
3305552	REC05851	deaD	N	646	4, 94, 210, 439, 558	P23304	Cold-shock DEAD-box protein A	b3162	UNC	0.88
3306565	REC05852	nlpI	N	294	244	P39833	Lipoprotein nlpI precursor	b3163	UNC	0.09
3308878	REC05853	pnp	E	734	-	P05055	Polyribonucleotide nucleotidyltransferase (EC 2.7.7.8)	b3164	NAM	0.97
3309325	REC05854	rpsO	E	89	-	P02371	30S ribosomal protein S15	b3165	PMS	1.00
3310418	REC06607	trub	N	314	72, 74, 177, 205, 267	P09171	tRNA pseudouridine synthase B (EC 4.2.1.70)	b3166	NAM	0.94
3310819	REC05856	rbfA	?	133	6	P09170	Ribosome-binding factor A	b3167	PMS	0.75
3313655	REC05857	infB	E	890	-	P02995	Translation initiation factor IF-2	b3168	PMS	1.00
3315167	REC05858	nusA	N	495	339	P03003	N utilization substance protein A	b3169	RCD	1.00
3315653	REC05859	yhbC	E	152	-	P03843	Hypothetical protein yhbC	b3170	UNC	0.78
3316278	REC03095	argG	N	447	62, 102, 119, 229, 384, 447	P22767	Argininosuccinate synthase (EC 6.3.4.5)	b3172	AAM	0.78
3319272	REC05860	yhbX	N	547	57, 168, 200, 214, 231, 279, 363, 386, 407, 422, 429, 430, 462, 483	P42640	Outer-membrane protein yhbX precursor	b3173	LPC	0.06
3320146	REC05861	secG	X	110	105	P33582	Protein-export membrane protein secG	b3175	PMS	0.31
3321711	REC05862	mrsA	N	445	58	P31120	Protein mrsA	b3176	UNC	0.84
3322597	REC05863	fo1P	N	297	190, 261	P26282	Dihydropterate synthase (EC 2.5.1.15)	b3177	NCM	0.84
3324576	REC05864	hflB	N	644	211, 555	P28691	Cell division protein ftsH (EC 3.4.24.-)	b3178	RCD	1.00
3325305	REC05865	rxmJ	N	209	5, 169	P28692	Ribosomal RNA large subunit methyltransferase J (EC 2.1.1.-)	b3179	NAM	0.47
3325431	REC03102	yhbY	N	97	42, 76	P42550	Hypothetical protein yhbY	b3180	UNC	0.38
3326341	REC05866	greA	N	153	4, 135	P21346	Transcription elongation factor greA	b3181	NAM	0.84
3326604	REC03104	dacB	N	477	62, 78, 95, 134, 246, 352, 452, 459	P24228	Penicillin-binding protein 4 precursor	b3182	LPC	0.34
3329395	REC05867	yhbZ	E	390	356, 385	P42641	Hypothetical GTP-binding protein yhbZ	b3183	UNC	1.00
3330376	REC05868	yhbE	N	321	133, 210, 292	P28636	Hypothetical transport protein yhbE	b3184	UNC	0.16
3330760	REC05869	rpsM	X	85	-	P02427	50S ribosomal protein L27	b3185	PMS	1.00
3331092	REC05870	rplU	X	103	-	P02422	50S ribosomal protein L21	b3186	PMS	0.97
3331351	REC03109	ispB	E	323	-	P19641	Octaprenyl-diphosphate synthase (EC 2.5.1.-)	b3187	LPC	0.84
3332550	REC03110	sfsB	N	92	76	P18837	Sugar fermentation stimulation protein B	b3188	RCD	0.03
3334135	REC05871	murA	N	419	55, 417	P28909	UDP-N-acetylglucosamine 1-carboxyvinyltransferase (EC 2.5.1.7)	b3189	LPC	0.97
3334459	REC05872	yrbA	N	89	21	P43781	Protein yrbA	b3190	UNC	0.22
3334993	REC05873	yrbB	N	129	2, 18, 44, 79	P45389	Hypothetical protein yrbB	b3191	UNC	0.09
3335532	REC05874	yrbC	N	211	13, 86, 102, 142, 150, 181, 198	P45390	Protein yrbC precursor	b3192	UNC	0.22
3336102	REC05875	yrbD	N	183	11, 73, 82, 136	P45391	Hypothetical protein yrbD precursor	b3193	UNC	0.53
3336889	REC05876	yrbE	N	260	195, 200, 236, 251	P45392	Hypothetical protein yrbE	b3194	UNC	0.84
3337706	REC05877	yrbF	N	269	159, 182	P45393	Hypothetical ABC transporter ATP-binding protein yrbF	b3195	UNC	0.56
3337916	REC03118	yrbG	N	325	92, 116, 148, 161, 255, 274, 289	P45394	Hypothetical protein yrbG	b3196	UNC	0.19
3338907	REC03119	yrbH	N	328	77, 122, 213, 215, 275	P45395	Hypothetical protein yrbH	b3197	UNC	0.56
3339914	REC03121	yrbI	X	188	-	P45396	Hypothetical protein yrbI	b3198	UNC	0.31
3340477	REC03122	yrbK	X	191	-	P45397	Hypothetical protein yrbK	b3199	UNC	0.19
3341021	REC03123	yhbN	X	185	-	P38685	Protein yhbN precursor	b3200	UNC	0.34
3341585	REC03124	yhbG	E	241	-	P31220	Probable ABC transporter ATP-binding protein yhbG	b3201	UNC	0.97
3342358	REC03125	rpsN	E	477	-	P24255	RNA polymerase sigma-54 factor	b3202	RCD	0.59
3343814	REC03126	yhbH	N	95	19	P31221	Probable sigma(54) modulation protein	b3203	UNC	0.50
3344219	REC03127	ptsN	E	163	-	P31222	Nitrogen regulatory IIA protein (EC 2.7.1.69)	b3204	CHM	0.41
3344756	REC03128	yhbJ	N	284	9, 100, 114, 230	P33995	Hypothetical protein yhbJ	b3205	UNC	0.50
3345607	REC03129	ptsO	N	90	51	P33996	Phosphocarrier protein NPr	b3206	MTR	0.28
3346093	REC03130	yrbL	N	210	4, 184	P46021	Hypothetical protein yrbL	b3207	UNC	0.00
3347450	REC05878	mtgA	N	242	48, 189	P46022	Monofunctional biosynthetic peptidoglycan transglycosylase (EC 2.b3208)	b3208	LPC	0.44
3348109	REC05879	e1bB	X	220	-	P26428	Enhancing lycopene biosynthesis protein 2	b3209	UNC	0.06
3350660	REC05880	arcB	N	776	9, 32, 187, 247, 248, 290, 320, 349, 365, 442, 467, 558, 675, 746, 771	P22763	Aerobic respiration control sensor protein arcB (EC 2.7.3.-)	b3210	RCD	0.47
3351685	REC06631	yhcC	N	309	289, 301	P45476	Hypothetical protein yhcC	b3211	UNC	0.28
3352267	REC03135	g1tB	N	1517	30, 84, 85, 90, 182, 224, 286, 315, 369, 394, 398, 434, 848, 1116, 1170, 1171	P09831	Glutamate synthase [NADPH] large chain precursor (EC 1.4.1.13)	b3212	MSM	0.66
3356833	REC03136	g1tD	N	472	358, 459	P09832	Glutamate synthase [NADPH] small chain (EC 1.4.1.13)	b3213	MSM	0.66
3358811	REC03137	g1tF	X	254	-	P28721	Protein gltF precursor	b3214	UNC	0.00
3359747	REC03138	yhcA	X	224	-	P28722	Hypothetical fimbrial chaperone yhcA precursor	b3215	UNC	0.00
3360442	REC03139	yhcD	N	793	703, 720, 773	P45420	Hypothetical outer membrane usher protein yhcD precursor	b3216	UNC	0.00
3362820	REC03140	yhcE	N	159	50, 51, 76, 96, 124	P45421	Hypothetical protein yhcE	b3217	UNC	0.00
3364353	REC06632	insH1I	N	338	59, 259	P03837	Transposase insH for insertion sequence element IS5	b3505	PHT	0.34
3364561	REC03142	yhcF	E	238	-	P45422	Hypothetical protein yhcF precursor	b3219	UNC	0.00
3365462	REC03143	yhcG	N	375	79, 111, 234, 344, 353	P45423	Hypothetical protein yhcG	b3220	UNC	0.06
3367113	REC05883	yhcH	N	154	10, 22, 59, 61	P45424	Hypothetical protein yhcH	b3221	UNC	0.16
3368018	REC05884	yhcI	N	302	131, 261	P45425	Hypothetical protein yhcI	b3222	UNC	0.09
3368671	REC05885	yhcJ	N	229	202, 218	P45426	Hypothetical protein yhcJ	b3223	UNC	0.28
3370239	REC05886	nanT	N	506	59, 88, 162, 230, 254, 262, 358	P41036	Putative sialic acid transporter	b3224	UNC	0.03

3371211	REC05887	nana	N	297	131, 188, 251, 276		P06995	N-acetylneuraminatase lyase subunit (EC 4.1.3.3)	b3225	CHM	0.19
3372124	REC05888	yhcK	E	263	-	< 0.05	P45427	Hypothetical transcriptional regulator yhcK	b3226	UNC	0.50
3372504	REC03150	dcuD	N	455	14, 35, 44, 60, 61, 86, 109, 118, 150, 154, 182, 232, 265, 333, 392		P45428	Putative cryptic C4-dicarboxylate transporter dcuD	b3227	UNC	0.06
3374411	REC05889	sspB	N	165	43, 161		P25663	Stringent starvation protein B	b3228	UNC	0.19
3375055	REC05890	sspA	X	212	-		P05838	Stringent starvation protein A	b3229	UNC	0.31
3375842	REC05891	rpsI	E	130	-	< 0.2	P02363	30S ribosomal protein S9	b3230	PMS	1.00
3376286	REC05892	rp1M	E	142	-	< 0.2	P02410	50S ribosomal protein L13	b3231	PMS	1.00
3377632	REC05893	yhcM	N	375	32, 75, 166, 211, 237, 256, 282, 287, 371		P46442	Hypothetical protein yhcM	b3232	UNC	0.38
3377820	REC03156	yhcB	N	134	6, 35		P39436	Hypothetical protein yhcB	b3233	UNC	0.06
3378378	REC03157	degQ	E	455	455	< 0.01	P39099	Protease degQ precursor (EC 3.4.21.-)	b3234	PMS	0.03
3379835	REC03158	degS	N	355	93, 231, 262, 306, 332		P31137	Protease degS precursor (EC 3.4.21.-)	b3235	UNC	0.09
3381903	REC05894	mdh	N	312	41, 93, 229		P06994	Malate dehydrogenase (EC 1.1.1.37)	b3236	CHM	0.81
3382338	REC03160	argR	E	156	139	< 0.2	P15282	Arginine repressor	b3237	RCD	0.16
3383122	REC03161	yhcN	?	104	-		P46477	Hypothetical protein yhcN precursor	b3238	UNC	0.00
3383764	REC05895	yhcO	E	90	-	0.43	P46480	Hypothetical protein yhcO	b3239	UNC	0.00
3385823	REC05896	yhcP	N	655	651		P46481	Hypothetical protein yhcP	b3240	UNC	0.13
3386761	REC05897	yhcQ	N	310	10, 61, 86, 109, 168, 195, 204, 220, 241, 259, 284		P46482	Hypothetical protein yhcQ	b3241	UNC	0.06
3387041	REC05898	yhcR	N	90	45		P46478	Hypothetical protein yhcR	b3242	UNC	0.00
3387155	REC03166	yhcS	N	309	62, 149		P45691	Hypothetical transcriptional regulator yhcS	b3243	UNC	0.72
3389663	REC05899	t1dD	N	481	82		P46473	T1dD protein	b3244	UNC	0.56
3393054	REC05900	yhdP	N	986	58, 119, 130, 161, 265, 408, 485, 580, 835, 874, 878, 895, 940		P46474	Hypothetical protein yhdP	b3245	UNC	0.13
3393895	REC05902	yhdR	N	282	14, 62, 96, 166, 169, 203, 229		P46476	Hypothetical protein yhdR precursor	b3246	UNC	0.00
3395450	REC05903	cafA	N	495	382, 393, 473		P25537	Ribonuclease G (EC 3.1.4.-)	b3247	RCD	0.41
3396015	REC05904	yhdE	N	197	15		P25536	Maf-like protein yhdE	b3248	UNC	0.75
3396512	REC05905	mreD	N	162	128		P16927	Rod shape-determining protein mreD	b3249	RCD	0.16
3397615	REC05906	mreC	E	367	-	< 0.01	P16926	Rod shape-determining protein mreC	b3250	RCD	0.50
3398784	REC05907	mreB	E	367	-	< 0.01	P13519	Rod shape-determining protein mreB	b3251	RCD	0.59
3400969	REC05908	yhdA	N	646	296, 564, 622		P13518	Hypothetical protein yhdA	b3252	UNC	0.03
3401121	REC03177	yhdH	X	324	-		P26646	Protein yhdH	b3253	UNC	0.75
3402254	REC05909		X	33	-		Q47712	ORF_F33	b3254	UNC	0.00
3403073	REC03179	accB	X	156	-		P02905	Biotin carboxyl carrier protein of acetyl-CoA carboxylase	b3255	LPC	0.75
3403554	REC03180	accC	X	449	-		P24182	Biotin carboxylase (EC 6.3.4.14) (A subunit of acetyl-CoA carboxy	b3256	LPC	0.81
3405012	REC03181	yhdT	X	80	-		P45566	Hypothetical protein yhdT	b3257	UNC	0.13
3405238	REC03182	panF	N	485	229, 231, 296, 298, 389		P16256	Sodium/pantothenate symporter	b3258	MTR	0.16
3406707	REC03184	pzmA	N	293	64, 162		P28637	Ribosomal protein L11 methyltransferase (EC 2.1.1.-)	b3259	PMS	0.75
3407917	REC03185	yhdG	N	321	167, 213		P25717	Hypothetical protein yhdG	b3260	UNC	0.91
3408908	REC03186	fis	E	98	-	< 0.3	P11028	DNA-binding protein fis	b3261	RCD	0.22
3409284	REC03187	yhdJ	N	296	15, 32, 81, 98, 132, 159, 273		P28638	Hypothetical adenine-specific methylase yhdJ (EC 2.1.1.72)	b3262	NAM	0.41
3410258	REC03188	yhdU	N	59	39, 41		P45764	Hypothetical protein yhdU	b3263	UNC	0.00
3411102	REC05910	envR	N	220	55, 112, 156		P31676	Potential acrEF/envCD operon repressor	b3264	UNC	0.25
3411501	REC03190	acrE	N	385	50, 97		P24180	Acriflavine resistance protein E precursor	b3265	UNC	0.47
3412670	REC03191	acrF	N	1034	20, 72, 182, 200, 204, 250, 326, 358, 365, 549, 758		P24181	Acriflavine resistance protein F	b3266	UNC	0.75
3416027	REC03192	yhdV	N	73	15, 49		P45765	Hypothetical protein yhdV	b3267	UNC	0.00
3416786	REC03193	yhdW	N	305	40, 152, 231, 303		P45766	Putative amino-acid ABC transporter binding protein yhdW precursor	b3268	UNC	0.22
3417753	REC03194	yhdX	X	368	-		P45767	Hypothetical amino-acid ABC transporter permease protein yhdX	b3269	UNC	0.19
3418958	REC03195	yhdY	N	368	308, 338		P45768	Hypothetical amino-acid ABC transporter permease protein yhdY	b3270	UNC	0.34
3420072	REC03196	yhdZ	N	252	50, 105, 141		P45769	Hypothetical amino-acid ABC transporter ATP-binding protein yhdZ	b3271	UNC	0.41
3426657	REC03197	yrdA	N	256	7, 23, 55, 81, 123, 123, 124, 188, 220		P45770	Protein yrdA	b3272	UNC	0.63
3427660	REC05911	yrdB	N	85	26, 35		P45795	Hypothetical protein yrdB	b3280	UNC	0.03
3428475	REC05912	aroE	N	272	219, 246		P15770	Shikimate 5-dehydrogenase (EC 1.1.1.25)	b3281	AAM	0.88
3429052	REC06645	yrdC	N	190	105		P45748	Protein yrdC	b3282	UNC	0.88
3429566	REC05914	yrdD	X	169	-		P45771	Hypothetical protein yrdD	b3283	UNC	0.06
3430102	REC05915	smg	N	157	59, 71, 115, 132, 149		P30853	Protein smg	b3284	UNC	0.13
3430382	REC05916	smf	N	102	32, 92		P30852	Smf protein	b3285	UNC	0.50
3431197	REC05917	smf	N	253	1, 17, 81, 149, 228		P30852	Smf protein	b3285	UNC	0.75
3431327	REC03205	def	E	169	-	< 0.05	P27251	Peptide deformylase (EC 3.5.1.88)	b3287	PMS	1.00
3431851	REC03206	fmt	E	315	-	< 0.01	P23882	Methionyl-tRNA formyltransferase (EC 2.1.2.9)	b3288	NAM	1.00
3432844	REC06646	sun	N	429	57, 68, 76, 112, 146, 171, 216, 278, 370		P36929	SUN protein	b3289	UNC	0.78
3434155	REC03208	trkA	N	458	6, 50, 78, 180, 224, 299		P23868	Trk system potassium uptake protein trkA	b3290	MTR	0.47
3435661	REC03209	mscL	E	136	-	< 0.1	P23867	Large-conductance mechanosensitive channel	b3291	MTR	0.56
3436286	REC06813	yhdL	?	72	-		P36675	Hypothetical protein yhdL	b3292	UNC	0.06
3436767	REC05918	zntR	N	141	66		P36676	Zn(II)-responsive regulator of zntA	b3292	RCD	0.38
3437146	REC05919	yhdN	X	122	-		P36677	Hypothetical protein yhdN	b3293	UNC	0.03
3437636	REC05920	rp1Q	X	127	-		P02416	50S ribosomal protein L17	b3294	PMS	1.00
3438666	REC05921	rpOA	X	329	-		P00574	DNA-directed RNA polymerase alpha chain (EC 2.7.7.6)	b3295	NAM	1.00
3439312	REC05922	rpsD	X	206	-		P02354	30S ribosomal protein S4	b3296	PMS	1.00
3439735	REC05923	rpsK	X	129	-		P02366	30S ribosomal protein S11	b3297	PMS	1.00
3440108	REC05924	rpsM	E	118	-	0.41	P02369	30S ribosomal protein S13	b3298	PMS	1.00
3440371	REC05925	rpsJ	?	38	-		P21194	50S ribosomal protein L36	b3299	PMS	0.66
3441734	REC05926	secY	E	443	-	< 0.001	P03844	Preprotein translocase secY subunit	b3300	PMS	1.00
3442176	REC05927	rp1O	E	144	-	0.39	P02413	50S ribosomal protein L15	b3301	PMS	1.00
3442359	REC05928	rpsD	?	59	-		P02430	50S ribosomal protein L30	b3302	PMS	0.69
3442866	REC05929	rpsE	E	167	-	0.37	P02356	30S ribosomal protein S5	b3303	PMS	1.00
3443234	REC05930	rp1R	E	117	-	0.53	P02419	50S ribosomal protein L18	b3304	PMS	1.00
3443777	REC05931	rp1F	E	177	-	0.35	P02390	50S ribosomal protein L6	b3305	PMS	1.00
3444182	REC05932	rpsH	E	130	-	0.49	P02361	30S ribosomal protein S8	b3306	PMS	1.00
3444521	REC05933	rpsN	E	101	-	0.59	P02370	30S ribosomal protein S14	b3307	PMS	1.00
3445075	REC05934	rp1E	N	179	49		P02389	50S ribosomal protein L5	b3308	PMS	1.00
3445404	REC05935	rp1X	E	104	-	0.58	P02425	50S ribosomal protein L24	b3309	PMS	1.00
3445786	REC05936	rp1N	E	123	111	0.49	P02411	50S ribosomal protein L14	b3310	PMS	1.00
3446205	REC05937	rpsQ	E	84	-	0.67	P02373	30S ribosomal protein S17	b3311	PMS	1.00
3446396	REC05938	rpsC	?	63	-		P02429	50S ribosomal protein L29	b3312	PMS	0.44
3446806	REC05939	rp1P	N	136	83		P02414	50S ribosomal protein L16	b3313	PMS	0.97
3447520	REC05940	rpsC	N	233	162		P02352	30S ribosomal protein S3	b3314	PMS	1.00
3447870	REC05941	rp1V	N	110	29		P02423	50S ribosomal protein L22	b3315	PMS	1.00
3448163	REC05942	rpsS	E	92	-	0.34	P02375	30S ribosomal protein S19	b3316	PMS	1.00
3449001	REC05943	rp1B	E	273	-	< 0.05	P02387	50S ribosomal protein L2	b3317	PMS	1.00
3449321	REC05944	rp1W	E	100	-	0.31	P02424	50S ribosomal protein L23	b3318	PMS	0.97
3449923	REC05945	rp1D	E	201	-	< 0.1	P02388	50S ribosomal protein L4	b3319	PMS	1.00
3450563	REC05946	rp1C	E	209	-	< 0.1	P02386	50S ribosomal protein L3	b3320	PMS	1.00
3450907	REC05947	rpsJ	E	103	-	< 0.3	P02364	30S ribosomal protein S10	b3321	PMS	1.00
3451564	REC05948	p1oO	N	139	6, 11, 86, 95		P03825	P1oO protein	b3322	UNC	0.00
3453035	REC05949	gspa	N	489	20, 112, 198, 382, 417, 431, 440, 440, 458		P45756	Probable general secretion pathway protein A	b3323	UNC	0.06

3453215	REC03242	<i>gspC</i>	X	271	-	P45757	Probable general secretion pathway protein C	b3324	UNC	0.03
3454002	REC03243	<i>gspD</i>	X	654	-	P45758	Probable general secretion pathway protein D precursor	b3325	UNC	0.44
3455976	REC03244	<i>gspE</i>	N	493	263, 264, 374, 391, 489	P45759	Probable general secretion pathway protein E	b3326	UNC	0.63
3457454	REC03245	<i>hofF</i>	N	398	97, 122, 150, 171, 367, 376	P41441	Putative general secretion pathway protein F	b3327	UNC	0.56
3458660	REC03246	<i>hofG</i>	N	145	10, 11, 118	P41442	Putative general secretion pathway protein G precursor	b3328	UNC	0.22
3459105	REC03247	<i>hofH</i>	N	169	124	P41443	Putative general secretion pathway protein H precursor	b3329	UNC	0.00
3459572	REC03248	<i>gspI</i>	X	138	-	P45760	Probable general secretion pathway protein I precursor	b3330	UNC	0.09
3459981	REC03249	<i>gspJ</i>	N	195	116, 144	P45761	Probable general secretion pathway protein J precursor	b3331	UNC	0.09
3460561	REC03250	<i>gspK</i>	N	327	55, 72, 97, 102, 126, 144, 286	P45762	Probable general secretion pathway protein K	b3332	UNC	0.16
3461556	REC03251	<i>gspL</i>	N	388	56, 148, 273	P45763	Probable general secretion pathway protein L	b3333	UNC	0.06
3462695	REC03252	<i>pshM</i>	X	161	-	P36678	Putative general secretion pathway protein M	b3334	UNC	0.00
3463180	REC03253	<i>hofD</i>	X	225	-	P25960	Type 4 prepilin-like proteins leader peptide processing enzyme	b3335	UNC	0.00
3464362	REC05950	<i>bfr</i>	X	158	-	P11056	Bacterioferritin	b3336	UNC	0.38
3464628	REC05951	<i>bfd</i>	X	64	-	P13655	Bacterioferritin-associated ferredoxin	b3337	UNC	0.06
3467490	REC05952	<i>chiA</i>	N	897	7, 15, 25, 39, 66, 82, 90, 110, 128	P13656	Probable bifunctional chitinase/lysozyme precursor	b3338	UNC	0.13
3468966	REC05953	<i>tufA</i>	E	394	-	P02990	Elongation factor Tu	b3339	PMS	1.00
3471151	REC05954	<i>fusa</i>	E	704	-	P02996	Elongation factor G	b3340	PMS	1.00
3471718	REC05955	<i>rpsG</i>	N	179	52	P02359	30S ribosomal protein S7	b3341	PMS	1.00
3472189	REC05956	<i>rpsL</i>	E	124	-	P02367	30S ribosomal protein S12	b3342	PMS	1.00
3472602	REC05957	<i>yheL</i>	E	95	-	P45530	Hypothetical protein yheL	b3343	UNC	0.09
3472969	REC05958	<i>yheM</i>	E	119	-	P45531	Hypothetical protein yheM	b3344	UNC	0.13
3473355	REC05959	<i>yheN</i>	E	128	107	P45532	Hypothetical protein yheN	b3345	UNC	0.13
3474089	REC05960	<i>yheO</i>	N	244	62	P45533	Hypothetical protein yheO	b3346	UNC	0.22
3475056	REC05961	<i>fkpA</i>	N	270	58, 83, 144, 150, 171, 203, 218, 220, 237	P45523	FKBP-type peptidyl-prolyl cis-trans isomerase fkpA precursor (EC	b3347	PMS	0.84
3475277	REC03266	<i>slyX</i>	N	72	35	P30857	SlyX protein	b3348	UNC	0.25
3476134	REC05962	<i>slyD</i>	E	196	5	P30856	FKBP-type peptidyl-prolyl cis-trans isomerase slyD (EC 5.2.1.8)	b3349	PMS	0.34
3476429	REC06997	<i>yheV</i>	X	66	-	P56622	Hypothetical protein yheV	b3350	UNC	0.06
3478244	REC05963	<i>kefB</i>	N	601	134, 174, 213	P45522	Glutathione-regulated potassium-efflux system protein kefB	b3350	MTR	0.47
3478798	REC05964	<i>yheR</i>	N	184	107, 162	P45534	Putative NAD(P)H oxidoreductase yheR (EC 1.6.99.-)	b3351	UNC	0.16
3478926	REC03270	<i>yheS</i>	N	637	27, 136	P45535	Hypothetical ABC transporter ATP-binding protein yheS	b3352	UNC	0.88
3480839	REC03271	<i>yheT</i>	N	340	51, 91, 124, 171, 174, 227, 305	P45524	Hypothetical protein yheT	b3353	UNC	0.19
3481855	REC03272	<i>yheU</i>	N	72	14, 63	P45536	Hypothetical protein yheU	b3354	UNC	0.09
3482127	REC06648	<i>prkB</i>	N	289	30, 46, 163, 217	P37307	Probable phosphoribulokinase (EC 2.7.1.19)	b3355	UNC	0.06
3483455	REC05965	<i>yhfa</i>	X	134	-	P24246	Hypothetical protein yhfa	b3356	UNC	0.31
3483757	REC03275	<i>crp</i>	X	210	-	P03020	Catabolite gene activator	b3357	RCD	0.44
3484440	REC03276	<i>yhfK</i>	N	696	186, 234, 269, 591	P45537	Hypothetical protein yhfK	b3358	UNC	0.25
3487817	REC05966	<i>argD</i>	?	406	30	P18335	Acetylornithine aminotransferase (EC 2.6.1.11)	b3359	AAM	0.69
3488466	REC05967	<i>paba</i>	N	187	51, 79	P00903	Para-aminobenzoate synthase glutamine amidotransferase comp	b3360	AAM	0.53
3489100	REC05968	<i>fic</i>	N	200	113	P20605	Cell filamentation protein fic	b3361	RCD	0.13
3489934	REC05970	<i>ppiA</i>	N	190	40	P20752	Peptidyl-prolyl cis-trans isomerase A precursor (EC 5.2.1.8)	b3363	PMS	0.84
3490205	REC03282	<i>yhfc</i>	N	393	317, 317, 347, 347, 396	P21229	Hypothetical protein yhfc	b3364	UNC	0.25
3491648	REC03283	<i>nirB</i>	N	847	11, 59, 75, 278, 431	P08201	Nitrite reductase [NAD(P)H] large subunit (EC 1.6.6.4)	b3365	BEN	0.47
3494188	REC03284	<i>nirD</i>	N	108	98	P23675	Nitrite reductase [NAD(P)H] small subunit (EC 1.6.6.4)	b3366	BEN	0.03
3494892	REC03285	<i>nirC</i>	X	184	-	P11097	Potential nitrite transporter	b3367	UNC	0.13
3495465	REC03286	<i>cysG</i>	X	457	-	P11098	Siroheme synthase	b3368	NCM	0.66
3497085	REC03287	<i>yhfl</i>	X	55	-	P45538	Hypothetical protein yhfl	b3369	UNC	0.00
3497496	REC06649	<i>yhfM</i>	N	462	198	P45539	Hypothetical transport protein yhfM	b3370	UNC	0.09
3498884	REC03289	<i>yhfN</i>	N	347	9, 18, 60, 133, 152, 183, 197, 243	P45540	Hypothetical protein yhfN	b3371	UNC	0.19
3498980	REC03290	<i>yhfO</i>	N	149	43, 44	P45541	Hypothetical protein yhfO	b3372	UNC	0.03
3500404	REC06650	<i>yhfp</i>	N	134	9, 85, 112	P45542	Hypothetical protein yhfp	b3373	UNC	0.03
3500805	REC03292	<i>yhfQ</i>	E	261	-	P45543	Hypothetical sugar kinase yhfQ	b3374	UNC	0.09
3501624	REC03293	<i>yhfr</i>	N	265	3, 84, 121	P45544	Hypothetical transcriptional regulator yhfr	b3375	UNC	0.53
3503658	REC05971	<i>yhfs</i>	N	361	298	P45545	Hypothetical protein yhfs	b3376	UNC	0.00
3504974	REC05972	<i>yhft</i>	X	434	8	P45546	Hypothetical protein yhft	b3377	UNC	0.00
3505378	REC05973	<i>yhfu</i>	N	130	42, 75, 100, 124	P45547	Hypothetical protein yhfu	b3378	UNC	0.00
3506228	REC05974	<i>php</i>	N	292	206, 281, 281	P45548	Phosphotriesterase homology protein	b3379	UNC	0.16
3507451	REC05975	<i>yhfW</i>	N	408	149, 192, 282, 356, 360	P45549	Hypothetical protein yhfW	b3380	UNC	0.41
3508614	REC05976	<i>yhfx</i>	N	387	47	P45550	Hypothetical protein yhfx	b3381	UNC	0.00
3509102	REC05977	<i>yhfy</i>	N	134	27, 101	P45551	Hypothetical protein yhfy	b3382	UNC	0.00
3509763	REC05978	<i>yh fz</i>	N	228	39, 48, 123, 176, 215	P45552	Hypothetical protein yhfz	b3383	UNC	0.00
3511276	REC05979	<i>trpS</i>	E	334	-	P00954	Tryptophanyl-tRNA synthetase (EC 6.1.1.2)	b3384	PMS	1.00
3512027	REC05980	<i>gph</i>	N	252	61	P32662	Phosphoglycolate phosphatase (EC 3.1.3.18)	b3385	CHM	0.81
3512697	REC05981	<i>rpe</i>	E	225	222	P32661	Ribulose-phosphate 3-epimerase (EC 5.1.3.1)	b3386	CHM	0.94
3513551	REC05982	<i>dam</i>	N	278	35, 197, 242	P00475	DNA adenine methylase (EC 2.1.1.72)	b3387	NAM	0.28
3514944	REC05983	<i>damX</i>	N	428	183, 358, 364, 426	P11557	DamX protein	b3388	UNC	0.03
3516124	REC05984	<i>aroB</i>	N	362	28, 158, 213	P07639	3-dehydroquinate synthase (EC 4.2.3.4)	b3389	AAM	0.84
3516903	REC05985	<i>aroK</i>	E	240	-	P24167	Shikimate kinase I (EC 2.7.1.71)	b3390	AAM	0.81
3518341	REC05986	<i>hofQ</i>	N	412	43, 324, 395	P34749	Protein transport protein hofQ precursor	b3391	UNC	0.28
3518696	REC05987	<i>yrfa</i>	?	147	-	P45750	Hypothetical protein yrfa	b3392	UNC	0.00
3519087	REC05988	<i>yrfb</i>	N	146	22, 95	P45751	Hypothetical protein yrfb	b3393	UNC	0.00
3519610	REC05989	<i>yrfc</i>	N	179	16, 68, 93, 121	P45752	Hypothetical protein yrfc	b3394	UNC	0.00
3520416	REC05990	<i>yrfD</i>	N	268	5, 79, 82	P45753	Hypothetical protein yrfD	b3395	UNC	0.00
3520485	REC03314	<i>mrcA</i>	N	858	51, 204, 253, 428, 569, 620, 625, 662, 699, 754, 792, 797	P02918	Penicillin-binding protein 1A	b3396	LPC	0.84
3523787	REC05991	<i>nudE</i>	N	186	50, 98, 129	P45799	ADP compounds hydrolase nudE (EC 3.6.1.-)	b3397	MMS	0.19
3524107	REC03316	<i>yfff</i>	N	711	86, 694	P45800	Putative membrane protein igaA homolog	b3398	UNC	0.00
3526262	REC03317	<i>yrfG</i>	N	237	3, 6, 55, 115, 125, 136, 173	P45801	Hypothetical protein yrfG	b3399	UNC	0.03
3526986	REC03318	<i>hslR</i>	N	133	8, 58, 63	P45802	Heat shock protein 15	b3400	SMC	0.34
3527406	REC03319	<i>hslO</i>	X	294	9	P45803	33 kDa chaperonin	b3401	PMS	0.69
3530077	REC05992	<i>yhgE</i>	N	574	6, 62, 72, 120, 146, 246, 287, 322, 347	P45804	Hypothetical protein yhgE	b3402	UNC	0.03
3530456	REC03321	<i>pckA</i>	N	540	42, 68, 216, 533	P22259	Phosphoenolpyruvate carboxykinase [ATP] (EC 4.1.1.49)	b3403	CHM	0.38
3533506	REC05993	<i>envZ</i>	N	450	112, 193, 222, 243, 297, 338	P02933	Osmolarity sensor protein envZ (EC 2.7.3.-)	b3404	SMC	0.34
3534222	REC05994	<i>ompR</i>	N	239	98, 133, 181, 222	P03025	Transcriptional regulatory protein ompR	b3405	SMC	0.69
3534414	REC03324	<i>greB</i>	N	170	63, 91	P30128	Transcription elongation factor greB	b3406	NAM	0.19
3535122	REC03325	<i>yhgF</i>	N	740	19, 115, 286, 291, 303, 307, 340, 471, 482, 651, 716	P46837	Protein yhgF	b3407	UNC	0.59
3537799	REC03326	<i>feoA</i>	N	75	22, 48	P33649	Ferrous iron transport protein A	b3408	UNC	0.03
3538043	REC03327	<i>feoB</i>	N	773	13, 86, 100, 153, 217, 431, 450, 484, 522, 683, 618, 690, 758, 766	P33650	Ferrous iron transport protein B	b3409	UNC	0.47
3540364	REC03328	<i>yhgG</i>	?	78	-	P46845	Hypothetical protein yhgG	b3410	UNC	0.00
3540803	REC03329	<i>yhgA</i>	N	292	111, 218, 256	P31667	Hypothetical protein yhgA	b3411	UNC	0.00
3542470	REC03331	<i>yhgH</i>	N	243	142	P46846	Hypothetical protein yhgH	b3413	UNC	0.50
3542480	REC05995	<i>bioH</i>	N	256	28	P13001	BioH protein	b3412	UNC	0.25
3543260	REC03332	<i>yhgI</i>	N	191	16, 175, 165	P46847	Protein yhgI	b3414	UNC	0.19
3544195	REC03333	<i>gntT</i>	N	437	31, 99, 166, 211, 342	P39835	High-affinity gluconate transporter	b3415	MTR	0.31
3547703	REC05996	<i>malQ</i>	N	694	35, 80, 118, 174, 275, 395, 430, 432, 478	P15977	4-alpha-glucanotransferase (EC 2.4.1.25)	b3416	CHM	0.41

3550106	REC06478	malP	N	797	745, 746	P00490	Maltodextrin phosphorylase (EC 2.4.1.1)	b3417	CHM	0.56	
3550718	REC06479	malT	N	901	847, 885	P06993	MalT regulatory protein	b3418	RCD	0.16	
3554071	REC05998	rtcA	N	201	78, 118	P46849	RNA 3'-terminal phosphate cyclase (EC 6.5.1.4)		NAM	0.13	
3554484	REC05999	yhgK	N	146	13, 47, 70			b3420	UNC	0.13	
3555711	REC06480	rtcB	N	408	237, 310, 400	P46850	Protein rtcB	b3421	UNC	0.31	
3555900	REC03340	rtcR	N	532	190, 204, 241, 252, 293, 315, 371, 456, 475, 526	P38035	Transcriptional regulatory protein rtcR	b3422	RCD	0.34	
3558238	REC06001	glpR	N	252	20, 32, 77, 197, 248	P09392	Glycerol-3-phosphate regulon repressor	b3423	RCD	0.34	
3559085	REC06002	glpG	N	276	222, 269	P09391	Protein glpG	b3424	UNC	0.13	
3559456	REC06003	glpE	X	108	-	P09390	Thiosulfate sulfurtransferase glpE (EC 2.8.1.1)	b3425	MSM	0.13	
3559646	REC06481	glpD	N	501	74, 414, 421, 457, 497	P13035	Aerobic glycerol-3-phosphate dehydrogenase (EC 1.1.99.5)	b3426	CHM	0.53	
3561650	REC06004	yzgJ	?	97	5	P76692	VERY HYPOTHETICAL 10.7 kDa PROTEIN IN GLPD-GLGP INT	b3427	UNC	0.00	
3564214	REC06482	glpP	N	815	52, 82, 172, 176, 247, 280, 315, 523, 648, 704, 807, 811	P13031	Glycogen phosphorylase (EC 2.4.1.1)	b3428	CHM	0.56	
3565666	REC06006	glgA	N	477	173, 230, 241, 373, 381, 434, 469	P08323	Glycogen synthase (EC 2.4.1.21)	b3429	CHM	0.53	
3566961	REC06007	glgC	N	431	31, 36, 60, 63, 80, 137	P00584	Glucose-1-phosphate adenylyltransferase (EC 2.7.7.27)	b3430	CHM	0.50	
3568952	REC06483	glgX	N	657	156, 351, 367, 418, 459, 614, 652	P15067	Glycogen operon protein glgX (EC 3.2.1.-)	b3431	UNC	0.53	
3571135	REC06009	glgB	N	728	49, 158, 163, 255, 290, 308, 317	P07762	1,4-alpha-glucan branching enzyme (EC 2.4.1.18)	b3432	CHM	0.53	
3572511	REC06010	asd	E	367	-	< 0.01	P00353	Aspartate-semialdehyde dehydrogenase (EC 1.2.1.11)	b3433	AAM	0.88
3572704	REC03352	yhgN	N	197	72	P46851	Hypothetical protein yhgN	b3434	UNC	0.56	
3573689	REC06011	gntU	N	111	1, 20	P46858	Low-affinity gluconate transporter	b3435	MTR	0.03	
3574693	REC06012	gntU	N	332	25, 244	P46858	Low-affinity gluconate transporter		MTR	0.00	
3575185	REC06013	gntK	X	162	-	P46859	Thermoresistant gluconokinase (EC 2.7.1.12)	b3437	CHM	0.31	
3576357	REC06014	gntR	X	313	-	P46860	Gluconate utilization system GNT-I transcriptional repressor	b3438	RCD	0.16	
3577276	REC06015	yhhW	N	231	2, 39, 52, 67, 100, 126, 196	P46852	Protein yhhW	b3439	UNC	0.38	
3578436	REC06016	yhhX	N	345	114, 172, 176, 268, 327	P46853	Putative oxidoreductase yhhX (EC 1.-.-.-)	b3440	UNC	0.06	
3578769	REC03359	yhhY	N	162	29	P46854	Hypothetical acetyltransferase yhhY (EC 2.3.1.-)	b3441	UNC	0.31	
3579494	REC03360	yhhZ	N	392	226, 250, 281	P46855	Hypothetical protein yhhZ	b3442	UNC	0.00	
3580669	REC03361	yrhA	N	138	1, 132	P46856	Hypothetical protein yrhA	b3443	UNC	0.00	
3581114	REC04294		E	91	26	0.33	P03827	Insertion element IS1 1/2/3/5/6 protein insA	b3442	PHT	0.00
3581308	REC04293	insB	?	167	142	P03830	Insertion element IS1 1/5/6 protein insB	b3445	PHT	0.00	
3582390	REC03364	yrhB	N	94	57	P46857	Hypothetical protein yrhB	b3446	UNC	0.00	
3584454	REC06017	ggt	N	580	13, 110, 171, 185, 567	P18956	Gamma-glutamyltranspeptidase precursor (EC 2.3.2.2)	b3447	AAM	0.56	
3584574	REC03366	yhhA	N	146	28, 35	P23850	Hypothetical protein yhhA precursor	b3448	UNC	0.00	
3585744	REC06018	ugpQ	N	247	111, 123, 224	P10908	Glycerophosphoryl diester phosphodiesterase (EC 3.1.4.46)	b3449	LPC	0.59	
3586850	REC06019	ugpC	X	369	340	P10907	SN-glycerol-3-phosphate transport ATP-binding protein ugpC	b3450	MTR	0.44	
3587658	REC06020	ugpE	N	281	16, 122, 151, 183	P10906	SN-glycerol-3-phosphate transport system permease protein ugpE	b3451	MTR	0.59	
3588542	REC06021	ugpA	N	295	25, 41, 131, 168, 211, 248	P10905	SN-glycerol-3-phosphate transport system permease protein ugpA	b3452	MTR	0.63	
3589956	REC06022	ugpB	N	438	154, 290	P10904	Glycerol-3-phosphate-binding periplasmic protein precursor	b3453	MTR	0.47	
3591080	REC06023	livF	N	241	30, 114	P22731	High-affinity branched-chain amino acid transport ATP-binding protein livF	b3454	MTR	0.53	
3591837	REC06024	livG	N	255	46, 74, 110, 120, 199, 247	P22730	High-affinity branched-chain amino acid transport ATP-binding protein livG	b3455	MTR	0.47	
3593111	REC06025	livM	N	425	96, 192, 420	P22729	High-affinity branched-chain amino acid transport system permease livM	b3456	MTR	0.38	
3594034	REC06026	livH	X	308	-	P08340	High-affinity branched-chain amino acid transport system permease livH	b3457	MTR	0.44	
3595191	REC06027	livK	N	369	3, 92, 112, 268, 280	P04816	Leucine-specific binding protein precursor	b3458	MTR	0.31	
3595615	REC03377	yhhK	N	127	48, 63	P37613	Hypothetical protein yhhK	b3459	UNC	0.00	
3597346	REC06028	livJ	N	386	219	P02917	Leu/Ile/Val-binding protein precursor	b3460	MTR	0.38	
3598414	REC06029	xpoH	E	284	-	< 0.1	P00580	RNA polymerase sigma-52 factor	b3461	RCD	0.50
3599717	REC06030	ftsX	N	352	317	P10122	Cell division protein ftsX	b3462	UNC	0.53	
3600378	REC06031	ftsE	E	222	-	< 0.1	P10115	Cell division ATP-binding protein ftsE	b3463	UNC	0.72
3601874	REC06032	ftsY	E	497	-	< 0.01	P10121	Cell division protein ftsY	b3464	PMS	1.00
3602024	REC03383	yhhF	E	198	181, 187	< 0.2	P10120	Putative methylase yhhF (EC 2.1.1.-)	b3465	UNC	0.94
3602610	REC03384	yhhL	E	89	72	0.44	P37614	Hypothetical protein yhhL	b3466	UNC	0.03
3603241	REC06033	yhhM	E	119	-	< 0.3	P37615	Hypothetical protein yhhM	b3467	UNC	0.00
3603382	REC03386	yhhN	N	208	143, 188	P37616	Hypothetical protein yhhN	b3468	UNC	0.03	
3604082	REC03387	zntA	N	732	72, 101, 204, 290, 378, 429, 511, 562, 638	P37617	Lead, cadmium, zinc and mercury transporting ATPase (EC 3.6.3.-)	b3469	MTR	0.47	
3606627	REC06034	sirA	X	81	-	P37618	SirA protein	b3470	UNC	0.38	
3606848	REC03389	yhhQ	X	221	-	P37619	Hypothetical protein yhhQ	b3471	UNC	0.47	
3607532	REC03390	dcrB	N	203	132, 166	P37620	DcrB protein precursor	b3472	UNC	0.00	
3609406	REC06035	yhhS	N	419	60, 70, 133, 160, 295, 309, 357, 376, 401	P37621	Hypothetical protein yhhS	b3473	UNC	0.19	
3609415	REC03392	yhhT	N	376	244	P37622	Hypothetical protein yhhT	b3474	UNC	0.34	
3610600	REC03393	yhhU	?	195	174	P37623	Hypothetical protein yhhU	b3475	UNC	0.03	
3611298	REC03394	nikA	N	524	105, 162, 171, 201, 236, 330, 485, 520	P33590	Nickel-binding periplasmic protein precursor	b3476	MTR	0.28	
3612872	REC03395	nikB	N	314	96, 112, 238	P33591	Nickel transport system permease protein nikB	b3477	MTR	0.19	
3613813	REC03396	nikC	N	277	228, 266	P33592	Nickel transport system permease protein nikC	b3478	MTR	0.16	
3614646	REC03397	nikD	N	254	109, 238, 245	P33593	Nickel transport ATP-binding protein nikD	b3479	MTR	0.03	
3615407	REC03398	nikE	N	268	12, 72, 101, 189, 225, 258	P33594	Nickel transport ATP-binding protein nikE	b3480	MTR	0.06	
3616219	REC03399	nikR	N	133	38, 49	P28910	Nickel responsive regulator	b3481	RCD	0.09	
3616823	REC03400	rhsB	N	1411	33, 75	P16917	RhsB protein precursor	b3482	UNC	0.03	
3621045	REC03401	yhhH	X	122	-	P28911	Hypothetical protein yhhH	b3483	UNC	0.00	
3622009	REC03402	yhhI	N	378	-	P28912	H repeat-associated protein yhhI	b3484	UNC	0.06	
3624437	REC06036	yhhJ	X	375	-	P31993	Hypothetical protein yhhJ	b3485	UNC	0.09	
3627118	REC06037	yhiH	N	894	10, 109, 212, 334, 336, 402, 425, 445, 493, 563, 651, 741	P37624	Hypothetical ABC transporter ATP-binding protein yhiH	b3486	UNC	0.97	
3628232	REC06039	yhiI	N	355	268	P37626	Hypothetical protein yhiI precursor	b3487	UNC	0.13	
3630220	REC06040	yhiJ	N	540	4, 153, 238, 263, 338, 393, 419, 443, 459, 492, 517, 540	P37627	Hypothetical protein yhiJ	b3488	UNC	0.00	
3630853	REC06041	yhiK	N	123	35, 42, 118	P37628		b3489	UNC	0.00	
3632088	REC06498	yhiL	N	412	23, 103, 147, 180	P37629	Hypothetical protein yhiL		UNC	0.00	
3632372	REC03410	yhiM	N	383	19, 39, 69, 110, 139, 143, 187, 204, 220, 256, 282, 284, 306, 320, 337	P37630	Hypothetical protein yhiM	b3491	UNC	0.00	
3635040	REC06499	yhiN	?	400	351	P37631	Hypothetical protein yhiN	b3492	UNC	0.47	
3635272	REC03412	pitA	N	499	34, 85, 99, 137, 210, 240, 265, 298, 362, 432	P37308	Low-affinity inorganic phosphate transporter 1	b3493	MTR	0.66	
3637350	REC06044	uspB	N	111	83	P37632	Universal stress protein B	b3494	UNC	0.03	
3637741	REC03414	uspA	N	144	114	P28242	Universal stress protein A	b3495	UNC	0.06	
3638492	REC03415	yhiP	N	489	237, 270, 358, 445	P36837	Hypothetical transporter yhiP	b3496	UNC	0.31	
3640762	REC06045	yhiQ	N	250	69, 180, 210	P37633	Hypothetical protein yhiQ	b3497	UNC	0.19	
3642812	REC06046	prlC	N	680	117, 204, 210, 246, 308, 472, 620	P27298	Oligopeptidase A (EC 3.4.24.70)	b3498	PMS	0.28	
3643015	REC03418	yhiR	N	280	55, 72, 108, 124	P37634	Hypothetical protein yhiR	b3499	UNC	0.34	
3643929	REC03419	gor	E	450	-	< 0.01	P06715	Glutathione reductase (EC 1.6.4.2)	b3500	BEN	0.44
3646158	REC03420	arsR	?	117	96	P37309	Arsenical resistance operon repressor	b3501	RCD	0.41	
3646544	REC03421	arsB	N	436	134, 170, 236, 301, 373, 389	P37310	Arsenical pump membrane protein	b3502	MTR	0.34	
3647867	REC03422	arsC	N	141	99	P37311	Arsenite reductase (EC 1.97.1.5)	b3503	MSM	0.66	
3648921	REC03423	yhiS	N	260	24, 41, 240	P37635	Hypothetical protein yhiS	b3504	UNC	0.00	
3650828	REC06501		N	338	218, 264, 302	P03837	Transposase insH for insertion sequence element IS5	b3505	PHT	0.34	
3651558	REC03425	slp	E	199	-	< 0.1	P37194	Outer membrane protein slp precursor	b3506	SMC	0.09
3652313	REC03426	yhiF	N	176	27, 172	P37195	Hypothetical transcriptional regulator yhiF	b3507	UNC	0.00	
3653532	REC06048	yhiD	X	215	-	P26606	Hypothetical protein yhiD	b3508	UNC	0.50	
3653934	REC06049	hdeB	X	112	-	P26605	Protein hdeB precursor	b3509	UNC	0.00	

3654370	REC06050	<i>hdeA</i>	X	110	-	P26604	Protein hdeA precursor	b3510	UNC	0.03
3654625	REC03430	<i>hdeD</i>	X	190	-	P26603	HdeD protein	b3511	UNC	0.22
3655996	REC03431	<i>yhiE</i>	N	175	21, 49, 71	P26688	Hypothetical protein yhiE	b3512	UNC	0.00
3656862	REC03432	<i>yhiU</i>	N	385	61	P37636	Hypothetical lipoprotein yhiU precursor	b3513	UNC	0.47
3658044	REC03433	<i>yhiV</i>	N	1037	256, 393, 472, 482, 531, 536, 689, 796, 810, 887, 916, 967	P37637	Hypothetical protein yhiV	b3514	UNC	0.75
3662248	REC06051	<i>yhiW</i>	N	242	96, 180	P37638	Hypothetical transcriptional regulator yhiW	b3515	UNC	0.00
3663440	REC06052	<i>gadX</i>	X	274	285	P37639	Transcriptional regulator gadX	b3516	UNC	0.00
3665210	REC06053	<i>gadA</i>	X	466	-	P80063	Glutamate decarboxylase alpha (EC 4.1.1.15)	b3517	AAM	0.16
3666818	REC06054	<i>yhjA</i>	X	465	-	P37197	Probable cytochrome C peroxidase (EC 1.1.1.5)	b3518	UNC	0.28
3667222	REC03438	<i>creF</i>	X	549	-	P37196	Probable cytoplasmic trehalase (EC 3.2.1.28)	b3519	UNC	0.00
3669524	REC06055	<i>yhjB</i>	X	200	-	P37640	Hypothetical transcriptional regulator yhjB	b3520	UNC	0.03
3669972	REC03440	<i>yhjC</i>	X	323	-	P37641	Hypothetical transcriptional regulator yhjC	b3521	UNC	0.72
3670992	REC03441	<i>yhjD</i>	X	337	-	P37642	Hypothetical protein yhjD	b3522	UNC	0.81
3672416	REC03442	<i>yhjE</i>	N	440	36, 103, 128, 184, 232, 293, 404	P37643	Hypothetical metabolite transport protein yhjE	b3523	UNC	0.41
3675995	REC060505	<i>yhjG</i>	N	691	25, 57, 71, 199, 262, 336, 473, 628	P37645	Hypothetical protein yhjG	b3524	UNC	0.06
3676820	REC06056	<i>yhjH</i>	N	256	104, 111, 194, 213	P37646	Hypothetical protein yhjH	b3525	UNC	0.00
3676830	REC03446	<i>kdgK</i>	N	382	6, 298	P37647	2-dehydro-3-deoxygluconokinase (EC 2.7.1.45)	b3526	CHM	0.56
3679570	REC06059	<i>yhjJ</i>	N	498	15, 261, 489, 497	P37648	Protein yhjJ precursor	b3527	UNC	0.03
3681077	REC06060	<i>dctA</i>	N	428	3, 90, 133, 284, 330, 341, 397	P37312	Aerobic C4-dicarboxylate transport protein	b3528	MTR	0.56
3683215	REC06061	<i>yhjK</i>	N	651	43, 69, 134, 267, 292, 380, 504, 505, 613, 618	P37649	Protein yhjK	b3529	UNC	0.00
3686830	REC06507	<i>yhjL</i>	N	1166	4, 45, 95, 144, 235, 283, 349, 509, 574, 597, 763, 882, 945, 1008, 1016	P37650	Hypothetical protein yhjL	b3530	UNC	0.03
3687890	REC06063	<i>bcsC</i>	N	368	110, 158, 208, 316, 357	P37651	Endoglucanase precursor (EC 3.2.1.4)	b3531	CHM	0.06
3690236	REC06064	<i>yhjN</i>	N	779	77, 81, 112, 208, 276, 561, 698, 761, 761	P37652	Hypothetical protein yhjN precursor	b3532	UNC	0.00
3692913	REC06065	<i>yhjO</i>	N	888	355, 428, 534, 605, 607, 676, 746, 793	P37653	Hypothetical protein yhjO	b3533	UNC	0.28
3693590	REC06067	<i>yhjQ</i>	N	242	95, 121, 144, 222	P37655	Hypothetical protein yhjQ	b3534	UNC	0.00
3693814	REC06068	<i>yhjR</i>	N	62	42	P37656	Hypothetical protein yhjR	b3535	UNC	0.00
3694087	REC03457	<i>yhjS</i>	N	523	30, 51, 90, 100, 351	P37657	Hypothetical protein yhjS	b3536	UNC	0.00
3695658	REC03458	<i>yhjT</i>	X	62	-	P37658	Hypothetical protein yhjT	b3537	UNC	0.00
3695843	REC03459	<i>yhjU</i>	N	559	119, 172, 233, 282, 322, 505, 532	P37659	Hypothetical protein yhjU	b3538	UNC	0.00
3698192	REC03460	<i>yhjV</i>	N	423	63, 71, 130, 153, 208, 329	P37660	Hypothetical transport protein yhjV	b3539	UNC	0.13
3700497	REC06069	<i>dppF</i>	N	334	90, 98, 222	P37313	Dipeptide transport ATP-binding protein dppF	b3540	MTR	0.53
3701477	REC06070	<i>dppD</i>	N	327	51, 86, 105, 146, 165, 202, 235, 265	P37314	Dipeptide transport ATP-binding protein dppD	b3541	MTR	0.59
3702390	REC06071	<i>dppC</i>	N	300	46, 218, 225	P37315	Dipeptide transport system permease protein dppC	b3542	MTR	0.59
3703419	REC06072	<i>dppB</i>	N	339	50, 94, 318	P37316	Dipeptide transport system permease protein dppB	b3543	MTR	0.72
3705334	REC06073	<i>dppA</i>	N	535	32, 36, 91, 152, 377, 423, 437, 489	P23847	Periplasmic dipeptide transport protein precursor	b3544	MTR	0.56
3708137	REC06511	<i>yhjW</i>	N	574	17, 40, 132, 236, 274, 393, 407, 425, 443, 476, 540	P37661	Membrane-protein yhjW	b3546	UNC	0.06
3709636	REC06075	<i>yhjX</i>	N	402	147, 182, 253, 350, 360	P37662	Hypothetical protein yhjX	b3547	UNC	0.38
3710569	REC06076	<i>yhjY</i>	N	234	27, 58, 68, 109, 113, 188	P37663	Hypothetical protein yhjY	b3548	UNC	0.00
3710721	REC03469	<i>tag</i>	N	187	8, 92, 185	P05100	DNA-3-methyladenine glycosylase I (EC 3.2.2.20)	b3549	NAM	0.47
3711281	REC03470	<i>yaAC</i>	N	146	36, 90, 117	P37664	Hypothetical acetyltransferase yaAC (EC 2.3.1.-)	b3550	UNC	0.13
3713909	REC06077	<i>bisC</i>	N	739	188, 312, 622, 692, 726	P20099	Biotin sulfoxide reductase (EC 1.-.-.-)	b3551	NCM	0.03
3714176	REC03472	<i>yaAD</i>	N	219	46, 54, 86, 110, 126, 167, 181	P37665	Hypothetical lipoprotein yaAD precursor	b3552	UNC	0.56
3714927	REC06512	<i>tkxA</i>	N	328	18, 152, 213, 277	P37666	2-ketoglucuronate reductase (EC 1.1.1.215)	b3553	CHM	0.47
3716793	REC06078	<i>yaEF</i>	?	276	268	P37667	Hypothetical protein yaEF	b3554	UNC	0.00
3717107	REC03475	<i>yaEG</i>	N	96	10, 11	P37668	Hypothetical protein yaEG	b3555	UNC	0.00
3717678	REC03476	<i>cspA</i>	N	70	23	P15277	Cold shock protein cspA	b3556	UNC	0.72
3718309	REC03477	<i>insJ</i>	N	173	3, 59, 135	P19768	Insertion element IS150 hypothetical 19.7 kDa protein	b3557	PHT	0.56
3718827	REC03478	<i>insK</i>	N	283	100, 221	P19769	Putative transposase insK for insertion sequence element IS150	b3558	UNC	0.56
3722026	REC06079	<i>glyS</i>	E	689	-	P00961	Glycyl-tRNA synthetase beta chain (EC 6.1.1.14)	b3559	PMS	0.72
3722947	REC06080	<i>glyQ</i>	E	303	-	P00960	Glycyl-tRNA synthetase alpha chain (EC 6.1.1.14)	b3560	PMS	0.75
3723516	REC03481	<i>yaIH</i>	N	331	61, 99, 101, 118, 165, 207, 208, 229, 231, 266	P37669	Hypothetical protein yaIH	b3561	UNC	0.06
3724993	REC06081	<i>yaIA</i>	N	146	5, 7, 13, 55, 87, 124	P11287	Hypothetical protein yaIA	b3562	UNC	0.03
3725389	REC06082	<i>yaIB</i>	N	117	1, 7, 78, 106	P11286	Hypothetical protein yaIB	b3563	UNC	0.00
3727000	REC06083	<i>xyiB</i>	?	484	-	P09099	Xylose kinase (EC 2.7.1.17)	b3564	CHM	0.47
3728394	REC06084	<i>xyiA</i>	N	440	46, 115, 253, 277, 341, 404	P09044	Xylose isomerase (EC 5.3.1.5)	b3565	CHM	0.22
3728760	REC03486	<i>xyiF</i>	N	330	5, 36	P37387	D-xylose-binding periplasmic protein precursor	b3566	MTR	0.19
3729830	REC03487	<i>xyiG</i>	N	513	253, 312, 338, 349, 370, 385, 464, 488	P37388	D-xylose transport ATP-binding protein xyiG	b3567	MTR	0.22
3731349	REC03488	<i>xyiH</i>	N	393	17, 150, 382	P37389	Xylose transport system permease protein xyiH	b3568	MTR	0.19
3732608	REC03489	<i>xyiR</i>	X	392	-	P37390	Xylose operon regulatory protein	b3569	RCD	0.06
3734806	REC06085	<i>bax</i>	N	274	24, 94, 115, 126, 188, 232	P27297	BAX protein	b3570	UNC	0.09
3735126	REC03491	<i>malS</i>	N	676	19, 56, 118, 173, 201, 265, 299	P25718	Alpha-amylase precursor (EC 3.2.1.1)	b3571	CHM	0.09
3737334	REC03492	<i>avtA</i>	N	417	59, 67, 96, 143, 196, 239, 364, 372, 407	P09053	Valine-pyruvate aminotransferase (EC 2.6.1.66)	b3572	AAM	0.09
3739211	REC06514	<i>ysaA</i>	N	157	112	P56256	Putative electron transport protein ysaA	b3573	UNC	0.00
3740161	REC06086	<i>yaJA</i>	N	282	115, 218	P37671	Hypothetical transcriptional regulator yaJA	b3574	UNC	0.19
3740362	REC03495	<i>yaIA</i>	N	332	114, 121, 163, 174, 177, 242, 314	P37672	Hypothetical oxidoreductase yaIA (EC 1.1.1.-)	b3575	UNC	0.06
3741372	REC03496	<i>yaIA</i>	N	155	25, 63, 87	P37673	Hypothetical protein yaIA	b3576	UNC	0.16
3741957	REC03497	<i>yaIA</i>	N	157	70	P37674	Hypothetical protein yaIA	b3577	UNC	0.13
3742433	REC03498	<i>yaIA</i>	?	424	18	P37675	Hypothetical protein yaIA	b3578	UNC	0.44
3743724	REC03499	<i>yaIO</i>	N	328	80, 130, 172, 202, 267, 323	P37676	Putative ABC transporter periplasmic binding protein yaIO precursor	b3579	UNC	0.41
3744714	REC03500	<i>lyx</i>	N	498	5, 14, 20, 59, 200, 210, 230, 329, 355, 365, 384	P37677	Cryptic L-xylose kinase (EC 2.7.1.53)	b3580	CHM	0.25
3746207	REC03501	<i>sgbH</i>	X	220	-	P37678	Probable hexulose-6-phosphate synthase (EC 4.1.2.-)	b3581	UNC	0.22
3746829	REC03502	<i>sgbU</i>	N	297	243, 247	P37679	Putative hexulose-6-phosphate isomerase (EC 5.-.-.-)	b3582	UNC	0.19
3747716	REC03503	<i>sgbE</i>	N	231	95, 130, 205	P37680	Probable sugar isomerase sgbE (EC 5.1.-.-)	b3583	UNC	0.19
3749498	REC06087	<i>yaIT</i>	N	246	30, 42, 94, 135, 163	P37681	Putative outer membrane protein yaIT precursor	b3584	UNC	0.03
3749622	REC03505	<i>yaIU</i>	N	324	38, 188	P37682	Hypothetical transcriptional regulator yaIU	b3585	UNC	0.00
3751729	REC06088	<i>yaIV</i>	N	378	17, 60, 76, 198, 207, 241, 267, 310	P37683	Hypothetical protein yaIV precursor	b3586	UNC	0.06
3752058	REC06089	<i>yaIW</i>	N	107	51, 75	P37684	Hypothetical protein yaIW	b3587	UNC	0.03
3754231	REC06090	<i>aldB</i>	X	542	-	P37685	Aldehyde dehydrogenase B (EC 1.2.1.22)	b3588	CHM	0.47
3755454	REC06091	<i>yaIY</i>	N	382	52, 76, 94, 100, 110, 142, 175, 215	P37686	Probable alcohol dehydrogenase (EC 1.1.1.1)	b3589	UNC	0.50
3757488	REC06528	<i>selB</i>	N	614	350, 538, 574, 606	P14081	Selenocysteine-specific elongation factor	b3590	PMS	0.16
3758876	REC06529	<i>selA</i>	N	463	123, 147, 198, 237, 256, 318, 344	P23328	L-seryl-tRNA(Sec) selenium transferase (EC 2.9.1.1)	b3591	NAM	0.25
3759582	REC06094	<i>yibF</i>	N	202	2, 54, 149, 150	P32105	Hypothetical GST-like protein yibF	b3592	UNC	0.22
3759810	REC03513	<i>rhsA</i>	N	1377	35, 150, 383, 453, 469, 491, 500, 533, 554, 596, 671, 705, 768, 1242, 130	P16916	RhsA protein precursor	b3593	UNC	0.03
3763964	REC03514	<i>yibA</i>	E	280	-	P24172	Hypothetical protein yibA	b3594	UNC	0.03
3764848	REC06531	<i>yibJ</i>	N	233	-	P32109	Hypothetical protein yibJ	b3595	UNC	0.00
3765804	REC03516	<i>yibG</i>	E	153	-	P32106	Hypothetical protein yibG precursor	b3596	UNC	0.00
3769006	REC06095	<i>yibH</i>	X	378	-	P32107	Hypothetical protein yibH	b3597	UNC	0.03
3769371	REC06096	<i>yibI</i>	X	120	-	P32108	Hypothetical protein yibI	b3598	UNC	0.00
3769908	REC03519	<i>mtLA</i>	N	637	601, 611	P00550	PTS system, mannitol-specific IIBC component (EC 2.7.1.69)	b3599	MTR	0.25
3772051	REC03520	<i>mtLD</i>	N	382	33, 73, 161, 162, 249, 272, 343, 371	P09424	Mannitol-1-phosphate 5-dehydrogenase (EC 1.1.1.17)	b3600	CHM	0.22
3773199	REC03521	<i>mtLR</i>	N	195	5, 166, 194	P36563	Mannitol operon repressor	b3601	RCD	0.03
3774292	REC03522	<i>yibL</i>	X	120	-	P36564	Hypothetical protein yibL	b3602	UNC	0.03
3775026	REC03523	<i>lidP</i>	N	551	16, 19, 138, 194, 278, 298, 348, 448, 456, 481	P33231	L-lactate permease	b3603	MTR	0.38

3776681	REC03524	<i>l1dR</i>	N	258	17, 94			P33233	Putative L-lactate dehydrogenase operon regulatory protein	b3604	UNC	0.03
3777454	REC03525	<i>l1dD</i>	N	396	160, 197, 319			P33232	L-lactate dehydrogenase (EC 1.1.2.3)	b3605	CHM	0.44
3778842	REC03526	<i>yibK</i>	N	157	95, 97			P33899	Hypothetical tRNA/rRNA methyltransferase yibK (EC 2.1.1.-)	b3606	UNC	0.78
3780189	REC06097	<i>cysE</i>	E	273	253		< 0.05	P05796	Serine acetyltransferase (EC 2.3.1.30)	b3607	AAM	0.72
3781288	REC06098	<i>gpsA</i>	N	339	303, 336			P37606	Glycerol-3-phosphate dehydrogenase [NAD(P)+] (EC 1.1.1.94)	b3608	CHM	0.94
3781755	REC06099	<i>secB</i>	E	155	155		< 0.1	P15040	Protein-export protein secB	b3609	PMS	0.41
3782069	REC06100	<i>grxC</i>	N	83	21			P37687	Glutaredoxin 3	b3610	AAM	0.47
3782642	REC06101	<i>yibN</i>	N	143	6, 13, 47, 72, 81, 98			P37688	Hypothetical protein yibN	b3611	UNC	0.31
3782887	REC03532	<i>yibO</i>	N	514	59, 136, 175, 238, 386			P37689	2,3-bisphosphoglycerate-independent phosphoglycerate mutase (I)	b3612	CHM	0.38
3784441	REC03533	<i>yibP</i>	N	427	266, 284, 290, 318, 402, 402			P37690	Hypothetical protein yibP	b3613	UNC	0.69
3785854	REC03534	<i>yibQ</i>	N	277	19, 65, 91, 119, 131, 184, 188			P37691	Hypothetical protein yibQ precursor	b3614	UNC	0.16
3787708	REC06102	<i>yibD</i>	N	344	142, 175, 192, 281, 292, 325			P11290	Putative glycosyl transferase yibD (EC 2.-.-.-)	b3615	UNC	0.44
3788972	REC06103	<i>tdh</i>	N	341	140, 160, 176, 210, 214, 235, 259			P07913	Threonine 3-dehydrogenase (EC 1.1.1.103)	b3616	AAM	0.19
3790178	REC06104	<i>kbI</i>	N	398	90, 184, 224, 249, 258, 287, 306, 313			P07912	2-amino-3-ketobutyrate coenzyme A ligase (EC 2.3.1.29)	b3617	AAM	0.59
3791325	REC06105	<i>htrL</i>	N	290	12, 97, 213, 241, 247			P25666	HtrL protein	b3618	UNC	0.00
3791614	REC03539	<i>rfaD</i>	N	310	1, 16, 68, 99, 117, 119, 234, 276, 299			P17963	ADP-L-glycero-D-manno-heptose-6-epimerase (EC 5.1.3.20)	b3619	CHM	0.38
3792556	REC03540	<i>rfaF</i>	N	348	11, 56, 62, 102, 119, 133, 156, 280			P37692	ADP-heptose-LPS heptosyltransferase II (EC 2.-.-.-)	b3620	LPC	0.41
3793606	REC03541	<i>rfaC</i>	E	319	-		< 0.01	P24173	Lipopolysaccharide heptosyltransferase-1 (EC 2.-.-.-)	b3621	LPC	0.22
3794575	REC03542	<i>rfaL</i>	N	419	17, 58, 225, 247, 361, 396			P27243	O-antigen ligase	b3622	MSM	0.00
3796939	REC06106	<i>rfaK</i>	N	357	91			P27242	Lipopolysaccharide 1,2-N-acetylglucosamintransferase (EC 2.4.1.3)	b3623	LPC	0.03
3797823	REC06107	<i>rfaZ</i>	N	283	-			P27241	Lipopolysaccharide core biosynthesis protein rfaZ	b3624	UNC	0.00
3798592	REC06108	<i>rfaY</i>	X	232	-			P27240	Lipopolysaccharide core biosynthesis protein rfaY	b3625	UNC	0.00
3799626	REC06109	<i>rfaJ</i>	X	338	-			P27129	Lipopolysaccharide 1,2-glycosyltransferase (EC 2.4.1.58)	b3626	LPC	0.00
3800685	REC06110	<i>rfaI</i>	X	339	-			P27128	Lipopolysaccharide 1,3-galactosyltransferase (EC 2.4.1.44)	b3627	LPC	0.09
3801794	REC06111	<i>rfaB</i>	X	369	-			P27127	Lipopolysaccharide 1,6-galactosyltransferase (EC 2.4.1.-)	b3628	LPC	0.19
3802743	REC06112	<i>rfaS</i>	N	311	42, 117, 153, 183, 212, 228			P27126	Lipopolysaccharide core biosynthesis protein rfaS	b3629	LPC	0.00
3803577	REC06113	<i>rfaP</i>	N	265	51, 74, 120, 132, 162, 177, 203, 220, 234			P25741	Lipopolysaccharide core biosynthesis protein rfaP	b3630	LPC	0.03
3804694	REC06114	<i>rfaG</i>	N	374	167, 173, 312			P25740	Lipopolysaccharide core biosynthesis protein rfaG	b3631	CHM	0.19
3805725	REC06115	<i>rfaQ</i>	N	344	4, 7, 68, 80, 131, 163		< 0.001	P25742	Lipopolysaccharide core biosynthesis glycosyl transferase rfaQ (E	b3632	LPC	0.19
3806167	REC03553	<i>kdtA</i>	E	425	-		< 0.001	P23282	3-deoxy-D-manno-octulosonic-acid transferase (EC 2.-.-.-)	b3633	LPC	0.53
3807452	REC03554	<i>coaD</i>	E	159	-		< 0.05	P23875	Phosphopantetheine adenyltransferase (EC 2.7.7.3)	b3634	NCM	0.91
3808779	REC06116	<i>mutM</i>	N	269	48, 89, 184			P05523	Formamidopyrimidine-DNA glycosylase (EC 3.2.2.23)	b3635	NAM	0.66
3809044	REC06117	<i>rpmG</i>	?	55	42			P02436	50S ribosomal protein L33	b3636	PMS	0.59
3809301	REC06118	<i>rpmB</i>	?	78	-			P02428	50S ribosomal protein L28	b3637	PMS	0.66
3810192	REC06119	<i>radC</i>	N	224	58, 65, 96, 107, 179			P25531	DNA repair protein radC	b3638	NAM	0.66
3810286	REC03559	<i>dfp</i>	E	430	41		< 0.0001	P24285	DNA/pantothenate metabolism flavoprotein	b3639	NCM	0.84
3811559	REC03560	<i>dut</i>	E	151	-		< 0.1	P06968	Deoxyuridine 5'-triphosphate nucleotidohydrolase (EC 3.6.1.23)	b3640	NCM	0.72
3812079	REC03561	<i>tkk</i>	N	212	29, 60, 108, 189, 192, 197			P06969	Ttk protein	b3641	UNC	0.09
3813395	REC06120	<i>pyrE</i>	N	213	35, 57			P00495	Orotate phosphoribosyltransferase (EC 2.4.2.10)	b3642	NCM	0.84
3814176	REC06121	<i>rph</i>	N	228	10, 16, 172			P03842	Ribonuclease PH (EC 2.7.7.56)	b3643	NAM	0.63
3814303	REC03564	<i>yicC</i>	X	287	-			P23839	Protein yicC	b3644	UNC	0.56
3815375	REC03565	<i>dinD</i>	N	278	56, 89, 111, 204, 244, 266			P23840	DNA-damage-inducible protein D	b3645	UNC	0.09
3816447	REC03566	<i>yicG</i>	N	223	38			P31432	Hypothetical protein yicG	b3646	UNC	0.41
3818803	REC06122	<i>yicF</i>	N	562	209, 247, 362, 461, 461, 556			P25772	Hypothetical DNA ligase-like protein yicF	b3647	UNC	1.00
3819055	REC03568	<i>gmk</i>	E	207	9		< 0.1	P24234	Guanylate kinase (EC 2.7.4.8)	b3648	NCM	0.94
3819733	REC03569	<i>rpoZ</i>	N	91	44, 58			P08374	DNA-directed RNA polymerase omega chain (EC 2.7.7.6)	b3649	NAM	0.38
3820027	REC03570	<i>spoT</i>	?	702	538, 554			P17580	Guanosine-3',5'-bis(Diphosphate) 3'-pyrophosphohydrolase (EC 3.6.1.15)	b3650	MSM	0.91
3822142	REC03571	<i>trmH</i>	N	229	58, 71, 76, 89, 99, 126, 155, 202			P19396	rRNA (Guanosine-2'-O)-methyltransferase (EC 2.1.1.34)	b3651	NAM	0.31
3822837	REC06537	<i>recG</i>	N	693	7, 22, 24, 44, 146, 167, 252, 295, 362, 470			P24230	ATP-dependent DNA helicase recG (EC 3.6.1.-)	b3652	NAM	0.91
3826292	REC06123	<i>gltS</i>	N	401	23, 25, 71, 168, 168, 282			P19533	Sodium/glutamate symport carrier protein	b3653	MTR	0.25
3826572	REC03574	<i>yicE</i>	N	463	28, 94, 117, 168, 212, 250, 285, 292			P27432	Putative purine permease yicE	b3654	UNC	0.06
3828084	REC03575	<i>yicH</i>	N	569	355, 378, 453, 486, 517, 523			P31433	Hypothetical protein yicH	b3655	UNC	0.03
3832164	REC06538	<i>yicI</i>	N	772	194, 331, 354, 424, 443, 651, 702, 734			P31434	Putative family 31 glucosidase yicI	b3656	UNC	0.22
3833613	REC06539	<i>yicJ</i>	N	479	11, 155, 174, 185, 217, 246, 311, 360, 378			P31435	Hypothetical symporter yicJ	b3657	UNC	0.16
3834580	REC03578	<i>setC</i>	N	394	149			P31436	Sugar efflux transporter C	b3659	MTR	0.00
3835875	REC03579	<i>yicL</i>	X	307	-			P31437	Hypothetical transport protein yicL	b3660	UNC	0.63
3837620	REC06126	<i>nlpA</i>	X	272	-			P04846	Lipoprotein-28 precursor	b3661	LPC	0.69
3839531	REC06127	<i>yicM</i>	X	451	-			P31438	Hypothetical protein yicM	b3662	UNC	0.22
3840056	REC06128	<i>yicN</i>	N	159	24, 56, 70, 121, 151			P31439	Hypothetical protein yicN	b3663	UNC	0.00
3841494	REC06129	<i>yicO</i>	N	470	206, 257, 257, 288, 323, 326, 398, 429, 452			P31440	Hypothetical protein yicO	b3664	UNC	0.66
3841591	REC03584	<i>yicP</i>	N	588	42, 86, 466, 505, 587			P31441	Probable adenine deaminase (EC 3.5.4.2)	b3665	UNC	0.28
3844794	REC06540	<i>uhpT</i>	N	463	59, 62, 101, 190, 246, 253, 292, 330, 441			P13408	Hexose phosphate transport protein	b3666	SMC	0.06
3846254	REC06541	<i>uhpC</i>	N	440	23, 240, 290, 306, 394			P09836	Regulatory protein uhpC	b3667	SMC	0.13
3847766	REC06132	<i>uhpB</i>	N	501	38, 84, 98, 123, 176, 210, 288, 311, 335, 388			P09835	Sensor protein uhpB (EC 2.7.3.-)	b3668	SMC	0.66
3848353	REC06133	<i>uhpA</i>	N	196	35, 128, 143			P10940	Transcriptional regulatory protein uhpA	b3669	SMC	0.25
3848719	REC06134	<i>ilvN</i>	X	96	-			P08143	Acetolactate synthase isozyme I small subunit (EC 4.1.3.18)	b3670	AAM	0.00
3850411	REC06135	<i>ilvB</i>	N	562	12, 49, 59, 63, 107, 136, 184, 202			P08142	Acetolactate synthase isozyme I large subunit (EC 4.1.3.18)	b3671	AAM	0.78
3850615	REC06136	<i>ilvL</i>	?	32	-			P03061	ilvN operon leader peptide	b3672	RCD	0.00
3851543	REC03592	<i>emrD</i>	N	396	88, 165, 187, 311			P31442	Multidrug resistance protein D	b3673	MTR	0.03
3853238	REC06137	<i>yidF</i>	?	165	91			P31443	Hypothetical protein yidF	b3674	UNC	0.00
3853597	REC06138	<i>yidG</i>	N	120	18, 52, 88, 117			P31444	Hypothetical protein yidG	b3675	UNC	0.00
3853934	REC06139	<i>yidH</i>	N	115	23, 29, 55, 105			P31445	Hypothetical protein yidH	b3676	UNC	0.06
3854042	REC03596	<i>yidI</i>	N	149	54, 70, 96, 98			P31446	Hypothetical protein yidI	b3677	UNC	0.00
3856031	REC06140	<i>yidJ</i>	N	497	55, 104, 257, 289, 447, 472			P31447	Putative sulfatase yidJ (EC 3.1.6.-)	b3678	UNC	0.22
3857743	REC06141	<i>yidK</i>	N	571	9, 49, 244, 258, 283, 288			P31448	Putative symporter yidK	b3679	UNC	0.16
3857880	REC03599	<i>yidL</i>	N	307	77, 91, 109, 129, 168, 223			P31449	Hypothetical transcriptional regulator yidL	b3680	UNC	0.00
3859614	REC06142	<i>glvG</i>	X	212	-			P31450	Probable 6-phospho-alpha-glucosidase (EC 3.2.1.122)	b3681	UNC	0.06
3860099	REC06143	<i>glvB</i>	X	161	-			P31451	PTS system, arbutin-like IIB component (EC 2.7.1.69)	b3682	CHM	0.16
3861491	REC06144	<i>glvC</i>	N	455	34, 56, 82, 120, 145, 191, 206, 270, 322, 341, 413, 443			P31452	PTS system, arbutin-like IIC component	b3683	MTR	0.16
3861526	REC03603	<i>yidP</i>	E	238	238		< 0.01	P31453	Hypothetical transcriptional regulator yidP	b3684	UNC	0.25
3863924	REC06145	<i>yidE</i>	N	561	15, 29, 50, 70, 92, 106, 348, 449, 501			P29211	Hypothetical membrane protein yidE	b3685	UNC	0.09
3864530	REC06146	<i>ibpB</i>	N	144	6, 42, 53, 140, 143			P29210	16 kDa heat shock protein B	b3686	UNC	0.25
3865049	REC06147	<i>ibpA</i>	N	137	26, 33, 55, 101			P29209	16 kDa heat shock protein A	b3687	UNC	0.25
3865280	REC03607	<i>yidQ</i>	N	135	37, 66, 103			P31454	Hypothetical protein yidQ precursor	b3688	UNC	0.00
3866939	REC06148	<i>yidR</i>	N	416	2, 91, 134, 201, 227, 279, 304			P31455	Hypothetical protein yidR	b3689	UNC	0.00
3866983	REC03609	<i>yidS</i>	N	361	53, 95, 121, 296, 339			P31456	Hypothetical protein yidS precursor	b3690	UNC	0.16
3869402	REC06149	<i>dgoT</i>	N	445	23, 42, 96, 143, 275, 345			P31457	D-galactonate transporter	b3691	MTR	0.34
3871240	REC06545	<i>dgoA</i>	N	587	27, 55, 77, 78, 118, 157, 171, 182, 196, 405, 582			P31458	DgoA protein	b3692	CHM	0.25
3872102	REC06151	<i>dgoK</i>	N	292	98, 185, 201, 217, 252			P31459	2-dehydro-3-deoxygalactonokinase (EC 2.7.1.58)	b3693	CHM	0.16
3872395	REC06546	<i>dgoR</i>	?	98	78			P31460	Galactonate operon transcriptional repressor	b3694	RCD	0.00
3872787	REC06547	<i>dgoR</i>	N	128	48, 119			P31460	Galactonate operon transcriptional repressor	b3694	RCD	0.13
3873122	REC03614</											

3875102	REC06154	<i>yidB</i>	N	135	7, 22, 50, 90	P09996	Hypothetical protein yidB	b3698	UNC	0.16
3877747	REC06155	<i>gyrB</i>	X	804	-	P06982	DNA gyrase subunit B (EC 5.99.1.3)	b3699	NAM	1.00
3878849	REC06156	<i>racF</i>	N	357	2, 70, 93, 148, 197, 198, 232, 257, 302	P03016	DNA replication and repair protein recF	b3700	NAM	0.72
3879949	REC06157	<i>dnaN</i>	X	366	-	P00583	DNA polymerase III, beta chain (EC 2.7.7.7)	b3701	NAM	1.00
3881357	REC06549	<i>dnaA</i>	E	467	-	P03004	Chromosomal replication initiator protein dnaA	b3702	NAM	0.97
3881965	REC03621	<i>rpmH</i>	?	46	-	P02437	50S ribosomal protein L34	b3703	PMS	0.56
3882122	REC03622	<i>rnpA</i>	?	119	-	P06277	Ribonuclease P protein component (EC 3.1.26.5)	b3704	NAM	0.25
3882475	REC06704	<i>yidD</i>	?	75	-	P22847	Hypothetical protein yidD	UNC	0.84	
3882705	REC03623	<i>yidC</i>	?	548	-	P25714	60 kDa inner-membrane protein	b3705	PMS	0.97
3884457	REC06550	<i>trmE</i>	E	454	-	P25522	Probable tRNA modification GTPase trmE	b3706	UNC	0.94
3886064	REC03625	<i>tnaL</i>	N	24	4, 14, 14	P09408	Tryptophanase leader peptide	b3707	NAM	0.00
3886344	REC03626	<i>tnaA</i>	N	476	50, 100, 128, 225, 360, 435, 443	P00913	Tryptophanase (EC 4.1.99.1)	b3708	AAM	0.06
3887865	REC03627	<i>tnaB</i>	N	415	71, 74, 127, 166, 170, 203, 244, 328, 381, 400	P23173	Low affinity tryptophan permease	b3709	MTR	0.00
3889244	REC03628	<i>yidY</i>	N	391	56, 78, 146	P31462	Hypothetical transport protein yidY	b3710	UNC	0.09
3890394	REC03629	<i>yidZ</i>	N	319	252	P31463	Hypothetical transcriptional regulator yidZ	b3711	UNC	0.72
3891498	REC03630	<i>yjeE</i>	N	253	125, 161, 168, 205	P31464	Hypothetical protein yjeE	b3712	UNC	0.00
3892281	REC03631	<i>yjeF</i>	N	188	27, 31, 59, 103, 133, 182	P31465	Hypothetical protein yjeF	b3713	UNC	0.28
3894238	REC06159	<i>yjeG</i>	N	445	101, 384	P31466	Hypothetical protein yjeG	b3714	UNC	0.66
3894403	REC03633	<i>yjeH</i>	N	221	125, 197, 214	P31467	Hypothetical protein yjeH	b3715	UNC	0.81
3895135	REC03634	<i>yjeI</i>	N	155	21, 52, 74, 85, 108, 122	P31468	Hypothetical protein yjeI	b3716	UNC	0.00
3895651	REC03635	<i>yjeJ</i>	N	195	22, 29, 72, 108	P31469	Hypothetical protein yjeJ	b3717	UNC	0.06
3896952	REC06160	<i>yjeK</i>	N	213	28, 195	P31470	Hypothetical protein yjeK	b3718	UNC	0.34
3898238	REC06161	<i>yjeL</i>	E	400	-	P31471	Hypothetical protein yjeL	b3719	UNC	0.00
3899848	REC06162	<i>yjeC</i>	N	538	377	P26218	Putative outer membrane protein yjeC precursor	b3720	UNC	0.00
3901329	REC06551	<i>bgIB</i>	X	470	-	P11988	6-phospho-beta-glucosidase bgIB (EC 3.2.1.86)	b3721	CHM	0.31
3903225	REC06164	<i>bgIF</i>	N	625	9, 31, 204, 240, 262, 327, 381, 387, 449, 482, 565, 598, 605	P08722	PTS system, beta-glucoside-specific IIABC component (EC 2.7.1.6)	b3722	MTR	0.47
3904195	REC06165	<i>bgIG</i>	N	278	115, 132	P11989	Cryptic beta-glucoside bgI operon anti terminator	b3723	RCD	0.19
3905206	REC06166	<i>phoU</i>	?	241	-	P07656	Phosphate transport system protein phoU	b3724	UNC	0.66
3905994	REC06167	<i>pstB</i>	N	257	60, 181, 254	P07655	Phosphate transport ATP-binding protein pstB	b3725	MTR	0.78
3907067	REC06168	<i>pstA</i>	N	296	202, 294	P07654	Phosphate transport system permease protein pstA	b3726	MTR	0.75
3908026	REC06169	<i>pstC</i>	N	319	253	P07653	Phosphate transport system permease protein pstC	b3727	MTR	0.75
3909153	REC06553	<i>pstS</i>	N	346	51, 113, 181, 200, 223, 265, 309, 310, 330	P06128	Phosphate-binding periplasmic protein precursor	b3728	MTR	0.75
3911296	REC06171	<i>glmS</i>	E	609	608	P17169	Glucosamine--fructose-6-phosphate aminotransferase [isomerizing]	b3729	CHM	0.91
3912828	REC06172	<i>glmU</i>	E	456	-	P17114	Bifunctional glmU protein	b3730	CHM	0.88
3913600	REC06173	<i>atpC</i>	E	139	-	P00832	ATP synthase epsilon chain (EC 3.6.3.14)	b3731	BEN	0.78
3915003	REC06174	<i>atpD</i>	N	460	7, 299, 371, 377, 432	P00824	ATP synthase beta chain (EC 3.6.3.14)	b3732	BEN	1.00
3915893	REC06175	<i>atpG</i>	N	287	47, 126, 144, 181, 211, 276	P00837	ATP synthase gamma chain (EC 3.6.3.14)	b3733	BEN	0.88
3917485	REC06176	<i>atpA</i>	N	513	185, 240, 508	P00822	ATP synthase alpha chain (EC 3.6.3.14)	b3734	BEN	1.00
3918031	REC06177	<i>atpH</i>	X	177	-	P00831	ATP synthase delta chain (EC 3.6.3.14)	b3735	BEN	0.72
3918516	REC06178	<i>atpF</i>	E	156	-	P00859	ATP synthase B chain (EC 3.6.3.14)	b3736	BEN	0.22
3918817	REC06179	<i>atpE</i>	N	79	29, 57, 72	P00844	ATP synthase C chain (EC 3.6.3.14)	b3737	BEN	0.22
3919679	REC06180	<i>atpB</i>	N	271	16, 30, 87, 112, 157, 182, 207, 271	P00855	ATP synthase A chain (EC 3.6.3.14)	b3738	BEN	0.84
3920080	REC06181	<i>atpI</i>	N	130	11, 39, 40	P03808	ATP synthase protein I	b3739	UNC	0.06
3921308	REC06182	<i>gidB</i>	N	207	40, 94, 198	P17113	Glucose inhibited division protein B	b3740	UNC	0.94
3923261	REC06555	<i>gida</i>	N	629	135, 200, 267, 433, 533	P17112	Glucose inhibited division protein A	b3741	UNC	0.94
3924083	REC06184	<i>mioc</i>	N	147	25, 58	P03817	Protein mioc	b3742	UNC	0.09
3924631	REC06185	<i>asnC</i>	N	152	59, 63, 141, 152	P03809	Regulatory protein asnC	b3743	RCD	0.16
3924783	REC03662	<i>asna</i>	N	330	89, 99, 115, 120, 161, 193, 198, 228, 236, 238, 284	P00963	Aspartate--ammonia ligase (EC 6.3.1.1)	b3744	AAM	0.13
3927063	REC06186	<i>yjeM</i>	N	427	19, 166, 186, 358, 425	P03818	Hypothetical protein yjeM	b3745	UNC	0.03
3928744	REC06556	<i>yjeN</i>	N	506	92, 169, 391, 485	P31473	Hypothetical protein yjeN	b3746	UNC	0.56
3928943	REC03666	<i>kup</i>	N	519	11, 28, 34, 47, 54, 83, 100, 129, 159, 199, 238, 250, 331, 392, 495	P30016	Kup system potassium uptake protein	b3747	MTR	0.31
3930941	REC03667	<i>rhsD</i>	N	151	40, 63	P04982	High affinity ribose transport protein rhsD	b3748	MTR	0.19
3931404	REC03668	<i>rhsA</i>	N	501	212, 227, 273, 305, 323, 331, 366	P04983	Ribose transport ATP-binding protein rhsA	b3749	MTR	0.66
3932914	REC03669	<i>rhsC</i>	N	321	34, 51, 74, 76, 133, 236, 299, 311	P04984	Ribose transport system permease protein rhsC	b3750	MTR	0.38
3933904	REC03670	<i>rhsB</i>	N	296	136	P02925	D-ribose-binding periplasmic protein precursor	b3751	MTR	0.41
3934920	REC03671	<i>rhsK</i>	N	309	166, 167, 221, 232, 255	P05054	Ribokinase (EC 2.7.1.15)	b3752	CHM	0.59
3935853	REC03672	<i>rhsR</i>	N	330	55, 92, 137, 260, 307	P25551	Ribose operon repressor	b3753	RCD	0.25
3938238	REC06189	<i>yjeO</i>	N	475	159, 265, 314, 319, 405, 409, 448	P31474	Hypothetical transport protein yjeO	b3754	UNC	0.41
3938806	REC06190	<i>yjeP</i>	N	181	37	P31475	Hypothetical transcriptional regulator yjeP	b3755	UNC	0.16
3945348	REC06191	<i>pssR</i>	N	198	41, 187	P27826	Possible regulatory protein pssR	UNC	0.72	
3945590	REC06192	<i>pssR</i>	N	133	5, 63, 80, 121	b3763	UNC	0.72		
3945709	REC06557	<i>yifE</i>	N	112	18, 31, 83, 99	P27827	Protein yifE	b3764	UNC	0.06
3947622	REC06193	<i>yifB</i>	N	516	29, 230, 248, 256, 296, 302, 318, 365, 387, 458, 493	P22787	Hypothetical protein yifB	b3765	UNC	0.75
3947945	REC03679	<i>ilvL</i>	?	32	-	P03060	IlvGEDA operon leader peptide	b3766	RCD	0.00
3948183	REC03680	<i>ilvG</i>	N	327	323	P00892	Acetolactate synthase isozyme II large subunit (EC 4.1.3.18)	b3767	AAM	0.78
3949824	REC06194	<i>ilvH</i>	N	87	6, 7, 49, 57	P13048	Acetolactate synthase isozyme II small subunit (EC 4.1.3.18)	b3769	AAM	0.00
3950107	REC03682	<i>ilvE</i>	N	309	91, 187, 209, 268	P00510	Branched-chain amino acid aminotransferase (EC 2.6.1.42)	b3770	CHM	0.78
3951132	REC03683	<i>ilvD</i>	N	605	188, 353, 372, 402, 459, 502, 566, 575	P05791	Dihydroxy-acid dehydratase (EC 4.2.1.9)	b3771	AAM	0.78
3952952	REC03684	<i>ilvA</i>	N	514	15, 32, 49, 121, 161, 244, 298, 508	P04968	Threonine dehydratase biosynthetic (EC 4.2.1.16)	b3772	AAM	0.75
3955441	REC06195	<i>ilvY</i>	N	297	174, 268	P05827	Transcriptional activator protein ilvY	b3773	RCD	0.06
3955591	REC03686	<i>ilvC</i>	N	491	7, 28, 44, 75, 82, 122, 158, 164, 208, 232, 290, 298, 310, 441, 464	P05793	Ketol-acid reductoisomerase (EC 1.1.1.86)	b3774	AAM	0.81
3957431	REC06196	<i>ppiC</i>	N	93	15	P39159	Peptidyl-prolyl cis-trans isomerase C (EC 5.2.1.8)	b3775	PMS	0.50
3957902	REC06558	<i>yifN</i>	N	91	19, 61	P56259	Hypothetical protein yifN	UNC	0.03	
3958117	REC06559		N	86	26	b3777	UNC	0.00		
3958292	REC03688	<i>rep</i>	E	673	8	P09980	ATP-dependent DNA helicase rep (EC 3.6.1.-)	b3778	NAM	0.28
3961844	REC06197	<i>gppA</i>	N	494	11, 112, 208, 336, 484	P25552	Guanosine-5'-triphosphate,3'-diphosphate pyrophosphatase (EC 3.6.1.15)	b3779	MSM	0.25
3963245	REC06198	<i>rhlB</i>	N	421	41, 46, 72, 99, 107, 122, 155, 157, 172, 353	P24229	Putative ATP-dependent RNA helicase rhlB	b3780	UNC	0.13
3963322	REC03691	<i>trxA</i>	N	127	16	P00274	Thioredoxin 1	b3781	MSM	0.97
3963846	REC03692	<i>rhoL</i>	?	33	-	P37324	Very hypothetical rho operon leader peptide	b3782	UNC	0.00
3964032	REC03693	<i>rho</i>	?	419	15	P03002	Transcription termination factor rho	b3783	RCD	0.88
3965531	REC03694	<i>wecA</i>	N	367	60, 148, 164, 210, 260, 315, 343	P24235	Undecaprenyl-phosphate alpha-N-acetylglucosaminyltransferase (b3784)	b3784	LPC	0.53
3966643	REC06569	<i>wzzE</i>	N	349	9, 56, 87, 167, 224, 260, 297	P25905	Lipopolysaccharide biosynthesis protein wzzE	b3785	LPC	0.03
3967706	REC06570	<i>wecB</i>	N	389	54, 113, 236	P27828	UDP-N-acetylglucosamine 2-epimerase (EC 5.1.3.14)	b3786	CHM	0.41
3968872	REC06571	<i>wecC</i>	N	420	8, 193, 203, 281, 303, 385, 398	P27829	UDP-N-acetyl-D-mannosamine dehydrogenase (EC 1.1.1.-)	b3787	CHM	0.34
3970134	REC03698	<i>rffG</i>	N	355	9, 10, 40, 120, 131, 216, 277, 317	P27830	dTDP-glucose 4,6-dehydratase (EC 4.2.1.46)	b3788	MSM	0.75
3971220	REC03699	<i>rffH</i>	N	293	4, 207, 255	P27831	Glucose-1-phosphate thymidyltransferase (EC 2.7.7.24)	b3789	MSM	0.59
3972208	REC03700	<i>rffC</i>	N	181	91	P27832	Lipopolysaccharide biosynthesis protein rffC	b3790	LPC	0.00
3972758	REC06572	<i>rffA</i>	N	376	182, 221	P27833	Lipopolysaccharide biosynthesis protein rffA	b3791	UNC	0.59
3973890	REC03702	<i>wzxE</i>	N	416	36, 78, 88, 125, 161, 240, 310	P27834	WzxE protein	b3792	UNC	0.00
3975137	REC06573		N	74	11	P56258	4-alpha-L-fucosyltransferase (EC 2.4.1.-)	b4404	LPC	0.00
3975603	REC06574	<i>wecF</i>	N	204	1, 168	P56258	4-alpha-L-fucosyltransferase (EC 2.4.1.-)	b4405	LPC	0.00
3976214	REC03703	<i>wzyE</i>	E	450	-	P27835	Putative ECA polymerase	b3793	UNC	0.00
3977569	REC06575	<i>wecG</i>	N	246	14, 31, 54, 107, 193, 223	P27836	Probable UDP-N-acetyl-D-mannosaminuronic acid transferase (EC 2.4.1.16)	b3794	UNC	0.44

3978500	REC06576	<i>yifK</i>	N	461	49, 365, 371	P27837	Probable transport protein yifK	b3795	UNC	0.09
3980571	REC06577	<i>aslB</i>	N	411	7, 83, 132, 214, 353	P25550	Putative arylsulfatase regulatory protein	b3800	UNC	0.09
3983620	REC06199	<i>asIA</i>	N	551	16, 110, 133, 241, 346, 444, 456, 476	P25549	Arylsulfatase (EC 3.1.6.1)	b3801	MSM	0.16
3985495	REC06200	<i>hemY</i>	N	398	108, 307, 368	P09128	HemY protein	b3802	NCM	0.09
3986679	REC06201	<i>hemX</i>	N	393	276	P09127	Putative uroporphyrin-III C-methyltransferase (EC 2.1.1.107)	b3803	UNC	0.16
3987441	REC06202	<i>hemD</i>	E	246	-	P09126	Uroporphyrinogen-III synthase (EC 4.2.1.75)	b3804	NCM	0.13
3988400	REC06578	<i>hemC</i>	E	320	-	P06983	Porphobilinogen deaminase (EC 4.3.1.8)	b3805	NCM	0.81
3988766	REC03712	<i>cyaA</i>	N	848	410, 436, 461, 483, 546, 662, 720, 790, 792	P00936	Adenylate cyclase (EC 4.6.1.1)	b3806	SMC	0.09
3991463	REC03714		N	161	3, 17, 48, 104, 137	P11291	Very hypothetical 17.3 kDa protein in <i>cyaA</i> region	b3808	UNC	0.00
3991672	REC06204	<i>cyaY</i>	N	106	23, 54, 68	P27838	CyaY protein	b3807	UNC	0.16
3992135	REC06705	<i>yifL</i>	N	67	27	P39166	Hypothetical protein yifL	UNC	0.00	
3992372	REC03715	<i>dapF</i>	E	275	-	P08885	Diaminopimelate epimerase (EC 5.1.1.7)	b3809	AAM	0.78
3993196	REC03716	<i>yigA</i>	N	235	68, 157, 158, 179, 181	P23305	Hypothetical protein yigA	b3810	UNC	0.13
3993900	REC03717	<i>xerC</i>	E	298	-	P22885	Integrase/recombinase xerC	b3811	NAM	0.34
3994796	REC06579	<i>yigB</i>	N	238	10, 120	P23306	Hypothetical protein yigB	b3812	UNC	0.06
3995596	REC06580	<i>uvrD</i>	N	720	80, 200, 382, 458, 476, 551, 563, 589, 591, 629, 667	P03018	DNA helicase II (EC 3.6.1.-)	b3813	NAM	1.00
3998204	REC06205		N	99	4	P27840	Hypothetical protein yigE	b3814	UNC	0.13
3998668	REC06206	<i>yigE</i>	N	161	48, 159	P27840	Hypothetical protein yigE	UNC	0.09	
3999038	REC06581	<i>corA</i>	E	316	-	P27841	Magnesium and cobalt transport protein corA	b3816	MTR	0.78
4000411	REC06207	<i>yigF</i>	N	126	74, 116	P27842	Hypothetical protein yigF	b3817	UNC	0.00
4000841	REC06208	<i>yigG</i>	N	138	5, 50, 89	P27843	Hypothetical protein yigG	b3818	UNC	0.00
4001802	REC06209	<i>rarD</i>	N	300	5, 93, 141, 193, 241, 265, 285	P27844	RarD protein	b3819	UNC	0.41
4002326	REC06582	<i>yigI</i>	?	161	16, 146	P27845	Hypothetical protein yigI	b3820	UNC	0.03
4002473	REC06583	<i>pldA</i>	N	289	46	P00631	Phospholipase A1 precursor (EC 3.1.1.32)	b3821	LPC	0.09
4003469	REC06584	<i>recQ</i>	N	610	30, 109, 185, 251, 316, 414, 429, 464, 494, 578, 602	P15043	ATP-dependent DNA helicase recQ (EC 3.6.1.-)	b3822	NAM	0.63
4005616	REC06585	<i>rhtC</i>	N	122	27	P27846	Threonine efflux protein	b3823	MTR	0.19
4006462	REC06211	<i>rhtB</i>	N	138	72, 134	P27847	Homoserine/homoserine lactone efflux protein	b3824	MTR	0.13
4006776	REC06586	<i>pldB</i>	N	340	103, 126, 149, 199, 243, 296	P07000	Lysophospholipase L2 (EC 3.1.1.5)	b3825	LPC	0.44
4007918	REC03732	<i>yigL</i>	N	171	18, 20, 121	P27848	Hypothetical protein yigL	b3826	UNC	0.03
4008666	REC03733	<i>yigM</i>	N	299	130, 147, 211	P27849	Hypothetical membrane protein yigM	b3827	UNC	0.13
4010406	REC06212	<i>metR</i>	N	317	39	P19797	Transcriptional activator protein metR	b3828	RCD	0.19
4010643	REC06587	<i>metE</i>	N	753	83, 89, 97, 115, 164, 242, 282, 292, 308, 312, 377, 391, 544, 591, 644	P25665	5-methyltetrahydropteroylglutamate-homocysteine methyltransferase	b3829	AAM	0.59
4013719	REC06588	<i>ysgA</i>	?	332	-	P56262	Putative carboxymethylglutaminolase (EC 3.1.1.145)	b3830	UNC	0.13
4014018	REC03736	<i>udp</i>	N	253	121, 127, 160, 223	P12758	Uridine phosphorylase (EC 2.4.2.3)	b3831	NCM	0.09
4014920	REC03737	<i>rmuC</i>	N	475	97, 152, 275, 329, 401, 449, 458	P27850	DNA recombination protein rmuC	b3832	NAM	0.41
4016442	REC06589	<i>ubiE</i>	E	251	-	P27851	Ubiquinone/menaquinone biosynthesis methyltransferase ubiE (EC 2.1.1.28)	b3833	NCM	0.78
4017211	REC06590	<i>yigP</i>	N	201	10, 78	P27852	Hypothetical protein yigP	b3834	UNC	0.13
4017813	REC03741	<i>ubiB</i>	E	546	-	P27854	Probable ubiquinone biosynthesis protein ubiB	b3835	UNC	0.47
4019490	REC06591	<i>tatA</i>	N	103	51	O69338	Sec-independent protein translocase protein tatA	b3836	PMS	0.09
4019665	REC06592		?	113	113	O32530	Hypothetical protein b3837	b3837	UNC	0.00
4019885	REC06593	<i>tatB</i>	N	145	40, 108	O69415	Sec-independent protein translocase protein tatB	b3838	PMS	0.06
4020325	REC03744	<i>tatC</i>	N	258	25, 30, 112, 113, 157, 171, 193	P27857	Sec-independent protein translocase protein tatC	b3839	PMS	0.72
4021131	REC03745	<i>tatD</i>	N	206	10, 60, 82, 93, 122, 192	P27859	Deoxyribonuclease tatD (EC 3.1.21.-)	b3840	UNC	0.06
4022411	REC06213	<i>rfaH</i>	N	162	43, 95, 132	P26614	Transcriptional activator rfaH	b3842	RCD	0.03
4022578	REC03748	<i>ubiD</i>	N	497	10, 69	P26615	3-octaprenyl-4-hydroxybenzoate carboxy-lyase (EC 4.1.1.-)	b3843	NCM	0.53
4024117	REC06594	<i>fre</i>	N	233	8, 27, 44, 113, 138, 153, 210, 213	P23486	NAD(P)H-flavin reductase (EC 1.6.8.-)	b3844	NCM	0.19
4026362	REC06595	<i>fadA</i>	N	387	74, 133, 186, 243, 244, 309, 351	P21151	3-ketoacyl-CoA thiolase (EC 2.3.1.16)	b3845	LPC	0.38
4028561	REC06215	<i>fadB</i>	N	729	69, 164, 206, 242, 327, 333, 356	P21177	Fatty acid oxidation complex alpha subunit	b3846	LPC	0.34
4028751	REC03752	<i>pepQ</i>	N	443	247, 248, 306, 313, 400, 401	P21165	Xaa-Pro dipeptidase (EC 3.4.13.9)	b3847	PMS	0.38
4030079	REC03753	<i>yigZ</i>	N	205	16, 94	P27862	Hypothetical protein yigZ	b3848	UNC	0.81
4030735	REC06596	<i>trkH</i>	N	432	25, 64, 91, 222, 241, 256, 288, 309, 377	P21166	Trk system potassium uptake protein trkH	b3849	MTR	0.31
4032197	REC03755	<i>hemG</i>	E	181	-	P27863	Protoporphyrinogen oxidase (EC 1.3.3.4)	b3850	NCM	0.06
4038998	REC06216	<i>mobB</i>	N	170	40, 67, 81	P32125	Molybdopterin-guanine dinucleotide biosynthesis protein B	b3856	UNC	0.25
4039579	REC06217	<i>mobA</i>	N	194	90, 136, 152, 181	P32173	Molybdopterin-guanine dinucleotide biosynthesis protein A	b3857	NCM	0.38
4039649	REC03758	<i>yihD</i>	N	89	18, 53	P32126	Protein yihD	b3858	UNC	0.06
4039996	REC03759	<i>yihE</i>	N	328	149	P32127	Hypothetical protein yihE	b3859	UNC	0.13
4040999	REC03760	<i>dsbA</i>	E	208	-	P24991	Thiol:disulfide interchange protein dsbA precursor	b3860	PMS	0.22
4041737	REC06597	<i>yihF</i>	X	490	36	P32128	Hypothetical protein yihF	b3861	UNC	0.03
4044182	REC06218	<i>yihG</i>	X	310	-	P32129	Hypothetical protein yihG	b3862	UNC	0.09
4044546	REC03763	<i>poIA</i>	N	928	6, 25, 503, 521, 641, 683	P00582	DNA polymerase I (EC 2.7.7.7)	b3863	NAM	1.00
4048312	REC06219	<i>engB</i>	E	199	-	P24253	Probable GTP-binding protein engB	b3865	UNC	0.75
4048927	REC03765	<i>yihI</i>	N	169	4, 136, 166	P32130	Hypothetical protein yihI	b3866	UNC	0.06
4049619	REC03766	<i>hemN</i>	N	459	27, 61, 157, 204, 280, 450	P32131	Oxygen-independent coproporphyrinogen III oxidase (EC 1.-.-.-)	b3867	NCM	0.47
4052858	REC06220	<i>glnG</i>	X	469	-	P06713	Nitrogen regulation protein NR(I)	b3868	SMC	0.66
4053919	REC06221	<i>glnL</i>	X	349	-	P06712	Nitrogen regulation protein NR(II) (EC 2.7.3.-)	b3869	SMC	0.31
4055614	REC06222	<i>glnA</i>	N	469	65, 92, 112, 124, 178, 205, 209	P06711	Glutamine synthetase (EC 6.3.1.2)	b3870	SMC	0.78
4055987	REC03770	<i>typA</i>	N	591	27, 51, 61, 332, 575	P32132	GTP-binding protein typA/BipA	b3871	UNC	0.81
4058026	REC03771	<i>yihL</i>	N	236	121, 224	P32133	Hypothetical transcriptional regulator yihL	b3872	UNC	0.53
4058744	REC03772	<i>yihM</i>	N	326	11, 51, 130, 133, 177, 242, 277, 308	P32134	Hypothetical protein yihM	b3873	UNC	0.06
4059826	REC03773	<i>yihN</i>	X	421	-	P32135	Hypothetical protein yihN	b3874	UNC	0.00
4061874	REC06223	<i>yshA</i>	N	230	3, 25	P76773	Hypothetical protein yshA precursor	b3875	UNC	0.00
4063352	REC06598	<i>yihO</i>	N	487	19, 98, 114, 144, 145, 173, 188, 240, 269, 303, 305, 340, 375, 389, 396	P32136	Hypothetical symporter yihO	b3876	UNC	0.06
4064795	REC06599	<i>yihP</i>	N	468	31	P32137	Hypothetical symporter yihP	b3877	UNC	0.03
4066856	REC06600	<i>yihQ</i>	N	678	99, 120, 352, 413, 563	P32138	Putative family 31 glucosidase yihQ	b3878	UNC	0.03
4067981	REC06227	<i>yihR</i>	N	308	151, 229	P32139	Hypothetical protein yihR	b3879	UNC	0.53
4069351	REC06228	<i>yihS</i>	N	418	42, 91, 107, 140, 265	P32140	Hypothetical protein yihS	b3880	UNC	0.09
4070231	REC06229	<i>yihT</i>	N	292	96, 107, 141, 156, 199	P32141	Hypothetical protein yihT	b3881	UNC	0.03
4071151	REC06230	<i>yihU</i>	N	298	216, 250	P32142	Hypothetical oxidoreductase yihU (EC 1.1.-.-)	b3882	UNC	0.38
4071313	REC03782	<i>yihV</i>	N	300	76, 156, 227, 267	P32143	Hypothetical sugar kinase yihV	b3883	UNC	0.59
4072225	REC03783	<i>yihW</i>	N	269	68, 117, 136, 155, 239, 250	P32144	Hypothetical transcriptional regulator yihW	b3884	UNC	0.25
4073112	REC03784	<i>yihX</i>	N	206	34, 91, 155	P32145	Hypothetical protein yihX	b3885	UNC	0.31
4073726	REC03785	<i>rbn</i>	N	290	15, 25, 56, 119, 189	P32146	Ribonuclease BN (EC 3.1.-.-)	b3886	NAM	0.81
4074595	REC03786	<i>tdt</i>	N	145	33	P32147	D-tyrosyl-tRNA(Tyr) deacylase (EC 3.1.-.-)	b3887	NAM	0.50
4075029	REC03787	<i>yiiD</i>	N	329	228, 253	P32148	Hypothetical protein yiiD	b3888	UNC	0.06
4076844	REC03788	<i>yiiE</i>	N	81	68	P32149	Hypothetical protein yiiE	b3889	UNC	0.03
4077307	REC03789	<i>yiiF</i>	X	80	-	P32150	Hypothetical protein yiiF	b3890	UNC	0.03
4078808	REC06231	<i>fdhE</i>	N	309	70, 91	P13024	Protein fdhE	b3891	UNC	0.13
4079440	REC06232	<i>fdoI</i>	N	211	58, 205	P32174	Formate dehydrogenase, cytochrome b556(FDO) subunit	b3892	BEN	0.13
4080339	REC06233	<i>fdoH</i>	N	300	43, 113, 119, 165, 207, 211, 234, 263	P32175	Formate dehydrogenase-O, iron-sulfur subunit	b3893	SMC	0.06
4083402	REC06611	<i>fdoG</i>	N	1016	13, 37, 101, 137, 206, 245, 339, 399, 408, 421, 455, 640, 726, 768, 831, 836	P32176	Formate dehydrogenase-O, major subunit (EC 1.2.1.2)	b3894	SMC	0.09
4083596	REC03794	<i>fdhD</i>	N	277	36, 149, 273	P32177	FdhD protein	b3895	UNC	0.47
4084582	REC03795	<i>yiiG</i>	N	351	37, 313	P32151	Hypothetical protein yiiG	b3896	UNC	0.00
4087436	REC06235	<i>fvvR</i>	X	582	551	P32152	Putative frv operon regulatory protein	b3897	UNC	0.00

4088506	REC06236	<i>frvX</i>	X	356	-	P32153	Putative frv operon protein frvX	b3898	UNC	0.25
4089953	REC06237	<i>frvB</i>	N	485	21, 43, 169, 215, 272, 277, 317	P32154	PTS system, fructose-like-1 IIBC component (EC 2.7.1.69)	b3899	CHM	0.47
4090404	REC06612	<i>frvA</i>	N	148	26, 80, 114, 124	P32155	PTS system, fructose-like-1 IIA component (EC 2.7.1.69)	b3900	CHM	0.47
4091019	REC06239	<i>yiiL</i>	N	104	43, 73	P32156	Hypothetical protein yiiL	b3901	UNC	0.16
4091853	REC06240	<i>rhaD</i>	E	274	-	P32169	Rhamnulose-1-phosphate aldolase (EC 4.1.2.19)	b3902	CHM	0.06
4093563	REC06241	<i>rhaA</i>	X	419	-	P32170	L-rhamnose isomerase (EC 5.3.1.14)	b3903	CHM	0.06
4095029	REC06242	<i>rhaB</i>	X	489	-	P32171	Rhamnulokinase (EC 2.7.1.5)	b3904	CHM	0.25
4095317	REC03804	<i>rhaS</i>	N	278	60, 82, 94, 172	P09377	L-rhamnose operon regulatory protein rhaS	b3905	RCD	0.28
4096137	REC03805	<i>rhaR</i>	N	312	99, 143, 223	P09378	L-rhamnose operon transcriptional activator rhaR	b3906	RCD	0.22
4098106	REC06243	<i>rhaT</i>	N	344	32, 33, 161	P27125	L-rhamnose-proton symport	b3907	MTR	0.00
4098391	REC03807	<i>sodA</i>	N	206	18, 193	P00448	Superoxide dismutase [Mn] (EC 1.15.1.1)	b3908	MSM	0.69
4099262	REC03808	<i>kdgT</i>	N	330	37, 40, 89, 143, 187, 203, 292, 330	P32172	2-keto-3-deoxygluconate permease	b3909	MTR	0.03
4100373	REC03809	<i>yiiM</i>	N	234	42, 51, 104	P32157	Hypothetical protein yiiM	b3910	UNC	0.34
4102556	REC06244	<i>cpxA</i>	X	457	2, 3	P08336	Sensor protein cpxA (EC 2.7.3.-)	b3911	SMC	0.28
4103251	REC06613	<i>cpXR</i>	N	232	40, 87, 106, 131, 149, 168, 177	P16244	Transcriptional regulatory protein cpXR	b3912	SMC	0.81
4103398	REC06614		N	49	21	P32158	Periplasmic protein cpX precursor	b3913	UNC	0.03
4103532	REC03812	<i>cpXP</i>	N	122	29, 42, 61	P32158	Periplasmic protein cpX precursor	b3914	UNC	0.03
4104049	REC03813	<i>yiiP</i>	N	300	3, 148, 198	P32159	Hypothetical protein yiiP	b3915	UNC	0.75
4105132	REC03814	<i>pfkA</i>	X	320	318	P06998	6-phosphofructokinase isozyme I (EC 2.7.1.11)	b3916	CHM	0.69
4106414	REC03815	<i>sbp</i>	N	329	21, 87, 174, 251, 299	P06997	Sulfate-binding protein precursor	b3917	MTR	0.41
4107510	REC03816	<i>cdh</i>	N	21	53	P06282	CDP-diacetylglucosyl pyrophosphatase (EC 3.6.1.26)	b3918	LPC	0.09
4109087	REC06246	<i>tpiA</i>	X	255	-	P04790	Triosephosphate isomerase (EC 5.3.1.1)	b3919	CHM	0.94
4109794	REC06247	<i>yiiQ</i>	N	199	5, 80	P32160	Hypothetical protein yiiQ precursor	b3920	UNC	0.00
4109895	REC03819	<i>yiiR</i>	N	146	9, 38, 108, 113	P32161	Hypothetical protein yiiR	b3921	UNC	0.06
4110547	REC03820	<i>yiiS</i>	N	99	5, 23, 36, 47, 91	P32162	Hypothetical protein yiiS	b3922	UNC	0.00
4110873	REC03821	<i>yiiT</i>	N	142	40, 56, 107	P32163	Hypothetical protein yiiT	b3923	UNC	0.06
4112052	REC06248	<i>fpr</i>	N	248	110	P28861	Ferredoxin--NADP reductase (EC 1.18.1.2)	b3924	BEN	0.31
4113159	REC06249	<i>glpX</i>	N	336	26, 153	P28860	Protein glpX	b3925	UNC	0.38
4114802	REC06250	<i>glpK</i>	N	502	23, 92, 139, 184, 189, 228, 253, 280, 287, 305, 339, 395, 422, 440	P08859	Glycerol kinase (EC 2.7.1.30)	b3926	CHM	0.78
4115670	REC06251	<i>glpF</i>	N	281	63, 168	P11244	Glycerol uptake facilitator protein	b3927	MTR	0.38
4116095	REC03826	<i>yiiU</i>	E	81	71	P32164	Hypothetical protein yiiU	b3928	UNC	0.00
4116910	REC06252	<i>menG</i>	N	161	8, 96, 111, 157	P32165	S-adenosylmethionine:2-demethylmenaquinone methyltransferase	b3929	NCM	0.22
4117929	REC06253	<i>menA</i>	N	308	43, 87, 118, 179, 226, 283	P32166	1,4-dihydroxy-2-naphthoate octaprenyltransferase (EC 2.5.1.-)	b3930	NCM	0.34
4119327	REC06254	<i>hslU</i>	N	443	4, 123, 303	P32168	ATP-dependent hsl protease ATP-binding subunit hslU	b3931	SMC	0.63
4119867	REC06255	<i>hslV</i>	N	176	15, 32, 45, 73, 79	P31059	ATP-dependent protease hslV (EC 3.4.25.-)	b3932	SMC	0.63
4120919	REC06256	<i>ftsN</i>	N	319	189, 248, 261, 300	P29131	Cell division protein ftsN	b3933	RCD	0.09
4122036	REC06257	<i>cytR</i>	N	341	14, 115, 120, 187, 259, 298	P06964	Transcriptional repressor cytR	b3934	RCD	0.59
4124390	REC06258	<i>priA</i>	E	732	725	P17888	Primosomal protein N'	b3935	NAM	0.51
4124593	REC03834	<i>rpmE</i>	?	70	-	P02432	50S ribosomal protein L31	b3936	PMS	0.63
4125474	REC06259	<i>yiiX</i>	N	202	49, 55, 110	P32167	Hypothetical protein yiiX precursor	b3937	UNC	0.00
4125975	REC06260	<i>metJ</i>	N	105	84	P08338	Met repressor	b3938	RCD	0.06
4126252	REC03837	<i>metB</i>	N	386	27, 50, 68, 87, 99, 176, 196, 236, 321, 364	P00935	Cystathionine gamma-synthase (EC 4.2.99.9)	b3939	AAM	0.69
4127415	REC03838	<i>metL</i>	N	810	128, 242, 381, 447, 508, 553, 717, 733, 759, 769	P00562	Bifunctional aspartokinase/homoserine dehydrogenase II	b3940	AAM	0.19
4130196	REC03839	<i>metF</i>	N	296	17, 78, 191	P00394	5,10-methylenetetrahydrofolate reductase (EC 1.7.99.5)	b3941	BEN	0.50
4131415	REC03840	<i>katG</i>	N	726	10, 26, 171, 383, 517, 527, 567, 578, 620, 708, 721, 726	P13029	Peroxidase/catalase HPI (EC 1.11.1.6)	b3942	MSM	0.28
4133655	REC03841	<i>yijE</i>	N	312	20, 39, 136, 149, 223	P32667	Hypothetical transport protein yijE	b3943	UNC	0.22
4135237	REC06261	<i>yijF</i>	N	205	4, 149, 154	P32668	Hypothetical protein yijF precursor	b3944	UNC	0.06
4136654	REC06262	<i>gldA</i>	N	380	5, 65, 338	P32665	Glycerol dehydrogenase (EC 1.1.1.6)	b3945	CHM	0.22
4137288	REC06263	<i>fsaB</i>	N	220	4, 65, 154, 180, 196, 216	P32669	Fructose-6-phosphate aldolase 2 (EC 4.1.2.-)	b3946	CHM	0.28
4139435	REC06264	<i>ptsA</i>	N	711	242, 248, 428, 463, 529, 574, 602, 633, 670	P32670	Phosphoenolpyruvate-protein phosphotransferase ptsA (EC 2.7.3.3)	b3947	MTR	0.75
4139437	REC03846	<i>yjiI</i>	X	109	-	Q923C7	Hypothetical protein YJI	b3948	UNC	0.00
4140109	REC03847	<i>frwC</i>	N	359	14, 86, 108, 116, 144, 198, 239, 262, 272	P32672	PTS system, fructose-like-2 IIC component	b3949	MTR	0.47
4141203	REC03848	<i>frwB</i>	N	106	26, 32	P32673	PTS system, fructose-like-2 IIB component 1 (EC 2.7.1.69)	b3950	CHM	0.09
4141574	REC03849	<i>pfLD</i>	N	765	353, 588, 639, 698, 764	P32674	Formate acetyltransferase 2 (EC 2.3.1.54)	b3951	CHM	0.22
4143837	REC03850	<i>pfIC</i>	N	292	9, 57, 98, 156, 178, 211, 253	P32675	Pyruvate formate-lyase 2 activating enzyme (EC 1.97.1.4)	b3952	CHM	0.28
4144717	REC03851	<i>frwD</i>	N	113	36, 96, 99	P32676	PTS system, fructose-like-2 IIB component 2 (EC 2.7.1.69)	b3953	CHM	0.09
4145896	REC06265	<i>yijO</i>	N	283	42, 215	P32677	Hypothetical transcriptional regulator yijO	b3954	UNC	0.13
4147844	REC06266	<i>yijP</i>	N	577	53, 82, 83, 104, 122, 135, 147, 156, 191, 199, 327, 450	P32678	Protein yijP	b3955	UNC	0.06
4150677	REC06267	<i>ppc</i>	N	883	3, 15, 82, 104, 123, 148, 171, 489, 624, 876, 881	P00864	Phosphoenolpyruvate carboxylase (EC 4.1.1.31)	b3956	CHM	0.34
4152426	REC06268	<i>argE</i>	X	383	363	P23908	Acetylmethionine deacetylase (EC 3.5.1.16)	b3957	AAM	0.44
4152580	REC03856	<i>argC</i>	E	334	317	P11446	N-acetyl-gamma-glutamyl-phosphate reductase (EC 1.2.1.38)	b3958	AAM	0.72
4153592	REC03857	<i>argB</i>	N	258	12, 53, 74, 98, 154, 190	P11445	Acetylglutamate kinase (EC 2.7.2.8)	b3959	AAM	0.72
4154429	REC03858	<i>argH</i>	N	457	13, 47, 58, 128, 130, 189, 374	P11447	Argininosuccinate lyase (EC 4.3.2.1)	b3960	AAM	0.75
4156069	REC03859	<i>oxyR</i>	N	305	181, 301	P11721	Hydrogen peroxide-inducible genes activator	b3961	RCD	0.50
4158303	REC06269	<i>sthA</i>	N	444	14, 53, 57, 81, 228, 280, 392	P27306	Soluble pyridine nucleotide transhydrogenase (EC 1.6.1.1)	b3962	BEN	0.19
4158646	REC03861	<i>yijC</i>	N	234	8, 111, 143, 207	P27307	Hypothetical protein yijC	b3963	UNC	0.09
4159350	REC03862	<i>yijD</i>	N	119	92, 102	P27308	Hypothetical protein yijD	b3964	UNC	0.03
4160849	REC06270	<i>trmA</i>	N	366	101, 115, 130, 177, 288	P23003	tRNA (Uracil-5-)-methyltransferase (EC 2.1.1.35)	b3965	NAM	0.16
4161218	REC03864	<i>btuB</i>	N	614	49, 109, 174, 273	P06129	Vitamin B12 receptor precursor	b3966	MTR	0.19
4162995	REC03865	<i>murI</i>	E	289	-	P22634	Glutamate racemase (EC 5.1.1.3)	b3967	AAM	0.84
4169636	REC03866	<i>murB</i>	N	342	7, 138, 296	P08373	UDP-N-acetylenolpyruvylglucosamine reductase (EC 1.1.1.158)	b3972	LPC	0.97
4170661	REC03867	<i>birA</i>	E	321	17	P06709	BirA bifunctional protein	b3973	NCM	0.88
4172605	REC06271	<i>coaA</i>	E	316	-	P15044	Pantothenate kinase (EC 2.7.1.33)	b3974	NCM	0.34
4172947	REC06272		N	51	4, 47	Q47715	COLI CHROMOSOMAL REGION FROM 89.2 TO 92.8 MINUTES	b3975	UNC	0.00
4173523	REC03870	<i>tufB</i>	E	394	-	P02990	Elongation factor Tu	b3980	PMS	1.00
4174937	REC03871	<i>secE</i>	N	127	86	P16920	Preprotein translocase secE subunit	b3981	PMS	0.22
4175322	REC03872	<i>nusG</i>	N	181	6, 57, 69	P16921	Transcription antitermination protein nusG	b3982	RCD	0.97
4176025	REC06615	<i>rpLK</i>	X	142	-	P02409	50S ribosomal protein L11	b3983	PMS	1.00
4176457	REC03874	<i>rpLA</i>	X	234	-	P02384	50S ribosomal protein L1	b3984	PMS	1.00
4177574	REC03875	<i>rpLJ</i>	E	165	-	P02408	50S ribosomal protein L10	b3985	PMS	1.00
4178138	REC03876	<i>rpLL</i>	E	121	-	P02392	50S ribosomal protein L7/L12	b3986	PMS	1.00
4178823	REC03877	<i>rpOB</i>	E	1342	-	P00575	DNA-directed RNA polymerase beta chain (EC 2.7.7.6)	b3987	NAM	1.00
4182928	REC06616	<i>rpOC</i>	E	1407	35	P00577	DNA-directed RNA polymerase beta' chain (EC 2.7.7.6)	b3988	NAM	1.00
4187364	REC03879	<i>htrC</i>	N	179	76, 108, 166	P27375	Heat shock protein C	b3989	UNC	0.00
4189446	REC06273	<i>thiH</i>	X	377	-	P30140	Thiazole biosynthesis protein thiH	b3990	NCM	0.16
4190288	REC06274	<i>thiG</i>	X	281	-	P30139	Thiazole biosynthesis protein thiG	b3991	NCM	0.63
4191136	REC06275	<i>thiF</i>	N	245	16, 39	P30138	Adenylyltransferase thiF (EC 2.7.7.-)	b3992	NCM	0.16
4191782	REC06276	<i>thiE</i>	N	211	64, 107, 150, 153	P30137	Thiamine-phosphate pyrophosphorylase (EC 2.5.1.3)	b3993	NCM	0.78
4193677	REC06277	<i>thiC</i>	N	631	43, 290, 429, 508	P30136	Thiamine biosynthesis protein thiC	b3994	NCM	0.63
4194386	REC06278	<i>rsd</i>	E	158	-	P31690	Regulator of sigma D	b3995	RCD	0.06
4194481	REC03886	<i>nudC</i>	N	257	13, 67, 84, 128, 187	P32664	NADH pyrophosphatase (EC 3.6.1.-)	b3996	MSM	0.38
4195294	REC06617	<i>hemE</i>	E	354	-	P29680	Uroporphyrinogen decarboxylase (EC 4.1.1.37)	b3997	NCM	0.72
4196362	REC03888	<i>nfi</i>	N	225	107, 204, 212	P32679	Endonuclease V (EC 3.1.-.-)	b3998	NAM	0.19

4197082	REC03889	yjaG	?	196	-	P32680	Hypothetical protein yjaG	b3999	UNC	0.06
4197859	REC03890	hupA	N	90	42, 74	P02342	DNA-binding protein HU-alpha	b4000	RCD	0.81
4198144	REC03891	yjaH	N	231	49, 60, 85, 89, 145, 168, 195	P32681	Hypothetical protein yjaH	b4001	UNC	0.03
4199407	REC06279	zraP	E	188	166	P32682	Zinc resistance-associated protein precursor	b4002	UNC	0.00
4199504	REC03893	zraS	N	465	20, 174, 310	P14377	Sensor protein zraS (EC 2.7.3.-)	b4003	SMC	0.16
4200898	REC03894	zraR	N	441	122, 142, 175, 350, 427	P14375	Transcriptional regulatory protein zraR	b4004	SMC	0.63
4203509	REC06280	purD	N	429	90, 191, 244, 307, 363	P15640	Phosphoribosylamine-glycine ligase (EC 6.3.4.13)	b4005	NCM	0.81
4205110	REC06281	purH	N	529	54, 79, 111, 226, 238, 249, 496	P15639	Bifunctional purine biosynthesis protein purH	b4006	NCM	0.81
4210813	REC03897	yjaA	N	127	83	P09162	Hypothetical protein yjaA	b4011	UNC	0.00
4211702	REC06282	yjaB	N	147	43, 79, 92	P09163	Hypothetical acetyltransferase yjaB (EC 2.3.1.-)	b4012	UNC	0.22
4211859	REC03899	metA	N	309	1, 172, 205, 270	P07623	Homoserine O-succinyltransferase (EC 2.3.1.46)	b4013	AAM	0.28
4213057	REC03900	aceB	N	533	164, 199, 269	P08997	Malate synthase A (EC 4.1.3.2)	b4014	CHM	0.13
4214688	REC03901	aceA	N	434	225, 289, 318, 369, 423	P05313	Iso citrate lyase (EC 4.1.3.1)	b4015	CHM	0.34
4216175	REC03902	aceK	N	578	12, 58, 64, 100, 353, 403, 505	P11071	Iso citrate dehydrogenase kinase/phosphatase (EC 2.7.1.116) (EC 2.7.1.116)	b4016	CHM	0.06
4220066	REC06283	arpA	N	728	126, 172, 196, 221, 244, 293, 346, 420, 510, 548, 554, 569, 580, 607, 639	P23325	Ankyrin-repeat protein A	b4017	RCD	0.00
4221246	REC06284	icrR	N	287	213	P16528	Acetate operon repressor	b4018	RCD	0.16
4221407	REC03905	metH	N	1227	21, 165, 193, 255, 332, 363, 488	P13009	5-methyltetrahydrofolate-homocysteine methyltransferase (EC 2.1.1.13)	b4019	AAM	0.56
4225310	REC03906	yjbB	N	543	93, 258, 321, 353, 380, 398	P32683	Hypothetical protein yjbB	b4020	UNC	0.34
4227721	REC06285	pepE	N	229	8, 86	P32666	Peptidase E (EC 3.4.-.-)	b4021	PMS	0.19
4227933	REC03908	yjbC	N	290	30, 180, 238, 282	P32684	Hypothetical protein yjbC	b4022	UNC	0.97
4229210	REC06286	yjbD	N	90	19, 44	P32685	Hypothetical protein yjbD	b4023	UNC	0.00
4230812	REC06287	lysC	N	449	384, 412, 443	P08660	Lysine-sensitive aspartokinase III (EC 2.7.2.4)	b4024	AAM	0.84
4231337	REC03911	pgi	N	549	210, 256, 264, 318, 357, 457, 531	P11537	Glucose-6-phosphate isomerase (EC 5.3.1.9)	b4025	CHM	0.94
4233485	REC03912	yjbE	N	80	20, 282	P32686	Hypothetical protein yjbE precursor	b4026	UNC	0.00
4233811	REC03913	yjbF	X	222	10	P32687	Hypothetical lipoprotein yjbF precursor	b4027	UNC	0.00
4234476	REC03914	yjbG	X	245	-	P32688	Hypothetical protein yjbG precursor	b4028	UNC	0.00
4235213	REC03915	yjbH	N	698	32, 52, 60, 140, 259, 439, 488, 526, 572, 595	P32689	Hypothetical lipoprotein yjbH precursor	b4029	UNC	0.00
4237904	REC03916	yjbA	E	136	-	P323896	Hypothetical protein yjbA	b4030	UNC	0.09
4239833	REC06288	xy1E	N	491	34, 54, 72, 168, 190, 198, 219	P09098	D-xylose-proton symporter	b4031	MTR	0.13
4241095	REC06289	malG	X	296	-	P07622	Maltose transport system permease protein malG	b4032	MTR	0.38
4242654	REC06290	malF	N	514	7, 19, 112, 128	P02916	Maltose transport system permease protein malF	b4033	MTR	0.25
4243998	REC06291	malE	N	396	186, 232, 304, 378	P02928	Maltose-binding periplasmic protein precursor	b4034	MTR	0.47
4244363	REC03921	malK	N	371	175, 327	P02914	Maltose/maltodextrin transport ATP-binding protein malK	b4035	MTR	0.28
4245550	REC03922	lamB	N	446	4, 36, 41, 58, 94, 126, 148, 214, 298, 330, 341	P02943	Maltoporin precursor	b4036	MTR	0.06
4247133	REC03923	malM	N	306	34, 88	P03841	Maltose operon periplasmic protein precursor	b4037	UNC	0.03
4248534	REC03924	yjbI	?	442	400	P32690	Hypothetical protein yjbI	b4038	UNC	0.00
4249974	REC03925	ubiC	N	202	-	P26602	Chorismate-pyruvate lyase (EC 4.-.-.-)	b4039	NCM	0.09
4250595	REC03926	ubiA	X	290	-	P26601	4-hydroxybenzoate octaprenyltransferase (EC 2.5.1.-)	b4040	NCM	0.66
4254105	REC06292	plsB	X	827	-	P00482	Glycerol-3-phosphate acyltransferase (EC 2.3.1.15)	b4041	LPC	0.16
4254216	REC03928	dgsA	X	122	-	P00556	Diacylglycerol kinase (EC 2.7.1.107)	b4042	LPC	0.44
4254694	REC03929	lexA	X	202	-	P03033	LexA repressor (EC 3.4.2.188)	b4043	NAM	0.63
4255321	REC03930	dinF	N	459	300, 357, 374, 389, 424, 434	P28303	DNA-damage-inducible protein F	b4044	UNC	0.88
4256816	REC03931	yjbJ	?	69	-	P32691	Protein yjbJ	b4045	UNC	0.13
4257642	REC06293	zur	N	191	24, 58, 120, 161, 183	P32692	Zinc uptake regulation protein	b4046	RCD	0.28
4257900	REC03933	yjbL	E	84	-	P32693	Hypothetical protein yjbL	b4047	UNC	0.00
4258178	REC03934	yjbM	E	235	225	P32694	Hypothetical protein yjbM	b4048	UNC	0.00
4259248	REC03935	yjbN	N	345	19, 22	P32695	Hypothetical protein yjbN	b4049	UNC	0.44
4260209	REC03936	yjbO	E	150	-	P32696	Hypothetical protein yjbO	b4050	UNC	0.03
4261810	REC06294	gor	N	327	-	P28304	Quinone oxidoreductase (EC 1.6.5.5)	b4051	BEN	0.47
4261893	REC03938	dnaB	E	471	-	P03005	Replicative DNA helicase (EC 3.6.1.-)	b4052	NAM	1.00
4263361	REC03939	alr	N	359	58, 61, 94, 106, 155, 307	P29743	Alanine racemase, biosynthetic (EC 5.1.1.1)	b4053	AAM	0.88
4264693	REC03940	tyrB	E	397	-	P04693	Aromatic-amino-acid aminotransferase (EC 2.6.1.57)	b4054	AAM	0.28
4266630	REC06772	yjbs	E	80	-	P58036	Hypothetical protein yjbs	b4055	UNC	0.00
4266993	REC03941	aphA	N	237	25, 54, 55, 80	P32697	Class B acid phosphatase precursor (EC 3.1.3.2)	b4056	MSM	0.03
4267817	REC03942	yjbQ	N	138	5, 32	P32698	Hypothetical protein yjbQ	b4057	UNC	0.34
4268237	REC06633	yjbr	N	118	75	P32699	Protein yjbr	b4058	UNC	0.00
4271450	REC06634	uvrA	N	940	106, 146, 245, 339, 372, 525	P07671	Excinuclease ABC subunit A	b4059	NAM	0.97
4271704	REC03945	ssb	X	178	-	P02339	Single-strand binding protein	b4060	NAM	0.91
4272689	REC06296	yjcb	X	116	-	P32700	Hypothetical protein yjcb	b4061	UNC	0.00
4273050	REC03947	yjcc	X	528	-	P32701	Hypothetical protein yjcc	b4062	UNC	0.31
4274962	REC06297	soxS	X	107	-	P22539	Regulatory protein soxS	b4063	RCD	0.06
4275048	REC03949	soxR	X	154	-	P22538	Redox-sensitive transcriptional activator soxR	b4064	RCD	0.16
4276058	REC03950	yjcd	N	449	60, 79, 120, 164, 194, 210, 249, 265, 382, 418	P32702	Hypothetical protein yjcd	b4065	UNC	0.66
4277559	REC03951	yjce	N	549	26, 28, 83, 287, 497	P32703	Putative Na(+)/H(+) exchanger yjce	b4066	UNC	0.44
4280654	REC06298	yjcf	N	430	377, 379	P32704	Hypothetical protein yjcf	b4067	UNC	0.03
4282481	REC06299	yjcg	N	549	-	P32705	Putative symporter yjcg	b4068	UNC	0.22
4282792	REC06300	yjch	X	104	-	P32706	Hypothetical protein yjch	b4069	UNC	0.06
4284950	REC06301	acs	N	652	116, 217, 252, 418, 453, 541, 609	P27550	Acetyl-coenzyme A synthetase (EC 6.2.1.1)	b4070	CHM	0.63
4285343	REC03956	nrfA	N	478	36, 122, 301, 326, 333, 340, 386, 387	P32050	Cytochrome C552 precursor	b4071	BEN	0.06
4286818	REC03957	nrfB	N	190	48, 85, 87, 127	P32707	Cytochrome c-type protein nrfB precursor	b4072	BEN	0.03
4287387	REC06635	nrfC	N	223	132	P32708	NrfC protein	b4073	UNC	0.06
4288055	REC03959	nrfD	N	318	55, 95, 190, 237	P32709	NrfD protein	b4074	UNC	0.03
4289091	REC03960	nrfE	N	552	132, 355, 439, 503, 504	P32710	Cytochrome c-type biogenesis protein nrfE	b4075	UNC	0.00
4290742	REC03961	nrfF	N	127	9, 31, 120	P32711	Cytochrome c-type biogenesis protein nrfF precursor	b4076	UNC	0.00
4291122	REC03962	nrfG	N	198	36, 88, 119, 127	P32712	NrfG protein	b4077	UNC	0.06
4292060	REC03963	gltP	N	437	3, 83, 104, 277, 378, 405	P21345	Proton glutamate symport protein	b4078	MTR	0.28
4294704	REC06302	yjco	N	229	83, 112	P32713	Hypothetical protein yjco precursor	b4079	UNC	0.00
4296945	REC06636	fdhF	N	715	35, 102, 401, 549	P07658	Formate dehydrogenase H (EC 1.2.1.2)	b4080	SMC	0.53
4298609	REC06637	yjcp	N	488	19, 29, 128, 190, 206, 275, 330	P32714	Hypothetical outer-membrane lipoprotein yjcp precursor	b4081	UNC	0.09
4300516	REC06305	yjqQ	N	636	18, 563	P32715	Hypothetical transporter yjqQ	b4082	UNC	0.00
4301688	REC06306	yjcr	N	343	112, 139, 247, 320	P32716	Hypothetical protein yjcr	b4083	UNC	0.50
4304188	REC06638	yjcs	N	665	608	P32717	Hypothetical protein yjcs	b4084	UNC	0.16
4305378	REC06308	alsK	N	309	239, 254, 274	P32718	D-allose kinase (EC 2.7.1.55)	b4085	CHM	0.09
4306057	REC06309	alsE	X	231	-	P32719	D-allose-6-phosphate 3-epimerase (EC 5.1.3.-)	b4086	CHM	0.03
4307048	REC06310	alsC	X	326	-	P32720	D-allose transport system permease protein alsC	b4087	MTR	0.13
4308559	REC06311	alsA	N	510	7, 91, 97, 152, 172, 201, 408, 430, 449	P32721	D-allose transport ATP-binding protein alsA	b4088	MTR	0.28
4309621	REC06312	alsB	N	311	234, 266	P39265	D-allose-binding periplasmic protein precursor	b4089	MTR	0.00
4310603	REC06313	rpiR	N	307	12, 18	P39266	Protein rpiR	b4090	CHM	0.56
4310929	REC03976	rpiB	N	149	54, 119, 142	P37351	Ribose 5-phosphate isomerase B (EC 5.3.1.6)	b4091	UNC	0.00
4311796	REC06314	phnQ	N	135	84, 90	P16693	Very hypothetical phnQ protein	b4092	UNC	0.28
4312680	REC06315	phnP	N	252	210, 237	P16692	PhnP protein	b4093	UNC	0.06
4313116	REC06316	phnO	X	144	-	P16691	PhnO protein	b4094	UNC	0.06
4313660	REC06317	phnN	X	185	-	P16690	ATP-binding protein phnN	b4094	UNC	0.16

4314796	REC06318	<i>phnM</i>	N	378	11, 111, 224, 266, 285			P16689	PhnM protein	b4095	UNC	0.19
4315473	REC06319	<i>phnL</i>	N	226	25, 53, 114			P16679	Phosphonates transport ATP-binding protein phnL	b4096	MSM	0.16
4316342	REC06320	<i>phnK</i>	X	252	-			P16678	Phosphonates transport ATP-binding protein phnK	b4097	MSM	0.75
4317184	REC06321	<i>phnJ</i>	X	281	-			P16688	PhnJ protein	b4098	UNC	0.16
4318241	REC06322	<i>phnI</i>	N	354	125, 202, 266			P16687	PhnI protein	b4099	UNC	0.16
4318825	REC06323	<i>phnH</i>	N	194	83, 95			P16686	PhnH protein	b4100	UNC	0.16
4319274	REC06324	<i>phnG</i>	N	150	25, 150			P16685	PhnG protein	b4101	UNC	0.16
4320000	REC06325	<i>phnF</i>	X	241	-			P16684	Probable transcriptional regulator phnF	b4102	UNC	0.19
4320242	REC06326		X	73	-			P16683	Phosphonates transport system permease protein phnE	b4103	MTR	0.00
4320859	REC06327	<i>phnE</i>	N	206	21			P16683	Phosphonates transport system permease protein phnE	b4105	MTR	0.25
4321930	REC06328	<i>phnD</i>	N	338	51, 118, 231, 309			P16682	Phosphonates-binding periplasmic protein precursor	b4106	MTR	0.25
4322743	REC06329	<i>phnC</i>	N	262	155, 203			P16677	Phosphonates transport ATP-binding protein phnC	b4107	MTR	0.34
4323319	REC06330	<i>phnB</i>	X	147	-			P16681	PhnB protein	b4107	UNC	0.22
4324312	REC06331	<i>phnA</i>	N	111	11, 33			P16680	PhnA protein	b4108	UNC	0.47
4324713	REC03995	<i>yjdA</i>	N	742	6, 41, 62, 137, 156, 241, 520, 575, 615			P16694	Hypothetical protein yjdA	b4109	UNC	0.00
4326971	REC03996	<i>yjcZ</i>	N	281	190, 220			P39267	Hypothetical protein yjcZ	b4110	UNC	0.00
4328080	REC03997	<i>proP</i>	N	500	14, 103, 132, 177, 245, 375, 499			P30848	Proline/betaine transporter	b4111	MTR	0.38
4330850	REC06332	<i>basS</i>	X	363	353			P30844	Sensor protein basS/pmrB (EC 2.7.3.-)	b4112	SMC	0.03
4331528	REC06333	<i>basR</i>	N	222	43, 60, 120, 166			P30843	Transcriptional regulatory protein basR/pmrA	b4113	SMC	0.00
4333198	REC06334	<i>yjdB</i>	N	557	125, 147, 226, 288, 362, 421			P30845	Hypothetical protein yjdB	b4114	UNC	0.31
4334609	REC06335	<i>yjdE</i>	X	445	-			P39269	Hypothetical transport protein yjdE	b4115	UNC	0.25
4335507	REC06337	<i>adiY</i>	X	253	-			P33234	Putative regulatory protein adiY	b4116	UNC	0.00
4338102	REC06338	<i>adiA</i>	N	756	39			P26629	Biodegradative arginine decarboxylase (EC 4.1.1.19)	b4117	AAM	0.31
4339206	REC06339	<i>melR</i>	N	302	46, 53			P10411	Melibiose operon regulatory protein	b4118	RCD	0.16
4339489	REC04006	<i>meLA</i>	N	451	181, 221, 390			P06720	Alpha-galactosidase (EC 3.2.1.22)	b4119	CHM	0.16
4340959	REC04007	<i>meLB</i>	N	469	110, 124, 126, 139, 168, 199, 223, 245, 292, 314, 319, 348, 384, 416, 436			P02921	Melibiose carrier protein	b4120	MTR	0.00
4343136	REC06340	<i>yjdF</i>	N	209	31, 71, 126			P39270	Hypothetical protein yjdF	b4121	UNC	0.03
4344904	REC06341	<i>fumB</i>	N	548	11, 394			P14407	Fumarate hydratase class I, anaerobic (EC 4.2.1.2)	b4122	CHM	0.31
4346322	REC06342	<i>dcuB</i>	N	446	1, 45, 74, 285, 421, 437			P14409	Anaerobic C4-dicarboxylate transporter dcuB	b4123	MTR	0.16
4347612	REC06343	<i>dcuR</i>	N	239	117			P39271	Transcriptional regulatory protein dcuR	b4124	SMC	0.03
4349240	REC06344	<i>dcuS</i>	N	543	152, 212			P39272	Sensor protein dcuS (EC 2.7.3.-)	b4125	SMC	0.03
4349421	REC04013	<i>yjdI</i>	N	76	35			P39273	Hypothetical protein yjdI	b4126	UNC	0.06
4349663	REC04014	<i>yjdJ</i>	N	90	31			P39274	Hypothetical protein yjdJ	b4127	UNC	0.22
4350162	REC04015	<i>yjdK</i>	N	98	15			P39275	Hypothetical protein yjdK	b4128	UNC	0.00
4350486	REC06711	<i>yjdO</i>	X	57	-			P58038	Hypothetical protein yjdO	b4129	UNC	0.00
4352295	REC06345	<i>lysU</i>	N	505	44, 73, 86, 136, 138, 196, 251, 272			P14825	Lysyl-tRNA synthetase, heat inducible (EC 6.1.1.6)	b4129	NAM	0.91
4353989	REC06346	<i>yjdL</i>	N	485	71, 206, 317, 340, 405, 433			P39276	Hypothetical transporter yjdL	b4130	UNC	0.31
4356195	REC06347	<i>cadA</i>	N	715	24, 65, 73, 170, 214, 258, 443, 464			P23892	Lysine decarboxylase, inducible (EC 4.1.1.18)	b4131	AAM	0.16
4357609	REC06348	<i>cadB</i>	N	444	391, 413, 431			P23891	Probable cadaverine/lysine antiporter	b4132	UNC	0.03
4359512	REC06349	<i>cadC</i>	X	512	-			P23890	Transcriptional activator cadC	b4133	RCD	0.06
4360910	REC06350	<i>yjdC</i>	X	199	-			P36656	Protein yjdC	b4135	UNC	0.09
4362620	REC06351	<i>dsbD</i>	N	565	97, 111, 146, 247, 267, 305			P36655	Thiol:disulfide interchange protein dsbD precursor	b4136	PMS	0.34
4362934	REC06352	<i>cutA</i>	N	112	41			P36654	Periplasmic divalent cation tolerance protein cutA	b4137	UNC	0.16
4364351	REC06353	<i>dcuA</i>	N	433	275, 343, 343, 414			P04539	Anaerobic C4-dicarboxylate transporter dcuA	b4138	MTR	0.16
4365950	REC06354	<i>aspA</i>	N	493	16, 90, 92, 208			P04422	Aspartate ammonia-lyase (EC 4.3.1.1)	b4139	AAM	0.41
4366341	REC04026	<i>fxsA</i>	N	125	20, 25			P37147	FxsA protein	b4140	UNC	0.22
4367990	REC06355	<i>yjeH</i>	N	418	250, 302, 389			P39277	Hypothetical protein yjeH	b4141	UNC	0.34
4368266	REC04028	<i>groS</i>	E	97	-	0.37		P05380	10 kDa chaperonin	b4142	PMS	0.97
4368603	REC04029	<i>groL</i>	E	548	-	< 0.01		P06139	60 kDa chaperonin	b4143	PMS	1.00
4370354	REC04030	<i>yjeI</i>	?	128	99			P39278	Hypothetical protein yjeI precursor	b4144	UNC	0.00
4371812	REC06356	<i>yjeJ</i>	N	289	28, 123, 137, 223			P39279	Hypothetical protein yjeJ	b4145	UNC	0.00
4373235	REC06357	<i>yjeK</i>	?	342	328			P39280	Hypothetical protein yjeK	b4146	UNC	0.41
4373277	REC04033	<i>efp</i>	E	188	-	< 0.2		P33398	Elongation factor P	b4147	PMS	1.00
4374131	REC06712	<i>ecnB</i>	?	48	-			P56549	Entericidin B precursor	b4148	UNC	0.00
4374303	REC04034	<i>sugE</i>	N	155	79			P30743	SugE protein	b4148	UNC	0.44
4375300	REC06358	<i>b1c</i>	?	177	155			P39281	Outer membrane lipoprotein b1c precursor	b4149	UNC	0.22
4376522	REC06359	<i>ampC</i>	N	377	17, 286			P00811	Beta-lactamase precursor (EC 3.5.2.6)	b4150	MSM	0.28
4376944	REC06360	<i>frdC</i>	?	119	105			P03806	Fumarate reductase 13 kDa hydrophobic protein	b4151	BEN	0.06
4377350	REC06361	<i>frdD</i>	N	131	18			P03805	Fumarate reductase 15 kDa hydrophobic protein	b4152	BEN	0.09
4378095	REC06362	<i>frdB</i>	N	244	78, 80, 181, 238			P00364	Fumarate reductase iron-sulfur protein (EC 1.3.99.1)	b4153	SMC	0.72
4379896	REC06363	<i>frdA</i>	N	602	106, 109, 189, 219, 273, 339, 373			P00363	Fumarate reductase flavoprotein subunit (EC 1.3.99.1)	b4154	SMC	0.78
4380191	REC04041	<i>poxA</i>	E	335	-	< 0.05		P30512	Putative lysyl-tRNA synthetase (EC 6.1.1.6)	b4155	UNC	0.31
4381375	REC04042	<i>yjeM</i>	N	514	28, 33, 215, 269, 296, 307, 330, 345, 514			P39282	Hypothetical transporter yjeM	b4156	UNC	0.00
4383282	REC04044	<i>yjeO</i>	E	104	-	0.35		P39284	Hypothetical protein yjeO	b4158	UNC	0.00
4386948	REC06477	<i>yjeP</i>	N	1107	27, 62, 179, 266, 425, 1051			P39285	Hypothetical protein yjeP precursor	b4159	UNC	0.88
4387938	REC06365	<i>psd</i>	X	322	318			P10740	Phosphatidylserine decarboxylase proenzyme (EC 4.1.1.65)	b4160	LPC	0.56
4389048	REC06366	<i>yjeQ</i>	X	337	-			P39286	Hypothetical protein yjeQ	b4161	UNC	0.66
4389113	REC04048	<i>orn</i>	N	204	15, 36, 59			P39287	Oligonucleotidase (EC 3.1.-.-)	b4162	NAM	0.28
4391644	REC04050	<i>yjeF</i>	N	515	132, 325, 342, 423, 454, 496			P31806	Hypothetical protein yjeF	b4167	UNC	0.75
4391645	REC06367	<i>yjeS</i>	N	379	296, 350			P39288	Putative electron transport protein yjeS	b4166	UNC	0.44
4393163	REC04051	<i>yjeE</i>	E	153	-	< 0.2		P31805	Hypothetical protein yjeE	b4168	UNC	0.91
4393643	REC04052	<i>amiB</i>	N	445	111, 117, 401			P26365	N-acetylmuramoyl-L-alanine amidase amiB precursor (EC 3.5.1.2)	b4169	LPC	0.84
4394990	REC04053	<i>mutL</i>	N	615	335, 337, 384, 407, 433, 494, 540, 547, 588			P23367	DNA mismatch repair protein mutL	b4170	NAM	0.84
4396830	REC04054	<i>miaA</i>	E	316	303	< 0.05		P16384	tRNA delta(2)-isopentenylpyrophosphate transferase (EC 2.5.1.8)	b4171	NAM	0.97
4397866	REC04055	<i>hfg</i>	E	102	-	0.31		P25521	Hfg protein	b4172	PHT	0.53
4398250	REC04056	<i>hflX</i>	N	426	62, 100, 351, 420, 424			P25519	GTP-binding protein hflX	b4173	UNC	0.75
4399616	REC04057	<i>hflK</i>	N	419	43, 49, 116, 167, 230, 290, 327			P25662	HflK protein	b4174	PMS	0.44
4400878	REC04058	<i>hflC</i>	N	334	151, 277			P25661	HflC protein (EC 3.4.-.-)	b4175	PMS	0.44
4401964	REC04059	<i>yjeT</i>	?	65	4			P39289	Hypothetical protein yjeT	b4176	UNC	0.03
4402265	REC04060	<i>purA</i>	N	432	238, 302, 413			P12283	Adenylosuccinate synthetase (EC 6.3.4.4)	b4177	NCM	0.84
4403768	REC04061	<i>yjeB</i>	N	141	21, 65, 81			P21498	Hypothetical protein yjeB	b4178	UNC	0.69
4404190	REC04062	<i>xnr</i>	N	827	76, 288			P21499	Ribonuclease R (EC 3.1.-.-)	b4179	NAM	0.88
4406853	REC04063	<i>yjfH</i>	N	243	9, 44, 137, 144, 189, 204			P39290	Hypothetical tRNA/rRNA methyltransferase yjfH (EC 2.1.1.-)	b4180	UNC	0.97
4407711	REC04064	<i>yjfI</i>	N	133	2, 73, 129			P39291	Hypothetical protein yjfI	b4181	UNC	0.06
4408131	REC04065	<i>yjfJ</i>	N	232	23, 28			P39292	Hypothetical protein yjfJ precursor	b4182	UNC	0.06
4408880	REC04066	<i>yjfK</i>	X	219	-			P39293	Hypothetical protein yjfK	b4183	UNC	0.00
4409557	REC04067	<i>yjfL</i>	X	132	-			P39294	Hypothetical protein yjfL	b4184	UNC	0.13
4409965	REC04068	<i>yjfM</i>	X	212	-			P39295	Hypothetical protein yjfM	b4185	UNC	0.00
4410606	REC04069	<i>yjfC</i>	X	387	-			P33222	Hypothetical protein yjfC	b4186	UNC	0.00
4411838	REC04070	<i>aidB</i>	N	546	421, 427, 438, 446, 523			P33224	AidB protein	b4187	UNC	0.28
4413897	REC06368	<i>yjfN</i>	N	100	49, 67			P39296	Hypothetical protein yjfN	b4188	UNC	0.00
4414447	REC06369	<i>yjfO</i>	N	142	20, 86, 112, 141			P39297	Hypothetical lipoprotein yjfO precursor	b4189	UNC	0.00
4414530	REC04073	<i>yjfP</i>	N	249	1, 37			P39298	Hypothetical protein yjfP	b4190	UNC	0.06

4416031	REC06370	yjfQ	X	251	-	P39299	Hypothetical transcriptional regulator yjfQ	b4191	UNC	0.13
4417209	REC06371	yjfr	N	356	69, 87, 280	P39300	Hypothetical protein yjfr	b4192	UNC	0.06
4417501	REC06484	sgaT	N	484	11, 87, 129, 139, 327, 371, 443	P39301	Putative transport protein sgaT	b4193	UNC	0.19
4418971	REC04077	sgaB	X	101	-	P39302	Unknown pentitol phosphotransferase enzyme II, B component (Ei	b4194	CHM	0.06
4419286	REC06485	sgaA	N	154	80, 130	P39303	Unknown pentitol phosphotransferase enzyme II, A component (Ei	b4195	CHM	0.16
4419764	REC04079	sgaH	N	216	62, 200	P39304	Probable hexulose-6-phosphate synthase (EC 4.1.2.-)	b4196	UNC	0.22
4420424	REC04080	sgaU	N	284	26, 57, 86, 135	P39305	Putative hexulose-6-phosphate isomerase (EC 5.-.-.-)	b4197	UNC	0.19
4421278	REC04081	sgaE	N	228	77, 181	P39306	Probable sugar isomerase sgaE (EC 5.1.-.-)	b4198	UNC	0.28
4422369	REC06372	yjfy	X	91	-	P39307	Hypothetical protein yjfy precursor	b4199	UNC	0.00
4422696	REC04083	rpsF	E	131	-	P02358	30S ribosomal protein S6	b4200	PMS	0.81
4423098	REC04084	prbB	E	104	-	P07013	Primosomal replication protein N	b4201	NAM	0.09
4423417	REC04085	rpsR	?	75	-	P02374	30S ribosomal protein S18	b4202	PMS	1.00
4423686	REC04086	rplI	N	149	67, 132	P02418	50S ribosomal protein L9	b4203	PMS	0.97
4425000	REC06373	yjfZ	N	264	49, 127, 181, 215, 232, 264	P39308	Hypothetical protein yjfZ	b4204	UNC	0.00
4425347	REC04088	ytfA	X	108	-	P39309	Hypothetical protein ytfA	b4205	UNC	0.03
4426331	REC06374	ytfB	X	224	-	P39310	Hypothetical protein ytfB	b4206	UNC	0.06
4426354	REC04090	fkIB	N	259	98, 112, 202, 228	P39311	FKBP-type 22 kDa peptidyl-prolyl cis-trans isomerase (EC 5.2.1.8)	b4207	MSM	0.84
4427442	REC04091	cycA	N	470	13, 24, 290	P39312	D-serine/D-alanine/glycine transporter	b4208	MTR	0.22
4429561	REC06375	ytfE	N	220	79, 151, 207	P39313	Hypothetical protein ytfE	b4209	UNC	0.19
4430643	REC06376	ytfF	N	324	70, 105, 150	P39314	Hypothetical protein ytfF	b4210	UNC	0.16
4431601	REC04095	ytfH	N	156	112, 145	P39316	Hypothetical protein ytfH	b4212	UNC	0.53
4431602	REC06377	ytfG	N	286	19, 60	P39315	Hypothetical protein ytfG	b4211	UNC	0.38
4434143	REC06378	cpdB	N	647	3, 51, 55, 89, 143, 185, 219, 520, 643	P08331	2',3'-cyclic-nucleotide 2'-phosphodiesterase precursor (EC 3.1.4.1)	b4213	NCM	0.34
4434333	REC04097	cysQ	N	246	29, 43, 200	P22255	CysQ protein	b4214	UNC	0.56
4435285	REC04098	ytfI	E	166	-	P39317	Hypothetical protein ytfI	b4215	UNC	0.00
4435692	REC06764	ytfI	E	176	-	P39317	Hypothetical protein ytfE	b4215	UNC	0.00
4436839	REC06379	ytfJ	N	184	113	P39187	Protein ytfJ precursor	b4216	UNC	0.06
4437125	REC04100	ytfK	N	81	21	P39318	Hypothetical protein ytfK	b4217	UNC	0.03
4438792	REC06380	ytfL	N	447	115, 220, 248, 293, 412	P39319	Hypothetical protein ytfL	b4218	UNC	0.94
4439753	REC06381	msrA	N	212	128, 212	P27110	Peptide methionine sulfoxide reductase msrA (EC 1.8.4.6)	b4219	PMS	0.81
4439959	REC04103	ytfM	N	577	201, 245, 383, 405, 450, 529	P39320	Hypothetical protein ytfM precursor	b4220	UNC	0.69
4441689	REC04104	ytfN	N	1259	112, 392, 414, 534, 644, 817, 871, 934, 973	P39321	Hypothetical protein ytfN	b4221	UNC	0.38
4445471	REC04105	ytfP	N	113	7, 62	P39323	Hypothetical protein ytfP	b4222	UNC	0.03
4446018	REC04107	chpS	E	85	-	P08365	PemI-like protein 2	b4224	UNC	0.00
4446269	REC04108	chpB	N	116	35	P33647	PemK-like protein 2	b4225	UNC	0.13
4447229	REC06383	ppa	E	176	-	P17288	Inorganic pyrophosphatase (EC 3.6.1.1)	b4226	MSM	0.66
4447539	REC04110	ytfQ	N	318	88, 115, 250	P39325	ABC transporter periplasmic binding protein ytfQ precursor	b4227	MTR	0.13
4448633	REC04111	ytfR	N	417	197, 242	P39326	Hypothetical ABC transporter ATP-binding protein ytfR	b4233	UNC	0.44
4449862	REC04112	ytfS	E	90	-	P39326	Hypothetical ABC transporter ATP-binding protein ytfR	b4229	UNC	0.00
4450145	REC04113	ytfT	N	341	71, 234, 292	P39328	Hypothetical ABC transporter permease protein ytfT	b4230	UNC	0.06
4451181	REC04114	yjfF	N	323	42, 85, 124, 206, 248	P37772	Hypothetical ABC transporter permease protein yjfF	b4231	UNC	0.09
4453183	REC06384	fbp	N	332	12, 112, 156, 178, 223, 318	P09200	Fructose-1,6-bisphosphatase (EC 3.1.3.11)	b4232	CHM	0.38
4453359	REC04116	mpI	N	457	66, 216, 287, 407	P37773	UDP-N-acetylmuramate:L-alanyl-gamma-D-glutamyl-meso-diamin	b4233	LPC	0.22
4454539	REC06385	yjgA	N	183	25	P26650	Hypothetical protein yjgA	b4234	UNC	0.19
4455533	REC04118	pmbA	N	450	9, 43, 66, 193, 277, 316	P24231	PmbA protein	b4235	UNC	0.53
4457127	REC04119	cybC	?	100	92	P00192	Soluble cytochrome b562 precursor	b4236	BEN	0.00
4457938	REC06386	nrdC	N	154	10, 10, 71	P39329	Anaerobic ribonucleoside-triphosphate reductase activating protein	b4237	NCM	0.28
4460234	REC06387	nrdD	N	712	50, 134, 273, 498, 532, 608, 656	P28903	Anaerobic ribonucleoside-triphosphate reductase (EC 1.17.4.2)	b4238	NCM	0.31
4462283	REC06388	treC	N	551	32, 74, 400, 527	P28904	Trehalose-6-phosphate hydrolase (EC 3.2.1.93)	b4239	CHM	0.44
4463754	REC06494	treB	N	473	28, 67, 122, 211, 322, 438	P36672	PTS system, trehalose-specific IIBC component (EC 2.7.1.69)	b4240	MTR	0.47
4464820	REC06390	treR	N	315	14, 94, 204	P36673	Trehalose operon repressor	b4241	RCD	0.06
4465199	REC06495	mgTA	N	898	15, 21, 33, 55, 72, 111, 119, 167, 223, 268, 850	P39168	Mg(2+) transport ATPase, P-type 1 (EC 3.6.3.2)	b4242	MTR	0.44
4468526	REC06391	yjgF	E	141	-	P39330	Protein yjgF	b4243	UNC	0.84
4469021	REC06392	pyrI	N	153	76, 78, 104	P00478	Aspartate carbamoyltransferase regulatory chain	b4244	RCD	0.13
4469669	REC06496	pyrB	N	311	105, 150, 206, 263	P00479	Aspartate carbamoyltransferase catalytic chain (EC 2.1.3.2)	b4245	NCM	0.81
4470087	REC04130	yjgG	N	110	75	P76807	HYPOTHETICAL 12.8 kDa PROTEIN IN PYRL-ARGI INTERGENE	b4247	UNC	0.00
4470107	REC06394	pyrL	?	44	-	P09150	PyrBI operon leader peptide	b4246	UNC	0.00
4470783	REC06395	yjgH	N	131	47	P39332	Hypothetical protein yjgH	b4248	UNC	0.19
4471627	REC06497	yjgI	N	237	30	P39333	Hypothetical oxidoreductase yjgI (EC 1.-.-.-)	b4249	UNC	0.13
4471801	REC04133	yjgJ	N	54	8, 37	P76808	FROM BASES 4471356 TO 4483288 (SECTION 386 OF 400) OF	b4250	UNC	0.00
4472037	REC04134	yjgK	E	84	82	P39334	Hypothetical protein yjgJ	b4251	UNC	0.00
4472427	REC04135	yjgK	N	153	13, 73, 98	P39335	Protein yjgK	b4252	UNC	0.16
4472975	REC04136	yjgL	N	616	3, 166, 482	P39336	Hypothetical protein yjgL	b4253	UNC	0.00
4475874	REC06397	argI	X	334	-	P04391	Ornithine carbamoyltransferase chain I (EC 2.1.3.3)	b4254	AAM	0.84
4476036	REC04138	yjgD	X	138	-	P37163	Hypothetical protein yjgD	b4255	UNC	0.06
4476890	REC06398	yjgM	X	97	-	P39337	Hypothetical acetyltransferase yjgM (EC 2.3.1.-)	b4256	UNC	0.06
4477310	REC06500	yjgN	N	393	338, 360, 365	P39338	Hypothetical protein yjgN	b4257	UNC	0.13
4481405	REC06399	valS	E	951	-	P07118	Valyl-tRNA synthetase (EC 6.1.1.9)	b4258	PMS	1.00
4481848	REC06400	hoIC	E	147	-	P28905	DNA polymerase III, chi subunit (EC 2.7.7.7)	b4259	NAM	0.13
4483519	REC06401	pepA	N	503	80, 106, 192, 227, 287, 342, 370, 399, 446, 449, 489, 497	P11648	Cytosol aminopeptidase (EC 3.4.11.1)	b4260	PMS	0.81
4483786	REC04145	yjgP	E	366	-	P39340	Hypothetical protein yjgP	b4261	UNC	0.41
4484883	REC04146	yjgQ	E	361	-	P39341	Hypothetical protein yjgQ	b4262	UNC	0.44
4487631	REC06402	yjgR	N	500	43, 88, 122	P39342	Hypothetical protein yjgR	b4263	UNC	0.25
4488707	REC06403	idnR	N	332	43, 69, 93, 112, 114, 125, 235	P39343	L-Idonate regulatory protein	b4264	RCD	0.06
4490093	REC06404	idnT	N	439	26, 145, 220, 234, 321, 332, 347, 375, 394, 409	P39344	Gnt-II system L-Idonate transporter	b4265	MTR	0.09
4490919	REC06405	idnO	N	254	4, 49, 150	P39345	Gluconate 5-dehydrogenase (EC 1.1.1.69)	b4266	CHM	0.44
4491974	REC06406	idnD	X	343	-	P39346	L-Idonate 5-dehydrogenase (EC 1.1.1.264)	b4267	CHM	0.09
4492191	REC04152	idnK	N	187	32, 63, 125	P39208	Thermosensitive gluconokinase (EC 2.7.1.12)	b4268	CHM	0.31
4493819	REC06407	yjgB	N	353	104, 157, 203, 240, 261, 342	P27250	Hypothetical zinc-type alcohol dehydrogenase-like protein yjgB	b4269	UNC	0.06
4494318	REC04154	intB	N	396	71, 156, 170	P39347	Prophage P4 integrase	b4271	PHT	0.09
4495795	REC00344		N	136	4, 42	P19776	Transposase insC for insertion element IS2A/D/F/H/I/K	b4272	PHT	0.56
4496163	REC06502		N	301	171	P19777	Transposase insD for insertion element IS2A/D/F/H/I/K	b4273	PHT	0.56
4497167	REC04157	yjgW	X	111	15, 110	Q9Z3A0	Hypothetical protein YJGW	b4274	UNC	0.00
4498057	REC06408	yjgX	X	148	-	P39349	Hypothetical protein yjgX precursor	b4276	UNC	0.00
4498449	REC06409	yjgY	X	149	-	P39350	Hypothetical protein yjgY	b4277	UNC	0.00
4498828	REC04160	yjgZ	N	109	1, 109	P39351	Hypothetical protein yjgZ	b4278	UNC	0.00
4500999	REC06410	insG	N	442	241, 369	P03835	Transposase insG for insertion sequence element IS4	b4278	PHT	0.00
4501566	REC04162	yjhB	N	425	1, 285, 308, 388, 409	P39352	Hypothetical metabolite transport protein yjhB	b4279	UNC	0.22
4502840	REC04163	yjhC	N	377	137, 237, 257, 306, 316, 338	P39353	Hypothetical oxidoreductase yjhC (EC 1.-.-.-)	b4280	UNC	0.44
4504568	REC06411	yjhD	N	124	4, 60	P39354	Hypothetical protein yjhD	b4281	UNC	0.00
4504729	REC04166	insN2	N	100	17, 43	P39212	Transposase insN for insertion sequence element IS911B	b4283	PHT	0.56
4506185	REC01364	insI3	N	383	147, 209, 287, 307, 326	P37246	Transposase insI for insertion sequence element IS30B/C/D	b4284	PHT	0.22
4506526	REC04168	insM	N	198	29, 33, 142	Q47718	Transposase insM for insertion sequence element IS600	b4285	PHT	0.56

4507288	REC04169	E	137	-	< 0.2	Q47719	Very hypothetical 15.1 kDa protein in intB-fecE intergenic region	b4286	UNC	0.03
4509025	REC06413	N	255	84		P15031	Iron(III) dicitrate transport ATP-binding protein fecE	b4287	MTR	0.09
4509982	REC06414	N	318	20, 279		P15029	Iron(III) dicitrate transport system permease protein fecD	b4288	MTR	0.13
4510977	REC06415	N	332	44, 117, 234, 309		P15030	Iron(III) dicitrate transport system permease protein fecC	b4289	MTR	0.69
4511882	REC06416	X	302	-		P15028	Iron(III) dicitrate-binding periplasmic protein precursor	b4290	MTR	0.31
4514245	REC06417	N	774	19, 25, 159, 277, 283, 341, 390, 446, 620, 626, 651, 687		P13036	Iron(III) dicitrate transport protein fecA precursor	b4291	MTR	0.16
4515285	REC06418	N	317	174		P23485	Protein fecR	b4292	SMC	0.16
4515803	REC06419	X	173	-		P23484	Probable RNA polymerase sigma factor fecI	b4293	UNC	0.16
4516095	REC04177	X	91	-		P19767	Insertion element IS17 protein insA	b4294	PHT	0.00
4517706	REC06420	X	266	-		P39356	Hypothetical transcriptional regulator yjhU	b4295	UNC	0.25
4519588	REC06508	N	449	13, 64, 118, 156, 168, 184, 231, 263, 292		P39357	Hypothetical permease yjhF	b4296	UNC	0.31
4521662	REC06509	N	437	522, 604, 624		P39358	Hypothetical protein yjhG	b4297	UNC	0.78
4522632	REC06423	N	319	75		P39359	Hypothetical protein yjhH	b4298	UNC	0.84
4523371	REC06424	N	262	19, 53, 89, 99, 122, 175, 202		P39360	Hypothetical transcriptional regulator yjhl	b4299	UNC	0.00
4524456	REC06425	X	260	258		P39361	Putative sgc region transcriptional regulator	b4300	UNC	0.00
4525105	REC06426	X	210	-		P39362	Protein sgcE (EC 5.1.3.-)	b4301	UNC	0.94
4525548	REC06427	E	143	-	< 0.2	P39363	Putative phosphotransferase enzyme II, A component sgcA (EC 2.7.1.69)	b4302	UNC	0.03
4526485	REC06428	N	268	52, 96		P39364	Putative sgc region protein sgcQ	b4303	UNC	0.13
4527811	REC06429	N	437	11, 85, 170, 258, 349, 373, 430		P39365	Putative phosphotransferase enzyme II, C component sgcC	b4304	UNC	0.09
4528104	REC06714	E	93	-	< 0.3	P58035	Putative phosphotransferase enzyme II, B component sgcB (EC 2.7.1.69)	b4305	UNC	0.06
4529249	REC06510	N	383	38, 64, 118		P39366	Putative sgc region protein sgcX	b4306	UNC	0.06
4530751	REC06431	N	248	32, 66, 73, 167, 187		P39367	Hypothetical protein yjhP	b4307	UNC	0.31
4531352	REC06432	N	181	132, 155		P39368	Hypothetical acetyltransferase yjhQ (EC 2.3.1.-)	b4308	UNC	0.34
4532583	REC04191	N	338	22, 49, 83, 97, 188, 207, 321, 335		P39369	Hypothetical protein yjhR	b4309	UNC	0.03
4535162	REC06433	N	326	50, 287		P39370	Hypothetical protein yjhS precursor	b4310	UNC	0.00
4536441	REC06434	N	404	66, 84, 151, 172, 215, 225		P39371	Hypothetical protein yjhT precursor	b4311	UNC	0.13
4537078	REC06435	N	241	21, 26, 108, 134, 208		P39372	Hypothetical protein yjhA precursor	b4312	UNC	0.00
4538525	REC04195	X	200	-		P04742	Type 1 fimbriae regulatory protein fimB	b4312	SMC	0.00
4539605	REC04196	X	198	-		P04741	Type 1 fimbriae regulatory protein fimE	b4313	RCD	0.00
4540683	REC04197	X	182	-		P04128	Type-1 fimbrial protein, A chain precursor	b4314	SMC	0.00
4541188	REC04198	X	215	-		P39264	Fimbrin-like protein fim precursor	b4315	SMC	0.00
4541872	REC04199	X	241	-		P31697	Chaperone protein fimC precursor	b4316	SMC	0.00
4542665	REC04200	N	878	82, 153, 185, 261, 287, 309, 327, 397, 437, 455, 576		P30130	Outer membrane usher protein fimD precursor	b4317	SMC	0.06
4545311	REC04201	X	176	-		P08189	FimF protein precursor	b4318	UNC	0.00
4545854	REC04202	?	167	144		P08190	FimG protein precursor	b4319	UNC	0.00
4546377	REC04203	N	300	8, 11, 79, 91, 98, 127, 147, 190, 221, 259		P08191	FimH protein precursor	b4320	UNC	0.00
4548865	REC06436	N	447	145, 331, 356, 402, 416		P39373	High-affinity gluconate transporter	b4321	MTR	0.31
4549205	REC04205	N	394	243, 260, 275		P24215	Mannonate dehydratase (EC 4.2.1.8)	b4322	CHM	0.25
4550470	REC04206	N	486	26, 51, 124, 294		P39160	D-mannonate oxidoreductase (EC 1.1.1.57)	b4323	CHM	0.09
4552145	REC04207	X	257	-		P39161	Uxu operon transcriptional regulator	b4324	RCD	0.09
4553889	REC06437	X	276	-		P39374	Hypothetical protein yjiC	b4325	UNC	0.00
4554553	REC04209	X	133	-		P39375	Hypothetical protein yjiD	b4326	UNC	0.00
4555858	REC06438	X	303	-		P39376	Hypothetical transcriptional regulator yjiE	b4327	UNC	0.13
4557095	REC06439	N	390	187, 209		P39377	Isoaspartyl dipeptidase (EC 3.4.19.-)	b4328	MSM	0.00
4557569	REC06440	N	153	47, 59, 123, 145		P39378	Hypothetical protein yjiG	b4329	UNC	0.03
4558261	REC06441	N	231	101		P39379	Hypothetical protein yjiH	b4330	UNC	0.03
4558397	REC04214	X	218	-		P39380	RNA 2'-phosphotransferase (EC 2.7.-.-)	b4331	NAM	0.13
4560244	REC06442	N	392	52, 87, 114, 153		P39381	Hypothetical protein yjiJ	b4332	UNC	0.19
4561283	REC06443	N	323	69, 104, 180, 189, 202, 297, 305		P39382	Hypothetical protein yjiK	b4333	UNC	0.03
4562264	REC06444	X	257	-		P39383	Hypothetical protein yjiL	b4334	UNC	0.16
4563440	REC06445	N	390	1, 67, 111		P39384	Hypothetical protein yjiM	b4335	UNC	0.00
4564815	REC06446	N	426	150, 153, 348		P39385	Hypothetical protein yjiN	b4336	UNC	0.16
4566088	REC06447	N	410	226, 296		P39386	Hypothetical transport protein yjiO	b4337	UNC	0.06
4566567	REC04221	N	103	13, 21, 38, 89, 96		P39387	Hypothetical protein yjiP	b4338	UNC	0.00
4566927	REC04222	N	186	4, 31, 72, 138, 166, 170		P39387	Hypothetical protein yjiQ	b4339	UNC	0.00
4569143	REC06448	N	470	438, 469		P39389	Hypothetical protein yjiR	b4340	UNC	0.56
4569320	REC04224	X	54	-		P39390	Hypothetical protein yjiS	b4341	UNC	0.00
4569935	REC04225	N	521	-		P39391	Hypothetical protein yjiT	b4342	UNC	0.00
4571704	REC06527	X	513	-		P39393	Hypothetical protein yjiV	b4343	UNC	0.00
4573163	REC04228	N	420	74, 115, 158, 251, 317, 401		P27301	McrD protein	b4344	RCD	0.00
4575528	REC06449	N	348	6, 76, 335		P15006	Protein mcrC	b4345	UNC	0.09
4576925	REC06450	N	465	16, 30, 80, 99, 332, 345		P15005	5-methylcytosine-specific restriction enzyme B (EC 3.1.21.-)	b4346	NAM	0.16
4577467	REC06451	N	132	8, 15, 130		P39394	Hypothetical protein yjiW	b4347	UNC	0.00
4579032	REC06452	N	464	18, 88, 191, 194, 258, 331, 407, 410		P05719	Type I restriction enzyme EcoKI specificity protein	b4348	NAM	0.47
4580618	REC06453	N	529	34		P08957	Type I restriction enzyme EcoKI M protein (EC 2.1.1.72)	b4349	NAM	0.50
4584385	REC06454	N	1188	2, 18, 84, 85, 242, 588, 836, 912, 1014, 1056, 1175		P08956	Type I restriction enzyme EcoKI R protein (EC 3.1.21.3)	b4350	NAM	0.09
4584519	REC04235	N	304	49, 172, 199		P24202	Mrr restriction system enzyme	b4351	NAM	0.19
4586333	REC06455	N	284	147		P24203	Hypothetical protein yjiA	b4352	UNC	0.34
4586649	REC06456	?	67	-		P39395	Hypothetical protein yjiX	b4353	UNC	0.06
4588864	REC06457	N	721	21, 93, 182, 211, 396, 459, 514, 516, 560, 562, 683		P39396	Hypothetical protein yjiY	b4354	UNC	0.41
4589227	REC06530	X	551	-		P02942	Methyl-accepting chemotaxis protein I	b4355	SMC	0.63
4592292	REC06458	N	453	46, 81, 163, 256, 363, 440		P39398	Hypothetical transport protein yjiL	b4356	UNC	0.38
4593313	REC06460	N	268	201		P39399	Hypothetical protein yjiM	b4357	UNC	0.09
4593544	REC04243	N	345	106, 117, 150, 181, 243		P39400	Hypothetical zinc-type alcohol dehydrogenase-like protein yjiN	b4358	UNC	0.56
4596971	REC06461	X	760	-		P39401	Phosphoglycerol transferase I (EC 2.7.8.20)	b4359	LPC	0.09
4597761	REC06462	N	165	20, 49, 76		P18390	Hypothetical protein yjiA precursor	b4360	UNC	0.00
4598544	REC06463	E	245	-	< 0.05	P07905	DNA replication protein dnaC	b4361	NAM	0.09
4599086	REC06464	E	179	-	< 0.1	P07904	Primosomal protein I	b4362	NAM	0.03
4599519	REC06465	?	108	84		P18389	Protein yjiB	b4363	UNC	0.34
4600490	REC06466	N	277	168		P39402	Hypothetical protein yjiP	b4364	UNC	0.34
4601046	REC04250	N	241	31, 51, 106, 126, 188, 237		P39403	Hypothetical protein yjiQ	b4365	UNC	0.00
4601729	REC04251	N	225	9, 16, 59, 79, 143, 224		P39404	Transcriptional activator protein bglJ	b4366	RCD	0.00
4603232	REC06467	X	262	-		P39405	Ferric iron reductase protein fluF	b4367	MSM	0.03
4603262	REC06716	X	115	-		P55914	Hypothetical protein yjiZ	b4368	UNC	0.00
4605269	REC06468	N	343	9, 28, 107, 167, 223, 237, 276		P39406	Ribosomal RNA small subunit methyltransferase C (EC 2.1.1.52)	b4371	NAM	0.47
4605372	REC04254	?	137	20		P28632	DNA polymerase III, psi subunit (EC 2.			

4614634	REC06470	<i>yjjI</i>	N	516	137, 233, 366	P37342	Hypothetical protein yjil	b4380	UNC	0.03
4614892	REC04263	<i>deoC</i>	N	259	20, 52, 114, 161, 185, 201, 223, 252	P00882	Deoxyribose-phosphate aldolase (EC 4.1.2.4)	b4381	CHM	0.59
4615798	REC04264	<i>deoA</i>	N	440	43, 87, 265, 286, 359, 374	P07650	Thymidine phosphorylase (EC 2.4.2.4)	b4382	NCM	0.44
4617172	REC04265	<i>deoB</i>	N	407	92, 202, 257, 305, 326, 360	P07651	Phosphopentomutase (EC 5.4.2.7)	b4383	CHM	0.41
4618452	REC04266	<i>deoD</i>	N	239	2, 104, 153, 160, 209	P09743	Purine nucleoside phosphorylase (EC 2.4.2.1)	b4384	NCM	0.41
4619338	REC04267	<i>yjjJ</i>	N	443	111, 192, 314	P39410	Hypothetical protein yjjJ	b4385	UNC	0.00
4621686	REC06471	<i>lpIA</i>	E	338	-	P32099	Lipoate-protein ligase A (EC 6.-.-.-)	b4386	NCM	0.31
4622358	REC06472	<i>smP</i>	N	214	24, 64, 74, 170	P18838	Protein smP precursor	b4387	UNC	0.03
4622464	REC04270	<i>serB</i>	N	322	13, 89, 191	P06862	Phosphoserine phosphatase (EC 3.1.3.3)	b4388	AAM	0.53
4623481	REC04271	<i>radA</i>	N	460	7, 185, 215, 446, 453	P24554	DNA repair protein radA	b4389	UNC	0.91
4624863	REC04272	<i>nadR</i>	N	417	87, 114, 236, 371	P27278	Transcriptional regulator nadR	b4390	NCM	0.06
4628091	REC06533	<i>yjjK</i>	N	555	25, 237	P37797	ABC transporter ATP-binding protein yjjK	b4391	MTR	0.63
4628275	REC04274	<i>slt</i>	N	654	41, 78, 128, 191, 283, 427, 499	P03810	Soluble lytic murein transglycosylase precursor (EC 3.2.1.-)	b4392	LPC	0.72
4630329	REC04275	<i>trpR</i>	N	108	29	P03032	Trp operon repressor	b4393	RCD	0.09
4631323	REC06474	<i>yjjX</i>	N	173	93	P39411	Hypothetical protein yjjX	b4394	UNC	0.03
4631366	REC04277	<i>gpmB</i>	N	215	31, 128, 161, 209	P36942	Probable phosphoglycerate mutase 2 (EC 5.4.2.1)	b4395	UNC	0.84
4632879	REC06475	<i>rob</i>	N	289	50, 85, 117, 149	P27292	Right origin-binding protein	b4396	NAM	0.19
4633090	REC04279	<i>creA</i>	N	157	12, 104, 135	P08367	CreA protein	b4397	UNC	0.25
4633576	REC04280	<i>creB</i>	N	229	75	P08368	Transcriptional regulatory protein creB	b4398	SMC	0.59
4634265	REC04281	<i>creC</i>	N	474	70, 208, 412, 444	P08401	Sensor protein creC (EC 2.7.3.-)	b4399	SMC	0.06
4635747	REC04282	<i>creD</i>	N	450	13, 57, 118, 134, 196, 198, 273, 334, 439	P08369	Inner membrane protein creD	b4400	SMC	0.09
4637875	REC06476	<i>arcA</i>	X	238	-	P03026	Aerobic respiration control protein arcA	b4401	SMC	0.81
4637971	REC04284	<i>yjjY</i>	X	46	-	P39412	Hypothetical protein yjjY	b4402	UNC	0.00
4638511	REC04285	<i>lasT</i>	N	228	49, 138, 183, 217	P37005	Hypothetical tRNA/rRNA methyltransferase lasT (EC 2.1.1.-)	b4403	UNC	0.44