

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	functional role	Blatner ID	ERGO	scale: 0 - 1
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		N	370	19, 107, 223, 295, 339		P08409	Putative transposase insL for insertion sequence element IS186A/B/C	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, 295, 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		E	91	-	< 0.2	P03827	Insertion element IS1 1/2/3/5/6 protein insA	b0022	PHT	0.00
21078	REC04295	<i>rpsT</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	316	203	< 0.05	P22565	ispH protein (<i>lytB</i>)	b0029	LPC	0.75
27293	REC00030	<i>yaaF</i>	N	304	96, 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, 328		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, 893		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 activatory 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		P1551	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, 181, 187, 223, 313, 409		P31575	FixC protein	b0043	UNC	0.34
45463	REC00044	<i>fixX</i>	N	95	68		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	64, 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	APA 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, 287, 320		P19624	4-hydroxythreonine-4-phosphate dehydrogenase (EC 1.1.1.262)	b0052	NCM	0.50
54702	REC04306	<i>surA</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	988	40, 73, 107, 225, 253, 301, 335, 429, 443, 483		P23852	RNA polymerase associated protein	b0059	UNC	0.25
65780	REC04310	<i>poIB</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	68, 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 penlplasmic 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/shl operon leader peptide	b0079	UNC	0.00
88028	REC00080	<i>fruR</i>	N	334	63, 104		P21168	Fructose repressor	b0080	RCD	0.16
89634	REC00081	<i>mraZ</i>	N	152	37		P22186	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-alar	b0086	LPC	0.91
96002	REC00087	<i>mraY</i>	N	360	89		P10876	Phospho-N-acetylmuramoyl-pentapeptide-transferase (EC 2.7.8.13)	b0087	LPC	0.97
97087	REC00088	<i>murD</i>	E	438	27, 102	< 0.05	P14900	UDP-N-acetylmuramoylalanine-D-glutamate ligase (EC 6			

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 (EC 3.6.1.-)	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 CC	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	Diphospho-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 2.4.2.19)	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, 286, 278		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	188		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	Dihydropolipoamide acetyltransferase component of pyruvate dehydrogenase complex	b0115	NCM	0.72
127912	REC00116	<i>lpaD</i>	E	474	-	< 0.01	P00391	Dihydropolipoamide 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, 850		P36683	Aconitate hydratase 2 (EC 4.2.1.3)	b0118	CHM	0.38
134340	REC00119	<i>yacL</i>	N	136	87, 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 [pyrroloquinoline-quinone] (EC 1.1.99.17)	b0124	CHM	0.13
141419	REC00125	<i>hpt</i>	N	182	10, 17, 89, 96, 143		P37666	Hypoxanthine phosphoribosyltransferase (EC 2.4.2.8)	b0125	NCM	0.75
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	0.00
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	283	146		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 fimbrial-like protein yadC precursor	b0135	UNC	0.00
151599	REC04343	<i>yadK</i>	N	198	18, 36, 48, 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
155426	REC04346	<i>htrE</i>	N	865	53, 60, 116, 184, 199, 232, 267, 300, 315, 330, 337, 361, 389, 395, 422, 587		P33129	Outer membrane usher protein htrE precursor	b0139	UNC	0.06
156201	REC04347	<i>ecpD</i>	N	246	221		P33128	Chaperone protein ecpD precursor	b0140	UNC	0.06
156883	REC04348	<i>yadN</i>	N	194	171		P37050	Hypothetical fimbrial-like protein yadN precursor	b0141	UNC	0.00
157732	REC04349	<i>foiK</i>	E	159	-	< 0.1	P26281	2-amino-4-hydroxy-6-hydroxymethylidihydropteridine pyrophosphokinase	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	NCM	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	36, 255, 271, 492, 695, 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, 129, 169, 212, 264, 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-tetrahydropyridine-2-carboxylate N-succinyltransferase (EC 2.6.1.16)	b0166	AAM	0.53
188650	REC04363	<i>glnD</i>	E	890	-	< 0.001	P27249	[Protein-Pil] 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>rpsB</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>frx</i>	E	185	-	< 0.2	P16174	Ribosome recycling factor	b0172	PMS	1.00
193521	REC00173	<i>dxx</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>cdaS</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 precursor	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 2.3.1.18)	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-acyltransferase	b0181	LPC	0.59
203348	REC00182	<i>lpxB</i>	E	382	-	n.d.	P10441	Lipid-A-disaccharide synthase (EC 2.4.1.182)	b0182	LPC	0.59
204493	REC00183	<i>rnhB</i>	E	198	188, 193	< 0.01	P10442	Ribonuclease HII (EC 3.1.26.4)	b0183	NAM	0.91
205126	REC00184	<i>dnaE</i>	E	1160	2	< 0.001	P10443	DNA polymerase III alpha subunit (EC 2.7.7.7)	b0184	NAM	1.00
208621	REC00185	<i>accA</i>	E	319	-	< 0.01	P30867	Acetyl-coenzyme A carboxyl transferase subunit alpha (E)	b0185	LPC	0.75
209679	REC00186	<i>ldcC</i>	N	713	67, 95, 121, 127, 159, 181, 219, 233, 337, 392, 402, 489, 680		P52095	Lysine decarboxylase, constitutive (EC 4.1.1.18)	b0186	AAM	

214291	REC00190	yaeQ	N	181	90,172	P52100	Hypothetical protein yaeQ	b0190	UNC	0.06
214833	REC00191	yaeJ	N	140	20,100	P40711	Hypothetical protein yaeJ	b0191	UNC	0.22
215269	REC00192	cutF	N	236	90,124,148,159,190,208	P40710	Copper homeostasis protein cutF precursor	b0192	UNC	0.03
217057	REC04366	yaeF	N	292	60,63,92,136,250,269,275	P37056	Hypothetical lipoprotein yaeF precursor	b0193	UNC	0.00
218775	REC04367	pros	E	572	664	P16659	Prolyl-tRNA synthetase (EC 6.1.1.15)	b0194	PMS	1.00
219594	REC04368	yaeB	?	235	24	P28634	Hypothetical protein yaeB	b0195	UNC	0.22
219995	REC04369	rscF	N	134	12,40,62,97	P28633	Protein rscF	b0196	SMC	0.00
220928	REC04370	yaeC	N	271	176,216,224,255	P28635	Putative lipoprotein yaeC precursor	b0197	UNC	0.69
221621	REC04371	yaeE	N	217	20,119,184,205	P31547	Hypothetical ABC transporter permease protein yaeE	b0198	UNC	0.69
222645	REC04372	abc	N	343	3,17,87,286	P30750	ATP-binding protein abc	b0199	UNC	0.97
222833	REC00200	yaeD	N	191	24,34,104	P31546	Hypothetical protein yaeD	b0200	UNC	0.75
229167	REC00201	dkgB	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	yafC	N	304	53,87,93,109,158,195,206,231,249,283,287	P30864	Hypothetical transcriptional regulator yafC	b0208	UNC	0.72
231122	REC00203	yafD	N	266	15,47,113,261	P30865	Hypothetical protein yafD	b0209	UNC	0.09
231926	REC00204	yafE	E	207	-	P30866	Hypothetical protein yafE	b0210	UNC	0.13
233955	REC04374	mltD	N	452	63,109,180,196,253,326	P23931	Membrane-bound lytic murein transglycosylase D precursor (EC 3.2.1.b0211)	b0211	LPC	0.38
234782	REC04375	gloB	N	251	224	Q47677	Probable hydroxyacylglutathione hydrolase (EC 3.1.2.6)	b0212	UNC	0.81
234798	REC00207	yafS	N	246	41,53,193,198	P75672	Hypothetical protein yafS	b0213	UNC	0.28
236002	REC04376	rnhA	E	155	42,72	P00647	Ribonuclease HI (EC 3.1.26.4)	b0214	NAM	0.56
236067	REC00209	dnaQ	E	243	138,240	P03007	DNA polymerase III, epsilon chain (EC 2.7.7.7)	b0215	NAM	0.75
237335	REC00210	yafT	N	261	5,47,102,248	P77339	Hypothetical lipoprotein yafT precursor	b0217	UNC	0.00
239084	REC04377	yafU	N	112	45	P77354	Hypothetical protein yafU	b0218	UNC	0.00
239154	REC06766	yhhI	N	74	66	Q47678	H repeat-associated protein in rnsB-pit intergenic region (orf-h), YhhI protein	b0219	UNC	0.00
240189	REC04378	yafV	N	256	25,87,93,126,146,175,191,203,226,246	Q47679	Hypothetical protein yafV	b0219	UNC	0.75
240343	REC00213	ivy	N	157	31,98,143	P45502	Inhibitor of vertebrate lysozyme precursor	b0220	MSM	0.00
243339	REC04379	yafH	N	826	18,42,118,403,431,528,563,647	Q47146	Hypothetical protein yafH	b0221	UNC	0.25
243543	REC00215	lpcA	N	192	25,49,161	P51001	Phosphoheptose isomerase (EC 5.-.-.-)	b0222	CHM	0.38
244327	REC00216	yafJ	N	255	69,102	Q47147	Hypothetical protein yafJ	b0223	UNC	0.25
245805	REC04380	yafK	N	246	21,52,175,229	Q47148	Hypothetical protein yafK precursor	b0224	UNC	0.13
246239	REC04381	yafQ	?	92	1	Q47149	Hypothetical protein yafQ	b0225	UNC	0.19
246502	REC04382	dinJ	N	86	30,31	Q47150	DNA-damage-inducible protein J	b0226	UNC	0.06
246712	REC00220	yafL	N	249	6,30,53,106,115,165,184,203	Q47151	Hypothetical lipoprotein yafL precursor	b0227	UNC	0.09
247637	REC00221	yafM	N	165	61,69,136	Q47152	Hypothetical protein yafM	b0228	UNC	0.16
250042	REC00223	mbhA	N	261	105,138,150,202,204	Q47154	MbhA protein	b0229	UNC	0.22
250097	REC04383	fhiA	N	579	330,439	Q47153	FhiA protein	b0229	UNC	0.13
250898	REC00224	dinP	N	351	45,78,236	Q47155	DNA-damage-inducible protein P	b0231	UNC	0.59
252005	REC00225	yafN	N	97	30,31	Q47156	Hypothetical protein yafN	b0232	UNC	0.00
252301	REC00226	yafO	N	132	52,53	Q47157	Hypothetical protein yafO	b0233	UNC	0.00
252709	REC00227	yafP	N	150	13,122,127,141	Q47158	Hypothetical acetyltransferase yafP (EC 2.3.1.-)	b0234	UNC	0.25
253467	REC00228	ykfJ	N	88	27,46	P75675	Hypothetical protein ykfJ	b0235	UNC	0.31
253702	REC00229	prfH	N	166	31,74,150	P28369	Peptide chain release factor homolog	b0236	UNC	0.09
255716	REC04384	pepD	N	485	36,59,269,277,361,442,452	P15288	Aminoacyl-histidine dipeptidase (EC 3.4.13.3)	b0237	PMS	0.16
255977	REC00231	gpt	?	152	122	P00501	Xanthine-guanine phosphoribosyltransferase (EC 2.4.2.22)	b0238	NCM	0.22
256527	REC00232	yafA	N	414	18,79,118,215,250,296,363,372	P04335	Hypothetical protein yafA	b0239	UNC	0.03
257829	REC00233	crI	N	133	12,88	P24251	Curlin genes transcriptional activatory protein	b0240	RCD	0.03
259324	REC04385	phoE	N	351	37,38,114,202,207,294	P02932	Outer membrane pore protein E precursor	b0241	SMC	0.00
259612	REC00235	proB	N	367	253,320	P07005	Glutamate 5-kinase (EC 2.7.2.11)	b0242	AAM	0.75
260727	REC00236	proA	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	ykfI	E	113	-	P77692	Hypothetical protein ykfI	b0245	UNC	0.00
263231	REC04387	yafW	N	105	86	Q47684	Hypothetical protein yafW	b0246	UNC	0.00
263956	REC06618	ykfG	N	158	17,52,64,86,99,101,122	Q47685	Putative radC-like protein ykfG	b0247	UNC	0.00
264430	REC04388	yafX	N	152	24,59,152	P75676	Hypothetical protein yafX	b0248	UNC	0.03
264767	REC04389	ykfF	N	79	34	P75677	Hypothetical protein ykfF	b0249	UNC	0.00
265311	REC04390	ykfB	N	155	54,145	P77162	Hypothetical protein ykfB precursor	b0250	UNC	0.00
266191	REC04391	yafY	N	285	16	P77365	Hypothetical transcriptional regulator yafY	b0251	UNC	0.03
267244	REC04392	yafZ	N	278	1,57,65,69,84,236	P77206	Hypothetical protein yafZ	b0252	UNC	0.03
268187	REC04393	ykfA	N	288	6,10,44,75,87,135,178	P75678	Hypothetical protein ykfA	b0253	UNC	0.00
269406	REC04394	perR	N	297	63,107,162,249	Q57083	Peroxide resistance protein perR	b0254	RCD	0.06
269466	REC00246	insN1	N	134	16,53	P75679	Transposase insN for insertion sequence element IS911A	b0255	PHT	0.56
269827	REC00247	insI1	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 THE C	b0257	UNC	0.56
272086	REC00249	ykfC	N	376	45,61,133,138	Q47688	Hypothetical protein ykfC	b0258	UNC	0.19
274341	REC06619		N	338	11,32,76,116,141,187	P03837	Transposase insH for insertion sequence element ISS	b0259	PHT	0.34
274525	REC00251	mmuP	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	mmuM	N	310	65,80	Q47690	Homocysteine S-methyltransferase (EC 2.1.1.10)	b0261	AAM	0.16
278038	REC04396	afuC	N	352	136,175,176,223,319	P37009	Putative ferric transport ATP-binding protein afuC	b0262	UNC	0.16
278400	REC04397	afuB	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	-	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	b0265	UNC	0.56
279986	REC04400	yagB	N	125	35,69,95	P37008	Hypothetical protein yagB	b0266	UNC	0.00
281207	REC04401	yagA	N	384	4,33,79,110,150,348	P37007	Hypothetical protein yagA	b0267	UNC	0.56
281481	REC00259	yagE	N	309	148,168,235	P75682	Hypothetical protein yagE	b0268	UNC	0.84
282425	REC00260	yagF	N	655	2,90,177,199,559,598,620,635	P77596	Hypothetical protein yagF	b0269	UNC	0.78
284619	REC00261	yagG	E	460	5	P75683	Hypothetical symporter yagG	b0270	UNC	0.00
286013	REC00262	yagH	E	536	223,532	P77713	Putative beta-xylosidase (EC 3.2.1.37)	b0271	UNC	0.13
288386	REC04402	yagI	N	252	19,77,196,208,227	P77300	Hypothetical transcriptional regulator yagI	b0272	UNC	0.38
289529	REC04403	argP	N	334	3,187,258	P06960	Ornithine carbamoyltransferase chain F (EC 2.1.3.3)	b0273	AAM	0.84
290376	REC06620	insB3	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	yagJ	N	243	140,168,233,235	P77169	Hypothetical protein yagJ	b0276	UNC	0.00
292172	REC04406	yagK	N	208	50,74,113,140,156	P77657	Hypothetical protein yagK	b0277	UNC	0.03
293142	REC04407	yagL	N	232	41,85,134,224	P77607	Hypothetical protein yagL	b0278	UNC	0.00
294023	REC06622	yagM	N	284	18,191	P71296	Hypothetical protein yagM	b0279	UNC	0.00
294803	REC06623	yagN	N	146	24,106,115	P71297	Hypothetical protein yagN	b0280	UNC	0.00
296320	REC06624	intP	N	466	91,151,226,308,387	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 1.1.b0285)	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	2,23,46,103,114,139,174,185	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	2,46,82,125,189,304,325,368,426	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	eaeH	N	295	35, 68, 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/IB	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 THE C	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, 183, 223	P77212	Probable pyridine nucleotide-disulfide oxidoreductase ykgC	b0304	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, 276	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	O65941	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	P77344	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	0.03
365529	REC04435	lacZ	N	1024	10, 162, 214, 237, 295, 315, 396, 420, 461, 863, 886, 1014, 1020	P00722	Beta-galactosidase (EC 3.2.1.23)	b0344	CHM	0.09
366734	REC04436	lacI	N	360	132, 138	P03023	Lactose operon repressor	b0345	RCD	0.00
367758	REC04437	mhpR	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-dihydroxyphenylpropanoate 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	mhpE	N	316	40, 123, 139, 177, 226, 244	P77580	Acetaldehyde dehydrogenase (EC 1.2.1.10)	b0351	CHM	0.06
373092	REC00336	mhpF	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 THE C	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 THE C	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 1.14.11.17)	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 THE C	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	N	288	43	P05822	Transposase insF for insertion sequence IS3A/B/C/D/E/FA	b2089	PHT	0.56
392134	REC06644	insE5	E	102	-	P77681	Transposase insE for insertion sequence IS3A/B/C/D/E/FA/IB	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, 128, 171, 175, 246, 320, 390	P24212	SbmA protein	b0377	UNC	0.16
397096	REC00362	yaiW	N	364	20, 329	P77562	Hypothetical protein yaiW	b0378	UNC	0.03
398557	REC04451	yaiY	E	102	72	P77669	Hypothetical protein yaiY	b0379	UNC	0.00
398685	REC00364	yaiZ	N	114	45	P77723	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	82	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, 131, 176	P21830	Hypothetical protein yaiC	b0385	UNC	0.13
404868	REC00371	yaiI	N	192	101	P52088	Hypothetical protein yaiI	b0387	UNC	0.38
404868	REC04453	proc	E	269	77	P00373	Pyroline-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	<i>aroM</i>	N	225	12, 136	P08403	AroM protein	b0390	UNC	0.00	
407401	REC00375	<i>yaiE</i>	N	94	44	P36768	Hypothetical protein yaiE	b0391	UNC	0.09	
407893	REC00376	<i>ykiA</i>	N	93	37, 69	P75704	Hypothetical protein ykiA	b0392	UNC	0.00	
409230	REC00378	<i>yajF</i>	N	348	2, 49, 71, 89, 113	P23917	Hypothetical protein yajF	b0394	UNC	0.19	
409243	REC04454	<i>rdgC</i>	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 THE C	b0395	UNC	0.00	
411705	REC04455	<i>araJ</i>	N	394	199, 215, 324, 366	P23910	Protein araJ precursor	b0396	UNC	0.00	
414977	REC04456	<i>sbpC</i>	N	1048	204, 278, 289, 376, 442, 487, 518, 522, 579, 758, 808, 878	P13458	Exonuclease sbpC	b0397	NAM	0.31	
416176	REC04457	<i>sbpD</i>	N	400	74, 85, 124, 327	P13457	Nuclease sbpC subunit D	b0398	NAM	0.41	
416366	REC00383	<i>phoB</i>	N	229	5, 44, 81, 115, 134, 178, 217	P08402	Phosphate regulon transcriptional regulatory protein phoB	b0399	RCD	0.75	
417113	REC00384	<i>phoR</i>	N	431	63, 117, 275, 292	P08400	Phosphate regulon sensor protein phoR (EC 2.7.3.-)	b0400	MSM	0.69	
418815	REC00385	<i>brnQ</i>	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	<i>proY</i>	N	457	41, 152, 158, 227, 295, 345, 413	P77327	Proline-specific permease proY	b0402	MTR	0.09	
421739	REC00387	<i>malZ</i>	N	605	86, 248, 304, 323, 347, 351, 460, 477, 507, 542, 594	P21517	Maltodextrin glucosidase (EC 3.2.1.20)	b0403	CHM	0.28	
424142	REC04458	<i>yajB</i>	N	193	8, 54, 156	P21515	Hypothetical protein yajB	b0404	UNC	0.06	
424235	REC00389	<i>queA</i>	N	356	256	P21516	S-adenosylmethionine:trRNA ribosyltransferase-isomerase (EC 5.--.-)	b0405	NAM	0.84	
425361	REC00390	<i>tgt</i>	N	375	218, 300, 332	P19675	Queuine tRNA-ribosyltransferase (EC 2.4.2.29)	b0406	NAM	0.91	
426511	REC00391	<i>yajC</i>	?	110	-	P19677	Hypothetical protein yajC	b0407	UNC	0.78	
426871	REC00392	<i>secD</i>	E	615	-	< 0.0001	P19673	Protein-export membrane protein secD	b0408	PMS	0.88
428729	REC00393	<i>secF</i>	E	323	-	< 0.05	P19674	Protein-export membrane protein secF	b0409	PMS	0.75
429829	REC00394	<i>yajD</i>	N	115	35, 101	P19678	Hypothetical protein yajD	b0410	UNC	0.00	
431237	REC04459	<i>tsx</i>	N	294	18, 69, 163, 224, 243, 269, 288	P22786	Nucleoside-specific channel-forming protein tsx precursor	b0411	MTR	0.03	
432135	REC04460	<i>yajI</i>	N	199	44, 55	P46122	Hypothetical lipoprotein yajI precursor	b0412	UNC	0.00	
432226	REC00397	<i>ybaD</i>	?	149	19	P25538	Hypothetical protein ybaD	b0413	UNC	0.72	
432679	REC00398	<i>ribD</i>	E	367	-	< 0.001	P25539	Riboflavin biosynthesis protein ribD	b0414	NCM	0.84
433871	REC00399	<i>ribH</i>	E	156	-	< 0.1	P25540	6,7-dimethyl-8-ribityllumazine synthase (EC 2.5.1.9)	b0415	NCM	0.84
434361	REC00400	<i>nusB</i>	E	139	-	< 0.1	P04381	N utilization substance protein B	b0416	RCD	0.88
434858	REC00401	<i>thiL</i>	E	325	-	< 0.01	P77785	Thiamine-monophosphate kinase (EC 2.7.4.16)	b0417	NCM	0.47
435813	REC00402	<i>pypA</i>	E	172	-	< 0.2	P18200	Phosphatidylglycerophosphatase A (EC 3.1.3.27)	b0418	LPC	0.31
437431	REC04461	<i>yajO</i>	N	348	170, 175, 237, 280, 299, 303	P77735	Hypothetical oxidoreductase yajO (EC 1.--.-)	b0419	UNC	0.41	
439401	REC04462	<i>dxs</i>	E	620	-	< 0.0001	P77488	1-deoxy-D-xylulose 5-phosphate synthase (EC 4.1.3.37)	b0420	NCM	0.88
440325	REC04463	<i>ispA</i>	E	299	-	< 0.05	P22939	Geranyltransferase (EC 2.5.1.10)	b0421	LPC	0.84
440567	REC04464	<i>xseB</i>	?	80	-	P22938	Exodeoxyribonuclease VII small subunit (EC 3.1.11.6)	b0422	NAM	0.16	
440773	REC00407	<i>thiI</i>	N	482	245, 325	P77718	Thiamine biosynthesis protein thiI	b0423	NCM	0.34	
442871	REC04465	<i>thiJ</i>	N	198	133	Q46948	4-methyl-5-(B-hydroxyethyl)-thiazole monophosphate biosynthesis enz	b0424	NCM	0.22	
443739	REC04466	<i>panE</i>	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	<i>yajQ</i>	N	169	30	P77482	Protein yajQ	b0426	UNC	0.25	
445896	REC04467	<i>yajR</i>	N	456	78, 129, 407	P77726	Hypothetical transport protein yajR	b0427	UNC	0.66	
446929	REC04468	<i>cyoE</i>	N	296	6, 96, 193, 276	P18404	Protoheme IX farnesyltransferase (EC 2.5.1.-)	b0428	NCM	0.59	
447270	REC04469	<i>cyoD</i>	E	109	-	< 0.3	P18403	Cytochrome O ubiquinol oxidase protein cyoD	b0429	BEN	0.28
447884	REC00470	<i>cyoC</i>	N	204	128	P18402	Cytochrome O ubiquinol oxidase subunit III (EC 1.10.3.-)	b0430	BEN	0.56	
449865	REC04471	<i>cyoB</i>	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	<i>cyoA</i>	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	<i>ampG</i>	N	491	136, 154, 266, 333, 335, 363, 442, 485	P36670	AmpG protein	b0433	UNC	0.31	
453493	REC04474	<i>yajG</i>	N	226	197	P36671	Hypothetical lipoprotein yajG precursor	b0434	UNC	0.03	
453663	REC00419	<i>bolA</i>	N	116	16, 92, 97	P15298	BolA protein	b0435	UNC	0.31	
454357	REC00420	<i>tig</i>	N	432	98, 145, 206, 276, 387	P22257	Trigger factor	b0436	UNC	0.97	
455901	REC00421	<i>clpP</i>	N	207	22, 91, 132	P19245	ATP-dependent Clp protease proteolytic subunit (EC 3.4.21.92)	b0437	PMS	0.97	
456650	REC00422	<i>clpX</i>	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	<i>lon</i>	N	784	276, 362, 363, 438, 484, 587	P08177	ATP-dependent protease La (EC 3.4.21.53)	b0439	PMS	0.78	
460675	REC00424	<i>hupB</i>	N	90	40, 42, 80	P02341	DNA-binding protein HU-beta	b0440	RCD	0.81	
461139	REC00425	<i>ppiD</i>	N	623	4, 168, 374, 495	P77241	Peptidyl-prolyl cis-trans isomerase D (EC 5.2.1.8)	b0441	PMS	0.56	
463161	REC00426	<i>ybaV</i>	E	123	-	< 0.2	P77415	Hypothetical protein ybaV precursor	b0442	UNC	0.13
463626	REC00427	<i>ybaW</i>	N	132	44, 91, 107	P77712	Hypothetical protein ybaW	b0443	UNC	0.03	
464771	REC04475	<i>ybaX</i>	N	231	2, 84, 197, 203	P77756	Hypothetical protein ybaX	b0444	UNC	0.63	
466536	REC04476	<i>ybaE</i>	N	566	51, 52, 185, 208, 397	P46890	Hypothetical protein ybaE	b0445	UNC	0.00	
466624	REC00430	<i>cof</i>	N	276	63	P46891	Cof protein	b0446	UNC	0.19	
467520	REC00431	<i>ybaO</i>	N	181	53	P54986	Hypothetical transcriptional regulator ybaO	b0447	UNC	0.44	
468095	REC00432	<i>mdlA</i>	N	590	9, 50, 129, 310, 340, 387	P77265	Multidrug resistance-like ATP-binding protein mdlA	b0448	MTR	0.91	
469860	REC00433	<i>mdlB</i>	N	593	76, 83, 298, 424, 487, 508	P75706	Multidrug resistance-like ATP-binding protein mdlB	b0449	MTR	0.91	
471822	REC00434	<i>glnK</i>	N	112	53, 59	P38504	Nitrogen regulatory protein P-II 2	b0450	SMC	0.66	
472190	REC00435	<i>amtB</i>	N	428	75, 160, 165, 253, 287	P37905	Probable ammonium transporter	b0451	UNC	0.66	
474385	REC04477	<i>tesB</i>	N	286	13, 15, 90, 155, 225	P23911	Acyl-CoA thioesterase II (EC 3.1.2.-)	b0452	LPC	0.34	
474603	REC00437	<i>ybaY</i>	N	190	14, 54	P77717	Hypothetical protein ybaY precursor	b0453	UNC	0.22	
475595	REC04478	<i>ybaZ</i>	N	129	103	P75707	Hypothetical protein ybaZ	b0454	UNC	0.16	
475896	REC00439	<i>ybaA</i>	E	117	-	< 0.2	P09161	Hypothetical protein ybaA	b0456	UNC	0.06
477847	REC04479	<i>ylaB</i>	N	518	18, 52, 71, 96, 321, 325, 448, 482	P77473	Hypothetical protein ylaB	b0457	UNC	0.31	
478514	REC04480	<i>ylaC</i>	N	169	7, 85, 98, 157	P77523	Hypothetical protein ylaC	b0458	UNC	0.00	
479142	REC04481	<i>maa</i>	N	183	3, 42, 50, 73, 94, 108, 182	P77791	Maltose O-acetyltransferase (EC 2.3.1.79)	b0459	CHM	0.25	
479532	REC04482	<i>hha</i>	N	72	10, 50	P23870	Haemolysin expression modulating protein	b0460	RCD	0.00	
479932	REC04483	<i>ybaJ</i>	N	124	3, 4, 73, 74	P37611	Hypothetical protein ybaJ	b0461	UNC	0.00	
483627	REC04484	<i>acrB</i>	N	1049	1, 71, 187, 198, 331, 444, 501, 515, 572, 582, 658, 678, 723, 770, 850, 903	P31224	Acriflavine resistance protein B	b0462	PMS	0.75	
484843	REC04485	<i>acrA</i>	N	397	20, 87, 107, 188, 204, 343	P31223	Acriflavine resistance protein A precursor	b0463	PMS	0.47	
484985	REC00447	<i>acrR</i>	N	215	43, 157, 173	P34000	Potential acrAB operon repressor	b0464	UNC	0.31	
485760	REC00448	<i>kefA</i>	N	1120	214, 412, 661, 739, 750, 789, 793, 918, 990, 1052	P77338	Potassium efflux system kefA	b0465	UNC	0.88	
489495	REC04486	<i>ybaM</i>	?	53	-	P45807	Hypothetical protein ybaM	b0466	UNC	0.00	
490036	REC04487	<i>prcC</i>	E	175	-	< 0.1	P23862	Primosomal replication protein N'	b0467	NAM	0.03
490106	REC00451	<i>ybaN</i>	E	125	121	< 0.2	P45808	Hypothetical protein ybaN	b0468	UNC	0.19
490636	REC00452	<i>apt</i>	E	183	-	< 0.1	P07672	Adenine phosphoribosyltransferase (EC 2.4.2.7)	b0469	NCM	0.78
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>adk</i>	E	214	-	< 0.05	P50582	Adenylylate kinase (EC 2.7.4.3)	b0474	MSM	1.00
497279	REC00458	<i>hemH</i>	E	320	-	< 0.01	P23871	Ferrocatalase (EC 4.99.1.1)	b0475	NCM	0.78
499197	REC04488	<i>aes</i>	N	319	107, 118, 163, 215, 244, 273	P23872	Acetyl estrase (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	REC00449	<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	68, 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	REC00491	<i>ybaK</i>	N	159	97	P37175	Protein ybaK	b0481	UNC	0.47	
507304	REC00492	<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	REC04494	<i>ybbJ</i>	N	151	26, 82, 97, 138	P75709	Hypothetical protein ybbJ	b0488	UNC	0.28
514997	REC04495	<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	REC04496	<i>ybbN</i>	N	296	56, 207	P77395	Hypothetical protein ybbN	b0492	UNC	0.97
518373	REC04497	<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	REC04498	<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, 481, 629, 787	P77504	Hypothetical protein ybbP	b0496	UNC	0.25
522485	REC00480	<i>rhsD</i>	N	1426	17, 26, 79, 203, 286, 331, 511, 516, 819, 1035, 1089, 1166, 1202, 1227, 125	P16919	RhsD protein precursor	b0497	UNC	0.03
526805	REC00481	<i>ybbc</i>	E	122	-	P33668	Hypothetical protein ybbc precursor	b0498	UNC	0.00
527173	REC00482		N	236	52, 119, 186	P77759	FROM BASES 522240 TO 533123 (SECTION 46 OF 400) OF THE C	b0499	UNC	0.00
527864	REC00483	<i>ybbD</i>	?	86	12	P33669	Hypothetical protein ybbD	b0500	UNC	0.00
528163	REC00484		N	63	24	P75710	FROM BASES 522240 TO 533123 (SECTION 46 OF 400) OF THE C	b0501	UNC	0.00
529276	REC04499		N	135	64, 94, 124	P77688	FROM BASES 522240 TO 533123 (SECTION 46 OF 400) OF THE C	b0502	UNC	0.00
530450	REC04500	<i>ybbB</i>	N	364	20, 51, 261, 290, 352	P33667	Hypothetical protein ybbB	b0503	UNC	0.06
531445	REC04501	<i>ybbS</i>	N	308	175	P77702	Hypothetical transcriptional regulator ybbS	b0504	UNC	0.03
531675	REC00488	<i>a11A</i>	E	160	-	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>gcI</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	Hydroxyppyruvate isomerase (EC 5.3.1.22)	b0508	CHM	0.25
535810	REC00492	<i>g1xR</i>	N	292	5, 5, 28, 40, 45, 55, 74, 130, 229, 270	P77161	2-hydroxy-3-oxopropionate reductase (EC 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, 188, 266, 340, 372, 406	P77328	Putative purine permease ybbY	b0513	UNC	0.03
541112	REC00497	<i>g1xK</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, 288, 324, 365, 394	P77425	Allantoate amidohydrolase (EC 3.5.3.-)	b0516	NCM	0.31
545557	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	P77518	Hypothetical protein y1bF	b0520	UNC	0.00
549662	REC00504	<i>arcC</i>	E	297	-	P37306	Carbamate kinase (EC 2.7.2.2)	b0521	MSM	0.25
551817	REC04505	<i>purK</i>	N	355	9, 84, 271, 311	P09029	Phosphoribosylaminimidazole carboxylase ATPase subunit (EC 4.1.	b0522	NCM	0.78
552323	REC04506	<i>purE</i>	N	169	77	P09028	Phosphoribosylaminimidazole carboxylase catalytic subunit (EC 4.1.	b0523	NCM	0.78
553163	REC04507	<i>ipxH</i>	E	240	19	P43341	UDP-2,3-diacylglucosamine hydrolase (EC 3.6.1.-)	b0524	CHM	0.31
553660	REC04508	<i>ppiB</i>	E	164	-	P23869	Peptidyl-prolyl cis-trans isomerase B (EC 5.2.1.8)	b0525	PMS	0.84
553834	REC00509	<i>cysS</i>	E	461	-	P21888	Cysteineyl-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 fibrial 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, 8	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	0.00
565195	REC00520		X	186	25	P77528	FROM BASES 555801 TO 565933 (SECTION 49 OF 400) OF THE C	b0538	UNC	0.03
565201	REC04513	<i>intD</i>	N	387	52, 246, 283, 288, 345, 378	P24218	Prophage DLP12 integrase	b0537	PHT	0.03
565584	REC04514		X	87	-	P75717	EXONUCLEASE (EC 3.1.11.3)	b0539	NAM	0.00
566056	REC00282	<i>insE3</i>	E	102	-	P77681	Transposase insE for insertion sequence IS3A/B/C/D/E/A/B	b0540	PHT	0.56
566361	REC00283	<i>insF3</i>	N	288	55, 65, 114, 148, 167, 173, 189, 235, 241, 271	P05822	Transposase insF for insertion sequence IS3A/B/C/D/E/A	b0541	PHT	0.56
567333	REC00524		?	45	-	P75718	FROM BASES 565876 TO 576392 (SECTION 50 OF 400) OF THE C	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	265	4, 98, 174, 213, 220	P77634	Hypothetical transcriptional regulator ybcM	b0546	UNC	0.09
571689	REC00529	<i>ybcN</i>	E	151	-	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	-	Q47271	Hypothetical protein ybcO in lambdaoid DLP12 prophage region	b0549	UNC	0.00
572594	REC00532	<i>rusA</i>	E	120	25	P40116	Crossover junction endodeoxyribonuclease 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		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	Probably lysozyme from lambdaoid prophage DLP12 (EC 3.2.1.17)	b0555	UNC	0.09
577330	REC00538	<i>rxdD</i>	N	153	6, 78, 109, 137	P75719	Putative Rz endopeptidase from lambdaoid prophage DLP12 (EC 3.4.-	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	-	P77598	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 ylcE	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 envY	b0566	RCD	0.00
587204	REC04522	<i>ybcH</i>								

609311	REC04532	<i>entD</i>	N	209	7, 103, 175	P19925	Enterobactin synthetase component D	b0583	UNC	0.22
611717	REC04533	<i>fepA</i>	N	746	145, 277, 306, 324, 351, 357, 365, 385, 519, 563, 695	P05825	Ferrienterobactin receptor precursor	b0584	MTR	0.06
612038	REC00566	<i>fes</i>	N	374	12, 36, 126, 338	P13039	Enterochelin esterase	b0585	NCM	0.03
613156	REC06664	<i>ybdZ</i>	?	75	39	P18393	Hypothetical protein ybdZ	b0586	UNC	0.09
613380	REC00567	<i>entF</i>	N	1293	100, 103, 136, 195, 248, 268, 324, 349, 633, 636, 744, 756, 880, 897, 1277	P11454	Enterobactin synthetase component F	b0586	RCD	0.16
617477	REC00568	<i>fepE</i>	N	377	1, 89, 170, 198, 213, 283, 284, 350, 369	P26266	Ferric enterobactin transport protein fepE	b0587	MTR	0.00
619422	REC04534	<i>fepC</i>	N	271	74, 172, 230	P23878	Ferric enterobactin transport ATP-binding protein fepC	b0588	MTR	0.81
620411	REC04535	<i>fepG</i>	X	330	237	P23877	Ferric enterobactin transport system permease protein fepG	b0589	MTR	0.69
621412	REC04536	<i>fepD</i>	N	334	91, 114, 177, 255	P23876	Ferric enterobactin transport system permease protein fepD	b0590	MTR	0.69
621523	REC00572	<i>ybdA</i>	X	416	-	P24077	Hypothetical membrane protein P43	b0591	UNC	0.09
623733	REC04537	<i>fepB</i>	E	318	-	< 0.01	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 entC (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 ybdB	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 ybdD	b0599	UNC	0.03
632700	REC04538	<i>ybdH</i>	N	362	10, 183	P45579	Hypothetical oxidoreductase ybdH (EC 1.1.-.-)	b0599	UNC	0.22
632809	REC00581	<i>ybdL</i>	N	386	175	P77806	Hypothetical aminotransferase ybdL (EC 2.6.1.-)	b0600	UNC	0.84
634599	REC04539	<i>ybdM</i>	N	209	29, 47, 84	P77174	Hypothetical protein ybdM	b0601	UNC	0.09
635792	REC04540	<i>ybdN</i>	N	406	52, 109, 206, 254, 339	P77216	Hypothetical protein ybdN	b0602	UNC	0.09
636841	REC04541	<i>ybdO</i>	N	300	7, 65, 150	P77746	Hypothetical transcriptional regulator ybdO	b0603	UNC	0.72
637856	REC04542	<i>dsbG</i>	N	268	15, 47, 53, 68, 79, 106, 147, 184	P77202	Thiol:disulfide interchange protein dsbG 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 ybdR	b0608	UNC	0.59
642630	REC00590	<i>?</i>	?	153	14, 153	P75725	FROM BASES 635836 TO 651340 (SECTION 56 OF 400) OF THE C	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>citT</i>	N	487	6, 167, 326, 349, 382, 399, 413, 433, 458, 461	P77405	Citrate carrier	b0612	MTR	0.09
646732	REC04547	<i>citG</i>	N	292	50, 251, 257	P77231	2-(5'-triphosphoribosyl)-3'-dephosphocoenzyme-A synthase (EC 4.2.-)	b0613	NCM	0.13
647258	REC04548	<i>citX</i>	N	183	108, 128	P77563	Apo-citrate lyase phosphoribosyl-dephospho-CoA transferase (EC 2.-)	b0614	CHM	0.06
648794	REC04549	<i>citF</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>citE</i>	N	307	26, 128, 212	P77170	Citrate lyase beta chain (EC 4.1.3.6) (EC 4.1.3.34)	b0616	CHM	0.38
650006	REC04551	<i>citD</i>	N	98	35	P77618	Citrate lyase acyl carrier protein	b0617	MTR	0.09
651166	REC04552	<i>citC</i>	N	381	13, 60, 93, 218, 267	P77390	[Citrate [pro-3S]-lyase] ligase (EC 6.2.1.22)	b0618	CHM	0.09
651458	REC00600	<i>dpiB</i>	N	552	19, 23, 83, 82, 137, 266, 298, 389, 505, 517	P77510	Sensor kinase dpiB (EC 2.7.3.-)	b0619	SMC	0.16
653085	REC00601	<i>dpiA</i>	N	226	147	Q54149	Transcriptional regulatory protein dpiA	b0620	SMC	0.09
655191	REC04553	<i>douc</i>	N	461	207, 209, 232, 312, 379	Q47134	Anaerobic C4-dicarboxylate transporter doucC	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 cspE	b0623	UNC	0.72
657161	REC04554	<i>crcB</i>	E	127	-	P37002	Protein crcB	b0624	UNC	0.16
657254	REC00606	<i>ybeM</i>	?	75	-	< 0.2	HYPOTHETICAL PROTEIN YBEM	b0625	UNC	0.00
657478	REC00607	<i>ybeH</i>	N	187	107, 109, 123	P39874	Hypothetical protein ybeH	b0626	UNC	0.75
658170	REC00608	<i>tatE</i>	?	67	-	P25895	Sec-independent protein translocase protein tatE	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 ybeF	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 ybeD	b0631	UNC	0.19
663186	REC04559	<i>dacA</i>	N	403	70, 78, 151, 175, 193, 269, 353, 394	P04287	Penicillin-binding protein 5 precursor (EC 3.4.16.4)	b0632	LPC	0.72
664413	REC04560	<i>rIpA</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 rodA	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	-	< 0.001	Hypothetical protein ybeA	b0636	UNC	0.66
668151	REC04564	<i>ybeB</i>	N	69	31	P05848	Hypothetical protein ybeB	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	-	< 0.01	DNA polymerase III, delta subunit (EC 2.7.7.7)	b0640	NAM	0.53
671409	REC04568	<i>rIpB</i>	E	193	186	< 0.1	Rare lipoprotein B precursor	b0641	UNC	0.19
674006	REC04569	<i>leuS</i>	E	860	732	< 0.001	Leucyl-tRNA synthetase (EC 6.1.1.4)	b0642	PMS	1.00
674241	REC00624	<i>ybeL</i>	?	160	129, 158	P46129	Hypothetical protein ybeL	b0643	UNC	0.03
675776	REC04570	<i>ybeQ</i>	N	327	30, 36, 74, 90, 93, 295	P77234	Hypothetical protein ybeQ	b0644	UNC	0.34
675934	REC00626	<i>ybeR</i>	N	235	63, 101, 120, 133, 157, 196, 234	P77627	Hypothetical protein ybeR	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 ybeS	b0646	UNC	0.00
678629	REC04571	<i>ybeT</i>	N	184	18, 55, 82, 82, 84, 91, 105, 130, 137, 158	P77296	Hypothetical protein ybeT	b0647	UNC	0.00
678731	REC00629	<i>ybeU</i>	N	235	1, 72, 98, 141, 143, 188, 221	P77427	Hypothetical protein ybeU	b0648	UNC	0.00
679435	REC00630	<i>ybeV</i>	N	483	29, 70, 149, 163, 237, 388, 404, 474	P77359	Hypothetical J-domain protein ybeV	b0649	UNC	0.00
682616	REC04572	<i>hscC</i>	N	556	17, 20, 65, 102	P77319	Chaperone protein hscC	b0650	UNC	0.06
683635	REC04573	<i>ybeK</i>	N	311	127, 193, 211, 287, 291	P41409	Hypothetical protein ybeK	b0651	UNC	0.41
684478	REC04574	<i>gltL</i>	E	241	-	< 0.05	Glutamate/aspartate transport ATP-binding protein gltL	b0652	MTR	0.69
685152	REC04575	<i>gltK</i>	E	224	1, 221	< 0.05	Glutamate/aspartate transport system permease protein gltK	b0653	MTR	0.25
685892	REC04576	<i>gltJ</i>	N	246	37, 86, 146, 183, 218	P41074	Glutamate/aspartate transport system permease protein gltJ	b0654	MTR	0.13
686970	REC04577	<i>gltI</i>	N	302	32, 201, 272	P37902	Glutamate/aspartate periplasmic binding protein precursor	b0655	MTR	0.16
688236	REC06525	<i>?</i>	N	338	148, 213, 222, 329	P03837	Transposase insH for insertion sequence element ISS	b0656	PHT	0.34
690104	REC04579	<i>lnt</i>	X	512	-	P23930	Apolipoprotein N-acyltransferase (EC 2.3.1.-)	b0657	LPC	0.69
691007	REC04580	<i>corC</i>	N	292	-	P77392	Magnesium and cobalt efflux protein corC	b0658	MTR	0.97
691564	REC04581	<i>ybeY</i>	E	155	-	< 0.2	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-octaprenyl-3-methyl-6-methoxy-1,4-benzoquinol hydroxylase (EC 1.	b0662	NCM	0.03
695581	REC00644	<i>?</i>	?	111	2, 36	P75729	FROM BASES 685948 TO 696574 (SECTION 60 OF 400) OF THE C	b0663	UNC	0.00
696065	REC00646	<i>?</i>	?	39	-	P75731	FROM BASES 685948 TO 696574 (SECTION 60 OF 400) OF THE C	b0669	UNC	0.00
696185	REC00647	<i>?</i>	?	50	-	P75732	FROM BASES 685948 TO 696574 (SECTION 60 OF 400) OF THE C	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, 126, 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	0.47
703167	REC00653	<i>nagE</i>	N	648	122, 141, 153, 177, 216, 354, 417, 431	P09323	PTS system, N-acetylglucosamine-specific IIABC component (EC 2.7	b0679	CHM	0.34
705316	REC00654	<i>glnS</i>	E	554	223	P00962	Glutaminyl-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	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	b0683	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>ybfP</i>	N	254	33, 68, 162, 219	P75736	Putative esterase/lipase ybfP (EC 3.1.-.)	b0686	UNC	0.25
712210	REC00661	<i>seqA</i>	E	181	-	P36658	SeqA protein	b0687	RCD	0.06
712781	REC00662	<i>pgm</i>	N	546	17, 41, 99, 170, 236, 256, 286	P36938	Phosphoglucomutase (EC 5.4.2.2)	b0688	CHM	0.44
714635	REC00663	<i>ybfP</i>	N	164	38, 49, 88, 128, 142	P75737	Hypothetical lipoprotein ybfP precursor	b0689	UNC	0.00
715532	REC04593	<i>ybfg</i>	?	120	86	P37003	Hypothetical protein ybfg	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	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	82, 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, 184, 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, 6	P16918	RhcS protein precursor	b0699	UNC	0.00
732999	REC00676	<i>ybfB</i>	E	108	85	P28914	Hypothetical protein ybfB	b0702	UNC	0.00
733443	REC00677	<i>ybfO</i>	N	477	262, 269, 308, 358, 309, 413	P77779	Hypothetical protein ybfO	b0703	UNC	0.00
734873	REC00678	<i>ybfC</i>	E	189	8	P28915	Hypothetical protein ybfC precursor	b0704	UNC	0.00
735688	REC06741	<i>ybfD</i>	X	84	-	Q9ZBC8	H repeat-associated protein in rhcS 3'region	UNC	0.00	
736327	REC00679	<i>ybfL</i>	N	285	46, 75, 150, 207, 216, 230, 267, 282	P75741	H REPEAT-ASSOCIATED PROTEIN IN RHSC-PHRB INTERGENIC Rb	b0705	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>phrB</i>	E	472	435	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	-	P75749	Hypothetical fimbrial 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 fimbrial-like protein ybgD precursor	b0719	UNC	0.00
753691	REC04608	<i>gltA</i>	N	427	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	<i>sdhB</i>	N	86	7, 34, 58	P75752	FROM BASES 747061 TO 762127 (SECTION 65 OF 400) OF THE C	b0725	UNC	0.00
757929	REC00700	<i>sucA</i>	E	933	74	P07015	2-oxoglutarate dehydrogenase E1 component (EC 1.2.4.2)	b0726	CHM	0.59
760745	REC00701	<i>sucB</i>	E	405	-	P07016	Dihydroloamide succinyltransferase component of 2-oxoglutarate de	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, 852	P54746	Hypothetical protein ybgG	b0732	UNC	0.19
770678	REC00707	<i>cydA</i>	E	523	-	P11026	Cytochrome D ubiquinol oxidase subunit I (EC 1.10.3.-)	b0733	BEN	0.63
772265	REC00708	<i>cydB</i>	E	379	-	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	UNC	0.09	
773532	REC00709	<i>ybgE</i>	N	97	28, 51, 92	P37343	Protein ybgE	b0735	UNC	0.03
773975	REC00710	<i>ybgC</i>	E	134	124	P08999	Protein ybgC	b0736	UNC	0.41
774376	REC00711	<i>tolQ</i>	N	230	148, 178	P05828	TolQ protein	b0737	MTR	0.44
775072	REC00712	<i>tolR</i>	N	142	49	P05829	TolR protein	b0738	MTR	0.41
775565	REC00713	<i>tolA</i>	N	421	27, 92, 242	P19934	TolA protein	b0739	MTR	0.03
776963	REC00714	<i>tolB</i>	N	430	80, 156, 195, 242, 274, 368	P19935	TolB protein precursor	b0740	MTR	0.44
778290	REC00715	<i>pal</i>	N	173	87, 116	P07176	Peptidoglycan-associated lipoprotein precursor	b0741	LPC	0.50
778821	REC00716	<i>ybgP</i>	N	263	20, 136, 186, 230	P45955	Hypothetical protein ybgP precursor	b0742	UNC	0.31
781308	REC00717	<i>nadA</i>	N	347	34, 82, 100, 120, 149, 167, 178, 213, 238, 282, 319	P11458	Quinolinate synthetase A	b0750	NCM	0.63
782389	REC00718	<i>pnuC</i>	N	239	41, 119, 183, 192	P31215	Protein pnuC	b0751	MTR	0.16
784046	REC04610	<i>zitB</i>	N	313	5, 11, 34, 183, 276, 294	P75757	Zinc transporter zitB	b0752	MTR	0.56
784540	REC04611	<i>ybgS</i>	N	126	21, 49, 76, 90, 104	P75758	Hypothetical protein ybgS precursor	b0753	UNC	0.00
784856	REC00721	<i>arog</i>	N	125	92, 120, 173	P00886	Phospho-2-dehydro-3-deoxyheptonate aldolase, Phe-sensitive (EC 4	b0754	AAM	0.41
786818	REC04612	<i>gpma</i>	N	250	122, 207	P31217	Phosphoglycerate mutase 1 (EC 5.4.2.1)	b0755	CHM	0.78
788060	REC04613	<i>galM</i>	N	346	200	P40681	Aldose 1-epimerase (EC 5.1.3.3)	b0756	CHM	0.53
789202	REC04614	<i>galK</i>	N	382	42, 52, 102, 241	P06976	Galactokinase (EC 2.7.1.6)	b0757	CHM	0.28
790252	REC04615	<i>galT</i>	N	348	31, 68, 117, 267, 268, 323	P09148	Galactose-1-phosphate uridylyltransferase (EC 2.7.7.10)	b0758	CHM	0.16
791278	REC04616	<i>galE</i>	N	338	16, 33, 140, 163, 266	P09147	UDP-glucose 4-epimerase (EC 5.1.3.2)	b0759	CHM	0.84
793011	REC04617	<i>modF</i>	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	<i>modE</i>	N	262	224	P46930	Transcriptional regulator modE	b0761	RCD	0.13
793996	REC00729	<i>ybhT</i>	?	49	-	P75759	Hypothetical protein ybhT precursor	b0762	UNC	0.00
794312	REC00730	<i>modA</i>	N	257	104	P37329	Molybdate-binding periplasmic protein precursor	b0763	MTR	0.66
795085	REC00731	<i>modB</i>	N	229	9, 48, 172, 204, 213	P09834	Molybdenum transport system permease protein modB	b0764	MTR	0.50
795777	REC00732	<i>modC</i>	N	352	33, 52	P09833	Molybdenum transport ATP-binding protein modC	b0765	MTR	0.34
797654	REC04619	<i>ybhA</i>	E	272	3	P21829	Hypothetical protein ybhA	b0766	UNC	0.66
797809	REC00734	<i>ybhE</i>	N	331	50, 156, 254	P52697	Hypothetical protein ybhE	b0767	UNC	0.25
799861	REC04620	<i>ybhD</i>	N	338	20, 89, 114, 141, 152, 209, 289	P52696	Hypothetical transcriptional regulator ybhD	b0768	UNC	0.25
799982	REC00736	<i>ybhH</i>	N	350	92, 104, 156, 193, 248, 284, 332	P75762	Hypothetical protein ybhH	b0769	UNC	0.28
801110	REC00737	<i>ybhI</i>	N	477	83, 121, 147, 235, 245, 292, 324, 383, 417, 433, 469, 473	P75763	Hypothetical protein ybhI	b0770	UNC	0.28
802702	REC00738	<i>ybhJ</i>	N	761	87, 100, 158	P75764	Hypothetical protein ybhJ	b0771	UNC	0.59
806504	REC04621	<i>ybhC</i>	N	427	107, 128, 167, 243, 316, 340, 384	P46130	Putative lipoprotein ybhC precursor	b0772	UNC	0.00
807132	REC04622	<i>ybhB</i>	N	158	45, 46	P12994	Protein ybhB	b0773	UNC	0.28
808480	REC04623	<i>bioA</i>	N	429	68, 413	P12995	Adenosylmethionine-8-amino-7-oxononoate aminotransferase (EC	b0774	NCM	0.66
808567	REC00742	<i>bioB</i>	N	346	95, 287, 340	P12996	Biotin synthase (EC 2.8.1.6)	b0775	NCM	0.72
809604	REC00743	<i>bioF</i>	N	384	23, 166, 227, 283, 347, 348	P12998	8-amino-7-oxononoate synthase (EC 2.3.1.47)	b0776	NCM	0.66
810745	REC00744	<i>bioC</i>	N	251	138, 214	P12999	Biotin synthesis protein bioC	b0777	NCM	0.47
811493	REC00745									

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, 78, 169, 190, 234	P75769	Hypothetical protein ybhM	b0787	UNC	0.00
821721	REC04625	ybhN	E	318	185	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	-	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, 67, 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	-	P30176	Hypothetical protein ybiA	b0798	UNC	0.06
832293	REC00766	dinG	N	716	322, 330, 404	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
838466	REC04636	ybiX	N	237	170, 211	P75779	Hypothetical protein ybiX	b0804	UNC	0.09
840754	REC04637	ybiL	N	760	7, 79, 96, 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	0.06
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	-	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, 238, 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 THE C	b0816	UNC	0.00
852406	REC00784	mntR	E	155	-	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	0.19
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, 283, 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, 689, 688, 700, 741, 781	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	418	118	P78055	Fructose-6-phosphate aldolase 1 (EC 4.1.2.-)	b0825	CHM	0.06
864352	REC04651	moeB	N	249	1, 82, 141, 210	P12282	Molybdopterin biosynthesis protein moeB	b0826	NCM	0.75
865587	REC04652	moeA	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, 167, 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	0.00
877258	REC04653	yliG	E	441	9	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	P75811	Hypothetical protein ybjK	b0846	UNC	0.03
889042	REC04660	ybjL	N	561	38, 122, 147, 200, 428, 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	E	85	-	P00277	Glutaredoxin 1	b0849	BEN	0.06
890136	REC00817	ybjC	?	95	7	P465119	Hypothetical protein ybjC	b0850	UNC	0.00
890407	REC00818	nfsA	N	240	14, 43, 115, 167	P17117	Oxygen-insensitive NADPH nitroreductase (EC 1.-.-.-)	b0851	NCM	0.25
891190	REC00819	rimK	N	300	4, 22, 194, 289	P17116	Ribosomal protein S6 modification protein	b0852	PMS	0.22
892180	REC00820	ybjN	?	158	11	P75815	Hypothetical protein ybjN	b0853	UNC	0.00
893007	REC00821	potP	N	370	90, 159, 329	P31133	Putrescine-binding periplasmic protein precursor	b0854	MTR	0.66
894133	REC00822	potG	N	404	29, 81, 256, 295, 371, 397	P31134	Putrescine transport ATP-binding protein potG	b0855	MTR	0.50
895357	REC00823	potH	N	317	95	P31135	Putrescine transport system permease protein potH	b0856	MTR	0.22
896307	REC00824	potI	N	281	187, 274	P31136	Putrescine transport system permease protein potI	b0857	MTR	0.25
897212	REC00825	ybjO	N	162	48, 89, 131	P75816	Hypothetical protein ybjO	b0858	UNC	0.00
897741	REC00826	ybjF	N	375	125, 206, 262, 338	P75817	Hypothetical RNA methyltransferase ybjF (EC 2.1.1.-)	b0859	UNC	0.72
899798	REC04662	artJ	N	243	140, 231	P30860	Arginine-binding periplasmic protein 2 precursor	b0860	MTR	0.38
900757	REC04663	artM	N	222	28, 61, 86, 112, 132	P30862	Arginine transport system permease protein artM	b0861	MTR	0.16
901473	REC04664	artQ	N	238	30, 64, 111, 114, 198, 235, 237	P30861	Arginine transport system permease protein artQ	b0862	MTR	0.66
902211	REC04665	artI	N	243	92, 195, 202	P30859	Arginine-binding periplasmic protein 1 precursor	b0863	MTR	0.34
902957	REC04666	artP	N	242	26, 209	P30858	Arginine transport ATP-binding protein artP	b0864	MTR	0.09
903690	REC04667	ybjP	E	171	147	P75818	Putative lipoprotein ybjP precursor	b0865	UNC	0.00
903816	REC00833	ybjQ	E	107	-	P75819	Hypothetical protein ybjQ	b0866	UNC	0.19
904136	REC00834	ybjR	E	276	-	P75820	Probable N-acetylmuramoyl-L-alanine amidase ybjR (EC 3.5.1.28)	b0867	UNC	0.34
906012	REC04668	ybjS	E	349	-	P75821	Hypothetical protein ybjS	b0868	UNC	0.25
907535	REC04669	ybjT	N	486	41, 282, 325	P75822	Hypothetical protein ybjT	b0869	UNC	0.31
908517	REC04670	ltaE	N	333	26, 36, 184, 213	P75823	Low-specificity L-threonine aldolase (EC 4.1.2.5)	b0870	AAM	0.47
910272	REC04671	poxB	N	572	110, 112, 198, 249, 295, 528, 551, 563	P07003	Pyruvate dehydrogenase [cytochrome] (EC 1.2.2.2)	b0871	CHM	0.22
911373	REC04672	hcr	N	322	41, 69, 223, 257, 299	P75824	NADH oxidoreductase hcr (EC 1.-.-.-)	b0872	UNC	0.09
913043	REC04673	hcp	N	552	138, 286	P75825	Prismase protein homolog	b0873	UNC	0.09
914128	REC04674	ybjE	N	315	39, 140, 149, 264	P75826	Hypothetical protein ybjE	b0874	UNC	0.13
915270	REC04675	aqpZ	N	231	4, 13, 21, 152	P48838	Aquaporin Z	b0875	MTR	0.22
915696	REC00843	ybjD	N	552	63, 77, 144, 154, 169, 189	P75828	Hypothetical protein ybjD	b0876	UNC	0.03
918343	REC04676	ybjX	N	330	46, 83, 133	P75829	Hypothetical protein ybjX	b0877	UNC	0.16
918431	REC00845	macA	N	380	34, 63, 87, 132, 135, 308	P75830	Macrolide-specific efflux protein macA precursor	b0878	MTR	0.38
919570	REC00846	macB	N	648	16, 56, 109, 191, 564	P75831	Macrolide-specific ABC-type efflux carrier	b0879	MTR	0.75
921813	REC04677	cspD	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	33, 79, 108, 169		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 1.8.99)		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	81, 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, 76, 138, 169, 209, 254, 270, 284			P75836	Hypothetical transcriptional regulator ycaN		b0900	UNC	0.72
948891	REC00866	<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>pf1A</i>	N	246	23, 205			P09374	Pyruvate formate-lyase 1 activating enzyme (EC 1.97.1.4)		b0902	CHM	0.31
952777	REC04686	<i>pf1B</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>rpsA</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-oculosonate 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>ybcC</i>	N	259	33, 74			P36565	Hypothetical protein ybcC		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	0.66
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	Nicotinate phosphoribosyltransferase (EC 2.4.2.11)		b0931	NCM	0.31
989845	REC00898	<i>pepN</i>	N	875	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	250	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	0.23
997082	REC00904	<i>ycbQ</i>	N	182	50, 58, 98, 173			P75855	Hypothetical fimbrial-like protein ycbQ precursor		b0938	UNC	0.05
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, 647			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	0.88
1009187	REC00915	<i>uup</i>	N	635	6, 121, 160, 296, 336, 374, 397, 493			P43672	ABC transporter ATP-binding protein uup		b0949	MTR	0.56
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, 259			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	-		< 0.1	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>su1A</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>he1D</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	-		< 0.2	P37066	Methylglucosyl 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		< 0.2	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	-		< 0.05	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								

1038519	REC00944	appB	N	378	23, 94, 211, 272	P26458	Cytochrome BD-II oxidase subunit II (EC 1.10.3.-)	b0979	BEN	0.03
1039840	REC00945	appA	N	432	127, 151	P07102	Periplasmic appA protein precursor	b0980	MSM	0.03
1043433	REC04712	etk	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	etp	N	152	9, 42, 152	P75880	Low molecular weight protein-tyrosine-phosphatase etp (EC 3.1.3.48)	b0982	CHM	0.59
1045026	REC04714	yccZ	N	379	41, 66, 88, 216, 272, 324	P75881	Putative polysaccharide export protein yccZ precursor	b0983	UNC	0.16
1047168	REC04715	ymcA	N	698	17, 213, 311, 598, 696	P75882	Hypothetical lipoprotein ymcA precursor	b0984	UNC	0.03
1047914	REC04716	ymcB	N	248	17, 51, 57, 122, 144, 168, 244	P75883	Hypothetical protein ymcB precursor	b0985	UNC	0.00
1048555	REC04717	ymcC	N	214	34, 82, 84, 129, 151	P75884	Hypothetical lipoprotein ymcC precursor	b0986	UNC	0.00
1048985	REC04718	ymcD	E	107	-	P75885	Hypothetical protein ymcD	b0987	UNC	0.00
1049250	REC00953	insB4	E	167	-	P57998	Insertion element IS1 4 protein insB	b0988	PHT	0.03
1050398	REC06609	cspH	?	70	-	P56253	Cold shock-like protein cspH	b0989	UNC	0.00
1050684	REC06610	cspG	N	70	3, 23, 44, 65	Q47130	Cold shock-like protein cspG	b0990	UNC	0.72
1051070	REC00954	sfa	N	76	23, 46, 55	P52634	Sfa protein	b0991	UNC	0.00
1051293	REC06673	gnsA	N	56	30	P52635	GnsA protein	b0992	UNC	0.00
1052585	REC04719	yccM	N	357	73, 168, 291, 327	P52636	Putative electron transport protein yccM	b0992	UNC	0.25
1055371	REC04720	torS	N	904	6, 109, 138, 280, 310, 362, 393, 437	P39453	Sensor protein torS (EC 2.7.3.-)	b0993	SMC	0.06
1055484	REC00957	torT	N	342	115, 289	P38683	Periplasmic protein torT precursor	b0994	MSM	0.03
1057177	REC04721	torR	E	230	-	P38684	TorCAD operon transcriptional regulatory protein torR	b0995	SMC	0.06
1057307	REC00959	torC	N	390	56, 80, 297, 337	P33226	Cytochrome c-type protein torC	b0996	SMC	0.06
1058479	REC00960	torA	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	torD	E	199	186	P36662	Chaperone protein torD	b0998	SMC	0.03
1062078	REC04722	yccD	E	101	-	P36660	Hypothetical protein yccD	b0999	UNC	0.00
1062998	REC04723	cbpA	N	306	18, 111	P36659	Curved DNA-binding protein	b1000	UNC	0.34
1063259	REC00964	yccE	N	418	21, 168, 393	P36661	Hypothetical protein yccE	b1001	UNC	0.00
1064808	REC00965	agp	N	413	23	P19926	Glucose-1-phosphatase precursor (EC 3.1.3.10)	b1002	MSM	0.00
1066314	REC04724	yccJ	?	75	-	P46131	Hypothetical protein yccJ	b1003	UNC	0.00
1066931	REC04725	wrbA	N	198	-	P30849	Flavoprotein wrbA	b1004	UNC	0.34
1067141	REC00968	ycdP	?	76	-	Q9ZN60	ORF, HYPOTHETICAL PROTEIN	b1005	UNC	0.00
1069128	REC04726	ycdG	N	464	125, 143, 172, 182, 254, 311, 381	P75892	Putative purine permease ycdG	b1006	UNC	0.47
1069541	REC04727	ycdH	N	152	33, 91, 126, 137	P75893	Putative flavin:NADH reductase ycdH (EC 1.6.8.-)	b1007	MSM	0.28
1070178	REC04728	ycdI	N	196	11, 150	P75894	Putative NADH dehydrogenase/NAD(P)H nitroreductase ycdI (EC 1.-)	b1008	UNC	0.13
1070988	REC04729	ycdJ	N	266	32	P75895	Hypothetical protein ycdJ	b1009	UNC	0.13
1071382	REC04730	ycdK	E	128	-	P75896	Hypothetical protein ycdK	b1010	UNC	0.81
1072128	REC04731	ycdL	E	244	233	P75897	Hypothetical isochorismatase family protein ycdL	b1011	UNC	0.34
1073234	REC04732	ycdM	N	382	92, 266, 334	P75898	Putative monooxygenase ycdM	b1012	UNC	0.13
1073465	REC00976	ydcC	N	212	70, 153	P75899	Hypothetical transcriptional regulator ydcC	b1013	UNC	0.28
1078105	REC04733	putA	N	1320	13, 17, 42, 230, 265, 363, 410, 428, 521, 610, 751, 770, 814, 823, 973, 984	P09546	Bifunctional putA protein	b1014	AAM	0.53
1078528	REC00978	putP	N	502	74, 151, 202, 287	P07117	Sodium/proline symporter	b1015	MTR	0.44
1080570	REC00979	yedY	N	39	17	P75901	Hypothetical protein yedY	b1016	UNC	0.00
1080677	REC00980	yedW	N	243	92	P75901	Hypothetical protein yedW	b1017	UNC	0.16
1081466	REC00981	yedO	N	375	171, 184, 354	P75902	Protein yedO	b1018	UNC	0.13
1082599	REC00982	yedB	N	423	19, 53, 149, 207, 320, 375	P31545	Hypothetical protein yedB precursor	b1019	UNC	0.16
1084215	REC00983	phoH	N	354	20, 183, 234, 327	P31544	PhoH protein	b1020	UNC	0.69
1085742	REC04734	yedP	N	137	78, 108, 127	P75904	Hypothetical protein yedP	b1021	UNC	0.00
1087069	REC04735	yedQ	N	441	11, 69, 110, 205, 266, 292, 298, 332, 343, 370, 396, 412, 440	P75905	Hypothetical protein yedQ	b1022	UNC	0.38
1089080	REC04736	yedR	N	672	24, 61, 85, 120, 165, 194, 202, 254, 260, 276, 299, 329, 652	P75906	Hypothetical lipoprotein yedR precursor	b1023	UNC	0.06
1091512	REC04737	yedS	N	807	135, 256, 358, 379, 433, 710, 782, 799	P75907	Hypothetical protein yedS precursor	b1024	UNC	0.03
1092099	REC00988	yedT	N	452	13, 31, 58, 158, 235, 272, 283, 307, 365, 374, 413, 424	P75908	Hypothetical protein yedT	b1025	UNC	0.59
1094364	REC06639	insP4	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	insE4	E	102	-	P77681	Transposase insE for insertion sequence IS3A/B/C/D/E/FA/FB	b1027	PHT	0.56
1094746	REC00991	yedU	N	107	12, 68	P75909	ORF_ID:O230#4	b1028	UNC	0.00
1095066	REC00992	yedU	N	328	27, 165, 196, 238, 270	P75910	Hypothetical protein yedU	b1029	UNC	0.00
1096171	REC00993	yedW	N	83	67, 76	P75911	FROM BASES 1094678 TO 1105023 (SECTION 95 OF 400) OF THE b1030	UNC	0.00	
1097070	REC00995	yedW	E	325	72	P75913	Putative 2-hydroxyacid dehydrogenase yedW	b1033	UNC	0.25
1098102	REC00996	yedX	E	245	-	P75914	Hypothetical protein yedX precursor	b1034	UNC	0.06
1098863	REC00997	yedY	N	184	38	P75915	Hypothetical protein yedY	b1035	UNC	0.03
1099471	REC00998	yedZ	E	179	-	P75916	Hypothetical protein yedZ	b1036	UNC	0.03
1100907	REC04740	csgG	N	277	2, 12, 47, 91, 228, 230	P52103	Curli production assembly/transport component csgG precursor	b1037	UNC	0.00
1101350	REC04741	csgF	N	138	31	P52104	Curli production assembly/transport component csgF precursor	b1038	UNC	0.00
1101764	REC04742	csgE	E	129	-	P52105	Curli production assembly/transport component csgE precursor	b1039	UNC	0.00
1102419	REC04743	csgD	N	216	101, 171	P52106	Probable csgAB operon transcriptional regulatory protein	b1040	UNC	0.06
1103174	REC01003	csgB	N	151	15, 27, 68, 114, 127	P39828	Minor curlin subunit precursor	b1041	SMC	0.03
1103670	REC01004	csgA	N	151	18, 52, 142	P28307	Major curlin subunit precursor	b1042	SMC	0.00
1104184	REC01005	csgC	N	110	71	P52107	Putative curli production protein csgC precursor	b1043	UNC	0.00
1104637	REC01006	ymdA	X	103	-	P75917	Hypothetical protein ymdA precursor	b1044	UNC	0.00
1105043	REC01007	ymdB	N	177	174	P75918	Hypothetical protein ymdB	b1045	UNC	0.28
1105518	REC01008	ymdC	N	493	16, 155, 162, 210, 366, 404, 450, 473	P75919	Hypothetical protein ymdC	b1046	UNC	0.63
1108164	REC04744	mdoC	N	385	15, 58, 79, 119, 165, 208, 262, 340	P75920	Glucans biosynthesis protein mdoC	b1047	CHM	0.03
1108558	REC01010	mdoG	N	511	201, 203, 241, 295, 334, 357, 467	P33136	Periplasmic glucans biosynthesis protein mdoG precursor	b1048	CHM	0.13
1110086	REC01011	mdoH	N	847	57, 167, 220, 377, 470, 484, 661	P33137	Periplasmic glucans biosynthesis protein mdoH	b1049	CHM	0.16
1112802	REC01012	yceK	N	75	29	P45806	Hypothetical protein yceK precursor	b1050	UNC	0.00
1113407	REC04745	msyB	E	125	-	P25738	Acidic protein msyB	b1051	UNC	0.00
1113532	REC04746	?	?	32	-	P75923	FROM BASES 1104966 TO 1115945 (SECTION 96 OF 400) OF THE b1052	UNC	0.00	
1114713	REC04747	yceE	N	408	11, 175, 202, 225, 340, 366	P25744	Hypothetical transport protein yceE	b1053	UNC	0.81
1115805	REC04748	htrB	N	306	43	P24187	Lipid A biosynthesis lauroyl acyltransferase (EC 2.3.1.-)	b1054	LPC	0.50
1116030	REC01017	yceA	N	350	25, 31, 75, 160, 267, 300, 348	P24188	Hypothetical protein yceA	b1055	UNC	0.63
1117699	REC04749	yceI	N	191	28, 123	P37904	Protein yceI precursor	b1056	UNC	0.44
1118269	REC04750	yceJ	N	188	140	P75925	Cytochrome b561 homolog 2	b1057	UNC	0.31
1118670	REC04751	yceO	?	46	-	P75926	Hypothetical protein yceO	b1058	UNC	0.00
1119809	REC04752	soIA	N	372	4, 49, 112, 275	P40874	N-methyl-L-tryptophan oxidase (EC 1.5.3.-)	b1059	AAM	0.22
1120178	REC04753	yceP	N	84	31	P75927	Hypothetical protein yceP	b1060	UNC	0.00
1120710	REC04754	dinI	N	81	64	Q47143	DNA-damage-inducible protein I	b1061	NAM	0.00
1121830	REC04755	pyrC	N	348	77, 206, 253, 328	P05020	Dihydroorotase (EC 3.5.2.3)	b1062	NCM	0.31
1122496	REC04756	yceB	N	186	12	P09995	Putative lipoprotein yceB precursor	b1063	UNC	0.00
1123277	REC04757	grxB	N	215	142	P39811	Glutaredoxin 2	b1064	AAM	0.06
1124579	REC04758	yceL	N	412	281	P77042	Hypothetical transport protein yceL	b1065	UNC	0.06
1124785	REC01028	rimJ	N	194	40, 45, 143	P09454	Ribosomal-protein-alanine acetyltransferase (EC 2.3.1.128)	b1066	PMS	0.41
1125380	REC01029	yceH	N	215	60, 177, 197	P29217	Hypothetical protein yceH	b1067	UNC	0.13
1126029	REC01030	mvIM	N	307	17, 111, 166, 182	P75931	Virulence factor mvIM homolog	b1068	UNC	0.13
1127062	REC01031	mvIN	E	511	-	P75932	Virulence factor mvIN homolog	b1069	UNC	0.00
1129053	REC04759	flgN	N	138	81	P43533	Flagella synthesis protein flgN	b1070	UNC	0.81
1129351	REC04760	flgM	N	97	32, 61	P43532	Negative regulator of flagellin synthesis	b1071	RCD	0.00
1130086	REC04761	flgA	N	219	114	P75933	Flagella basal body P-ring formation protein flgA precursor	b1072	SMC	0.13
1130241	REC01035	flgB	N	138	9, 112	P75934	Flagellar basal-body rod protein flgB	b1073	SMC	0.34
1130661	REC01036	flgC	N	134	26	P75935	Flagellar basal-body rod protein flgC	b1074	SMC	0.56
1131077	REC01037	flgD	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	8, 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	350, 485, 489	P32325	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	-	P21513	Ribonuclease E (EC 3.1.4.-)	b1084	NAM	0.56
1143671	REC01047	-	E	124	-	P75943	FROM BASES 1137539 TO 1147976 (SECTION 99 OF 400) OF THE	b1085	UNC	0.00
1144163	REC01048	<i>rJuc</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>yceP</i>	N	207	142, 160	P27244	Maf-like protein yceP	b1087	UNC	0.75
1146017	REC01050	<i>ycdD</i>	N	173	92, 158	P14189	Hypothetical protein ycdD	b1088	UNC	0.19
1146590	REC01051	<i>rpmF</i>	?	57	-	P02435	50S ribosomal protein L32	b1089	PMS	0.69
1146874	REC01052	<i>plsX</i>	N	346	15, 124, 162, 233, 307	P27247	Fatty acid/phospholipid synthesis protein plsX	b1090	UNC	0.72
1147982	REC01053	<i>fabH</i>	E	317	-	P24249	3-oxoacyl-[acyl-carrier-protein] synthase III (EC 2.3.1.41)	b1091	LPC	0.84
1148951	REC01054	<i>fabD</i>	E	309	-	P25715	Malonyl CoA-acyl carrier protein transacylase (EC 2.3.1.39)	b1092	LPC	0.84
1149893	REC01055	<i>fabG</i>	E	244	-	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>fabP</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	-	P37345	Thymidylate kinase (EC 2.7.4.9)	b1098	NCM	0.88
1154985	REC01061	<i>hoLB</i>	E	334	-	P28631	DNA polymerase III, delta' subunit (EC 2.7.7.7)	b1099	NAM	0.75
1156000	REC01062	<i>ycfH</i>	N	265	205, 259	P37346	Putative deoxyribonuclease ycfH (EC 3.1.21.-)	UNC	1.00	0.00
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>fhuE</i>	N	729	98, 166, 290, 479, 583, 716	P16869	FhuE receptor precursor	b1102	MTR	0.13
1161108	REC01065	<i>ycfP</i>	N	119	66	P36950	HIT-like protein ycfP	b1103	UNC	0.94
1161470	REC01066	<i>ycfL</i>	N	125	7, 33	P75946	Hypothetical protein ycfL	b1104	UNC	0.03
1161861	REC01067	<i>ycfM</i>	N	213	3, 117	P75947	Hypothetical protein ycfM	b1105	UNC	0.03
1162483	REC01068	<i>ycfN</i>	N	274	13	P75948	Hypothetical protein ycfN	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>ycfP</i>	E	199	-	P75950	Hypothetical protein ycfP	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>ycfJ</i>	N	179	135	P37796	Hypothetical protein ycfJ	b1110	UNC	0.06
1168133	REC04765	<i>ycfQ</i>	N	236	191	P75952	Hypothetical transcriptional regulator ycfQ	b1111	UNC	0.22
1168296	REC01074	<i>ycfR</i>	N	85	22	P75953	Hypothetical protein ycfR precursor	b1112	UNC	0.00
1169597	REC04766	<i>ycfS</i>	N	320	233, 282, 299	P75954	Hypothetical protein ycfS precursor	b1113	UNC	0.16
1173187	REC04767	<i>mfd</i>	N	1148	36, 164, 305, 498, 571, 578, 667, 746, 960	P30958	Transcription-repair coupling factor	b1114	NAM	0.94
1174388	REC04768	<i>ycfT</i>	N	357	88, 89, 176, 209, 286	P75955	Hypothetical protein ycfT	b1115	UNC	0.00
1174650	REC01078	<i>loIC</i>	E	399	-	P75956	Lipoprotein releasing system transmembrane protein loIC	b1116	LPC	0.31
1175857	REC01079	<i>loID</i>	E	228	-	P75957	Lipoprotein releasing system ATP-binding protein loID	b1117	MTR	0.84
1176543	REC01080	<i>loIE</i>	E	414	-	P75958	Lipoprotein releasing system transmembrane protein loIE	b1118	LPC	0.66
1177816	REC01081	<i>ycfX</i>	N	303	233	P75959	Hypothetical protein ycfX	b1119	UNC	0.53
1178743	REC01082	<i>cobB</i>	N	279	148	P75960	CobB protein	b1120	UNC	0.50
1180490	REC04769	<i>ycfZ</i>	N	262	1, 47, 91, 171, 234	P75961	Hypothetical protein ycfZ	b1121	UNC	0.00
1180957	REC04770	<i>ymfA</i>	N	156	10, 118	P75962	Hypothetical protein ymfA	b1122	UNC	0.00
1182052	REC04771	<i>potD</i>	E	348	326	P23861	Spermidine/putrescine-binding periplasmic protein precursor	b1123	MTR	0.69
1182843	REC04772	<i>potC</i>	E	264	-	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, 268, 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>ycfD</i>	E	376	-	P27431	Hypothetical protein ycfD	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)	b1131	NCM	0.84
1191854	REC04779	<i>ycfC</i>	N	213	103, 124	P25746	Hypothetical protein ycfC	b1132	UNC	0.16
1193041	REC04780	<i>trmJ</i>	E	383	333	P25745	tRNA (5-methylaminomethyl-2-thiouridylate)-methyltransferase (EC 2.3.1.33)	b1133	NAM	0.97
1193511	REC04781	<i>ymfB</i>	N	153	40	P75965	Putative Nudix hydrolase ymfB (EC 3.6.-.-)	b1134	UNC	0.09
1194144	REC04782	<i>ymfC</i>	N	207	4, 14, 66, 76, 175	P75966	Hypothetical protein ymfC	b1135	UNC	0.97
1194346	REC01098	<i>icd</i>	N	416	24, 71, 280, 385	P08200	Isocitrate dehydrogenase [NADP] (EC 1.1.1.42)	b1136	CHM	0.38
1196755	REC04783	<i>ymfD</i>	N	221	180, 221	P75967	Hypothetical protein ymfD	b1137	UNC	0.00
1197460	REC04784	<i>ymfE</i>	X	234	-	P75968	Hypothetical protein ymfE	b1138	UNC	0.00
1197918	REC01101	<i>lit</i>	X	297	-	P11072	Bacteriophage T4 late gene expression blocking protein	b1139	RCD	0.00
1200029	REC04785	<i>intE</i>	N	375	-	P75969	Prophage lambda integrase	b1140	PHT	0.00
1200255	REC04786	<i>ymfG</i>	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	<i>ymfI</i>	E	128	-	P75972	Hypothetical protein ymfI	b1143	UNC	0.00
1201283	REC04788	<i>ymfJ</i>	E	94	-	P75973	Hypothetical protein ymfJ	b1144	UNC	0.00
1201944	REC01108	-	E	167	-	P75975	FROM BASES 1195814 TO 1209543 (SECTION 104 OF 400) OF TH	b1146	UNC	0.00
1202156	REC04789	<i>ymfK</i>	E	224	-	P75974	Putative lambdoid prophage e14 repressor protein C2	b1145	UNC	0.00
1202479	REC01109	<i>ymfL</i>	N	189	114, 159	P75976	Hypothetical protein ymfL	b1147	UNC	0.00
1203045	REC01110	<i>ymfM</i>	N	112	47, 80	P75977	Hypothetical protein ymfM	b1148	UNC	0.00
1203393	REC01111	<i>ymfN</i>	N	455	99, 131, 326, 424	P75978	Hypothetical protein ymfN	b1149	UNC	0.13
1204772	REC01112	<i>ymfR</i>	?	60	-	P75979	Hypothetical protein ymfR	b1150	UNC	0.00
1204954	REC01113	<i>ymfO</i>	N	157	13	P75980	Hypothetical protein ymfO	b1151	UNC	0.03
1205354	REC01114	<i>ymfP</i>	N	263	64, 96, 147, 163	P75981	Hypothetical protein ymfP in lambdoid prophage e14 region	b1152	UNC	0.06
1206136	REC01115	<i>ymfQ</i>	N	194	106, 115	P75982	Hypothetical protein ymfQ in lambdoid prophage e14 region precursor	b1153	UNC	0.00
1206724	REC01116	<i>ycfK</i>	N	209	23, 46, 105	P45581	Hypothetical protein ycfK	b1154	UNC	0.00
1207355	REC01117	<i>ymfS</i>	N	137	57	P09154	Hypothetical protein ymfS	b1155	UNC	0.00
1208342	REC04790	<i>tfafE</i>	N	200	22, 41, 51, 96, 121, 130, 156, 170	P09153	Tail fiber assembly protein homolog from lambdoid prophage e14	b1156	UNC	0.03
1208881	REC04791	<i>stfE</i>	N	179	38, 71, 86, 119	P33227	Side tail fiber protein homolog from lambdoid prophage e14	b1157	UNC	0.03
1208908	REC01120	<i>pinE</i>	N	184	22, 32, 176	P03014	DNA-invertase from lambdoid prophage e14	b1158	PHT	0.44
1209569	REC01121	<i>mcrA</i>	N	277	96, 260	P24200	5-methylcytosine-specific restriction enzyme A (EC 3.1.21.-)	b1159	NAM	0.00
1211226	REC04792	<i>e1bA</i>	E	107	-	P75987	Enhancing lycopene biosynthesis protein 1	b1160	UNC	0.00
1212330	REC04793	<i>ycgX</i>	E	134	-	P75988	Hypothetical protein ycgX	b1161	UNC	0.00
1213282	REC04794	<i>ycgE</i>	N	243	18, 129, 132	P75989	Hypothetical transcriptional regulator ycgE	b1162	UNC	0.09
1214698	REC04795	<i>ycgF</i>	N	403	38, 158, 318, 390	P75990	Hypothetical protein ycgF	b1163	UNC	0.06
1215012	REC01126	<i>ycgZ</i>	N	78	44, 61	P75991	Hypothetical protein ycgZ	b1164	UNC	0.00
1215291	REC01127	<i>ymgA</i>	N	90	2, 36, 57	P75992	Hypothetical protein ymgA	b1165	UNC	0.00
1215592	REC01128	<i>ymgB</i>	N	88	72	P75993	Hypothetical protein ymgB	b1166	UNC	0.00
1215971	REC01129	<i>ymgC</i>	N	82	44	P75994	Hypothetical protein ymgC	b1167	UNC	0.00
1216509	REC01130	<i>ycgG</i>	N	521	24, 60, 133, 264, 403, 432, 464, 497	P75995	Hypothetical protein ycgG	b1168	UNC	0.31
1218170	REC06761	<i>ymgP</i>	N	84	36, 61	P58034	Hypothetical protein ymgP	UNC	0.00	0.00
1218824	REC01131	-	N	506	34, 45, 77, 130, 146, 191, 241, 354	P75996	O56 WAS O411 AND O104	b1169	UNC	0.00
1220429	REC01132									

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 TH	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, 230, 284	P77335	Hemolysin E, chromosomal	b1182	UNC	0.00	
1229990	REC01145	umuD	N	139	46, 127	P04155	UmuD protein (EC 3.4.21.-)	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, 108, 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)	b1347	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	lolB	X	207	-	P24208	Outer-membrane lipoprotein lolB precursor	b1209	LPC	0.09	
1262937	REC01172	hemA	X	418	-	P13580	Glutaryl-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-deoxyphosphoacetate 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	28	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	narG	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	narH	N	512	4, 215, 433	P11349	Respiratory nitrate reductase 1 beta chain (EC 1.7.99.4)	b1225	SMC	0.22	
1284362	REC01188	narJ	N	236	178	P11351	Respiratory nitrate reductase 1 delta chain (EC 1.7.99.4)	b1226	SMC	0.13	
1285072	REC01189	narI	N	225	29, 205	P11350	Respiratory nitrate reductase 1 gamma chain (EC 1.7.99.4)	b1227	SMC	0.22	
1285932	REC01190		E	91	-	0.53	P76023	FROM BASES 1278800 TO 1289447 (SECTION 111 OF 400) OF TH	b1228	UNC	0.00
1286411	REC04824	tpr	?	33	-	P02338	Protamine-like protein	b1229	UNC	0.00	
1287847	REC04825	purU	E	280	-	< 0.2	P37051	Formyltetrahydrofolate deformylase (EC 3.5.1.10)	b1232	NCM	0.56
1288355	REC04826	ychJ	N	152	60, 97, 98	P37052	Hypothetical protein ychJ	b1233	UNC	0.22	
1288429	REC01194	ychK	N	314	218	P37053	Hypothetical protein ychK	b1234	UNC	0.56	
1289465	REC01195	hnr	E	337	-	< 0.2	P37055	Hnr protein	b1235	UNC	0.16
1290680	REC01196	galU	E	302	-	< 0.3	P25520	UTP--glucose-1-phosphate uridylyltransferase (EC 2.7.7.9)	b1236	CHM	0.78
1292145	REC04827	hns	E	137	-	0.52	P08936	DNA-binding protein H-NS	b1237	UNC	0.09
1292750	REC01198	tdk	E	205	-	< 0.3	P23331	Thymidine kinase (EC 2.7.1.21)	b1238	NCM	0.41
1294239	REC04828	ychG	N	196	84	P30192	Hypothetical protein ychG	b1239	UNC	0.00	
1297344	REC04830	adhE	N	891	10, 55, 123, 232, 280, 848	P17547	Aldehyde-alcohol dehydrogenase	b1241	MSM	0.50	
1297821	REC01202	ychE	N	215	78, 121, 184	P25743	Hypothetical protein ychE	b1242	UNC	0.56	
1299206	REC01203	oppA	N	543	8, 184, 221, 244, 276, 310, 453, 500, 525	P23843	Periplasmic oligopeptide-binding protein precursor	b1243	MTR	0.72	
1300923	REC01204	oppB	N	306	122, 147, 222	P31132	Oligopeptide transport system permease protein oppB	b1244	MTR	0.72	
1301858	REC01205	oppC	E	302	79	< 0.05	P77664	Oligopeptide transport system permease protein oppC	b1245	MTR	0.81
1302778	REC01206	oppD	E	337	-	< 0.05	P76027	Oligopeptide transport ATP-binding protein oppD	b1246	MTR	0.75
1303788	REC01207	oppF	N	334	17, 233, 301	P77737	Oligopeptide transport ATP-binding protein oppF	b1247	MTR	0.47	
1305252	REC04831	yciU	N	135	42	P76028	Hypothetical protein yciU	b1248	UNC	0.06	
1306669	REC04832	cIs	N	486	281	P31071	Cardiolipin synthetase (EC 2.7.8.-)	b1249	LPC	0.63	
1308293	REC04833	kch	N	417	118, 138, 209, 254, 317, 327, 412	P31069	Putative potassium channel protein	b1250	UNC	0.34	
1308985	REC04834	yciI	N	130	73	P31070	Protein yciI	b1251	UNC	0.22	
1309113	REC01212	tonB	E	239	-	< 0.05	P02929	TonB protein	b1252	MTR	0.06
1310270	REC04835	yciA	E	132	-	< 0.2	P04379	Putative acyl-CoA thioester hydrolase yciA (EC 3.1.2.-)	b1253	UNC	0.59
1310914	REC04836	ispZ	E	179	168	< 0.1	P21366	Probable intracellular septation protein	b1254	UNC	0.38
1311687	REC04837	yciC	N	247	61, 183	P21365	Hypothetical protein yciC	b1255	UNC	0.03	
1312044	REC01216	ompW	N	212	81	P21364	Outer membrane protein W precursor	b1256	SMC	0.25	
1313248	REC04838	yciE	N	168	13, 27, 146	P21363	Protein yciE	b1257	UNC	0.06	
1313794	REC04839	yciF	N	166	20, 39, 63, 64, 97, 134	P21362	Protein yciF	b1258	UNC	0.09	
1314116	REC04840	yciG	N	78	40, 65	P21361	Hypothetical protein yciG	b1259	UNC	0.03	
1315246	REC04841	trpA	N	268	37, 161, 206, 250, 265	P00928	Tryptophan synthase alpha chain (EC 4.2.1.20)	b1260	AAM	0.84	
1316439	REC04842	trpB	N	397	262, 306, 365, 391	P00932	Tryptophan synthase beta chain (EC 4.2.1.20)	b1261	AAM	0.88	
1317812	REC04843	trpC	N	453	231, 236, 271, 314, 344, 388	P00909	Tryptophan biosynthesis protein trpCF	b1262	AAM	0.84	
1319408	REC04844	trpD	N	531	117, 171, 181, 314, 365, 497	P00904	Anthranilate synthase component II (EC 4.1.3.27)	b1263	AAM	0.84	
1320970	REC04845	trpE	N	520	29, 377	P00895	Anthranilate synthase component I (EC 4.1.3.27)	b1264	AAM	0.81	
1321244	REC01226	trpH	N	293	17, 48, 101	P77766	Protein trpH	b1266	UNC	0.19	
1322086	REC01227	yciO	N	218	28, 159	P45847	Protein yciO	b1267	UNC	0.31	
1322770	REC01228	yciQ	N	631	28, 75, 172, 200, 240, 277, 288, 344, 369, 391, 413, 418, 474, 483, 546, 568	P45848	Hypothetical protein yciQ	b1268	UNC	0.06	
1324876	REC01229	yciL	E	291	237	< 0.01	P37765	Hypothetical protein yciL	b1269	UNC	0.97
1326381	REC04847	btuR	E	196	107	< 0.05	P13040	COB(I)alamin adenosyltransferase (EC 2.5.1.17)	b1270	NCM	0.41

1327136	REC04848	<i>yciK</i>	E	252	125	< 0.01	P31808	Hypothetical oxidoreductase <i>yciK</i> (EC 1.-.-.-)	b1271	UNC	0.78
1327356	REC01232	<i>sohB</i>	N	349	43, 56, 201, 213, 231, 252, 302		P24213	Possible protease <i>sohB</i> (EC 3.4.21.-)	b1272	UNC	0.78
1328692	REC04849	<i>yciN</i>	N	83	29		P46132	Protein <i>yciN</i>	b1273	UNC	0.03
1329072	REC01234	<i>topA</i>	E	865	-	< 0.001	P06612	DNA topoisomerase I (EC 5.99.1.2)	b1274	NAM	0.97
1331879	REC01235	<i>cysB</i>	N	324	18, 89, 96, 249, 315		P06613	Cys regulon transcriptional activator	b1275	RCD	0.19
1333148	REC06676	<i>yciX</i>	N	54	18		P58094	Hypothetical protein <i>yciX</i>		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>rihA</i>	E	196	-	< 0.1	P25523	GTP cyclohydrolase II (EC 3.5.4.25)	b1277	NCM	0.84
1337354	REC01238	<i>pgpB</i>	N	254	32, 56, 221		P18201	Phosphatidylglycerophosphate B (EC 3.1.3.27)	b1278	LPC	0.06
1338267	REC01239	<i>yciS</i>	E	102	-	0.33	P77614	Hypothetical protein <i>yciS</i>	b1279	UNC	0.06
1338582	REC06490	<i>yciM</i>	N	389	260, 347, 379		P45576	Hypothetical protein <i>yciM</i> precursor	b1280	UNC	0.16
1339945	REC01241	<i>pyrP</i>	E	245	170	< 0.1	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 <i>yciH</i>	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 <i>yciT</i>	b1284	UNC	0.09
1344766	REC04853	<i>yciR</i>	N	661	11, 63, 132, 325, 603		P77334	Hypothetical protein <i>yciR</i>	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 <i>yciW</i>	b1287	UNC	0.00
1349063	REC04856	<i>fabI</i>	E	262	-	< 0.1	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 <i>ycjD</i>	b1289	UNC	0.22
1350658	REC04858	<i>sapF</i>	N	268	148, 165		P36637	Peptide transport system ATP-binding protein <i>sapF</i>	b1290	MTR	0.06
1351652	REC04859	<i>sapD</i>	N	330	105, 129		P36635	Peptide transport system ATP-binding protein <i>sapD</i>	b1291	MTR	0.06
1352542	REC04860	<i>sapC</i>	N	296	19, 125, 148, 203		Q47624	Peptide transport system permease protein <i>sapC</i>	b1292	MTR	0.06
1353494	REC04861	<i>sapB</i>	N	321	160, 248, 266		Q47623	Peptide transport system permease protein <i>sapB</i>	b1293	MTR	0.06
1355134	REC04862	<i>sapA</i>	N	547	169, 203, 310		Q47622	Peptide transport periplasmic protein <i>sapA</i> precursor	b1294	MTR	0.06
1355692	REC04863	<i>ymjA</i>	N	81	37		P76036	Hypothetical protein <i>ymjA</i>	b1295	UNC	0.00
1357265	REC04864	<i>ycjJ</i>	N	479	100, 179, 291, 306, 422		P76037	Hypothetical transport protein <i>ycjJ</i>	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	61, 144, 153		P76038	Hypothetical protein <i>ycjL</i>	b1298	UNC	0.38
1359935	REC01259	<i>ycjC</i>	N	185	93, 110		P38522	Hypothetical protein <i>ycjC</i>	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 <i>ordL</i> (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	-	0.38	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	0.43	P23857	Phage shock protein E precursor	b1308	UNC	0.06
1368213	REC01269	<i>ycjM</i>	N	568	59, 97, 107, 186, 221, 229, 266, 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 <i>ycjN</i> precursor	b1310	UNC	0.22
1371246	REC01271	<i>ycjO</i>	N	293	84		P77653	Hypothetical ABC transporter permease protein <i>ycjO</i>	b1311	UNC	0.41
1372114	REC01272	<i>ycjP</i>	N	280	81, 132, 251		P77716	Hypothetical ABC transporter permease protein <i>ycjP</i>	b1312	UNC	0.47
1372987	REC01273	<i>ycjQ</i>	N	350	59, 253		P76043	Hypothetical zinc-type alcohol dehydrogenase-like protein <i>ycjQ</i>	b1313	UNC	0.03
1374049	REC01274	<i>ycjR</i>	?	265	248		P76044	Hypothetical protein <i>ycjR</i>	b1314	UNC	0.16
1374856	REC01275	<i>ycjS</i>	N	351	194		P77503	Hypothetical oxidoreductase <i>ycjS</i> (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 <i>ycjT</i>	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, 292		P77481	Hypothetical ABC transporter ATP-binding protein <i>ycjV</i>	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 <i>ycjW</i>	b1320	UNC	0.03
1382141	REC01281	<i>ycjX</i>	N	465	24, 401		P76046	Hypothetical protein <i>ycjX</i>	b1321	UNC	0.19
1383535	REC01282	<i>ycjF</i>	E	353	-	< 0.05	P45525	Hypothetical protein <i>ycjF</i>	b1322	UNC	0.16
1384744	REC01283	<i>tyrR</i>	N	513	265, 391, 465		P07604	Transcriptional regulatory protein <i>tyrR</i>	b1323	RCD	0.59
1386835	REC04868	<i>tpx</i>	N	168	67		P37901	Thiol peroxidase (EC 1.1.1.1-)	b1324	MSM	0.44
1386912	REC01285	<i>ycjG</i>	N	335	65, 78, 137, 317		P51981	Hypothetical protein <i>ycjG</i>	b1325	UNC	0.31
1386882	REC04869	<i>ycjI</i>	E	262	-	< 0.05	P51983	Hypothetical protein <i>ycjI</i>	b1326	UNC	0.00
1389899	REC04870	<i>ycjY</i>	N	310	102, 173, 219, 291		P76049	Hypothetical protein <i>ycjY</i>	b1327	UNC	0.13
1390015	REC01288	<i>ycjZ</i>	N	299	127, 136, 244, 298		P77333	Hypothetical transcriptional regulator <i>ycjZ</i>	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 <i>ynaI</i>	b1330	UNC	0.13
1394100	REC06520	-	X	338	-		P03837	Transposase <i>insH</i> for insertion sequence element ISS	b1331	PHT	0.34
1395389	REC01292	<i>ynaJ</i>	E	85	-	0.48	P76050	Hypothetical protein <i>ynaJ</i>	b1332	UNC	0.00
1396646	REC04872	<i>ydaA</i>	N	316	-		P03807	Protein <i>ydaA</i>	b1333	UNC	0.47
1397550	REC04873	<i>fnr</i>	N	250	-		P03019	Fumarate and nitrate reduction 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 <i>abgR</i>	b1339	UNC	0.06
1404003	REC01300	<i>ydaL</i>	E	187	-	< 0.2	P76053	Hypothetical protein <i>ydaL</i>	b1340	UNC	0.28
1405879	REC04878	<i>ydaM</i>	N	430	7, 29, 40, 59, 155, 374		P77302	Hypothetical protein <i>ydaM</i>	b1341	UNC	0.13
1406074	REC01302	<i>ydaN</i>	N	327	57, 71, 99, 141, 262, 280		P76054	Hypothetical protein <i>ydaN</i>	b1342	UNC	0.78
1407535	REC01303	<i>dbpA</i>	N	457	32, 157, 327, 453		P21693	ATP-independent RNA helicase <i>dbpA</i>	b1343	SMC	0.28
1409972	REC04879	<i>ydaO</i>	N	311	35, 167, 250, 278		P76055	Hypothetical protein <i>ydaO</i>	b1344	UNC	0.50
1411259	REC04880	<i>intrR</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 <i>ydaQ</i>	b1346	UNC	0.00
1411764	REC04882	<i>ydaC</i>	X	69	-		P33230	Hypothetical protein <i>ydaC</i>	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, 678, 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>kil</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 TH1354	b1354	UNC	0.00
1418265	REC04889	<i>racR</i>	E	158	140	< 0.1	P76062	Rac prophage repressor			

1424079	REC01327	N	77	49	P76070	FROM BASES 1415432 TO 1425731 (SECTION 123 OF 400) OF THb1367	UNC	0.00	
1424478	REC01328	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 THb1371	UNC	0.00	
1426750	REC04890	E	326	-	P76071	Transposase insH for insertion sequence element ISSY	b1370	PHT	0.34
1427067	REC01332	N	1122	24, 128, 165, 329, 598, 708, 814, 1029, 1038, 1110	P76072	Side tail fiber protein homolog from lambdoid prophage Rac	b1372	UNC	0.00
1430435	REC01333	N	191	16, 62, 86, 121, 146, 179	P77163	Tail fiber assembly protein homolog from lambdoid prophage Rac	b1373	UNC	0.03
1431698	REC04891	N	196	5, 44, 75, 142, 173	P77574	Putative DNA-invertase from lambdoid prophage Rac	b1374	UNC	0.03
1432281	REC04892	N	88	27	P76073	Hypothetical protein ynaE	b1375	UNC	0.00
1433715	REC04893	N	168	14, 27, 45, 54, 94, 145	P73903	Unknown protein 2D_000B3L from 2D-page	b1376	UNC	0.13
1434917	REC04894	N	377	74, 114, 126, 180, 199, 228, 300, 345	P77747	Outer membrane protein N precursor	b1377	UNC	0.06
1438808	REC04895	N	1174	36, 222, 299, 624, 861, 1092, 1138	P52647	Probable pyruvate-flavodoxin oxidoreductase (EC 1.2.7.-)	b1378	UNC	0.34
1439082	REC06678	?	88	-	P52644	Hypothetical protein ydbJ precursor	-	UNC	0.00
1439767	REC04896	E	140	-	P52644	Heat shock protein hslJ	b1379	UNC	0.03
1440867	REC04897	N	329	121, 224, 280, 325	P52643	D-lactate dehydrogenase (EC 1.1.1.28)	b1380	CHM	0.47
1441075	REC01341	N	879	10, 105, 249, 321, 770, 838, 853, 872	P52645	Hypothetical protein ydbH	b1381	UNC	0.03
1443711	REC01342	N	61	12, 36	P76075	Hypothetical protein ynbE	b1382	UNC	0.03
1443898	REC01343	N	110	47	P76076	Hypothetical protein ydbL precursor	b1383	UNC	0.03
1445307	REC04898	N	301	183, 198, 230	Q47129	Transcriptional activator feaR	b1384	RCD	0.22
1445540	REC01345	N	500	32, 347, 357, 424	P80668	Phenylacetaldehyde dehydrogenase (EC 1.2.1.39)	b1385	AAM	0.19
1449373	REC04899	N	757	33, 197, 417, 545, 719	P46883	Copper amine oxidase precursor (EC 1.4.3.6)	b1386	AAM	0.06
1451666	REC04900	N	681	16, 188	P77455	MaoC protein	b1387	UNC	0.19
1451951	REC01348	N	309	140, 245, 249	P76077	Phenylacetic acid degradation protein paaA	b1388	MSM	0.09
1452892	REC01349	X	95	-	P76078	Phenylacetic acid degradation protein paaB	b1389	MSM	0.09
1453188	REC01350	E	248	-	P76079	Phenylacetic acid degradation protein paaC	b1390	MSM	0.09
1453943	REC01351	N	167	36, 78	P76080	Phenylacetic acid degradation protein paaD	b1391	MSM	0.09
1454454	REC01352	N	356	23, 48, 78, 98	P76081	Probable phenylacetic acid degradation NADH oxidoreductase paaE	b1392	UNC	0.38
1455521	REC01353	N	255	32, 59, 146, 186, 250	P76082	Probable enoyl-CoA hydratase paaF (EC 4.2.1.17)	b1393	UNC	0.28
1456288	REC01354	N	262	222	P77467	Probable enoyl-CoA hydratase paaG (EC 4.2.1.17)	b1394	UNC	0.44
1457078	REC01355	N	475	284, 337	P76083	Probable 3-hydroxybutyryl-CoA dehydrogenase (EC 1.1.1.157)	b1395	UNC	0.41
1458495	REC01356	N	140	79, 105	P76084	Phenylacetic acid degradation protein paaI	b1396	UNC	0.13
1458917	REC01357	N	401	60	P77525	Probable beta-ketoadipyl CoA thiolase (EC 2.3.1.-)	b1397	UNC	0.28
1460149	REC01358	N	437	284	P76085	Phenylacetate-coenzyme A ligase (EC 6.2.1.30)	b1398	MSM	0.13
1461563	REC01359	E	316	-	P76086	Phenylacetic acid degradation operon negative regulatory protein paaJ	b1399	RCD	0.00
1462495	REC01360	E	196	167	P77181	Phenylacetic acid degradation protein paaY	b1400	UNC	0.16
1463416	REC01361	N	852	48, 138, 180, 419, 759, 795	P76858	RtoA protein	b1401	UNC	0.03
1466850	REC06523	X	301	-	P19777	Transposase insD for insertion element IS2A/D/F/H/I/K	b1402	PHT	0.56
1467218	REC06524	X	136	-	P19776	Transposase insC for insertion element IS2A/D/F/H/I/K	b1403	PHT	0.56
1467382	REC06526	X	383	-	P37246	Transposase insI for insertion sequence element IS30B/C/D	b4284	PHT	0.22
1468714	REC01365	N	1107	647, 805	P33666	Hypothetical protein ydbA	UNC	0.06	
1472245	REC01366	N	286	176	P25906	Hypothetical oxidoreductase ydbC (EC 1.-.-)	b1406	UNC	0.25
1473162	REC01367	N	770	37, 60, 310, 360, 376, 414, 435, 450, 472, 529, 531, 579, 607, 675, 698, 705	P25907	Hypothetical protein ydbD	b1407	UNC	0.00
1475639	REC01368	N	203	72	P76090	Hypothetical protein ynbA	b1408	UNC	0.06
1476250	REC01369	X	298	-	P76091	Hypothetical protein ynbB	b1409	UNC	0.94
1477162	REC01370	N	585	233, 248, 292, 299, 388, 467, 544	P76092	Hypothetical protein ynbC	b1410	UNC	0.25
1478933	REC01371	N	430	36, 136, 218	P76093	Hypothetical protein ynbD	b1411	UNC	0.09
1480884	REC04903	E	201	-	P41407	Acyl carrier protein phosphodiesterase (EC 3.1.4.14)	b1412	LPC	0.34
1481142	REC01373	N	1281	17, 114, 169, 228, 265, 397, 420, 890, 1022, 1103	P43329	ATP-dependent helicase hrpA	b1413	UNC	0.28
1485259	REC01374	N	266	94, 207	P34209	Protein ydcF	b1414	UNC	0.00
1486256	REC01375	N	479	312, 464	P25553	Aldehyde dehydrogenase A (EC 1.2.1.22)	b1415	CHM	0.13
1487988	REC04904	?	83	-	P33898	Glyceraldehyde 3-phosphate dehydrogenase C (EC 1.2.1.12)	b1416	CHM	0.97
1488389	REC04905	N	134	94	P33898	Glyceraldehyde 3-phosphate dehydrogenase C (EC 1.2.1.12)	b1418	CHM	0.97
1488890	REC01378	N	188	83, 181	P08732	Cytochrome b561	b1418	BEN	0.31
1489701	REC01379	N	57	34	P23864	Hypothetical protein ydcA precursor	b1419	UNC	0.03
1489940	REC06875	N	76	36	P77193	SIMILAR TO	UNC	0.00	
1490494	REC01381	E	546	-	P05704	Methyl-accepting chemotaxis protein III	b1421	SMC	0.63
1493236	REC04907	N	354	89, 267	P77171	Hypothetical transcriptional regulator ydcI	b1422	UNC	0.22
1493312	REC01383	N	447	29, 441	P76097	Hypothetical protein ydcJ	b1423	UNC	0.09
1494880	REC01384	N	551	17, 246, 376, 432	P40120	Protein ydcG precursor	b1424	UNC	0.06
1496732	REC01386	?	55	-	P46135	Hypothetical protein ydcH	b1426	UNC	0.00
1496962	REC01387	E	179	-	P13857	Ribosomal-protein-serine acetyltransferase (EC 2.3.1.-)	b1427	PMS	0.19
1498473	REC04909	N	326	105, 157, 310	P76100	Hypothetical protein ydcK	b1428	UNC	0.00
1498597	REC01389	N	330	181, 301, 328	P25396	Tellurite resistance protein tehA	b1429	UNC	0.13
1499586	REC01390	N	197	158	P25397	Tellurite resistance protein tehB	b1430	UNC	0.09
1500481	REC01391	N	222	57	P76101	Hypothetical lipoprotein ydcL precursor	b1431	UNC	0.00
1501681	REC01392	N	402	26, 105, 170	P76102	Hypothetical protein ydcM	b1432	UNC	0.31
1504196	REC01394	E	178	-	P77626	Hypothetical protein ydcN	b1434	UNC	0.09
1504365	REC04910	N	478	100, 267, 311, 446, 453	P76103	Hypothetical protein ydcO	b1433	UNC	0.25
1504763	REC01395	N	667	135, 363, 458, 583, 659	P76104	Putative protease ydcP precursor (EC 3.4.-)	b1435	UNC	0.16
1507088	REC04911	N	76	45	P76105	Hypothetical protein yncJ precursor	b1436	UNC	0.00
1507471	REC04912	N	65	22	P76106	FROM BASES 1506783 TO 1516942 (SECTION 131 OF 400) OF THb1437	UNC	0.00	
1507511	REC01398	E	145	44	P76107	Hypothetical protein ydcQ	b1438	UNC	0.00
1508027	REC01399	N	468	114, 171, 467	P77730	Hypothetical protein ydcR	b1439	UNC	0.31
1509678	REC01400	N	381	10, 53, 90, 165	P76108	Putative ABC transporter periplasmic binding protein ydcS precursor	b1440	UNC	0.06
1510841	REC01401	E	337	-	P77795	Hypothetical ABC transporter ATP-binding protein ydcT	b1441	UNC	0.09
1511855	REC01402	E	313	-	P77156	Hypothetical ABC transporter permease protein ydcU	b1442	UNC	0.06
1512786	REC01403	E	264	207	P77505	Hypothetical ABC transporter permease protein ydcV	b1443	UNC	0.06
1513602	REC01404	N	474	208	P77674	Putative betaine aldehyde dehydrogenase (EC 1.2.1.8)	b1444	UNC	0.25
1515338	REC01405	?	82	-	P76109	Hypothetical protein ydcX	b1445	UNC	0.00
1515672	REC01406	N	77	34	P76110	Hypothetical protein ydcY	b1446	UNC	0.00
1516355	REC04913	E	149	-	P76111	Hypothetical protein ydcZ	b1447	UNC	0.03
1516870	REC04914	E	172	172	P76112	Hypothetical acetyltransferase yncA (EC 2.3.1.-)	b1448	UNC	0.50
1516958	REC01409	N	376	10, 54, 114, 312, 325	P76113	Putative NADP-dependent oxidoreductase yncB (EC 1.-.-)	b1449	UNC	0.44
1518229	REC01410	N	240	98, 175, 198, 215, 216, 236	P76114	Hypothetical transcriptional regulator yncC	b1450	UNC	0.16
1521089	REC04915	N	700	258, 320, 377, 415, 481, 556, 573, 587, 614, 642, 672	P76115	Probable tonB-dependent receptor yncD precursor	b1451	UNC	0.28
1521331	REC01412	E	353	-	P76116	Hypothetical protein yncE precursor	b1452	UNC	0.00
1524055	REC04916	N	516	151, 379	P77610	L-asparagine permease	b1453	MTR	0.22
1524271	REC01414	N	205	151	P76117	Hypothetical GST-like protein yncG	b1454	UNC	0.13
1524964	REC01415	N	70	-	P76118	Hypothetical protein yncH	b1455	UNC	0.00
1525914	REC01416	N	682	-	P24211	RhsE protein	b1456	UNC	0.00
1527946	REC01417	?	160	-	P31991	Hypothetical protein ydcD	b1457	UNC	0.00
1528610	REC01418	N	248	-	P76119	FROM BASES 1528490 TO 1540683 (SECTION 133 OF 400) OF THb1458	UNC	0.00	
1529400	REC01419	?	66	-	P76120	FROM BASES 1528490 TO 1540683 (SECTION 133 OF 400) OF THb1459	UNC	0.00	
1529840	REC01420	N	378	-	P28917	H repeat-associated protein ydcC	b1460	UNC	0.03
1531076	REC01421	N	77	-	P31992	Hypothetical protein ydcE	b1461	UNC	0.00
1531923	REC04917	N	205	13, 57	P76121	Hypothetical protein ydcH	b1462	UNC	0.06
1532048	REC01423	E	281	-	P77567	N-hydroxyarylamino O-acetyltransferase (EC 2.3.1.118)	b1463	MSM	0.19

1533882	REC04918	ydeE	E	274	-	< 0.2	P37757	Hypothetical protein ydeE	b1464	UNC	0.47
1534641	REC04919	narV	N	226	101		P19316	Respiratory nitrate reductase 2 gamma chain (EC 1.7.99.4)	b1465	SMC	0.22
1535333	REC04920	narW	N	231	18, 94		P19317	Respiratory nitrate reductase 2 delta chain (EC 1.7.99.4)	b1466	SMC	0.09
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)	b1467	SMC	0.22
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)	b1468	SMC	0.22
1542084	REC04923	narU	N	462	2, 72, 95		P37758	Nitrite extrusion protein 2	b1469	SMC	0.25
1542743	REC04924	yddJ	N	111	73, 100		P76122	Hypothetical protein yddJ	b1470	UNC	0.00
1543738	REC04925	yddK	E	318	306	< 0.05	P76123	Hypothetical protein yddK	b1471	UNC	0.03
1544052	REC04926	E	E	96	-	0.34	P77519	FROM BASES 1540626 TO 1550846 (SECTION 134 OF 400) OF THb1472	b1472	UNC	0.00
1545193	REC04927	yddG	N	293	19, 177, 230, 252		P46136	Hypothetical protein yddG	b1473	UNC	0.13
1545425	REC01434	fdnG	N	1015	73, 322, 383, 426, 543, 669, 678, 787, 787		P24183	Formate dehydrogenase, nitrate-inducible, major subunit (EC 1.2.1.2)	b1474	SMC	0.09
1548485	REC01435	fdnH	N	294	67, 176, 229		P24184	Formate dehydrogenase, nitrate-inducible, iron-sulfur subunit	b1475	BEN	0.06
1549362	REC01436	fdnI	N	217	88		P24185	Formate dehydrogenase, nitrate-inducible, cytochrome b556(FDN) su	b1476	SMC	0.13
1550784	REC04928	yddM	E	120	-	0.39	P76125	Hypothetical protein yddM	b1477	UNC	0.00
1551892	REC04929	adhP	N	346	72, 154, 189, 289		P39451	Alcohol dehydrogenase, propanol-preferring (EC 1.1.1.1)	b1478	CHM	0.75
1553720	REC04930	sfcA	N	574	45, 187		P26616	NAD-dependent malic enzyme (EC 1.1.1.38)	b1479	BEN	0.22
1553987	REC04931	rpsV	N	45	10		P28690	30S ribosomal protein S22	b1480	PMS	0.00
1554367	REC04932	bdm	N	92	6, 18		P76127	Bdm protein	b1481	UNC	0.00
1554649	REC01442	osmC	N	143	32, 46		P23929	Osmotically inducible protein C	b1482	UNC	0.22
1556062	REC04933	yddO	N	308	47, 107		P77622	Hypothetical ABC transporter ATP-binding protein yddO	b1483	UNC	0.28
1557041	REC04934	yddP	N	328	86, 242, 279		P77268	Hypothetical ABC transporter ATP-binding protein yddP	b1484	UNC	0.03
1557934	REC04935	yddQ	E	298	-	< 0.05	P77463	Hypothetical ABC transporter permease protein yddQ	b1485	UNC	0.06
1558953	REC04936	yddR	N	340	37, 185, 242		P77308	Hypothetical ABC transporter permease protein yddR	b1486	UNC	0.03
1560505	REC04937	yddS	N	516	46, 62, 102, 141, 152, 207, 281, 299, 312, 339, 368, 398, 444, 464, 465, 466		P76128	Putative ABC transporter periplasmic binding protein yddS precursor	b1487	UNC	0.09
1561100	REC04938	ddpX	N	193	157, 182		P77790	D-alanyl-D-alanine dipeptidase (EC 3.4.13.-)	b1488	SMC	0.16
1563781	REC04939	yddU	N	807	36, 87, 129, 228, 673		P76129	Hypothetical protein yddU	b1489	UNC	0.25
1565164	REC04940	yddV	N	460	81, 175, 276, 288, 351, 362		P77793	Hypothetical protein yddV	b1490	UNC	0.34
1566847	REC04941	yddW	N	439	29, 368, 379		P76130	Hypothetical lipoprotein yddW precursor	b1491	UNC	0.19
1568513	REC04942	xasA	N	511	70		P39183	Amino acid antiporter	b1492	UNC	0.13
1570069	REC04943	gadB	N	466	8, 42, 66, 103, 110, 185, 252, 271, 286, 310		P28302	Glutamate decarboxylase beta (EC 4.1.1.15)	b1493	AAM	0.19
1573226	REC04944	pqqL	N	931	55, 153, 185, 211, 596, 752, 803, 831, 921, 924		P31828	Probable zinc protease pqqL (EC 3.4.99.-)	b1494	UNC	0.84
1575643	REC04945	yddB	N	790	24, 116, 163, 282, 298, 349, 399, 438, 462, 565, 581, 601, 612, 634, 661, 70		P31827	Hypothetical protein yddB	b1495	UNC	0.03
1577366	REC04946	yddA	N	561	98, 131, 193, 193, 224, 251, 282, 320, 328, 347, 382, 413, 417, 447, 487, 49		P31826	Hypothetical ABC transporter ATP-binding protein yddA	b1496	UNC	0.31
1578829	REC04947	ydeM	N	390	60, 128, 280, 361, 369		P76134	Hypothetical protein ydeM	b1497	UNC	0.06
1580581	REC04948	ydeN	N	571	47, 98, 158, 169, 197, 246, 274, 285, 310, 341, 362, 380, 400, 412, 435, 533		P77318	Putative sulfatase ydeN precursor (EC 3.1.6.-)	b1498	UNC	0.06
1581711	REC04949	ydeO	N	253	14, 141, 152, 212, 230		P76135	Hypothetical transcriptional regulator ydeO	b1499	UNC	0.00
1581983	REC04950	?	?	65	-		P76136	FROM BASES 1577448 TO 1588149 (SECTION 137 OF 400) OF THb1500	b1500	UNC	0.00
1584510	REC04951	ydeP	N	759	12, 35, 48, 197, 481, 689, 757		P77561	Hypothetical protein ydeP	b1501	UNC	0.50
1585758	REC04952	ydeQ	N	304	62		P77588	Hypothetical fimbrial-like protein ydeQ precursor	b1502	UNC	0.00
1586320	REC04953	ydeR	N	167	33, 131		P77294	Hypothetical fimbrial-like protein ydeR precursor	b1503	UNC	0.00
1586863	REC04954	ydeS	N	176	27, 74, 117, 120		P77789	Hypothetical fimbrial-like protein ydeS precursor	b1504	UNC	0.00
1588025	REC04955	?	X	59	-		P76137	FROM BASES 1577448 TO 1588149 (SECTION 137 OF 400) OF THb1505	b1505	UNC	0.09
1588560	REC04956	?	X	59	-		P76138	FROM BASES 1588092 TO 1598300 (SECTION 138 OF 400) OF THb1506	b1506	UNC	0.00
1590200	REC04957	hipA	N	440	178, 179		P23874	Protein hipA	b1507	UNC	0.19
1590466	REC04958	hipB	?	88	-		P23873	Protein hipB	b1508	RCD	0.00
1592089	REC04959	ydeU	N	466	70, 236, 351		P77286	Hypothetical protein ydeU	b1509	UNC	0.16
1596110	REC04960	ydeX	N	1325	200, 235, 254, 309, 311, 399, 432, 479, 507, 555, 571, 582, 615, 779, 1116		P32051	Hypothetical lipoprotein ydeX precursor	b1510	UNC	0.19
1598233	REC04961	ydeV	N	530	57, 522		P77432	Hypothetical sugar kinase ydeV	b1511	UNC	0.41
1599265	REC04962	ydeW	N	317	226, 232		P76141	Hypothetical transcriptional regulator ydeW	b1512	UNC	0.16
1599514	REC01473	ego	N	511	242, 396, 497		P77257	Putative ABC transporter ATP-binding protein ego	b1513	UNC	0.06
1601043	REC01474	ydeY	N	342	177, 312		P77672	Hypothetical ABC transporter permease protein ydeY	b1514	UNC	0.03
1602071	REC01475	ydeZ	N	330	187		P77651	Hypothetical ABC transporter permease protein ydeZ	b1515	UNC	0.38
1603075	REC01476	yneA	N	340	76, 135, 171, 187		P76142	Hypothetical protein yneA precursor	b1516	UNC	0.09
1604124	REC01477	yneB	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	yneC	N	96	79		P76144	Hypothetical protein yneC	b1518	UNC	0.09
1605370	REC01479	tam	N	252	204		P76145	Trans-aconitate methyltransferase (EC 2.1.1.-)	b1519	CHM	0.28
1607097	REC04963	yneE	N	321	62		P76146	Hypothetical protein yneE	b1520	UNC	0.13
1608704	REC04964	uxaB	N	483	239		P24214	Altronate oxidoreductase (EC 1.1.1.58)	b1521	CHM	0.13
1609878	REC04965	yneF	N	315	186, 308		P76147	Hypothetical protein yneF	b1522	UNC	0.44
1610349	REC04966	yneG	E	119	-	0.41	P76148	Hypothetical protein yneG	b1523	UNC	0.00
1611275	REC04967	yneH	N	308	113, 208		P77470	Probable glutaminase yneH (EC 3.5.1.2)	b1524	UNC	0.41
1612751	REC04968	yneI	N	470	69, 130		P76149	Aldehyde-dehydrogenase like protein yneI (EC 1.2.1.-)	b1525	UNC	0.63
1612828	REC01486	yneJ	N	293	28, 77, 209, 269		P77309	Hypothetical transcriptional regulator yneJ	b1526	UNC	0.72
1613787	REC01487	yneK	N	371	3, 13, 33, 137, 310, 352, 370		P76150	Hypothetical protein yneK	b1527	UNC	0.00
1615052	REC01488	soxB	N	396	100, 269, 331		P31122	Sugar efflux transporter	b1528	MTR	0.34
1616932	REC04969	marC	N	221	171		P31123	Multiple antibiotic resistance protein marC	b1529	MTR	0.56
1617201	REC01490	marR	N	125	14, 28, 41, 49, 71, 73, 102		P27245	Multiple antibiotic resistance protein marR	b1530	NAM	0.09
1617592	REC01491	marA	E	129	-	< 0.1	P27246	Multiple antibiotic resistance protein marA	b1531	RCD	0.06
1618013	REC01492	marB	?	72	51		P31121	Multiple antibiotic resistance protein marB	b1532	MSM	0.00
1619062	REC04970	eama	N	266	54, 206, 251		P31125	Probable amino acid metabolite efflux pump	b1533	UNC	0.25
1619356	REC01494	ydeE	E	395	323, 370	< 0.001	P31126	Hypothetical protein ydeE	b1534	UNC	0.81
1621874	REC04971	ydeH	N	296	27, 39, 64, 81, 121, 170, 185, 219, 249, 296		P31129	Hypothetical protein ydeH	b1535	UNC	0.00
1622521	REC04972	ydeI	N	130	49, 126		P31130	Hypothetical protein ydeI precursor	b1536	UNC	0.06
1622797	REC01497	ydeJ	X	172	-		P31131	Hypothetical protein ydeJ	b1537	UNC	0.03
1625404	REC04973	dcp	N	681	33, 41, 203, 301, 429		P24171	Peptidyl-dipeptidase dcp (EC 3.4.15.5)	b1538	PMS	0.22
1625541	REC01499	ydfG	N	248	1, 186		P39831	Probable oxidoreductase ydfG (EC 1.-.-.-)	b1539	UNC	0.78
1626376	REC01500	ydfH	N	228	35, 87		P77577	Hypothetical transcriptional regulator ydfH	b1540	UNC	0.53
1627239	REC01501	ydfZ	?	67	-		P76153	Hypothetical protein ydfZ	b1541	UNC	0.00
1628937	REC04974	ydfI	N	486	23, 33, 80, 198, 241, 261		P77260	Hypothetical oxidoreductase ydfI (EC 1.-.-.-)	b1542	UNC	0.03
1630309	REC04975	ydfJ	N	427	49, 188, 254, 306, 398, 412		P77228	Hypothetical metabolite transport protein ydfJ	b1543	UNC	0.41
1631063	REC01504	ydfK	N	88	10, 51, 58		P76154	Hypothetical protein ydfK	b1544	UNC	0.00
1631646	REC01505	pinQ	N	196	7, 58, 74, 103, 118, 180, 192		P77170	Putative DNA-invertase from lambdoid prophage Qin	b1545	UNC	0.00
1632909	REC06567	tfaQ	N	191	25, 77, 112, 166, 180		P76155	Tail fiber assembly protein homolog from lambdoid prophage Qin	b1546	UNC	0.03
1633871	REC04977	stfQ	?	320	267		P77515	Side tail fiber protein homolog from lambdoid prophage Qin	b1547	UNC	0.00
1634391	REC04978	nohA	?	189	165		P31061	Prophage Qin DNA packaging protein NU1 homolog	b1548	UNC	0.00
1635056	REC01509	ydfO	N	141	7, 66		P76156	Hypothetical protein ydfO	b1549	UNC	0.00
1635809	REC04979	gnsB	?	58	-		P77695	GnsB protein	b1550	UNC	0.00
1636169	REC04980	ynfN	?	63	4		P76157	Hypothetical protein ynfN	b1551	UNC	0.00
1636691	REC04981	cspI	?	70	66		P77605	Cold shock-like protein cspI	b1552	UNC	0.72
1637551	REC04982	ydfP	X	165	-		P76158	Hypothetical protein ydfP precursor	b1553	UNC	0.00
1638081	REC04983	ydfQ	N	177	46, 74, 85, 158		P76159	Probable lysozyme from lambdoid prophage Qin (EC 3.2.1.17)	b1554	UNC	0.00
1638389	REC04984	ydfR	E	103	-	< 0.3	P76160	Hypothetical protein ydfR	b1555	UNC	0.00
1638684	REC04985	essQ	E	96	82, 88	< 0.3	P77237	Lysis protein S homolog from lambdoid prophage Qin	b1556	UNC	0.00
1639578	REC04986	cspB	N	71	53		P36995	Cold shock-like protein cspB	b1557	UNC	0.72
1639879	REC01518	cspP	N	70	8, 30		P39819	Cold shock-like protein cspP	b1558	UNC	0.00
1641295	REC04987	ydfT	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	-	P07009	HokD protein	b1562	UNC	0.00
1643657	REC04991	<i>reIE</i>	E	95	-	P07008	Hypothetical relE protein	b1563	UNC	0.06
1643896	REC04992	<i>reIB</i>	E	79	-	P07007	RelB protein	b1564	UNC	0.00
1643921	REC01525	<i>ydfV</i>	E	101	-	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	-	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	-	P19777	Transposase insD for insertion element IS2A/D/F/H/I/K	b1579	PHT	0.56
1649536	REC01538	<i>intQ</i>	N	398	50, 92, 129, 152, 171, 243, 273, 366	P76168	Putative lambdaoid 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	-	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	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 1.8.9.1)	b1587	UNC	0.09
1658577	REC01547	<i>ynfF</i>	N	808	25, 63, 202, 206, 289, 403, 500, 605, 806	P77783	Probable dimethyl sulfoxide reductase chain ynfF precursor (EC 1.8.9.1)	b1588	UNC	0.03
1661014	REC01548	<i>ynfG</i>	E	205	-	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 eriC-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	-	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	P07001	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 protein ydgC	b1607	UNC	0.06
1680174	REC01567	<i>rstA</i>	N	242	65, 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	261, 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>maLI</i>	N	342	320, 342	P18811	Maltose regulon regulatory protein mall	b1620	RCD	0.00
1697379	REC01580	<i>maLX</i>	N	530	45, 149, 628	P19642	PTS system, maltose and glucose-specific IIBC component (EC 2.7.1.40)	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>ydgJ</i>	N	359	4, 41, 71, 89, 146, 154	P77376	Hypothetical oxidoreductase ydgJ (EC 1.-.-)	b1624	UNC	0.38
1702500	REC06681	<i>b1r</i>	N	66	23, 52	P56976	Beta-lactam resistance protein	b1625	MSM	0.00
1702973	REC01584	<i>ydgT</i>	N	71	57	P76179	Hypothetical protein ydgT	b1626	UNC	0.00
1703250	REC01585	<i>ydgK</i>	N	154	26, 38, 78, 141, 151	P76180	Hypothetical protein ydgK	b1626	UNC	0.00
1703791	REC01586	<i>rnfA</i>	N	193	10, 108, 170, 182	P76181	Electron transport complex protein rnfA	b1627	BEN	0.25
1704372	REC01587	<i>rnfB</i>	X	192	-	P77223	Electron transport complex protein rnfB	b1628	BEN	0.28
1704943	REC01588	<i>rnfC</i>	N	740	139, 293, 334, 556, 644	P77611	Electron transport complex protein rnfC	b1629	BEN	0.25
1707166	REC01589	<i>rnfD</i>	N	352	44, 151, 250, 299	P76182	Electron transport complex protein rnfD	b1630	BEN	0.22
1708228	REC01590	<i>rnfG</i>	N	206	73	P77285	Electron transport complex protein rnfG	b1631	BEN	0.13
1708852	REC01591	<i>rnfE</i>	N	231	52, 61, 124	P77179	Electron transport complex protein rnfE	b1632	BEN	0.25
1709547	REC01592	<i>nth</i>	N	211	88, 164, 187	P20625	Endonuclease III (EC 4.2.99.18)	b1633	NAM	0.97
1710793	REC01593	<i>ydgR</i>	E	500	-	P77304	Hypothetical transporter ydgR	b1634	UNC	0.31
1712401	REC01594	<i>gst</i>	N	201	102, 191	P39100	Glutathione S-transferase (EC 2.5.1.18)	b1635	BEN	0.44
1713913	REC05017	<i>pxdY</i>	N	287	38, 153, 180, 197, 242	P77150	Pyridoxamine kinase (EC 2.7.1.35)	b1636	NCM	0.34
1715246	REC05018	<i>tyrS</i>	E	424	160	P00951	Tyrosyl-tRNA synthetase (EC 6.1.1.1)	b1637	PMS	1.00
1716031	REC05019	<i>pxdX</i>	N	218	67, 171	P28225	Pyridoxamine 5'-phosphate oxidase (EC 1.4.3.5)	b1638	NCM	0.47
1716338	REC05020	<i>ydhA</i>	?	82	-	P28224	Hypothetical protein ydhA	b1639	UNC	0.03
1717626	REC05021	<i>ydhH</i>	N	369	70, 145, 212, 300	P77570	Hypothetical protein ydhH	b1640	UNC	0.41
1717900	REC01600	<i>slyB</i>	N	155	64, 102, 133	P55741	Outer membrane lipoprotein slyB precursor	b1641	UNC	0.06
1718854	REC05022	<i>slyA</i>	N	146	7	P55740	Transcriptional regulator slyA	b1642	RCD	0.19
1719049	REC01602	<i>ydhI</i>	?	78	-	P76184	Hypothetical protein ydhI	b1643	UNC	0.00
1719246	REC01603	<i>ydhJ</i>	N	299	188, 294	P76185	Hypothetical protein ydhJ	b1644	UNC	0.06
1720145	REC01604	<i>ydhK</i>	N	670	21, 122, 184, 272, 378, 465, 492, 586	P76186	Hypothetical protein ydhK	b1645	UNC	0.13
1722679	REC05023	<i>sodC</i>	N	173	127, 163	P53635	Superoxide dismutase [Cu-Zn] precursor (EC 1.15.1.1)	b1646	MSM	0.28
1723656	REC05024	<i>ydhP</i>	N	298	141	P76187	Hypothetical oxidoreductase ydhP (EC 1.-.-)	b1647	UNC	0.34
1724047	REC01608	<i>ydhM</i>	N	199	105	P76189	Hypothetical transcriptional regulator ydhM	b1649	UNC	0.13
1724082	REC05025	<i>ydhL</i>	E	125	-	P76188	Hypothetical protein ydhL precursor	b1648	UNC	0.25
1724683	REC01609	<i>nema</i>	N	365	86, 219, 301	P77258	N-ethylmaleimide reductase (EC 1.-.-)	b1650	BEN	0.50
1725861	REC01610	<i>gloA</i>	?	135	76	Q59384	Lactoylglutathione lyase (EC 4.4.1.5)	b1651	CHM	0.53
1726371	REC01611	<i>rnt</i>	E	215						

1735868	REC01617	<i>purR</i>	N	341	19, 289	P15039	Purine nucleotide synthesis repressor	b1658	RCD	0.22
1737822	REC05028	<i>ydhB</i>	N	310	99	P37598	Hypothetical transcriptional regulator ydhB	b1659	UNC	0.06
1737935	REC01619	<i>ydhC</i>	N	403	147, 203, 306	P37597	Hypothetical transport protein ydhC	b1660	UNC	0.59
1739437	REC01620	<i>cfa</i>	N	382	127, 263, 302	P30010	Cyclopropane-fatty-acyl-phospholipid synthase (EC 2.1.1.79)	b1661	LPC	0.47
1741266	REC05029	<i>ribE</i>	E	213	-	P29015	Riboflavin synthase alpha chain (EC 2.5.1.9)	b1662	NCM	0.84
1741481	REC01622	<i>norM</i>	N	457	133, 335, 456	P37340	Multidrug resistance protein norM	b1663	MTR	0.88
1744151	REC05030	<i>ydhQ</i>	N	418	260, 309, 310, 352, 405	P77552	Hypothetical protein ydhQ	b1664	UNC	0.00
1744724	REC01624	<i>ydhR</i>	E	101	-	P77225	Protein ydhR precursor	b1667	UNC	0.00
1745155	REC01625	<i>ydhs</i>	N	534	27, 109, 189, 381, 382, 400	P77148	Hypothetical protein ydhs	b1668	UNC	0.00
1747583	REC05031	<i>ydht</i>	N	270	78	P77147	Hypothetical protein ydht	b1669	UNC	0.00
1748372	REC05032	<i>ydhu</i>	N	261	77, 82, 184, 207	P77409	PhsC protein homolog	b1670	UNC	0.00
1749088	REC05033	<i>ydhx</i>	E	239	222	P77375	Putative ferredoxin-like protein ydHX	b1671	UNC	0.00
1749748	REC05034	<i>ydhw</i>	?	215	15	P77564	Hypothetical protein ydhw	b1672	UNC	0.00
1751854	REC05035	<i>ydhv</i>	N	700	31, 173, 424, 665	P76192	Hypothetical protein ydhV	b1673	UNC	0.03
1752501	REC05036	<i>ydhy</i>	N	208	36, 65, 186	P77186	Putative ferredoxin-like protein ydHY	b1674	UNC	0.00
1753165	REC05037	<i>ydhz</i>	N	69	10, 29, 45, 64	P77274	Hypothetical protein ydHZ	b1675	UNC	0.00
1753722	REC01633	<i>pykF</i>	N	470	139, 405	P14178	Pyruvate kinase I (EC 2.7.1.40)	b1676	CHM	0.88
1755445	REC01634	<i>lpp</i>	X	78	-	P02937	Major outer membrane lipoprotein precursor	b1677	LPC	0.00
1756749	REC05038	<i>ynhG</i>	N	334	182	P76193	Hypothetical protein ynhG precursor	b1678	UNC	0.19
1757314	REC05039	<i>sufE</i>	N	138	105	P76194	SufE protein	b1679	UNC	0.31
1758547	REC05040	<i>csdB</i>	N	406	103, 286, 300, 337, 345, 391	P77444	Selenocysteine lyase (EC 4.4.1.16)	b1680	NCM	0.94
1759815	REC05041	<i>sufD</i>	N	423	64, 379	P77689	SufD protein	b1681	UNC	0.59
1760536	REC05042	<i>sufC</i>	N	248	88, 118	P77499	Probable ATP-dependent transporter sufC	b1682	UNC	0.59
1762072	REC05043	<i>sufB</i>	N	508	9, 88, 247	P77522	SufB protein	b1683	UNC	0.59
1762410	REC05044	<i>sufA</i>	E	122	122	P77667	SufA protein	b1684	UNC	0.66
1763227	REC05045	<i>ydiH</i>	?	89	-	P76195	Hypothetical protein ydiH	b1685	UNC	0.00
1763656	REC05046	<i>ydiI</i>	E	136	-	P77781	Hypothetical protein ydiI	b1686	UNC	0.28
1766709	REC05047	<i>ydiJ</i>	N	1018	19, 38, 59, 76, 273, 321, 361, 486	P77748	Hypothetical protein ydiJ	b1687	UNC	0.16
1767098	REC01645	<i>ydiK</i>	N	370	127, 298	P77175	Hypothetical protein ydiK	b1688	UNC	0.69
1768612	REC01646	<i>ydiL</i>	N	127	60, 68	P76196	Hypothetical protein ydiL	b1689	UNC	0.00
1769095	REC01647	<i>ydiM</i>	N	404	55, 330, 365	P76197	Hypothetical transport protein ydiM	b1690	UNC	0.06
1770530	REC01648	<i>ydiN</i>	N	423	118, 151, 169, 195, 231, 262, 301, 322, 391	P76198	Hypothetical transport protein ydiN	b1691	UNC	0.06
1771813	REC01649	<i>ydiB</i>	N	288	131	P28244	Hypothetical shikimate 5-dehydrogenase-like protein ydiB	b1692	UNC	0.88
1772710	REC01650	<i>aroD</i>	N	252	14, 190, 223, 227	P05194	3-dehydroquinate dehydratase (EC 4.2.1.10)	b1693	AAM	0.19
1773611	REC01651	<i>ydiF</i>	N	531	14, 19, 82, 117, 132, 173, 210, 224, 255, 287, 289, 321, 330, 393, 508	P37766	Hypothetical protein ydiF	b1694	UNC	0.22
1775166	REC01652	<i>ydiO</i>	E	401	55	P76200	Hypothetical protein ydiO	b1695	UNC	0.44
1777325	REC05048	<i>ydiP</i>	N	303	54, 80, 84, 128, 174, 219	P77402	Hypothetical transcriptional regulator ydiP	b1696	UNC	0.31
1777641	REC01654	<i>ydiQ</i>	N	254	32, 128, 208	P76201	Putative electron transfer flavoprotein subunit ydiQ	b1697	UNC	0.09
1778425	REC01655	<i>ydiR</i>	E	312	19	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 ydiS	b1699	UNC	0.22
1780705	REC01657	<i>ydiT</i>	E	97	-	P77714	Ferredoxin-like protein ydiT	b1700	UNC	0.13
1781001	REC01658	<i>ydiD</i>	N	566	192, 198, 283, 427, 468, 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	-	P00887	Phospho-2-dehydro-3-deoxyheptonate aldolase, Trp-sensitive (EC 4.1.1.1)	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	-	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>rplT</i>	E	118	-	P02421	50S ribosomal protein L20	b1716	PMS	1.00
1798023	REC05061	<i>rplM</i>	?	65	56	P07085	50S ribosomal protein L35	b1717	PMS	0.28
1798662	REC05062	<i>infC</i>	E	180	-	P02999	Translation initiation factor IF-3	b1718	PMS	1.00
1800594	REC05063	<i>thrs</i>	E	642	-	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, 365, 446	P76205	Ankyrin-repeat protein B	b1721	UNC	0.00
1804107	REC05064	<i>ydiY</i>	E	252	3	P76206	Hypothetical protein ydiY precursor	b1722	UNC	0.06
1804394	REC01680	<i>pfkB</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	-	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, 293, 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>ydiC</i>	N	249	55	P37794	Hypothetical protein ydiC	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)	b1734	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	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	-	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	-	P18843	NH(3)-dependent NAD(+) synthetase (EC 6.3.5.1)	b1740	NCM	0.91
1821539	REC01698	<i>ydiQ</i>	E	295	-	P76213	Hypothetical protein ydiQ	b1741	UNC	0.00
1823024	REC05075	<i>ydiR</i>	E	212	-	P76214	Hypothetical protein ydiR	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	-	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	P76218	Arginine N-succinyltransferase (EC 2.3.1.109)	b1747	AAM	0.09
1830006	REC05081	<i>argM</i>	N	406	30, 100, 221, 226, 348	P77581	Succinylomithine transaminase (EC 2.6.1.-)	b1748	AAM	0.34
1830452	REC01706	<i>xthA</i>	N	288	90, 94, 214	P09030	Exodeoxyribonuclease III (EC 3.1.11.2)	b1749	NAM	0.81
1831377	REC01707	<i>ydiX</i>	N	252	41, 210, 224	P76219	Hypothetical protein ydiX	b1750	UNC	0.00
1831978	REC01708	<i>ydiY</i>	N	279	10, 24, 105	P76220	Hypothetical protein ydiY precursor	b1751	UNC	0.03
1832832	REC01709	<i>ydiZ</i>	N	235	4, 52	P76221	Hypothetical protein ydiZ	b1752	UNC	0.28
1833539	REC01710	<i>ynjA</i>	E	182	-	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	-	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 pyrophosphohydrolase (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	-	P16456	Selenide, water dikinase (EC 2.7.9.3)	b1764	MSM	0.16
1846700	REC05087	<i>ydjA</i>	E	183	-	P24250	Protein ydjA	b1765	UNC	0.31
1846861	REC01723	<i>sppA</i>	N	618	36, 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 3.5.1.1)	b1767	AAM	0.56
1849893	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, 288	P77280	Hypothetical zinc-type alcohol dehydrogenase-like protein ydjJ	b1774	UNC	0.56
1858253	REC05094	<i>ydjK</i>	N	459	387	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	-	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, 388, 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 TH1788	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	-	P76242	Hypothetical transport protein yeaN	b1791	UNC	0.53
1874912	REC01749	<i>yeaO</i>	E	122	-	P76243	Hypothetical protein yeaO	b1792	UNC	0.25
1875556	REC05102	<i>yeaP</i>	?	84	-	P76244	Hypothetical protein yeaP	b1793	UNC	0.00
1875610	REC01751	<i>yeaQ</i>	N	384	193, 232, 286, 299, 336, 378	P76245	Hypothetical protein yeaQ	b1794	UNC	0.00
1877279	REC05103	<i>yeaR</i>	N	82	6, 14, 67, 79	P76246	Hypothetical protein yeaR	b1795	UNC	0.09
1877609	REC05104	<i>yeaG</i>	?	60	-	P76247	Hypothetical protein yeaG	b1796	UNC	0.00
1877972	REC05105	<i>yeaR</i>	?	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	-	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	-	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>yoaB</i>	X	192	-	P43337	Hypothetical protein yoaB	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>yoeA</i>	N	518	71, 280, 390, 446	P76262	Hypothetical protein yoeA	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>yobN</i>	N	206	139	P76264	Hypothetical protein yobN	b1821	UNC	0.25
1905084	REC05115	<i>rrmA</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>yobO</i>	N	95	55	P76266	Hypothetical protein yobO	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	-	P45577	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	-	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	-	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	-	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/KDGP 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	-	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, 288	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 (KDO2)-(lauroyl)-lipid IVA acyltransferase (EC 2.3.1.17)	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 endonuclease 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, 87	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 biosynthetic 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	P07364	Chemotaxis protein methyltransferase (EC 2.1.1.80)	b1884	SMC	0.47
1969008	REC05156	<i>tap</i>	N	533	54, 161, 205, 213, 320, 349, 481	P07018	Methyl-accepting chemotaxis protein IV	b1885	SMC	0.63	
1970715	REC05157	<i>tar</i>	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	<i>cheW</i>	E	167	166	< 0.1	P07365	Chemotaxis protein cheW	b1887	SMC	0.41
1973348	REC05159	<i>cheA</i>	N	654	90, 186, 233, 319, 322, 515, 527	P07363	Chemotaxis protein cheA (EC 2.7.3.-)	b1888	MSM	0.56	
1974279	REC05160	<i>motB</i>	N	308	168, 283	P09349	Chemotaxis motB protein	b1889	SMC	0.50	
1975163	REC05161	<i>motA</i>	E	295	-	< 0.05	P09348	Chemotaxis motA protein	b1890	SMC	0.53
1975868	REC05162	<i>flhC</i>	N	192	108	P11165	Flagellar transcriptional activator flhC	b1891	RCD	0.03	
1976230	REC05163	<i>flhD</i>	N	119	14, 20, 67	P11164	Flagellar transcriptional activator flhD	b1892	RCD	0.03	
1977045	REC06654	<i>insB6</i>	N	167	67, 158	P03830	Insertion element IS1 1/5/6 protein insB	b3445	PHT	0.00	
1977239	REC06655	<i>insA6</i>	X	91	-	P03827	Insertion element IS1 1/2/3/5/6 protein insA	b3444	PHT	0.00	
1977777	REC01852	<i>yecG</i>	E	142	-	0.33	P46888	Hypothetical protein yecG	b1896	UNC	0.06
1979636	REC05166	<i>otsA</i>	N	474	-	P31677	Alpha,alpha-trehalose-phosphate synthase [UDP-forming] (EC 2.4.1.1)	b1896	CHM	0.19	
1980411	REC05167	<i>otsB</i>	N	266	-	P31678	Trehalose-phosphatase (EC 3.1.3.12)	b1897	CHM	0.13	
1980838	REC05168	<i>araH</i>	N	86	-	P08532	L-arabinose transport system permease protein araH	b1898	MTR	0.00	
1981566	REC05169	<i>araB</i>	N	234	14, 74, 205, 214	P08533	L-arabinose transport system permease protein araH	b1899	MTR	0.13	
1983092	REC05170	<i>araG</i>	E	504	-	< 0.01	P08531	L-arabinose transport system permease protein araG	b1900	MTR	0.06
1984151	REC05171	<i>araF</i>	E	329	174, 308	< 0.05	P02924	L-arabinose-binding periplasmic protein precursor	b1901	MTR	0.00
1984948	REC01859	<i>ftnB</i>	N	167	18, 47, 70, 124	P52009	Ferritin-like protein 2	b1902	UNC	0.09	
1985467	REC01860		N	112	65	P76307	FROM BASES 1975196 TO 1986052 (SECTION 173 OF 400) OF TH	b1903	UNC	0.00	
1986245	REC01861	<i>yecR</i>	N	107	66	P76308	Hypothetical protein yecR	b1904	UNC	0.00	
1986739	REC01862	<i>ftnA</i>	N	165	51, 76, 153	P23887	Ferritin 1	b1905	NCM	0.28	
1987513	REC05172	<i>yecH</i>	?	79	-	P46887	Hypothetical protein yecH	b1906	UNC	0.00	
1987704	REC01864	<i>tyrP</i>	N	403	10, 34, 56, 223, 244, 334, 335, 360	P18199	Tyrosine-specific transport protein	b1907	MTR	0.16	
1989642	REC05173	<i>yecA</i>	N	221	166	P06979	Hypothetical protein yecA	b1908	UNC	0.09	
1990840	REC05174	<i>pgsA</i>	E	182	-	< 0.1	P06978	CDP-diacylglycerol-glycerol-3-phosphate 3-phosphatidyltransferase	b1912	LPC	0.94
1992663	REC05175	<i>uvrC</i>	N	588	94, 145, 163, 257, 297, 442	P07028	Excinuclease ABC subunit C	b1913	NAM	0.97	
1993382	REC05176	<i>uvrY</i>	N	218	8, 38, 96, 147, 173	P7027	UvrY protein	b1914	UNC	0.31	
1993841	REC01869	<i>yecF</i>	N	74	1, 13, 69	P46120	Hypothetical protein yecF	b1915	UNC	0.00	
1994855	REC05177	<i>sdiA</i>	N	240	51, 55, 74, 80, 97, 106, 118, 204	P07026	Regulatory protein sdiA	b1916	RCD	0.19	
1995837	REC05178	<i>yecC</i>	N	250	27, 106, 194	P37774	Hypothetical amino-acid ABC transporter ATP-binding protein yecC	b1917	UNC	0.34	
1996502	REC05179	<i>yecS</i>	N	222	47, 170, 207	P76315	Hypothetical amino-acid ABC transporter permease protein yecS	b1918	UNC	0.66	
1997599	REC05180	<i>yedO</i>	X	360	-	P76316	Putative 1-aminocyclopropane-1-carboxylate deaminase (EC 4.1.99.-)	b1919	UNC	0.19	
1998408	REC05181	<i>fliY</i>	?	266	17	P39174	Cystine-binding periplasmic protein precursor	b1920	MTR	0.53	
1999083	REC05182	<i>fliZ</i>	N	195	24, 165, 190	P52627	FliZ protein	b1921	UNC	0.00	
1999812	REC05183	<i>fliA</i>	N	239	50, 84, 127, 154	P31804	RNA polymerase sigma factor for flagellar operon	b1922	RCD	0.44	
2001629	REC05184	<i>fliC</i>	N	498	17, 21, 43, 114, 130, 166, 212, 297, 414	P04949	Flagellin	b1923	SMC	0.53	
2001895	REC01878	<i>fliD</i>	N	468	24, 62, 139, 166, 208, 278, 325, 465	P24216	Flagellar hook-associated protein 2	b1924	SMC	0.28	
2003326	REC01879	<i>fliS</i>	N	136	61	P26608	Flagellar protein flis	b1925	UNC	0.31	
2003736	REC01880	<i>fliT</i>	N	121	73	P26610	Flagellar protein flit	b1926	UNC	0.00	
2004179	REC01881	<i>amyA</i>	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	<i>yedD</i>	N	137	94	P31063	Hypothetical lipoprotein yedD precursor	b1928	UNC	0.00	
2006300	REC01883	<i>yedE</i>	E	401	249	< 0.001	P31064	Hypothetical protein yedE	b1929	UNC	0.06
2007502	REC01884	<i>yedF</i>	N	77	50	P31065	Hypothetical protein yedF	b1930	UNC	0.09	
2007844	REC01885	<i>yedK</i>	?	217	152	P76318	Hypothetical protein yedK	b1931	UNC	0.22	
2008622	REC01886	<i>yedL</i>	N	159	18, 34, 77, 110, 142	P76319	Hypothetical acetyltransferase yedL (EC 2.3.1.-)	b1932	UNC	0.19	
2009561	REC05186	<i>yedN</i>	?	63	-	P76321	Hypothetical protein yedN	b1933	UNC	0.00	
2009891	REC05187	<i>yedM</i>	N	106	20	P76322	Hypothetical protein yedM	b1935	UNC	0.00	
2010373	REC05188	<i>yedM</i>	N	116	56	P76323	FROM BASES 2008529 TO 2019581 (SECTION 176 OF 400) OF TH	b1936	UNC	0.00	
2010524	REC01890		N	92	33	P76323	FROM BASES 2008529 TO 2019581 (SECTION 176 OF 400) OF TH	b1936	UNC	0.00	
2011036	REC05189	<i>fliE</i>	X	104	-	P25797	Flagellar hook-basal body complex protein flie	b1937	SMC	0.28	
2011251	REC01892	<i>fliF</i>	N	552	183, 226, 452	P25798	Flagellar M-ring protein	b1938	SMC	0.56	
2012902	REC01893	<i>fliG</i>	N	331	92, 211, 261	P31067	Flagellar motor switch protein flig	b1939	SMC	0.56	
2013869	REC01894	<i>fliH</i>	N	235	106, 167	P31068	Flagellar assembly protein flih	b1940	SMC	1.00	
2014576	REC01895	<i>fliI</i>	N	457	195, 269, 408	P52612	Flagellum-specific ATP synthase (EC 3.6.3.14)	b1941	SMC	0.13	
2015968	REC01896	<i>fliJ</i>	E	147	146	< 0.3	P52613	Flagellar flij protein	b1942	SMC	0.09
2016408	REC01897	<i>fliK</i>	N	375	62, 136, 221, 244, 328, 338	P52614	Flagellar hook-length control protein	b1943	SMC	0.13	
2017640	REC01898	<i>fliL</i>	E	154	-	< 0.2	P06973	Flagellar filL protein	b1944	SMC	0.28
2018109	REC01899	<i>fliM</i>	N	334	27, 195, 245	P06974	Flagellar motor switch protein flim	b1945	SMC	0.53	
2019110	REC01900	<i>fliN</i>	E	137	-	< 0.2	P15070	Flagellar motor switch protein flin	b1946	SMC	0.56
2019586	REC01901	<i>fliO</i>	N	101	42	P22586	Flagellar protein flio	b1947	SMC	0.06	
2019891	REC01902	<i>fliP</i>	N	245	10, 32, 217	P33133	Flagellar biosynthetic protein flip precursor	b1948	UNC	0.59	
2020638	REC01903	<i>fliQ</i>	N	89	48	P33134	Flagellar biosynthetic protein fliq	b1949	SMC	0.41	
2020915	REC01904	<i>fliR</i>	N	261	184, 233	P33135	Flagellar biosynthetic protein flir	b1950	SMC	0.53	
2021990	REC01905	<i>rcsA</i>	N	207	12, 63, 142	P24210	Colanic acid capsular biosynthesis activation protein A	b1951	SMC	0.00	

2022993	REC01907	yodD	?	80	-	P76328	Hypothetical protein yodD	b1953	UNC	0.00
2023533	REC01908	yedP	N	271	53, 55, 153	P76329	Hypothetical protein yedP	b1955	UNC	0.00
2026054	REC05191	yedQ	N	569	74, 87	P76330	Hypothetical protein yedQ	b1956	UNC	0.22
2026392	REC05192	yodC	?	60	-	P76331	Hypothetical protein yodC	b1957	UNC	0.00
2027388	REC05193	yedI	N	305	74, 211, 239, 298	P46125	Hypothetical protein yedI	b1958	UNC	0.25
2027561	REC01912	yedA	N	306	125	P09185	Hypothetical transport protein yedA	b1959	UNC	0.16
2028940	REC05194	vsr	N	156	90	P09184	Very short patch repair protein (EC 3.1.-.-)	b1960	UNC	0.09
2030339	REC05195	dcm	E	472	452	P11876	DNA-cytosine methyltransferase (EC 2.1.1.73)	b1961	NAM	0.16
2031101	REC05196	yedJ	N	231	3, 26, 170	P46144	Hypothetical protein yedJ	b1962	UNC	0.19
2031524	REC05197	yedR	?	127	5	P76334	Hypothetical protein yedR	b1963	UNC	0.00
2032043	REC01917	yedS	N	171	79, 85, 106, 118	P76335	Potential outer membrane protein yedS precursor	b1964	UNC	0.00
2032568	REC01918	yedS	?	69	-	P76335	Potential outer membrane protein yedS precursor	b1965	UNC	0.00
2032861	REC01919	yedS	N	134	79, 129	P76335	DE: POTENTIAL OUTER MEMBRANE PROTEIN YEDS PRECURSOR	b1966	UNC	0.00
2033857	REC01920	yedU	N	283	3, 22, 44, 67, 98, 162, 228, 279	P31658	Protein yedU	b1967	UNC	0.16
2036174	REC05198	yedV	N	452	397, 438	P76339	Putative sensor-like histidine kinase yedV (EC 2.7.3.-)	b1968	UNC	0.03
2036893	REC05199	yedW	N	239	-	P76340	Probable transcriptional regulatory protein yedW	b1969	UNC	0.81
2036978	REC01923	yedX	N	137	-	P76341	Transthyretin-like protein precursor	b1970	UNC	0.31
2037500	REC01924	yedY	N	334	-	P76342	Hypothetical protein yedY	b1971	UNC	0.31
2038505	REC01925	yedZ	N	211	135, 173, 189	P76343	Hypothetical protein yedZ	b1972	UNC	0.25
2039397	REC01926	yodA	N	216	54, 61, 127, 208	P76344	Hypothetical protein yodA	b1973	UNC	0.13
2040360	REC01927	yodB	N	186	37, 104, 115, 154	P76345	Cytochrome b561 homolog 1	b1974	UNC	0.31
2041634	REC01928	yeeI	E	278	259	P76346	Hypothetical protein yeeI	b1976	UNC	0.13
2042885	REC01929	yeeJ	N	2383	69, 219, 370, 463, 595, 645, 758, 963, 1084, 1198, 1243, 1361, 1419, 1612	P76347	Hypothetical protein yeeJ	b1978	UNC	0.00
2050624	REC05200	yeeL	?	108	80	P76349	Hypothetical protein yeeL	b1979	UNC	0.00
2051350	REC05201	yeeL	X	234	-	P76349	Hypothetical protein yeeL	b1980	UNC	0.00
2051665	REC01932	shiA	N	438	135, 360, 378	P76350	Shikimate transporter	b1981	MTR	0.41
2053083	REC01933	amn	N	484	24, 60, 82, 117, 285, 293, 406, 424	P15272	AMP nucleosidase (EC 3.2.2.4)	b1982	NCM	0.28
2054880	REC01934	yeeN	N	238	79	P76351	Hypothetical protein yeeN	b1983	UNC	0.16
2057868	REC06488	yeeO	?	547	-	P76352	Hypothetical protein yeeO	b1985	UNC	0.22
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	57, 117, 271, 323	P36562	Nicotinate-nucleotide-dimethylbenzimidazole phosphoribosyltransferase	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	yeeP	N	338	247	P03837	Transposase insH for insertion sequence element ISS	b1994	PHT	0.34
2066630	REC01943	yeeP	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	yeeP	X	86	-	P76358	FROM BASES 2060088 TO 2072764 (SECTION 181 OF 400) OF TH	b1998	UNC	0.00
2068523	REC01947	yeeP	N	236	106, 135	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	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	-	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	0.00
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	b2017	UNC	0.16
2087762	REC05221	yefM	X	92	59	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.-)	b2023	AAM	0.75
2093144	REC01972	hisA	N	246	123, 146, 216	P10371	1-(5-phosphoribosyl)-5-[(5-phosphoribosylamino)methylideneamino]ri	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, 63, 83, 119, 147, 180, 210, 217, 254, 268, 289, 311, 328, 349	P76373	UDP-glucose 6-dehydrogenase (EC 1.1.1.12)	b2028	SMC	0.59
2099290	REC05224	gnd	N	468	103, 374, 401	P00350	6-phosphogluconate dehydrogenase, decarboxylating (EC 1.1.1.44)	b2029	CHM	0.69
2100933	REC04395	yeeP	?	338	284	P03837	Transposase insH for insertion sequence element ISS	b2030	PHT	0.34
2101411	REC05226	wbbL	N	157	26, 40, 109, 132	P36667	Putative lipopolysaccharide biosynthesis glycosyl transferase wbbL (b2031	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, 189	P37750	Putative lipopolysaccharide biosynthesis O-acetyl transferase wbbJ (b2033	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-dehydrodihydroxymethyl-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 thymidyllyltransferase (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-dehydrodihydroxymethyl-3,5-epimerase 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	galP	E	297	297	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 guanylyltransferase (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 mannosyl hydrolase (EC 3.6.1.-)	b2051	CHM	0.03
2125212	REC05247	fcl1	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, 126, 175	P71240	Putative colanic acid biosynthesis acetyltransferase wcaF (EC 2.3.1. b2054	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	13, 31	P77558	Putative colanic acid biosynthesis acetyltransferase wcaB (EC 2.3.1.)	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	P77153	Low molecular weight protein-tyrosine-phosphatase wzb (EC 3.1.3.48)	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	20, 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	aIka	N	282	7, 18, 212, 265	P04395	DNA-3-methyladenine glycosylase II (EC 3.2.2.21)	b2068	NAM	0.41
2145633	REC02017	yegD	N	471	16, 22, 98, 112, 156, 208, 354, 396	P36928	Hypothetical chaperone protein yegD	b2069	UNC	1.00
2149007	REC05262	yegI	N	648	156, 299, 343, 359, 450	P76393	Hypothetical protein yegI	b2070	UNC	0.06
2149207	REC02019	yegJ	N	153	89, 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	-	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, 87, 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	-	P76402	Hypothetical protein yegP	b2080	UNC	0.06
2163690	REC02029	yegQ	N	453	118, 289, 338, 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	?	N	48	-	P76404	FROM BASES 2163066 TO 2175408 (SECTION 188 OF 400) OF THb2083	b2083	UNC	0.00
2166023	REC05267	?	N	88	53, 68	P76405	FROM BASES 2163066 TO 2175408 (SECTION 188 OF 400) OF THb2084	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	b2087	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	56	O07943	GALACTITOL UTILIZATION OPERON REPRESSOR	b2090	RCD	0.00
2170895	REC05271	gatD	E	346	9	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	flaB	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, 187, 206	P76420	Hypothetical transcriptional regulator yegW	b2101	UNC	0.53
2181680	REC05279	yegX	N	275	19, 50, 51, 96, 127, 255, 283	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	-	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, 506	P33341	Hypothetical outer membrane usher protein yehB precursor	b2109	UNC	0.13
2189665	REC05285	yehC	E	239	-	P33342	Hypothetical fimbrial chaperone yehC precursor	b2110	UNC	0.00
2190242	REC05286	yehD	E	180	-	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	-	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	0.60
2195430	REC02064	moIR	N	645	34, 65, 68, 103, 104, 164, 204, 206, 253, 264, 327, 612	P33345	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, 236, 282, 383, 422, 425, 468, 545, 555, 761, 785, 857, 1130	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, 128, 153, 190, 214, 263	P33348	Hypothetical protein yehL	b2120	UNC	0.03
2203715	REC02068	yehM	N	759	272, 478, 566, 734, 751	P33349	Hypothetical protein yehM	b2121	UNC	0.03
2205987	REC02069	yehP	N	378	6, 70, 74, 130, 132, 182, 242	P33352	Hypothetical protein yehP	b2122	UNC	0.00
2207096	REC02070	yehQ	N	622	469, 606, 607	P33353	Hypothetical protein yehQ	b2123	UNC	0.06
2209233	REC02071	yehR	N	157	2, 45, 103	P33354	Hypothetical lipoprotein yehR precursor	b2124	UNC	0.00
2210216	REC05289	yehS	N	156	13, 72, 117	P33355	Hypothetical protein yehS	b2125	UNC	0.06
2210997	REC05290	yehT	N	244	25, 138	P33356	Hypothetical protein yehT	b2126	UNC	0.16
2212664	REC05292	yehU	N	561	64, 102, 107, 235, 268, 296, 442, 507	P33357	Hypothetical protein yehU precursor	b2127	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, 256	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	201, 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	b2138	UNC	0.00
2226859	REC05302	yohH	N	96	2, 31, 74	P33370	?	b2139	UNC	0.00
2228405	REC05303	yohI	N	315	84, 163, 168, 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	cdt	N	294	164, 215, 253	P13652	Cytidine deaminase (EC 3.5.4.5)	b2143	NCM	0.06
2230898	REC02093	sana	N	239	81, 87, 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
2232379	REC02096	yehI	N	413	89, 229, 301, 310, 407, 412	P25889	Hypothetical transport protein yehI	b2147	UNC	0.31
2235773	REC05304	mgIC	?	336	13, 32	P23200	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, 298, 322, 322, 345, 364, 387	P23199	Galactoside transport ATP-binding protein mgIA	b2149	MTR	0.59

2238368	REC05306	<i>mgIB</i>	E	332	-	< 0.01	P02927	D-galactose-binding periplasmic protein precursor	b2150	MTR	0.19
2239688	REC05307	<i>galS</i>	N	346	4, 24, 56, 63, 150, 170		P25748	MgI repressor and galactose ultrainduction factor	b2151	RC	0.03
2240987	REC05308	<i>yeiB</i>	N	385	201, 225, 240, 260, 318, 362		P25747	Hypothetical protein yeiB	b2152	UNC	0.16
2241672	REC05309	<i>foIE</i>	E	222	-	< 0.1	P27511	GTP cyclohydrolase 1 (EC 3.5.4.16)	b2153	NCM	0.75
2241930	REC02103	<i>yeiG</i>	N	278	143		P33018	Hypothetical protein yeiG	b2154	UNC	0.28
2244789	REC05310	<i>cirA</i>	N	663	-		P17315	Colicin I receptor precursor	b2155	UNC	0.34
2246552	REC05311	<i>lysp</i>	N	489	-		P25737	Lysine-specific permease	b2156	MTR	0.34
2247638	REC05312	<i>yeiE</i>	N	293	-		P32484	Hypothetical transcriptional regulator yeiE	b2157	UNC	0.72
2247737	REC02107	<i>yeiH</i>	N	349	-		P33019	Hypothetical protein yeiH	b2158	UNC	0.44
2248860	REC02108	<i>nfo</i>	N	285	-		P12638	Endonuclease IV (EC 3.1.21.2)	b2159	NAM	0.31
2249720	REC02109	<i>yeiI</i>	N	362	-		P33020	Hypothetical sugar kinase yeiI	b2160	UNC	0.59
2252165	REC05313	<i>yeiJ</i>	E	416	-	< 0.05	P33021	Hypothetical transport protein yeiJ	b2161	UNC	0.22
2253206	REC05314	<i>yeiK</i>	N	313	-		P33022	Hypothetical protein yeiK	b2162	UNC	0.41
2253375	REC02112	<i>yeiL</i>	E	219	-	< 0.05	P33023	Hypothetical protein yeiL	b2163	UNC	0.00
2253535	REC05315	<i>yeiM</i>	E	416	-	< 0.01	P33024	Hypothetical transport protein yeiM	b2164	UNC	0.22
2256387	REC05316	<i>yeiN</i>	?	312	136, 213, 216, 275		P33025	Hypothetical protein yeiN	b2165	UNC	0.22
2257316	REC05317	<i>yeiC</i>	N	313	-		P30235	Hypothetical sugar kinase yeiC	b2166	UNC	0.59
2259430	REC05318	<i>fruA</i>	N	563	144, 184, 235, 287, 302, 383, 411, 455, 549		P20966	PTS system, fructose-specific IIBC component (EC 2.7.1.69)	b2167	MTR	0.47
2260385	REC05319	<i>fruK</i>	N	312	95, 311		P23539	1-phosphofructokinase (EC 2.7.1.56)	b2168	CHM	0.50
2261515	REC05320	<i>fruB</i>	N	376	41, 107, 164, 172		P24217	PTS system, fructose-specific IIA/FPF component (EC 2.7.1.69)	b2169	MTR	0.09
2261883	REC02119	<i>setB</i>	N	393	80, 157, 200		P33026	Sugar efflux transporter B	b2170	MTR	0.00
2263215	REC02120	<i>yeiP</i>	N	275	55, 190, 217, 243, 250, 265		P33028	Protein yeiP	b2171	UNC	1.00
2264265	REC02121	<i>yeiQ</i>	N	488	67, 176, 248, 328, 483		P33029	Hypothetical oxidoreductase yeiQ (EC 1.-.-.-)	b2172	UNC	0.28
2265849	REC02122	<i>yeiR</i>	N	328	25, 83, 312		P33030	Hypothetical protein yeiR	b2173	UNC	0.56
2266838	REC02123	<i>yeiU</i>	N	249	38, 70, 90, 92, 204, 224		P76445	Hypothetical protein yeiU	b2174	UNC	0.03
2267999	REC02124	<i>spr</i>	N	188	30, 38, 66, 80, 139		P77685	Lipoprotein spr precursor	b2175	LPC	0.16
2268746	REC02125	<i>rtn</i>	N	518	107, 213, 402, 452		P76446	Rtn protein	b2176	UNC	0.31
2270378	REC02126	<i>yejA</i>	N	606	67, 170, 301, 302, 404, 497, 499		P33913	Hypothetical protein yejA precursor	b2177	UNC	0.25
2272199	REC02127	<i>yejB</i>	N	364	69, 210, 313, 344, 345		P33914	Hypothetical ABC transporter permease protein yejB	b2178	UNC	0.28
2273293	REC02128	<i>yejE</i>	E	341	295	< 0.05	P33915	Hypothetical ABC transporter permease protein yejE	b2179	UNC	0.81
2274320	REC02129	<i>yejF</i>	N	529	23, 43, 80, 363, 479		P33916	Hypothetical ABC transporter ATP-binding protein yejF	b2180	UNC	0.31
2276257	REC05321	<i>yejG</i>	N	114	28		P33917	Hypothetical protein yejG	b2181	UNC	0.00
2277780	REC05322	<i>bcr</i>	N	396	66, 221, 244, 272		P28246	Bicyclicmycin resistance protein	b2182	MTR	0.99
2278503	REC05323	<i>rsuA</i>	N	231	85, 142		P33918	Ribosomal small subunit pseudouridine synthase A (EC 4.2.1.70)	b2183	NAM	0.57
2278652	REC02133	<i>yejH</i>	N	586	128, 178, 248, 378, 552, 574		P33919	Hypothetical protein yejH	b2184	UNC	0.16
2280537	REC02134	<i>rpLY</i>	E	94	-	0.32	P02426	50S ribosomal protein L25	b2185	PMS	0.81
2281967	REC05324	<i>yejK</i>	N	335	67, 132, 156, 203, 217, 249, 265		P33920	37 kDa nucleoid-associated protein	b2186	UNC	0.13
2282149	REC02136	<i>yejL</i>	?	75	-		P33921	Hypothetical protein yejL	b2187	UNC	0.06
2282396	REC02137	<i>yejM</i>	N	586	328, 470, 514, 539		P33922	Hypothetical protein yejM	b2188	UNC	0.09
2286920	REC05325	<i>yejO</i>	N	836	12, 195, 249, 251, 267, 299, 338, 406, 477, 577, 610, 660, 668, 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 TH	b2191	UNC	0.00
2288101	REC06543		N	338	27, 294, 295		P03837	Transposase insH for insertion sequence element ISS	b2192	PHT	0.34
2288520	REC02142	<i>narP</i>	N	215	64, 103, 184		P31802	Nitrate/nitrite response regulator protein narP	b2193	SMC	0.63
2290430	REC05327	<i>cmhF</i>	N	350	43, 112, 276, 324		P33925	Cytochrome c-type biogenesis protein cmhF precursor	b2194	UNC	0.25
2290984	REC05328	<i>dsbE</i>	N	185	90		P33926	Thiol:disulfide interchange protein dsbE	b2195	UNC	0.59
2292924	REC05329	<i>cmfF</i>	N	647	242, 291, 384, 430, 608, 609		P33927	Cytochrome c-type biogenesis protein cmfF	b2196	UNC	0.41
2293400	REC05330	<i>cmfE</i>	E	159	-	< 0.2	P33928	Cytochrome c-type biogenesis protein cmfE	b2197	UNC	0.31
2293606	REC05331	<i>cmfD</i>	N	69	24		P36770	Heme exporter protein D	b2198	MTR	0.06
2294340	REC05332	<i>cmfC</i>	N	245	49, 194		P33929	Heme exporter protein C	b2199	MTR	0.34
2295044	REC05333	<i>cmfB</i>	N	220	135		P33930	Heme exporter protein B	b2200	MTR	0.25
2295658	REC05334	<i>cmfA</i>	N	205	44, 169		P33931	Heme exporter protein A	b2201	MTR	0.31
2296279	REC05335	<i>napC</i>	N	200	139, 165		P33932	Cytochrome c-type protein napC	b2202	BEN	0.19
2296759	REC05336	<i>napB</i>	N	156	95, 133		P33933	Diheme cytochrome c napB precursor	b2203	BEN	0.19
2297598	REC05337	<i>napH</i>	N	287	74, 86, 107		P33934	Ferredoxin-type protein napH	b2204	UNC	0.06
2298280	REC05338	<i>napG</i>	N	231	43, 173, 173, 200		P33936	Ferredoxin-type protein napG	b2205	UNC	0.06
2300773	REC05339	<i>napA</i>	N	828	344, 641, 701, 826		P33937	Periplasmic nitrate reductase precursor (EC 1.7.99.4)	b2206	SMC	0.34
2301033	REC05340	<i>napD</i>	N	67	55		P33938	NapD protein	b2207	UNC	0.16
2301517	REC05341	<i>napF</i>	N	164	101, 127, 135		P33939	Ferredoxin-type protein napF	b2208	UNC	0.16
2301925	REC02158	<i>eco</i>	N	162	7, 48, 61		P23827	Ecotin precursor	b2209	MSM	0.03
2304774	REC05342	<i>mgo</i>	N	548	20, 57, 258		P33940	Malate:quinone oxidoreductase (EC 1.1.99.16)	b2210	CHM	0.25
2306635	REC05343	<i>yojI</i>	N	547	45, 138, 195, 328, 490		P33941	Hypothetical ABC transporter ATP-binding protein yojI	b2211	UNC	0.09
2307361	REC05344	<i>alkB</i>	N	216	151		P05050	Alkylated DNA repair protein alkB	b2212	NAM	0.19
2308425	REC05345	<i>ada</i>	N	354	66, 91, 278		P06134	ADA regulatory protein	b2213	NAM	0.78
2309554	REC05346	<i>apbE</i>	N	351	10, 105, 197, 251		P33944	Thiamine biosynthesis lipoprotein apbE precursor	b2214	NCM	0.56
2310769	REC05347	<i>ompC</i>	N	367	6, 249, 296		P06996	Outer membrane protein C precursor	b2215	SMC	0.00
2311508	REC02165	<i>yojN</i>	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	<i>rscB</i>	N	216	146, 199		P14374	Capsular synthesis regulator component B	b2217	SMC	0.06
2317848	REC05348	<i>rscC</i>	N	933	60, 356, 611, 644, 648, 762, 900		P14376	Sensor protein rscC (EC 2.7.3.-)	b2218	SMC	0.06
2318063	REC02168	<i>atoS</i>	N	608	6, 10, 31, 59, 79, 87, 105, 130, 133, 201, 280, 318, 336, 363, 440, 500		Q06067	Sensor protein atoS (EC 2.7.3.-)	b2219	SMC	0.63
2319886	REC02169	<i>atoC</i>	N	461	425, 455		Q06065	Acetoacetate metabolism regulatory protein atoC	b2200	SMC	0.75
2321467	REC02170	<i>atoD</i>	N	220	42, 80		P76458	Acetate CoA-transferase alpha subunit (EC 2.8.3.8)	b2221	LPC	0.41
2322129	REC02171	<i>atoA</i>	N	216	10, 50, 184		P76459	Acetate CoA-transferase beta subunit (EC 2.8.3.8)	b2222	LPC	0.41
2322776	REC02172	<i>atoE</i>	N	440	107, 177, 212, 262		P76460	Short-chain fatty acids transporter	b2223	MTR	0.16
2324129	REC02173	<i>atoB</i>	N	394	147, 290, 365		P76461	Acetyl-CoA acetyltransferase (EC 2.3.1.9)	b2224	LPC	0.66
2326163	REC05349	<i>yfaP</i>	N	258	94, 157, 205, 255		P76462	Hypothetical protein yfaP precursor	b2225	UNC	0.06
2327817	REC05350	<i>yfaQ</i>	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	<i>yfaS</i>	N	1337	6, 139, 161, 188, 220, 376, 455, 546, 712, 812, 846, 904, 957, 1015, 1029, 1		P76464	Hypothetical protein yfaS precursor	b2227	UNC	0.13
2333006	REC05353	<i>yfaT</i>	N	216	25, 41		P76466	Hypothetical protein yfaT precursor	b2229	UNC	0.09
2334712	REC05354	<i>yfaA</i>	N	578	234, 284, 469, 497, 523, 560		P17994	Hypothetical protein yfaA	b2230	UNC	0.06
2337440	REC05355	<i>gyrA</i>	E	875	-	< 0.001	P09097	DNA gyrase subunit A (EC 5.99.1.3)	b2231	NAM	1.00
2337587	REC02181	<i>ubiG</i>	E	240	-	< 0.05	P17993	3-demethylubiquinone-9 3-methyltransferase (EC 2.1.1.64)	b2232	NCM	0.44
2342189	REC05356	<i>yfaL</i>	N	1250	12, 34, 34, 55, 125, 128, 143, 200, 225, 337, 404, 436, 524, 563, 661, 725, 7		P45508	Hypothetical protein yfaL precursor	b2233	UNC	0.16
2342885	REC06544	<i>nrda</i>	E	761	-	< 0.001	P00452	Ribonucleoside-diphosphate reductase 1 alpha chain (EC 1.17.4.1)	b2234	NCM	0.88
2345404	REC02184	<i>nrdb</i>	E	376	-	< 0.01	P00453	Ribonucleoside-diphosphate reductase 1 beta chain (EC 1.17.4.1)	b2235	NCM	0.75
2346534	REC02185	<i>yfaE</i>	N	84	49, 78		P37910	Hypothetical ferredoxin-like protein yfaE	b2236	UNC	0.13
2347492	REC05357	<i>inaA</i>	N	216	159, 206, 209		P27294	Protein inaA	b2237	UNC	0.03
2347707	REC02187	<i>yfaH</i>	?	68	-		P45505	Hypothetical protein yfaH	b2238	UNC	0.00
2349031	REC05358	<i>gfpQ</i>	N	358	45, 283, 349		P09394	Glycerophosphoryl diester phosphodiesterase, periplasmic precursor	b2239	LPC	0.41
2350394	REC05359	<i>gfpT</i>	N	452	39, 121, 154, 182		P08194	Glycerol-3-phosphate transporter	b2240	MTR	0.22
2350667	REC02190	<i>gfpA</i>	N	542	244, 320		P13032	Anaerobic glycerol-3-phosphate dehydrogenase subunit A (EC 1.1.99.b2241)	b2241	CHM	0.09
2352285	REC02191	<i>gfpB</i>	N	419	106, 136		P13033	Anaerobic glycerol-3-phosphate dehydrogenase subunit B (EC 1.1.99.b2242)	b2242	CHM	0.06
2353541	REC02192	<i>gfpC</i>	N	396	96, 121, 206, 252, 316, 334, 385		P13034	Anaerobic glycerol-3-phosphate dehydrogenase subunit C	b2243	BEN	0.09
2354924	REC02193	<i>yfaD</i>	E	299	280	< 0.05	P37014	Hypothetical protein yfaD	b2244	UNC	0.00
2356865	REC05360	<i>yfaU</i>	N	267	42, 84, 201, 257		P76469	Hypothetical protein yfaU	b2245	UNC	0.09
2358211	REC05361	<i>yfaV</i>	E	442	432	< 0.01	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	269, 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		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-succinylbenzoate-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	-	P17109	Menaquinone biosynthesis protein menD	b2264	NCM	0.28
2378438	REC05373	menP	N	356	21, 57, 232, 245, 280	P38051	Menaquinone-specific isochorismate synthase (EC 5.4.99.6)	b2265	NCM	0.34
2379047	REC05374	elaB	N	101	2, 25, 100	P52084	ElaB protein	b2266	UNC	0.06
2379563	REC05375	elaA	E	153	-	P52077	Protein elaA	b2267	UNC	0.38
2379610	REC02217	elaC	N	311	89, 111, 159, 170, 222, 232, 284	Q47012	Protein elaC	b2268	UNC	0.31
2380733	REC02218	elaD	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	-	P77727	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	-	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	28, 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 yccG	b2302	UNC	0.44
2419345	REC02252	foI1X	N	120	9, 15, 65, 111	P80449	D-erythro-7,8-dihydrooneopterin triphosphate epimerase (EC 5.-.-.-)	b2303	NCM	0.03
2419728	REC02253	yfcH	E	297	-	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	280	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	-	P09550	3-oxopentenyl-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	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 (Eib)	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	tRNA 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	-	P14926	3-oxoacyl-[acyl-carrier-protein] synthase I (EC 2.3.1.41)	b2323	LPC	0.75
2439724	REC02273	yfcK	N	688	29, 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, 130	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, 259, 273	P76498	Hypothetical protein yfcO precursor	b2332	UNC	0.00
2448610	REC05424	yfcP	N	179	6, 80, 88, 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	11, 25, 69, 126, 149, 171, 250, 283, 304, 336, 441, 559	P77196	Hypothetical outer membrane usher protein yfcU precursor	b2337	UNC	0.06
2453666	REC05430	yfcY	N	187	111, 132, 186	P77288	Hypothetical fimbrial-like protein yfcY precursor	b2339	UNC	0.00
2454832	REC05431	sixA	X	161	-	P76502	Phosphatidyl phosphate 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	yfdP	N	352	280, 314	P76505	Hypothetical protein yfdP	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	intsS	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 CPS-	b2350	UNC	0.00
2466234	REC02299	yfdH	X	306	-	P77293	Bactoprenol glucosyl transferase homolog from prophage CPS-53 (E	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, 166	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	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, 235, 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, 588, 629, 682, 798, 819	P77439	Putative phosphoenolpyruvate-protein phosphotransferase ypdD (EC	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	9, 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	-	P76525	Putative PTS system IIB component ypdH (EC 2.7.1.69)	b2387	UNC	0.09
2507446	REC05456	gIk	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	38, 137	P33031	Nucleoside permease nupC	b2393	MTR	0.22
2512345	REC06606	insL3	N	372	201, 218, 225, 246, 252, 285, 296, 309, 330, 332	P08409	Putative transposase insL for insertion sequence element IS186A/(b	b2394	UNC	0.00
2515969	REC05458	yfeA	N	768	134, 220, 238, 290, 308, 424, 458, 549, 567, 604, 611, 642, 651, 691, 695, 7	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	gltX	E	471	449	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	0.00
2522005	REC05461	xapB	N	418	48, 50, 155, 276, 311, 337, 353, 379, 415	P45562	Xanthosine permease	b2406	MTR	0.06
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, 138, 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	-	P15042	DNA ligase (EC 6.5.1.2)	b2411	NAM	1.00
2529253	REC05465	zipA	E	328	-	P77173	Cell division protein zipA	b2412	RCD	0.13
2529483	REC02354	cysZ	N	253	102, 151, 232	P12610	CysZ protein	b2413	UNC	0.09
2530429	REC02355	cysK	N	323	96, 170, 182, 206, 264, 281	P11096	Cysteine synthase A (EC 4.2.9.8)	b2414	AAM	0.84
2531784	REC02356	ptsH	N	85	15, 58	P70006	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	128, 240	P16703	Cysteine synthase B (EC 4.2.9.8)	b2421	AAM	0.84
2538834	REC05467	cysA	N	365	128, 169, 253, 263, 280, 342	P16676	Sulfate transport ATP-binding protein cysA	b2422	MTR	0.91
2539273	REC05468	cysW	E	149	-	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, 226	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	0.06
2550372	REC02375	amiA	N	289	113, 163, 202	P36548	Probable N-acetylmuramoyl-L-alanine amidase amiA precursor (EC 3	b2435	UNC	0.84
2551245	REC02376	hemF	N	299	36, 60, 115, 238, 294	P36553	Coroporphyrinogen 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	-	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	-	P76544	Hypothetical protein yffM	b2444	UNC	0.00

2559630	REC02385	<i>yffN</i>	N	127	9, 68		P76545	Hypothetical protein yffN	b2445	UNC	0.00
2560131	REC02386	<i>yffO</i>	E	138	-	< 0.3	P76546	Hypothetical protein yffO	b2446	UNC	0.00
2560544	REC02387	<i>yffP</i>	N	197	29		P76547	Hypothetical protein yffP	b2447	UNC	0.00
2561597	REC02388	<i>yffQ</i>	N	130	77		P76548	Hypothetical protein yffQ	b2448	UNC	0.00
2562000	REC02389	<i>yffR</i>	?	130	18		P76549	Hypothetical protein yffR precursor	b2449	UNC	0.00
2562513	REC02390	<i>yffS</i>	E	279	-	< 0.1	P76550	Hypothetical protein yffS	b2450	UNC	0.00
2564904	REC05482	<i>eutA</i>	N	467	74, 88, 333		P76551	Ethanolamine utilization protein eutA	b2451	UNC	0.06
2566127	REC05483	<i>eutH</i>	N	408	79, 302, 338		P76552	Ethanolamine utilization protein eutH	b2452	UNC	0.13
2567558	REC05484	<i>eutG</i>	N	404	217		P76553	Ethanolamine utilization protein eutG	b2453	UNC	0.50
2568357	REC05485	<i>eutJ</i>	N	278	114, 146, 162, 198, 201		P77277	Ethanolamine utilization protein eutJ	b2454	UNC	0.06
2569771	REC05486	<i>eutE</i>	N	467	201, 297		P77445	Ethanolamine utilization protein eutE	b2455	UNC	0.03
2570070	REC05487	<i>eutN</i>	E	95	76	0.43	P77633	Ethanolamine utilization protein eutN	b2456	UNC	0.09
2570512	REC05488	<i>eutM</i>	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 2.5.1.17)	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>ta1A</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>yffH</i>	N	191	152		P73128	Hypothetical protein yffH	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	-	< 0.3	P24178	Protein yffB	b2471	UNC	0.38
2589627	REC02412	<i>dapE</i>	E	375	-	< 0.01	P24176	Succinyl-diaminopimelate desuccinylase (EC 3.5.1.18)	b2472	AAM	0.75
2590758	REC0691	<i>?</i>	?	74	-		P77259	SIMILAR TO	b2473	UNC	0.00
2591814	REC05498	<i>ypfH</i>	N	240	151, 224		P76561	Hypothetical protein ypfH	b2474	UNC	0.38
2593879	REC05499	<i>ypfI</i>	N	671	220, 223, 251, 291, 301, 352, 484, 519, 630		P76562	Hypothetical protein ypfI	b2475	UNC	0.06
2594757	REC05500	<i>ypfJ</i>	N	287	117		P76563	Hypothetical protein ypfJ	b2476	UNC	0.28
2595638	REC05501	<i>purC</i>	N	237	23, 43, 44, 77, 150, 177, 180		P21155	Phosphoribosylaminoimidazole-succinocarboxamide synthase (EC 6.3.3.1)	b2477	NCM	0.59
2596888	REC05502	<i>n1pB</i>	N	345	4, 52, 91, 134, 172, 200, 291, 314, 343		P21167	Lipoprotein-34 precursor	b2478	UNC	0.66
2597780	REC05503	<i>dapA</i>	E	292	-	< 0.05	P05640	Dihydrodipicolinate synthase (EC 4.2.1.52)	b2479	AAM	0.84
2597860	REC02419	<i>gcvR</i>	E	212	-	< 0.05	P23483	Glycine cleavage system transcriptional repressor	b2480	RCD	0.09
2598498	REC02420	<i>bcp</i>	N	156	46, 63, 84, 101, 116, 143		P23480	Bacterioferritin comigratory protein	b2481	UNC	0.72
2599182	REC02421	<i>hyfA</i>	N	218	12, 45, 109		P23482	Hydrogenase-4 component A (EC 1.-.-.-)	b2482	BEN	0.00
2599838	REC02422	<i>hyfB</i>	N	672	467, 561		P77858	Hydrogenase-4 component B (EC 1.-.-.-)	b2483	BEN	0.00
2601846	REC02423	<i>hyfC</i>	N	322	87, 95, 114, 185, 254		P77416	Hydrogenase-4 component C (EC 1.-.-.-)	b2484	BEN	0.22
2602831	REC02424	<i>hyfD</i>	N	479	1, 448		P77524	Hydrogenase-4 component D (EC 1.-.-.-)	b2485	LPC	0.03
2604282	REC02425	<i>hyfE</i>	N	216	120		P77437	Hydrogenase-4 component E (EC 1.-.-.-)	b2486	BEN	0.03
2604937	REC02426	<i>hyfF</i>	N	526	197, 315, 369, 481, 499		P77329	Hydrogenase-4 component F (EC 1.-.-.-)	b2487	BEN	0.00
2606507	REC02427	<i>hyfG</i>	N	555	122, 147, 499		P77423	Hydrogenase-4 component G (EC 1.-.-.-)	b2488	BEN	0.03
2608184	REC02428	<i>hyfH</i>	X	181	-		P77668	Hydrogenase-4 component H (EC 1.-.-.-)	b2489	BEN	0.00
2608726	REC02429	<i>hyfI</i>	N	252	55, 244		P77453	Hydrogenase-4 component I (EC 1.-.-.-)	b2490	LPC	0.00
2609414	REC02430	<i>hyfJ</i>	N	158	15, 33, 108		P71229	Hydrogenase-4 component J (EC 1.-.-.-)	b2491	RCD	0.03
2609941	REC02431	<i>hyfR</i>	N	663	18, 139, 285, 321, 429, 446, 557, 661		P77733	Hydrogenase-4 transcriptional activator	b2492	UNC	0.16
2611954	REC02432	<i>focB</i>	N	282	6, 119, 122, 152, 195, 204, 229, 252		P77406	Probable formate transporter 2	b2493	UNC	0.34
2613901	REC05504	<i>perM</i>	N	353	54, 84, 130, 198, 331		P76568	Putative permease perM	b2494	UNC	0.38
2614114	REC02434	<i>yfgC</i>	?	487	92		P76569	Hypothetical protein yfgC precursor	b2495	UNC	0.19
2615598	REC02435	<i>yfgD</i>	N	119	42		P76570	Protein yfgD	b2496	UNC	0.16
2616841	REC05505	<i>yfgE</i>	E	248	-	< 0.05	P33780	Hypothetical protein yfgE	b2497	MTR	0.47
2618180	REC05506	<i>uraA</i>	N	429	20, 107, 279, 423		P25532	Uracil permease	b2498	NCM	0.81
2618919	REC05507	<i>upp</i>	N	217	176		P08178	Uracil phosphoribosyltransferase (EC 2.4.2.9)	b2499	NCM	0.78
2619217	REC02439	<i>purM</i>	N	345	51, 107, 235		P08179	Phosphoribosylformylglycinamide cyclo-ligase (EC 6.3.3.1)	b2500	NCM	0.78
2620254	REC02440	<i>purN</i>	N	212	8, 94, 135, 182		P28688	Phosphoribosylglycinamide formyltransferase (EC 2.1.2.2)	b2501	MSM	0.50
2621064	REC02441	<i>ppk</i>	N	688	15, 484, 520, 533, 640, 655		P29014	Polyphosphate kinase (EC 2.7.4.1)	b2502	MSM	0.69
2623135	REC02442	<i>ppx</i>	N	513	42, 125, 322, 339, 478		P77172	Exopolysphatase (EC 3.6.1.11)	b2503	UNC	0.53
2626958	REC05508	<i>yfgF</i>	N	747	9, 74, 87, 120, 134, 135, 161, 170, 213, 282, 318, 328, 561, 622		P76572	Hypothetical protein yfgF	b2504	UNC	0.00
2627812	REC02445	<i>yfgH</i>	?	172	7, 166		P04079	Hypothetical lipoprotein yfgH precursor	b2505	UNC	0.00
2628346	REC02446	<i>yfgI</i>	X	179	-		P06981	Hypothetical protein yfgI	b2506	UNC	0.00
2630555	REC05509	<i>guaA</i>	N	525	60, 76, 365		P04994	GMP synthase [glutamine-dehydrolyzing] (EC 6.3.5.2)	b2507	NCM	0.84
2632090	REC05510	<i>guaB</i>	N	488	14, 321, 373, 440, 456		P76575	Inosine-5'-monophosphate dehydrogenase (EC 1.1.1.205)	b2508	NCM	0.78
2632252	REC02449	<i>xseA</i>	N	456	174, 412		P77254	Exodeoxyribonuclease VII large subunit (EC 3.1.11.6)	b2509	NAM	0.81
2633870	REC05511	<i>yfgJ</i>	N	83	45		P77574	Hypothetical protein yfgJ	b2510	UNC	0.03
2635415	REC05512	<i>engA</i>	E	503	-	< 0.001	P77774	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		P76576	Hypothetical protein yfgL	b2512	UNC	0.19
2637303	REC05514	<i>yfgM</i>	N	206	22, 72, 115, 181		P04804	Hypothetical protein yfgM	b2513	UNC	0.16
2638595	REC05515	<i>hisS</i>	E	424	-	< 0.001	P27433	Histidyl-tRNA synthetase (EC 6.1.1.21)	b2514	PMS	1.00
2639824	REC05516	<i>ispG*</i>	E	372	-	< 0.01	P27434	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		P36979	Hypothetical protein yfgA	b2516	UNC	0.09
2642303	REC05518	<i>yfgB</i>	N	384	53, 112, 194, 198		P24233	Hypothetical protein yfgB	b2517	UNC	0.88
2642884	REC05519	<i>ndk</i>	E	143	-	< 0.2	P76577	Nucleoside diphosphate kinase (EC 2.7.4.6)	b2518	MSM	0.84
2645345	REC05520	<i>pbpC</i>	N	770	126, 127, 184, 356, 731, 757		P76578	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, 1374, 1441, 1580		P31142	Hypothetical lipoprotein yfhM precursor	b2520	UNC	0.22
2650355	REC02461	<i>sseA</i>	N	334	49, 65, 101, 239, 260, 319, 321		P31143	3-mercaptopyruvate sulfurtransferase (EC 2.8.1.2)	b2521	MSM	0.41
2652962	REC05522	<i>sseB</i>	N	261	204, 245		P37095	Protein sseB	b2522	UNC	0.00
2654465	REC05523	<i>pepB</i>	N	456	71, 122, 144, 151, 171, 197, 267, 339, 369		P37096	Peptidase B (EC 3.4.11.-)	b2523	AAM	0.09
2654756	REC05524	<i>yfhJ</i>	N	66	40		P25528	Hypothetical protein yfhJ	b2524	UNC	0.16
2655103	REC05525	<i>fdx</i>	E	111	-	< 0.2	P36541	Ferredoxin, 2Fe-2S	b2525	BEN	0.44
2656955	REC05526	<i>hscA</i>	E	616	-	< 0.001	P36540	Chaperone protein hscA	b2526	UNC	0.25
2657487	REC05527	<i>hscB</i>	E	171	-	< 0.05	P36539	Chaperone protein hscB	b2527	PMS	0.19
2657906	REC05528	<i>yfhF</i>	?	107	14		P77310	Protein yfhF	b2528	UNC	0.66
2658309	REC05529	<i>nifS</i>	E	128	-	< 0.2	P39171	NifU-like protein	b2529	UNC	0.69
2659575	REC05530	<i>iscS</i>	E	412	-	< 0.001	P77484	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		P77484	Hypothetical tRNA/rRNA methyltransferase yfhQ (EC 2.1.1.-)	b2532	UNC	0.44
2661462	REC02473	<i>shbB</i>	E	267	-	< 0.05	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	0.00
2663434	REC02475	<i>csiE</i>	N	433	56, 78, 276, 311, 401		P54901	Stationary phase inducible protein csiE	b2535	UNC	0.09
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 dioxygenase alpha subunit (EC 1.14.1.-)	b2538	MSM	0.16
2668410	REC02479	<i>hca</i>									

2669245	REC02481	hcaB	N	270	70, 80, 183	P77646	2,3-dihydroxy-2,3-dihydroxy-phenylpropionate dehydrogenase (EC 1.3.1.2)	b2541	MSM	0.00	
2670067	REC02482	hcaD	N	400	147, 180, 348, 369	P77650	3-phenylpropionate dioxxygenase ferredoxin-NAD(+) reductase complex	b2542	MSM	0.28	
2671294	REC02483	yphA	N	164	7, 55, 57, 78, 84, 98, 153	P77751	Hypothetical protein yphA	b2543	UNC	0.19	
2672708	REC05535	yphB	N	290	26, 34, 166, 221, 268	P76584	Hypothetical protein yphB	b2544	UNC	0.53	
2673814	REC05536	yphC	N	364	47, 183, 200, 331	P77360	Hypothetical zinc-type alcohol dehydrogenase-like protein yphC	b2545	UNC	0.53	
2674845	REC05537	yphD	N	332	84, 121, 196, 219, 253, 288, 308	P77315	Hypothetical ABC transporter permease protein yphD	b2546	UNC	0.00	
2676381	REC05538	yphE	N	503	256, 319, 348, 366, 419	P77509	Hypothetical ABC transporter ATP-binding protein yphE	b2547	UNC	0.03	
2677387	REC05539	yphF	N	327	18, 19, 28, 162, 191, 318	P77269	ABC transporter periplasmic binding protein yphF precursor	b2548	UNC	0.03	
2680858	REC05540	yphG	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	yphH	N	399	347	P76586	Hypothetical protein yphH	b2550	UNC	0.03	
2683527	REC05541	glyA	E	417	-	< 0.01	P00477	Serine hydroxymethyltransferase (EC 2.1.2.1)	b2551	AAM	0.97
2683855	REC02492	hmp	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	glnB	N	112	37, 90	P05826	Nitrogen regulatory protein P-II 1	b2553	SMC	0.66	
2686823	REC05543	yfhA	N	444	42, 136, 225, 244, 344, 412	P21712	Hypothetical protein yfhA	b2554	UNC	0.09	
2687526	REC05544	yfhG	?	237	2	P37328	Hypothetical protein yfhG	b2555	UNC	0.00	
2689181	REC05545	yfhK	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	purL	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	yfhD	N	472	61, 211, 230, 248, 260, 408, 417, 449	P30135	Hypothetical protein yfhD	b2558	UNC	0.13	
2695910	REC05547	yfhC	E	178	-	< 0.1	P30134	Hypothetical protein yfhC	b2559	UNC	0.78
2696507	REC05548	yfhB	N	190	2, 91, 177	P30133	Hypothetical protein yfhB	b2560	UNC	0.00	
2696707	REC02501	yfhH	?	306	46	P37767	Hypothetical protein yfhH	b2561	UNC	0.53	
2697683	REC02502	yfhL	N	86	52, 54, 66	P52102	Putative ferredoxin-like protein yfhL	b2562	UNC	0.38	
2699018	REC05549	acpS	E	126	109	< 0.2	P24224	Holo-[acyl-carrier protein] synthase (EC 2.7.8.7)	b2563	NCM	0.75
2699749	REC05550	pxdJ	E	243	-	< 0.05	P24223	Pyridoxal phosphate biosynthetic protein pxdJ	b2564	NCM	0.47
2700489	REC06647	recO	N	242	46, 100	P15027	DNA repair protein recO	b2565	NAM	0.50	
2701406	REC05552	era	E	301	-	< 0.01	P06616	GTP-binding protein era	b2566	UNC	0.97
2702083	REC05553	rnc	E	226	-	< 0.05	P05797	Ribonuclease III (EC 3.1.26.3)	b2567	NAM	0.97
2703329	REC05554	lepB	E	324	314	< 0.01	P00803	Signal peptidase I (EC 3.4.21.89)	b2568	PMS	0.91
2705144	REC05555	lepA	N	599	175, 331, 454	P07682	GTP-binding protein lepA	b2569	UNC	1.00	
2705821	REC05556	rseC	N	159	7, 54, 156	P46187	Sigma-E factor regulatory protein rseC	b2570	RCD	0.09	
2706774	REC05557	rseB	N	318	25, 108, 159, 251, 296, 303	P46186	Sigma-E factor regulatory protein rseB precursor	b2571	RCD	0.13	
2707424	REC05558	rseA	N	216	88, 96, 144, 197	P38106	Sigma-E factor negative regulatory protein	b2572	RCD	0.06	
2708032	REC05559	rpoE	?	191	-	P34086	RNA polymerase sigma-E factor	b2573	RCD	0.50	
2708440	REC02514	nadB	N	540	50, 70, 77, 155, 239, 359, 448, 505, 527	P10902	L-aspartate oxidase (EC 1.4.3.16)	b2574	NCM	0.53	
2710904	REC05560	yfiC	N	285	29, 43	P31825	Hypothetical protein yfiC	b2575	UNC	0.50	
2710916	REC02516	srnB	?	444	-	P21507	ATP-dependent RNA helicase srnB	b2576	SMC	0.16	
2713385	REC05561	yfiE	N	308	168, 255	P33634	Hypothetical transcriptional regulator yfiE	b2577	UNC	0.72	
2713443	REC02518	yfiK	N	195	73, 120	P38101	Hypothetical protein yfiK	b2578	UNC	0.31	
2714469	REC05562	yfiD	E	127	-	< 0.3	P33633	Protein yfiD	b2579	UNC	0.06
2714774	REC02520	ung	N	229	144, 162	P12295	Uracil-DNA glycosylase (EC 3.2.2.-)	b2580	NAM	0.69	
2716548	REC05563	yfiF	N	345	78, 150, 172, 205, 206	P33635	Hypothetical tRNA/rRNA methyltransferase yfiF (EC 2.1.1.-)	b2581	UNC	0.97	
2716755	REC02522	trxC	E	139	-	< 0.3	P33636	Thioredoxin 2	b2582	MSM	0.97
2717219	REC02523	yfiP	N	240	107, 110, 212	Q47319	Hypothetical protein yfiP	b2583	UNC	0.06	
2717973	REC02524	yfiQ	N	886	58, 61, 104, 104, 107, 416, 453, 481, 792, 838	P76594	Hypothetical protein yfiQ	b2584	UNC	0.25	
2720744	REC02525	pssA	E	452	-	< 0.05	P23830	CDP-diacylglycerol-serine O-phosphatidyltransferase (EC 2.7.8.8)	b2585	LPC	0.61
2722199	REC02526	yfiM	N	90	7, 20	P46126	Hypothetical protein yfiM	b2586	UNC	0.03	
2723766	REC05564	kytP	N	432	110, 227, 331, 372	P17448	Alpha-ketoglutarate permease	b2587	MTR	0.31	
2732193	REC05565	clpB	N	857	88, 802	P03815	ClpB protein	b2592	UNC	0.94	
2733054	REC05566	yfiH	N	243	11, 21, 147	P33644	Hypothetical protein yfiH	b2593	UNC	0.69	
2734031	REC05567	rluD	E	326	312	< 0.1	P33643	Ribosomal large subunit pseudouridine synthase D (EC 4.2.1.70)	b2594	NAM	1.00
2734166	REC02531	yfiO	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 TH	b2596	UNC	0.00	
2735174	REC02533	yfiA	N	113	51, 111	P11285	Protein yfiA	b2597	UNC	0.06	
2735765	REC02535	pheA	N	386	6, 70, 100, 139, 267, 349	P07022	P-protein	b2599	AAM	0.78	
2738089	REC05568	tyrA	N	373	65, 188	P07023	T-protein	b2600	AAM	0.13	
2739170	REC05569	aroF	N	356	7, 15, 34, 58, 63, 121, 270	P00888	Phospho-2-dehydro-3-deoxyheptonate aldolase, Tyr-sensitive (EC 4.2.1.24)	b2601	AAM	0.41	
2739341	REC02538	yfiL	N	134	50, 63, 88	P11289	Hypothetical protein yfiL	b2602	UNC	0.03	
2739895	REC02539	yfiR	N	172	4, 58, 89, 170, 172	P76597	Hypothetical protein yfiR precursor	b2603	UNC	0.03	
2740403	REC02540	yfiN	N	408	1, 2, 326	P46139	Hypothetical protein yfiN	b2604	UNC	0.19	
2741645	REC02541	yfiB	N	160	87, 117, 119	P07021	Putative lipoprotein yfiB precursor	b2605	UNC	0.03	
2742550	REC05570	rplS	E	115	-	< 0.3	P02420	50S ribosomal protein L19	b2606	PMS	1.00
2743359	REC05571	trnM	E	255	-	< 0.05	P07020	tRNA (Guanine-N(1)-methyltransferase (EC 2.1.1.31)	b2607	NAM	1.00
2743947	REC05572	rimM	E	185	-	< 0.1	P21504	16S rRNA processing protein rimM	b2608	NAM	0.88
2744205	REC05573	rpsP	E	82	-	< 0.3	P02372	30S ribosomal protein S16	b2609	PMS	0.97
2745815	REC05574	fth	E	453	-	< 0.001	P07019	Signal recognition particle protein	b2610	PMS	1.00
2745907	REC02547	ypjD	N	288	80, 208	P76599	Hypothetical protein ypjD	b2611	UNC	0.16	
2746818	REC02548	?	?	194	-	< 0.1	P37908	Hypothetical protein ypjD	b2612	UNC	0.03
2747398	REC02549	yfiJ	N	227	1, 103, 145, 197	P37908	Hypothetical protein yfiJ	b2613	UNC	0.91	
2748729	REC05575	grpE	E	197	-	< 0.1	P09372	GrpE protein	b2614	PMS	1.00
2748852	REC02551	ppnK	E	292	-	< 0.05	P37768	Probable inorganic polyphosphate/ATP-NAD kinase (EC 2.7.1.23)	b2615	MSM	0.94
2749816	REC02552	recN	N	553	46, 76, 89, 103, 276, 432, 464, 530, 534	P05824	DNA repair protein recN	b2616	NAM	0.84	
2751815	REC02553	smpA	?	50	-	< 0.2	P23089	Small protein A precursor	b2617	UNC	0.06
2752337	REC05576	yfiF	E	102	-	0.30	P52119	Protein yfiF	b2618	UNC	0.16
2752785	REC05577	yfiG	E	158	-	< 0.2	P52121	Hypothetical protein yfiG	b2619	UNC	0.34
2752917	REC02556	smpB	N	160	83, 114	P32052	SsrA-binding protein	b2620	NAM	1.00	
2754180	REC02557	intA	N	413	31, 138, 143	P32053	Prophage CP4-57 integrase	b2622	PHT	0.22	
2756621	REC05578	yfiH	X	318	-	P52123	Hypothetical protein yfiH	b2623	UNC	0.00	
2756665	REC02559	aIpA	X	70	-	P33997	Prophage CP4-57 regulatory protein aIpA	b2624	RCD	0.06	
2757006	REC02560	yfiI	X	469	-	P52124	Hypothetical protein yfiI	b2625	UNC	0.00	
2758568	REC02561	yfiJ	X	208	-	P52125	Hypothetical protein yfiJ	b2626	UNC	0.03	
2761561	REC05579	yfiK	N	729	-	P52126	Hypothetical protein yfiK	b2627	UNC	0.00	
2763174	REC05580	yfiL	N	538	16, 119, 194, 248	P52127	Hypothetical protein yfiL	b2628	UNC	0.00	
2763797	REC05581	yfiM	N	87	13, 38, 46	P52128	Hypothetical protein yfiM	b2629	UNC	0.00	
2763939	REC02565	yfiN	N	357	81, 135, 172, 249	P52129	Hypothetical protein yfiN	b2630	UNC	0.00	
2765056	REC02566	yfiO	?	106	-	P52130	Hypothetical protein yfiO	b2631	UNC	0.00	
2765725	REC02567	yfiP	N	289	116, 155, 156, 192	P52131	Hypothetical protein yfiP	b2632	UNC	0.00	
2766866	REC02568	yfiQ	N	273	96, 153, 226, 229	P52132	Hypothetical protein yfiQ	b2633	UNC	0.00	
2767724	REC02569	yfiR	N	233	131, 154	P52133	Hypothetical transcriptional regulator yfiR	b2634	UNC	0.03	
2768310	REC06651	ypjK	N	130	84, 104	P52134	Hypothetical protein ypjK precursor	b2635	UNC	0.03	
2768453	REC06652	yfiS	?	230	37, 56	O52982	Hypothetical lipoprotein yfiS precursor	b2636	UNC	0.03	
2769169	REC02571	yfiT	N	155	123	P52135	Hypothetical protein yfiT precursor	b2637	UNC	0.00	
2770175	REC05582	yfiU	N	104	62	P52136	Putative arsenate reductase (EC 1.97.1.5)	b2638	UNC	0.00	
2770706	REC05583	yfiV	N	172	27, 64, 65, 105, 144, 170	P52137	Putative arsenical pump membrane protein	b2639	UNC	0.31	
2771057	REC05584	yfiW	?	66	49	P77014	PUTATIVE ARSENICAL PUMP MEMBRANE PROTEIN	b2640	UNC	0.31	
2771339	REC06653	yfiX	N	567	1, 3, 333	P52138	Hypothetical protein yfiW	b2642	UNC	0.00	
2773940	REC02577	yfiX	X	152	-	P52139	Hypothetical protein yfiX	b2643	UNC	0.03	

2774407	REC02578	<i>yfjY</i>	X	160	-	P52140	Putative radC-like protein yfjY	b2644	UNC	0.03
2774886	REC06877	<i>ypjJ</i>	X	70	-	P58033	Hypothetical protein ypjJ	UNC	UNC	0.00
2775136	REC02579	<i>yfjZ</i>	X	105	-	P52141	Hypothetical protein yfjZ	b2645	UNC	0.00
2775474	REC02580	<i>ypjF</i>	E	109	-	Q46953	Hypothetical protein ypfF	b2646	UNC	0.00
2780876	REC05586	<i>ypjA</i>	N	1569	412, 559, 669, 741, 817, 919, 1045, 1170, 1262, 1274, 1407, 1467, 1524, 15	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	UNC	UNC	0.00
2783031	REC05589	<i>ypjC</i>	E	160	-	P76613	Hypothetical protein ypjC	b2650	UNC	0.00
2783241	REC06656	<i>N</i>	X	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	<i>X</i>	X	164	-	Q9ZAZ7	Subunit 1 of the gab-activator protein	UNC	RCD	0.00
2785267	REC02589	<i>X</i>	X	62	-	P76618	FROM BASES 2775730 TO 2786129 (SECTION 240 OF 400) OF THb2656	b2656	UNC	0.00
2785627	REC02590	<i>X</i>	X	210	-	Q9R7D4	Subunit 2 of the gab-activator protein	UNC	RCD	0.00
2786398	REC02591	<i>yqaD</i>	N	90	-	P76620	Hypothetical protein yqaD	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	UNC	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, 255	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	-	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	-	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	0.89
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	-	Q47414	Glutaredoxin-like protein nrhH	b2673	AAM	0.19
2798986	REC02607	<i>nrhI</i>	E	136	-	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	155, 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	<i>X</i>	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>yqaA</i>	N	142	56, 141	P76631	Hypothetical protein yqaA	b2689	UNC	0.25
2815525	REC05598	<i>yqaB</i>	N	188	10, 136, 144, 163, 174	P77475	Hypothetical protein yqaB	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	-	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 3.2.1.2)	b2701	LPC	0.31
2823855	REC02630	<i>srIA</i>	N	187	27, 122, 138, 144, 152	P56579	PTS system, glucitol/sorbitol-specific IIC2 component	b2702	MTR	0.06
2824415	REC02631	<i>srIE</i>	N	319	47, 143, 229, 260	P56580	PTS system, glucitol/sorbitol-specific IIB component (EC 2.7.1.69)	b2703	MTR	0.06
2825385	REC02632	<i>srIB</i>	?	123	111	P05706	PTS system, glucitol/sorbitol-specific IIA component (EC 2.7.1.69)	b2704	MTR	0.06
2825760	REC02633	<i>srID</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>srIR</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	GuoQ 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>flrD</i>	N	475	145, 154, 382, 401, 450, 456	Q46877	Flavouredoxin	b2710	BEN	0.34
2831935	REC02640	<i>flrR</i>	N	377	50, 97, 99	P37596	FIRd-NAD(+) reductase (EC 1.18.1.-)	b2711	BEN	0.69
2835448	REC06486	<i>hypF</i>	N	750	22, 86, 96, 148, 202, 215, 265, 266, 298, 332, 365, 497, 588, 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 component	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	-	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	-	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>fhIA</i>	N	692	88, 134, 281, 366, 434, 563	P19323	Formate hydrogenlyase transcriptional activator	b2731	RCD	0.06
2854829	REC05619	<i>yghA</i>	E	117	-	P25728	Hypothetical protein yghA	b2732	UNC	0.00
2855116	REC02662	<i>mutS</i>	N	853	125, 170, 176, 255, 307, 472, 499, 586, 684, 792, 852	P23909	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)	b2734	PMS	0.15
2859287	REC05620	<i>ygbI</i>	N	265	108, 246, 260, 262	P52598	Hypothetical transcriptional regulator ygbI	b2735	UNC	0.26
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	19	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, 189	Q46891	Hypothetical protein ygbM	b2739	UNC	0.22
2863124	REC02669	<i>ygbN</i>	N	454	43, 96, 347, 398, 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, 848, 156, 178, 220, 315, 384, 372	P33648	Lipoprotein nlpD precursor	b2742	LPC	0.38
2867542	REC05623	<i>pcm</i>	N	208	100	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	2-C-methyl-D-erythritol 2,4-cyclodiphosphate synthase (EC 4.6.1.12)	b2746	LPC	0.72
2870513	REC05627	<i>ispD</i>	E	236	-	< 0.05	Q46893	2-C-methyl-D-erythritol 4-phosphate cytidyltransferase (EC 2.7.7.60)	b2747	LPC	0.72
2870843	REC05628	<i>ygbQ</i>	E	103	-	< 0.3	Q46894	Hypothetical protein ygbQ	b2748	UNC	0.19
2871360	REC05629	<i>ygbE</i>	N	107	22		P46141	Hypothetical protein ygbE	b2749	UNC	0.00
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, 465		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 3.4.1.1)	b2753	MSM	0.00
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>ygcI</i>	N	226	181, 188		Q46898	Hypothetical protein ygcI precursor	b2757	UNC	0.00
2880165	REC05637	<i>ygcJ</i>	N	363	80, 202, 236, 240, 255, 313, 343		Q46899	Hypothetical protein ygcJ	b2758	UNC	0.00
2880660	REC05638	<i>ygcK</i>	N	160	8, 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	0.00
2886335	REC05641	<i>cysH</i>	N	244	132, 147, 337		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 1.8.1.2)	b2763	MSM	0.38
2889921	REC05643	<i>cysJ</i>	N	599	9, 137, 184, 212, 456		P38038	Sulfite reductase [NADPH] flavoprotein alpha-component (EC 1.8.1.2)	b2764	MSM	0.38
2890237	REC02694	<i>ygcM</i>	N	121	57, 105		Q46903	Putative 6-pyruvoyl tetrahydrobiopterin 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 ygcN	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	REC06503	<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 ygcU	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	186, 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>	N	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	-	< 0.001	P08398	CTP synthase (EC 6.3.4.2)	b2780	NCM	0.94
2908707	REC05654	<i>mazG</i>	N	263	10, 21, 48		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	30, 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	0.47
2932257	REC02732	<i>fucP</i>	N	438	41, 173, 211		P11551	L-fucose permease	b2801	MTR	0.22
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 desulfinate (EC 4.4.1.-)	b2810	NCM	0.94
2942564	REC02742	<i>ygdK</i>	E	147	-	< 0.2	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>mltA</i>	N	365	44, 129, 129, 289		P46885	Membrane-bound lytic murein transglycosylase A precursor (EC 3.2.1.1)	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 3.5.1.28)	b2817	LPC	0.84
2947264	REC02746	<i>argA</i>	N	443	71, 86, 107, 109, 133, 154, 197, 222, 223, 255, 433		P08205	Amino-acid acetyltransferase (EC 2.3.1.1)	b2818	AAM	0.47
2950483	REC05675	<i>recD</i>	N	608	46, 117, 205, 335, 468, 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	184, 358, 388, 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	-	< 0.05	P00470	Thymidylate synthase (EC 2.1.1.45)	b2827	NCM	0.81
2964059	REC05684	<i>lgt</i>	E	291	-	< 0.05	P37149	Protoporphyrin diacylglycerol transferase (EC 2.4.99.-)	b2828	PMS	0.97
2966456	REC05685	<i>ptsP</i>	N	748	29, 158, 194, 355, 399, 406, 453, 456, 482, 580, 663		P37177	Phosphoenolpyruvate-protein phosphotransferase ptsP (EC 2.7.3.9)	b2829	CHM	0.75

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	-	P04425	Glutathione synthetase (EC 6.3.2.3)	b2947	AAM	0.41
3090884	REC02870	yggE	E	211	-	P52049	Protein yggE	b2948	UNC	0.50
3091519	REC02871	yggF	E	138	-	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	-	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	-	P38521	Hypothetical protein yggL	b2959	UNC	0.06
3100870	REC05753	yggH	N	239	154,180	P32049	Hypothetical methyltransferase yggH (EC 2.1.1.-)	b2970	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	mItc	N	360	28,70,184,199,279,304,359	P52066	Membrane-bound lytic murein transglycosylase C precursor (EC 3.2.1b2963)	b2963	LPC	0.09
3103684	REC02887	nupG	N	434	63,160,164,254,372,400	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	0.41
3115113	REC05760	yghJ	N	848	107,200,412,415,457,464,648,669,721,775,795	Q46837	Putative lipoprotein acdD 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	493	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 ISS	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	294,570	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	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	-	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	hyb0	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	yqhA	E	164	-	P52082	Hypothetical protein yqhA	b3002	UNC	0.28
3147677	REC02925	yqhA	N	294	22,38,57,107,202	P25887	Hypothetical oxidoreductase yqhA (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	83,263	Q46855	Hypothetical transcriptional regulator yqhC	b3010	UNC	0.31
3154754	REC02934	dkgA	N	236	17,21,80	Q46857	2,5-diketo-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	plsC	E	245	-	P26647	1-acyl-sn-glycerol-3-phosphate acyltransferase (EC 2.3.1.51)	b3018	NAM	0.91
3163989	REC05793	parC	E	752	-	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	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	b3024	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	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	-	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	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	tolC	N	495	196	Q02930	Outer membrane protein tolC precursor	b3035	PMS	0.28
3177612	REC02959	yqiA	N	86	61	Q92363	Hypothetical protein YqiA	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	-	< 0.1	P24199	3,4-dihydroxy-2-butanone 4-phosphate synthase	b3041	NCM	0.53
3182796	REC02965	yqiC	N	116	14		Q48688	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, 288, 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.-.-)	b3052	LPC	0.44
3197282	REC05809	glnE	N	946	271, 393, 487, 764, 777		P30870	Glutamate-ammonia-ligase adenylyltransferase (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	-	< 0.01	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	folB	N	123	53		P31055	Dihydropyrimidinase (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, 69, 92, 115, 192, 240, 290		P45463	Hypothetical transcriptional regulator ygiP	b3060	UNC	0.72
3204104	REC02984	tcdA	X	303	-		P05847	L(+)-tartrate dehydratase alpha subunit (EC 4.2.1.32)	b3061	CHM	0.09
3205012	REC02985	tcdB	N	201	14, 43, 145		P05851	L(+)-tartrate dehydratase beta subunit (EC 4.2.1.32)	b3062	CHM	0.00
3205665	REC02986	ygiE	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	-	< 0.0001	P02923	DNA primase (EC 2.7.7.-)	b3066	NAM	0.97
3210688	REC02990	rpoD	E	613	-	< 0.0001	P00579	RNA polymerase sigma factor rpoD	b3067	RCD	0.97
3213114	REC05815	mug	N	168	62, 145		P43342	GU 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, 166, 243, 436, 447, 460		P50466	Aerotaxis receptor	b3072	SMC	0.25
3217024	REC02995	yqjG	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, 960, 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	yqjI	N	477	1, 171		P42590	Hypothetical transporter yqjI	b3078	UNC	0.00
3225442	REC03001	yqjJ	N	356	43, 66, 94, 96, 185, 241, 248, 321		P42591	Hypothetical protein yqjJ precursor	b3079	UNC	0.00
3226529	REC03002	yqjK	N	783	47, 57, 93, 159, 206, 261, 441, 442		P42592	Hypothetical protein yqjK 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	yqjM	X	138	-		P42594	Hypothetical protein yqjM	b3082	UNC	0.00
3232096	REC05820	yqjN	X	104	-		P42595	Hypothetical protein yqjN	b3083	UNC	0.13
3233546	REC05821	yqjO	N	388	112, 134, 204, 223, 244, 252, 278, 324, 369		P42596	Putative ribosomal RNA small subunit methyltransferase D (EC 2.1.1.-)	b3084	UNC	0.09
3233565	REC03007	yqjP	N	179	46, 132		P42597	Hypothetical protein yqjP	b3085	UNC	0.06
3234181	REC03008	yqjQ	E	230	-	< 0.1	P42598	Hypothetical protein yqjQ	b3086	UNC	0.06
3234394	REC03010	yqjR	N	334	158, 258, 299		P42599	Hypothetical oxidoreductase yqjR (EC 1.1.-.-)	b3087	UNC	0.56
3236222	REC03011	yqjT	N	321	88, 182, 245, 284, 319		P42601	Hypothetical protein yqjT	b3088	UNC	0.31
3237584	REC03012	yqjU	N	414	53, 87, 252, 280		P42602	Hypothetical symporter yqjU	b3089	UNC	0.28
3239384	REC05822	yqjV	N	183	15		P42603	Hypothetical protein yqjV	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	0.25
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	283	122, 242		P42608	Exu regulon transcriptional regulator	b3094	RCD	0.09
3245413	REC03020	yqjA	E	220	-	< 0.05	P42614	Hypothetical protein yqjA	b3095	UNC	0.50
3246079	REC03021	yqjB	E	127	-	< 0.2	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	-	< 0.2	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, 284		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	b3107	UNC	0.06
3254292	REC05829	yhaN	N	187	18, 130		P42627		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	< 0.3	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	-	0.32	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	garR	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	garL	N	256	51, 184		P23522	2-dehydro-3-deoxyglucuronate 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	agaV	E	169	-	< 0.2	P42904	PTS system, N-acetylgalactosamine-specific IIB component 2 (EC 2. b3133	CHM	0.03	
3278342	REC03058	agaW	E	133	121	< 0.3	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 3.5.1.1)	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	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 2.2.1.15)	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 fibrial-like protein yraH precursor	b3142	UNC	0.00
3285731	REC03067	yraI	N	231	25, 127	P42914	Hypothetical fibrial chaperone yral precursor	b3143	UNC	0.00
3286455	REC03068	yraJ	N	838	260, 378, 407, 439, 467, 532, 593, 682, 767	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	folP	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	rpmA	X	85	-	P02427	50S ribosomal protein L27	b3185	PMS	1.00
3331092	REC05870	rpU	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	0.56
3337706	REC05877	yrbF	N	269	159, 182	P45393	Hypothetical ABC transporter ATP-binding protein yrbF	b3195	UNC	0.84
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	rpoN	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	0.40
3344756	REC03128	yhbJ	N	284	9, 100, 114, 230	P33995	Hypothetical protein yhbJ	b3205	UNC	0.51
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 2.4.1.13)	b3208	LPC	0.44
3348109	REC05879	e1hb	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	gltB	N	1517	30, 64, 85, 90, 182, 224, 286, 315, 369, 394, 398, 434, 848, 1116, 1170, 1179	P09831	Glutamate synthase [NADPH] large chain precursor (EC 1.4.1.13)	b3212	MSM	0.66
3356833	REC03136	gltD	N	472	358, 459	P09832	Glutamate synthase [NADPH] small chain (EC 1.4.1.13)	b3213	MSM	0.66
3358811	REC03137	gltF	X	254	-	P28721	Protein gltF precursor	b3214	UNC	0.00
3359747	REC03138	yhcA	X	224	-	P28722	Hypothetical fibrial 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	insH11	N	338	59, 259	P03837	Transposase insH for insertion sequence element ISS	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-acetylneuraminate lyase subunit (EC 4.1.3.3)	b3225	CHM	0.19
3372124	REC05888	yhcK	E	263	-	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	-	P02363	30S ribosomal protein S9	b3230	PMS	1.00
3376286	REC05892	rpmL	E	142	-	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	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

3467490	REC05952	chiA	N	897	7, 15, 25, 39, 66, 82, 90, 110, 128		P13656	Probable bifunctional chitinase/lysozyme precursor	b3338	UNC	0.13
3468966	REC05953	tufA	E	394	-	< 0.05	P02990	Elongation factor Tu	b3339	PMS	1.00
3471151	REC05954	fusa	E	704	-	< 0.001	P02996	Elongation factor G	b3340	PMS	1.00
3471718	REC05955	rpsG	N	179	62		P02359	30S ribosomal protein S7	b3341	PMS	1.00
3472189	REC05956	rpsL	E	124	-	< 0.2	P02367	30S ribosomal protein S12	b3342	PMS	1.00
3472602	REC05957	yjeL	E	95	-	< 0.3	P45530	Hypothetical protein yjeL	b3343	UNC	0.09
3472969	REC05958	yjeM	E	119	-	< 0.3	P45531	Hypothetical protein yjeM	b3344	UNC	0.13
3473355	REC05959	yjeN	E	128	107	< 0.2	P45532	Hypothetical protein yjeN	b3345	UNC	0.13
3474089	REC05960	yjeO	N	244	62		P45533	Hypothetical protein yjeO	b3346	UNC	0.22
3475056	REC05961	fkpA	N	270	58, 83, 144, 150, 171, 203, 218, 220, 237		P45523	FKBP-type peptidyl-prolyl cis-trans isomerase fkpA precursor (EC 5.2.1.1)	b3347	PMS	0.84
3475277	REC03266	slyX	N	72	35		P30857	SlyX protein	b3348	UNC	0.25
3476134	REC05962	slyD	E	196	5	< 0.1	P30856	FKBP-type peptidyl-prolyl cis-trans isomerase slyD (EC 5.2.1.8)	b3349	PMS	0.34
3476429	REC06697	yjeV	X	66	-		P56622	Hypothetical protein yjeV	b3350	UNC	0.06
3478244	REC05963	kefB	N	601	134, 174, 213		P45522	Glutathione-regulated potassium-efflux system protein kefB	b3350	MTR	0.47
3478798	REC05964	yjeR	N	184	107, 162		P45534	Putative NAD(P)H oxidoreductase yjeR (EC 1.6.99.-)	b3351	UNC	0.16
3478926	REC03270	yjeS	N	637	27, 136		P45535	Hypothetical ABC transporter ATP-binding protein yjeS	b3352	UNC	0.88
3480839	REC03271	yjeT	N	340	51, 91, 124, 171, 174, 227, 305		P45524	Hypothetical protein yjeT	b3353	UNC	0.19
3481855	REC03272	yjeU	N	72	14, 63		P45536	Hypothetical protein yjeU	b3354	UNC	0.09
3482127	REC06648	prkB	N	289	30, 46, 163, 217		P37307	Probable phosphoribulokinase (EC 2.7.1.19)	b3355	UNC	0.06
3483455	REC05965	yhfA	X	134	-		P24246	Hypothetical protein yhfA	b3356	UNC	0.31
3483757	REC03275	crp	X	210	-		P03020	Catabolite gene activator	b3357	RCD	0.44
3484440	REC03276	yhfK	N	696	186, 234, 269, 591		P45537	Hypothetical protein yhfK	b3358	UNC	0.25
3487817	REC05966	argD	?	406	30		P18335	Acetylornithine aminotransferase (EC 2.6.1.11)	b3359	AAM	0.69
3488466	REC05967	paba	N	187	51, 79		P00903	Para-aminobenzoate synthase glutamine amidotransferase component	b3360	AAM	0.53
3489100	REC05968	fic	N	200	113		P20605	Cell filamentation protein fic	b3361	RCD	0.13
3489934	REC05970	ppiA	N	190	40		P20752	Peptidyl-prolyl cis-trans isomerase A precursor (EC 5.2.1.8)	b3363	PMS	0.84
3490205	REC03282	yhfC	N	393	317, 317, 347, 347, 386		P21229	Hypothetical protein yhfC	b3364	UNC	0.25
3491648	REC03283	nirB	N	847	11, 69, 75, 278, 431		P08201	Nitrite reductase [NAD(P)H] large subunit (EC 1.6.6.4)	b3365	BEN	0.47
3494188	REC03284	nirD	N	108	56		P23675	Nitrite reductase [NAD(P)H] small subunit (EC 1.6.6.4)	b3366	BEN	0.03
3494892	REC03285	nirC	X	184	-		P11097	Potential nitrite transporter	b3367	UNC	0.13
3495465	REC03286	cysG	X	457	-		P11098	Siroheme synthase	b3368	NCM	0.66
3497085	REC03287	yhfL	X	55	-		P45538	Hypothetical protein yhfL	b3369	UNC	0.00
3497496	REC06649	yhfM	N	462	198		P45539	Hypothetical transport protein yhfM	b3370	UNC	0.09
3498884	REC03289	yhfN	N	347	9, 18, 60, 133, 152, 183, 197, 243		P45540	Hypothetical protein yhfN	b3371	UNC	0.19
3498990	REC03290	yhfO	N	149	43, 44		P45541	Hypothetical protein yhfO	b3372	UNC	0.03
3500404	REC06650	yhfP	N	134	8, 65, 112		P45542	Hypothetical protein yhfP	b3373	UNC	0.03
3500805	REC03292	yhfQ	E	261	-	< 0.05	P45543	Hypothetical sugar kinase yhfQ	b3374	UNC	0.09
3501624	REC03293	yhfR	N	265	3, 84, 121		P45544	Hypothetical transcriptional regulator yhfR	b3375	UNC	0.53
3503658	REC05971	yhfS	N	361	298		P45545	Hypothetical protein yhfS	b3376	UNC	0.00
3504974	REC05972	yhfT	X	434	8		P45546	Hypothetical protein yhfT	b3377	UNC	0.00
3505378	REC05973	yhfU	N	130	42, 75, 100, 124		P45547	Hypothetical protein yhfU	b3378	UNC	0.00
3506228	REC05974	php	N	292	206, 281, 281		P45548	Phosphotriesterase homology protein	b3379	UNC	0.16
3507451	REC05975	yhfW	N	408	149, 192, 282, 356, 360		P45549	Hypothetical protein yhfW	b3380	UNC	0.41
3508614	REC05976	yhfX	N	387	47		P45550	Hypothetical protein yhfX	b3381	UNC	0.00
3509102	REC05977	yhfY	N	134	27, 101		P45551	Hypothetical protein yhfY	b3382	UNC	0.00
3509763	REC05978	yhfZ	N	228	39, 48, 123, 176, 215		P45552	Hypothetical protein yhfZ	b3383	UNC	0.00
3511276	REC05979	trpS	E	334	-	< 0.05	P00954	Tryptophanyl-tRNA synthetase (EC 6.1.1.2)	b3384	PMS	1.00
3512027	REC05980	gph	N	252	61		P32662	Phosphoglycolate phosphatase (EC 3.1.3.18)	b3385	CHM	0.81
3512697	REC05981	rpe	E	225	222		P32661	Ribulose-phosphate 3-epimerase (EC 5.1.3.1)	b3386	CHM	0.94
3513551	REC05982	dam	N	278	35, 197, 242	< 0.2	P00475	DNA adenine methylase (EC 2.1.1.72)	b3387	NAM	0.28
3514944	REC05983	damX	N	428	183, 358, 364, 426		P11557	DamX protein	b3388	UNC	0.03
3516124	REC05984	aroB	N	362	28, 158, 213		P07639	3-dehydroquinate synthase (EC 4.2.3.4)	b3389	AAM	0.84
3516903	REC05985	aroK	E	240	-	< 0.1	P24167	Shikimate kinase I (EC 2.7.1.71)	b3390	AAM	0.81
3518341	REC05986	hofQ	N	412	43, 324, 395		P33479	Protein transport protein hofQ precursor	b3391	UNC	0.28
3518696	REC05987	yrfA	?	147	-		P45750	Hypothetical protein yrfA	b3392	UNC	0.00
3519087	REC05988	yrfB	N	146	22, 95		P45751	Hypothetical protein yrfB	b3393	UNC	0.00
3519610	REC05989	yrfC	N	179	16, 68, 93, 121		P45752	Hypothetical protein yrfC	b3394	UNC	0.00
3520416	REC05990	yrfD	N	268	5, 79, 82		P45753	Hypothetical protein yrfD	b3395	UNC	0.00
3520485	REC03314	mrcA	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	nudE	N	186	50, 98, 129		P45799	ADP compounds hydrolase nudE (EC 3.6.1.-)	b3397	MSM	0.19
3524107	REC03316	yrfE	N	711	86, 694		P45800	Putative membrane protein igaA homolog	b3398	UNC	0.00
3526262	REC03317	yrfG	N	237	3, 6, 55, 115, 125, 136, 173		P45801	Hypothetical protein yrfG	b3399	UNC	0.03
3526986	REC03318	hslR	N	133	8, 58, 63		P45802	Heat shock protein 15	b3400	SMC	0.34
3527406	REC03319	hslO	X	294	9		P45803	33 kDa chaperonin	b3401	PMS	0.69
3530077	REC05992	yhgE	N	574	6, 62, 72, 120, 146, 246, 287, 322, 347		P45804	Hypothetical protein yhgE	b3402	UNC	0.03
3530456	REC03321	pckA	N	540	42, 68, 216, 533		P22259	Phosphoenolpyruvate carboxykinase [ATP] (EC 4.1.1.49)	b3403	CHM	0.38
3533506	REC05993	envZ	N	450	112, 193, 222, 243, 297, 338		P02933	Osmolarity sensor protein envZ (EC 2.7.3.-)	b3404	SMC	0.34
3534222	REC05994	ompR	N	239	98, 133, 181, 222		P03025	Transcriptional regulatory protein ompR	b3405	SMC	0.69
3534414	REC03324	greB	N	170	63, 91		P30128	Transcription elongation factor greB	b3406	NAM	0.19
3535122	REC03325	yhgP	N	740	19, 115, 286, 291, 303, 307, 340, 471, 482, 651, 716		P46837	Protein yhgP	b3407	UNC	0.59
3537799	REC03326	feoA	N	75	22, 48		P33649	Ferrous iron transport protein A	b3408	UNC	0.03
3538043	REC03327	feoB	N	773	13, 86, 100, 153, 217, 431, 450, 484, 522, 583, 618, 690, 758, 766		P33650	Ferrous iron transport protein B	b3409	UNC	0.47
3540364	REC03328	yhgG	?	78	-		P46845	Hypothetical protein yhgG	b3410	UNC	0.00
3540803	REC03329	yhgA	N	292	111, 218, 256		P31667	Hypothetical protein yhgA	b3411	UNC	0.00
3542470	REC03331	yhgH	N	243	142		P46846	Hypothetical protein yhgH	b3413	UNC	0.50
3542480	REC05995	bioH	N	256	26		P13001	BioH protein	b3412	UNC	0.25
3543260	REC03332	yhgI	N	191	16, 175, 185		P46847	Protein yhgI	b3414	UNC	0.19
3544195	REC03333	gntT	N	437	31, 99, 166, 211, 342		P39835	High-affinity gluconate transporter	b3415	MTR	0.31
3547703	REC05996	malQ	N	694	35, 60, 116, 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)	b3420	NAM	0.13
3554484	REC05999	yhgK	N	146	13, 47, 70				b3421	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, 457		P13035	Aerobic glycerol-3-phosphate dehydrogenase (EC 1.1.99.5)	b3426	CHM	0.53
3561650	REC06004	yglL	?	97	5		P76692	VERY HYPOTHETICAL 10.7 kDa PROTEIN IN GLPD-GLGP INTERG	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, 183, 255, 290, 306, 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

3686830	REC06507	yhjL	N	1166	4, 45, 95, 144, 235, 283, 349, 509, 574, 597, 763, 882, 945, 1008, 1016, 1017	P37650	Hypothetical protein yhjL	b3530	UNC	0.03
3687890	REC06063	bosc	N	368	110, 158, 208, 316, 357	P37651	Endoglucanase precursor (EC 3.2.1.4)	b3531	CHM	0.06
3690236	REC06064	yhjN	N	779	77, 81, 112, 208, 276, 561, 698, 761, 761	P37652	Hypothetical protein yhjN precursor	b3532	UNC	0.00
3692913	REC06065	yhjO	N	888	355, 428, 534, 605, 607, 676, 746, 793	P37653	Hypothetical protein yhjO	b3533	UNC	0.28
3693590	REC06067	yhjQ	N	242	95, 121, 144, 222	P37655	Hypothetical protein yhjQ	b3534	UNC	0.00
3693814	REC06068	yhjR	N	62	42	P37656	Hypothetical protein yhjR	b3535	UNC	0.00
3694087	REC03457	yhjS	N	523	30, 51, 90, 100, 351	P37657	Hypothetical protein yhjS	b3536	UNC	0.00
3695658	REC03458	yhjT	X	62	-	P37658	Hypothetical protein yhjT	b3537	UNC	0.00
3695843	REC03459	yhjU	N	559	119, 172, 233, 282, 322, 505, 532	P37659	Hypothetical protein yhjU	b3538	UNC	0.00
3698192	REC03460	yhjV	N	423	63, 71, 130, 153, 208, 329	P37660	Hypothetical transport protein yhjV	b3539	UNC	0.13
3700497	REC06069	dppF	N	334	90, 98, 222	P37313	Dipeptide transport ATP-binding protein dppF	b3540	MTR	0.53
3701477	REC06070	dppD	N	327	51, 86, 105, 146, 165, 202, 235, 265	P37314	Dipeptide transport ATP-binding protein dppD	b3541	MTR	0.59
3702390	REC06071	dppC	N	300	46, 218, 225	P37315	Dipeptide transport system permease protein dppC	b3542	MTR	0.59
3703419	REC06072	dppB	N	339	50, 94, 318	P37316	Dipeptide transport system permease protein dppB	b3543	MTR	0.72
3705334	REC06073	dppA	N	535	32, 36, 91, 152, 377, 423, 437, 489	P23847	Periplasmic dipeptide transport protein precursor	b3544	MTR	0.56
3708137	REC06511	yhjW	N	574	17, 40, 132, 236, 274, 393, 407, 425, 443, 476, 540	P37661	Membrane-protein yhjW	b3546	UNC	0.06
3709636	REC06075	yhjX	N	402	147, 182, 253, 350, 360	P37662	Hypothetical protein yhjX	b3547	UNC	0.38
3710569	REC06076	yhjY	N	234	27, 58, 68, 109, 113, 188	P37663	Hypothetical protein yhjY	b3548	UNC	0.00
3710721	REC03469	tag	N	187	8, 92, 185	P05100	DNA-3-methyladenine glycosylase I (EC 3.2.2.20)	b3549	NAM	0.47
3711281	REC03470	yaiaC	N	146	36, 90, 117	P37664	Hypothetical acetyltransferase yaiaC (EC 2.3.1.-)	b3550	UNC	0.13
3713909	REC06077	bisc	N	739	188, 312, 622, 692, 726	P20099	Biotin sulfoxide reductase (EC 1.-.-.-)	b3551	NCM	0.03
3714176	REC03472	yaiaD	N	219	46, 54, 86, 110, 126, 167, 181	P37665	Hypothetical lipoprotein yaiaD precursor	b3552	UNC	0.56
3714927	REC06512	tkrA	N	328	18, 152, 213, 277	P37666	2-ketoglucanate reductase (EC 1.1.1.215)	b3553	CHM	0.47
3716793	REC06078	yaiaF	?	276	268	P37667	Hypothetical protein yaiaF	b3554	UNC	0.00
3717107	REC03475	yaiaG	N	96	10, 11	P37668	Hypothetical protein yaiaG	b3555	UNC	0.00
3717678	REC03476	cspA	N	70	23	P15277	Cold shock protein cspA	b3556	UNC	0.72
3718309	REC03477	insJ	N	173	3, 59, 135	P19768	Insertion element IS150 hypothetical 19.7 kDa protein	b3557	PHT	0.56
3718827	REC03478	insK	N	283	100, 221	P19769	Putative transposase insK for insertion sequence element IS150	b3558	UNC	0.56
3722026	REC06079	glys	E	689	-	P00961	Glycyl-IRNA synthetase beta chain (EC 6.1.1.14)	b3559	PMS	0.72
3722947	REC06080	glyyQ	E	303	-	P00960	Glycyl-IRNA synthetase alpha chain (EC 6.1.1.14)	b3560	PMS	0.75
3723516	REC03481	yaiaH	N	331	61, 99, 101, 118, 165, 207, 208, 229, 231, 266	P37669	Hypothetical protein yaiaH	b3561	UNC	0.06
3724993	REC06081	yaiaA	N	146	5, 7, 13, 55, 87, 124	P11287	Hypothetical protein yaiaA	b3562	UNC	0.03
3725389	REC06082	yaiaB	N	117	1, 7, 78, 106	P11286	Hypothetical protein yaiaB	b3563	UNC	0.00
3727000	REC06083	xyiB	?	484	-	P09099	Xylulose kinase (EC 2.7.1.17)	b3564	CHM	0.47
3728394	REC06084	xyiA	N	440	46, 115, 253, 277, 341, 404	P00944	Xylose isomerase (EC 5.3.1.5)	b3565	CHM	0.22
3728760	REC03486	xyiF	N	330	5, 36	P37387	D-xylose-binding periplasmic protein precursor	b3566	MTR	0.19
3729830	REC03487	xyiG	N	513	253, 312, 338, 349, 370, 385, 464, 488	P37388	D-xylose transport ATP-binding protein xyiG	b3567	MTR	0.22
3731349	REC03488	xyiH	N	393	17, 150, 392	P37389	Xylose transport system permease protein xyiH	b3568	MTR	0.19
3732608	REC03489	xyiR	X	392	-	P37390	Xylose operon regulatory protein	b3569	RCD	0.06
3734806	REC06085	bax	N	274	24, 94, 115, 126, 188, 232	P27297	BAX protein	b3570	UNC	0.09
3735126	REC03491	malS	N	676	19, 56, 118, 173, 201, 265, 299	P25718	Alpha-amylase precursor (EC 3.2.1.1)	b3571	CHM	0.09
3737334	REC03492	avtA	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	ysaA	N	157	112	P56256	Putative electron transport protein ysaA	b3573	UNC	0.00
3740161	REC06086	yaiaJ	N	282	115, 218	P37671	Hypothetical transcriptional regulator yaiaJ	b3574	UNC	0.09
3740362	REC03495	yaiaK	N	332	114, 121, 163, 174, 177, 242, 314	P37672	Hypothetical oxidoreductase yaiaK (EC 1.1.1.-)	b3575	UNC	0.16
3741372	REC03496	yaiaL	N	155	25, 63, 87	P37673	Hypothetical protein yaiaL	b3576	UNC	0.16
3741957	REC03497	yaiaM	N	157	70	P37674	Hypothetical protein yaiaM	b3577	UNC	0.13
3742433	REC03498	yaiaN	?	424	18	P37675	Hypothetical protein yaiaN	b3578	UNC	0.44
3743724	REC03499	yaiaO	N	328	80, 130, 172, 202, 267, 323	P37676	Putative ABC transporter periplasmic binding protein yaiaO precursor	b3579	UNC	0.41
3744714	REC03500	lyx	N	498	5, 14, 20, 59, 200, 210, 230, 329, 355, 365, 384	P37677	Cryptic L-xylulose kinase (EC 2.7.1.53)	b3580	CHM	0.25
3746207	REC03501	sgbH	X	220	-	P37678	Probable hexulose-6-phosphate synthase (EC 4.1.2.-)	b3581	UNC	0.22
3746829	REC03502	sgbU	N	293	247, 247	P37679	Putative hexulose-6-phosphate isomerase (EC 5.-.-.-)	b3582	UNC	0.19
3747716	REC03503	sgbE	N	231	95, 130, 205	P37680	Probable sugar isomerase sgbE (EC 5.1.-.-)	b3583	UNC	0.19
3749498	REC06087	yaiaT	N	246	30, 42, 94, 135, 163	P37681	Putative outer membrane protein yaiaT precursor	b3584	UNC	0.03
3749622	REC03505	yaiaU	N	324	38, 188	P37682	Hypothetical transcriptional regulator yaiaU	b3585	UNC	0.00
3751729	REC06088	yaiaV	N	378	17, 60, 76, 198, 207, 241, 267, 310	P37683	Hypothetical protein yaiaV precursor	b3586	UNC	0.06
3752058	REC06089	yaiaW	N	107	51, 75	P37684	Hypothetical protein yaiaW	b3587	UNC	0.03
3754231	REC06090	aldB	X	542	-	P37685	Aldehyde dehydrogenase B (EC 1.2.1.22)	b3588	CHM	0.47
3755454	REC06091	yaiaY	N	382	52, 76, 84, 100, 110, 142, 175, 215	P37686	Probable alcohol dehydrogenase (EC 1.1.1.1)	b3589	UNC	0.50
3757488	REC06528	selB	N	614	350, 538, 574, 606	P14081	Selenocysteine-specific elongation factor	b3590	PMS	0.16
3758876	REC06529	selA	N	463	123, 147, 198, 237, 256, 318, 344	P23328	L-seryl-IRNA(Sec) selenium transferase (EC 2.9.1.1)	b3591	NAM	0.25
3759582	REC06094	yibP	N	202	2, 54, 149, 150	P32105	Hypothetical GST-like protein yibP	b3592	UNC	0.22
3759810	REC03513	rhsA	N	1377	35, 150, 393, 453, 468, 491, 500, 533, 554, 596, 671, 705, 768, 1242, 1305	P16916	RhsA protein precursor	b3593	UNC	0.03
3763964	REC03514	yibA	E	280	-	P24172	Hypothetical protein yibA	b3594	UNC	0.03
3764848	REC06531	yibJ	N	233	-	P32109	Hypothetical protein yibJ	b3595	UNC	0.00
3765804	REC03516	yibG	E	153	-	P32106	Hypothetical protein yibG precursor	b3596	UNC	0.00
3769006	REC06095	yibH	X	378	-	P32107	Hypothetical protein yibH	b3597	UNC	0.03
3769371	REC06096	yibI	X	120	-	P32108	Hypothetical protein yibI	b3598	UNC	0.00
3769908	REC03519	mtiA	N	637	501, 611	P00550	PTS system, mannitol-specific IIABC component (EC 2.7.1.69)	b3599	MTR	0.25
3772051	REC03520	mtiD	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	mtiR	N	195	5, 166, 194	P36563	Mannitol operon repressor	b3601	RCD	0.03
3774292	REC03522	yibL	X	120	-	P36564	Hypothetical protein yibL	b3602	UNC	0.03
3775026	REC03523	ltdP	N	551	16, 19, 136, 194, 278, 298, 348, 448, 456, 491	P33231	L-lactate permease	b3603	MTR	0.38
3776681	REC03524	ltdR	N	258	17, 94	P33233	Putative L-lactate dehydrogenase operon regulatory protein	b3604	UNC	0.03
3777454	REC03525	ltdD	N	396	160, 197, 319	P33232	L-lactate dehydrogenase (EC 1.1.2.3)	b3605	CHM	0.44
3778842	REC03526	yibK	N	157	95, 97	P33899	Hypothetical tRNA/rRNA methyltransferase yibK (EC 2.1.1.-)	b3606	UNC	0.78
3780189	REC06097	cysE	E	273	-	P05796	Serine acetyltransferase (EC 2.3.1.30)	b3607	AAM	0.72
3781288	REC06098	gpsA	N	339	303, 336	P37606	Glycerol-3-phosphate dehydrogenase [NAD(P)+] (EC 1.1.1.94)	b3608	CHM	0.94
3781755	REC06099	secB	E	155	-	P15040	Protein-export protein secB	b3609	PMS	0.41
3782069	REC06100	grxX	N	83	21	P37687	Glutaredoxin 3	b3610	AAM	0.47
3782642	REC06101	yibN	N	143	6, 13, 47, 72, 81, 98	P37688	Hypothetical protein yibN	b3611	UNC	0.31
3782887	REC03532	yibo	N	514	59, 138, 175, 236, 386	P37689	2,3-bisphosphoglycerate-independent phosphoglycerate mutase (EC 3.1.1.3)	b3612	CHM	0.38
3784441	REC03533	yibP	N	427	266, 284, 290, 318, 402, 402	P37690	Hypothetical protein yibP	b3613	UNC	0.69
3785854	REC03534	yibQ	N	277	19, 65, 91, 119, 131, 184, 188	P37691	Hypothetical protein yibQ precursor	b3614	UNC	0.16
3787708	REC06102	yibD	N	344	142, 175, 192, 281, 292, 325	P11290	Putative glycosyl transferase yibD (EC 2.-.-.-)	b3615	UNC	0.44
3788972	REC06103	tdh	N	341	140, 160, 176, 210, 214, 235, 259	P07913	Threonine 3-dehydrogenase (EC 1.1.1.103)	b3616	AAM	0.19
3790178	REC06104	klb	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	htrL	N	290	12, 97, 213, 241, 247	P25666	HtrL protein	b3618	UNC	0.00
3791614	REC03539	rfaD	N	310	1, 16, 68, 79, 117, 119, 234, 278, 299	P17963	ADP-L-glycero-D-manno-heptose-6-epimerase (EC 5.1.3.20)	b3619	CHM	0.38
3792556	REC03540	rfaF	N	348	11, 56, 62, 102, 119, 133, 156, 280	P37692	ADP-heptose-LPS heptosyltransferase II (EC 2.-.-.-)	b3620	LPC	0.41
3793606	REC03541	rfaC	E	319	-	P24173</				

3800685	REC06110	rfaI	X	339	-	P27128	Lipopolysaccharide 1,3-galactosyltransferase (EC 2.4.1.44)	b36228	LPC	0.09
3801794	REC06111	rfaB	X	369	-	P27127	Lipopolysaccharide 1,6-galactosyltransferase (EC 2.4.1.-)	b36228	LPC	0.19
3802743	REC06112	rfaS	N	311	42, 117, 153, 183, 212, 228	P27126	Lipopolysaccharide core biosynthesis protein rfaS	b36229	LPC	0.00
3803577	REC06113	rfaP	N	265	51, 74, 120, 132, 162, 177, 203, 220, 234	P25741	Lipopolysaccharide core biosynthesis protein rfaP	b36300	LPC	0.03
3804694	REC06114	rfaG	N	374	167, 173, 312	P25740	Lipopolysaccharide core biosynthesis protein rfaG	b36301	CHM	0.19
3805725	REC06115	rfaQ	N	344	-	P25742	Lipopolysaccharide core biosynthesis glycosyl transferase rfaQ (EC 3.1.1.11)	b36302	LPC	0.19
3806167	REC03553	kdtA	E	425	4, 7, 68, 80, 131, 163	P23282	3-deoxy-D-manno-octulosonic-acid transferase (EC 2.-.-.-)	b36333	LPC	0.53
3807452	REC03554	coaD	E	159	-	P23875	Phosphopantetheine adenylyltransferase (EC 2.7.7.3)	b36334	NCM	0.91
3808779	REC06116	mutM	N	269	48, 89, 184	P05523	Formamidopyrimidine-DNA glycosylase (EC 3.2.2.23)	b36335	NAM	0.66
3809044	REC06117	rpmG	?	55	42	P02436	50S ribosomal protein L33	b36336	PMS	0.59
3809301	REC06118	rpmB	?	78	-	P02428	50S ribosomal protein L28	b36337	PMS	0.66
3810192	REC06119	radC	N	224	58, 65, 96, 107, 179	P25531	DNA repair protein radC	b36338	NAM	0.66
3810286	REC03559	dfp	E	430	41	P24285	DNA/pantothenate metabolism flavoprotein	b36339	NCM	0.84
3811559	REC03560	dut	E	151	-	P06968	Deoxyuridine 5'-triphosphate nucleotidohydrolase (EC 3.6.1.23)	b36340	NCM	0.72
3812079	REC03561	tkk	N	212	29, 60, 108, 189, 192, 197	P06969	Ttk protein	b36341	UNC	0.09
3813395	REC06120	pyrE	N	213	35, 57	P00495	Orotate phosphoribosyltransferase (EC 2.4.2.10)	b36342	NCM	0.84
3814176	REC06121	rph	N	228	10, 16, 172	P03842	Ribonuclease PH (EC 2.7.7.56)	b36343	NAM	0.63
3814303	REC03564	yicC	X	287	-	P23839	Protein yicC	b36344	UNC	0.56
3815375	REC03565	dinD	N	278	56, 89, 111, 204, 244, 296	P23840	DNA-damage-inducible protein D	b36345	UNC	0.09
3816447	REC03566	yicG	N	223	38	P31432	Hypothetical protein yicG	b36346	UNC	0.41
3818803	REC06122	yicF	N	562	209, 247, 362, 461, 461, 556	P25772	Hypothetical DNA ligase-like protein yicF	b36347	UNC	1.00
3819055	REC03568	gmk	E	207	9	P24234	Guanylate kinase (EC 2.7.4.8)	b36348	NCM	0.94
3819733	REC03569	rpoZ	N	91	44, 58	P08374	DNA-directed RNA polymerase omega chain (EC 2.7.7.6)	b36349	NAM	0.38
3820027	REC03570	spoT	?	702	538, 554	P17580	Guanosine-3',5'-bis(Diphosphate) 3'-pyrophosphohydrolase (EC 3.1.7.1)	b36350	MSM	0.91
3822142	REC03571	trmH	N	229	58, 71, 76, 89, 99, 126, 155, 202	P19396	tRNA (Guanosine-2'-O)-methyltransferase (EC 2.1.1.34)	b36351	NAM	0.31
3822837	REC06537	recG	N	693	7, 22, 24, 44, 146, 167, 252, 295, 362, 470	P24230	ATP-dependent DNA helicase recG (EC 3.6.1.-)	b36352	NAM	0.91
3826292	REC06123	gltS	N	401	23, 25, 71, 168, 168, 282	P19933	Sodium/glutamate symport carrier protein	b36353	MTR	0.25
3826572	REC03574	yicE	N	463	28, 94, 117, 168, 212, 250, 265, 292	P27432	Putative purine permease yicE	b36354	UNC	0.06
3828084	REC03575	yicH	N	569	395, 378, 453, 486, 517, 523	P31433	Hypothetical protein yicH	b36355	UNC	0.03
3832164	REC06538	yicI	N	772	194, 331, 354, 424, 443, 651, 702, 734	P31434	Putative family 31 glucosidase yicI	b36356	UNC	0.22
3833613	REC06539	yicJ	N	479	11, 155, 174, 185, 217, 246, 311, 360, 378	P31435	Hypothetical symporter yicJ	b36357	UNC	0.16
3834580	REC03578	setC	N	394	149	P31436	Sugar efflux transporter C	b36358	MTR	0.00
3835875	REC03579	yicL	X	307	-	P31437	Hypothetical transport protein yicL	b36359	UNC	0.63
3837620	REC06126	nlpA	X	272	-	P04846	Lipoprotein-28 precursor	b36360	LPC	0.69
3839531	REC06127	yicM	X	451	-	P31438	Hypothetical protein yicM	b36361	UNC	0.22
3840056	REC06128	yicN	N	159	24, 56, 70, 121, 151	P31439	Hypothetical protein yicN	b36362	UNC	0.00
3841494	REC06129	yicO	N	470	206, 257, 257, 288, 323, 326, 398, 429, 452	P31440	Hypothetical protein yicO	b36363	UNC	0.66
3841591	REC03584	yicP	N	588	42, 86, 466, 505, 587	P31441	Probable adenine deaminase (EC 3.5.4.2)	b36364	UNC	0.28
3844794	REC06540	uhpT	N	463	59, 62, 101, 190, 246, 253, 292, 330, 441	P13408	Hexose phosphate transport protein	b36365	SMC	0.06
3846254	REC06541	uhpC	N	440	23, 240, 290, 306, 394	P09836	Regulatory protein uhpC	b36366	SMC	0.13
3847766	REC06132	uhpB	N	501	38, 84, 98, 123, 176, 210, 288, 311, 335, 388	P09835	Sensor protein uhpB (EC 2.7.3.-)	b36367	SMC	0.06
3848353	REC06133	uhpA	N	196	35, 128, 143	P10940	Transcriptional regulatory protein uhpA	b36368	SMC	0.25
3848719	REC06134	ilvN	X	96	-	P08143	Acetolactate synthase isozyme I small subunit (EC 4.1.3.18)	b36369	AAM	0.00
3850411	REC06135	ilvB	N	562	12, 49, 59, 63, 107, 136, 184, 202	P08142	Acetolactate synthase isozyme I large subunit (EC 4.1.3.18)	b36370	AAM	0.78
3850615	REC06136	ilvL	?	32	-	P03061	ilvBN operon leader peptide	b36371	RCD	0.00
3851543	REC03592	emrD	N	396	88, 165, 187, 311	P31442	Multidrug resistance protein D	b36372	MTR	0.03
3853238	REC06137	yidF	?	165	91	P31443	Hypothetical protein yidF	b36373	UNC	0.00
3853597	REC06138	yidG	N	120	18, 52, 88, 117	P31444	Hypothetical protein yidG	b36374	UNC	0.00
3853934	REC06139	yidH	N	115	23, 29, 55, 105	P31445	Hypothetical protein yidH	b36375	UNC	0.06
3854042	REC03596	yidI	N	149	54, 70, 96, 98	P31446	Hypothetical protein yidI	b36376	UNC	0.00
3856031	REC06140	yidJ	N	497	55, 104, 257, 289, 447, 472	P31447	Putative sulfatase yidJ (EC 3.1.6.-)	b36377	UNC	0.22
3857743	REC06141	yidK	N	571	9, 49, 244, 258, 283, 288	P31448	Putative symporter yidK	b36378	UNC	0.16
3857880	REC03599	yidL	N	307	77, 91, 109, 129, 198, 223	P31449	Hypothetical transcriptional regulator yidL	b36379	UNC	0.00
3859614	REC06142	glvG	X	212	-	P31450	Probable 6-phospho-alpha-glucosidase (EC 3.2.1.122)	b36380	UNC	0.06
3860099	REC06143	glvB	X	161	-	P31451	PTS system, arbutin-like IIB component (EC 2.7.1.69)	b36381	CHM	0.16
3861491	REC06144	glvC	N	455	34, 56, 82, 120, 145, 191, 206, 270, 322, 341, 413, 443	P31452	PTS system, arbutin-like IIC component	b36382	MTR	0.16
3861526	REC03603	yidP	E	238	238	P31453	Hypothetical transcriptional regulator yidP	b36383	UNC	0.25
3863924	REC06145	yidE	N	561	15, 26, 50, 70, 92, 106, 348, 449, 501	P29211	Hypothetical membrane protein yidE	b36384	UNC	0.09
3864530	REC06146	ibpB	N	144	6, 42, 53, 140, 143	P29210	16 kDa heat shock protein B	b36385	UNC	0.25
3865049	REC06147	ibpA	N	137	26, 33, 55, 101	P29209	16 kDa heat shock protein A	b36386	UNC	0.25
3865280	REC03607	yidQ	N	135	37, 66, 103	P31454	Hypothetical protein yidQ precursor	b36387	UNC	0.00
3866939	REC06148	yidR	N	416	2, 91, 134, 201, 227, 279, 304	P31455	Hypothetical protein yidR	b36388	UNC	0.00
3866983	REC03609	yidS	N	361	53, 95, 121, 296, 339	P31456	Hypothetical protein yidS precursor	b36389	UNC	0.16
3869402	REC06149	dgoT	N	445	23, 42, 96, 143, 275, 345	P31457	D-galactonate transporter	b36390	MTR	0.34
3871240	REC06545	dgoA	N	587	27, 55, 77, 78, 118, 157, 171, 182, 196, 405, 582	P31458	DgoA protein	b36391	CHM	0.25
3872102	REC06151	dgoK	N	292	98, 185, 201, 217, 252	P31459	2-dehydro-3-deoxygalactonokinase (EC 2.7.1.58)	b36392	CHM	0.16
3872395	REC06546	dgoR	?	98	76	P31460	Galactonate operon transcriptional repressor	b36393	RCD	0.00
3872787	REC06547	dgoR	N	128	48, 119	P31461	Galactonate operon transcriptional repressor	b36394	RCD	0.13
3873122	REC03614	yidX	N	223	19, 39, 134	P31462	Hypothetical protein yidX	b36395	UNC	0.00
3874580	REC06548	yidA	N	270	2, 32, 42, 42, 65, 121, 157, 170, 219, 244	P09997	Hypothetical protein yidA	b36396	UNC	0.66
3875102	REC06154	yidB	N	135	7, 22, 50, 90	P09996	Hypothetical protein yidB	b36397	UNC	0.16
3877747	REC06155	gyrB	X	804	-	P06982	DNA gyrase subunit B (EC 5.99.1.3)	b36398	NAM	1.00
3878849	REC06156	recF	N	357	2, 70, 93, 148, 197, 198, 232, 257, 302	P03016	DNA replication and repair protein recF	b37000	NAM	0.72
3879949	REC06157	dnaN	X	366	-	P00583	DNA polymerase III, beta chain (EC 2.7.7.7)	b37001	NAM	1.00
3881357	REC06549	dnaA	E	467	-	P03004	Chromosomal replication initiator protein dnaA	b37002	NAM	0.97
3881965	REC03621	rpmH	?	46	-	P02437	50S ribosomal protein L34	b37003	PMS	0.56
3882122	REC03622	rnpA	?	119	-	P06277	Ribonuclease P protein component (EC 3.1.26.5)	b37004	NAM	0.25
3882475	REC06704	yidD	?	75	-	P22847	Hypothetical protein yidD	b37005	UNC	0.84
3882705	REC03623	yidC	?	548	-	P25714	60 kDa inner-membrane protein	b37006	PMS	0.97
3884457	REC06550	trmE	E	454	-	P25522	Probable tRNA modification GTPase trmE	b37007	UNC	0.94
3886064	REC03625	tnaL	N	24	4, 14, 14	P09408	Tryptophanase leader peptide	b37008	NAM	0.00
3886344	REC03626	tnaA	N	476	50, 100, 128, 225, 360, 435, 443	P00913	Tryptophanase (EC 4.1.99.1)	b37009	AAM	0.06
3887865	REC03627	tnaB	N	415	71, 74, 127, 166, 170, 203, 244, 328, 381, 400	P23173	Low affinity tryptophan permease	b37010	MTR	0.00
3889244	REC03628	yidY	N	391	56, 76, 146	P31462	Hypothetical transport protein yidY	b37011	UNC	0.09
3890394	REC03629	yidZ	N	319	292	P31463	Hypothetical transcriptional regulator yidZ	b37012	UNC	0.72
3891498	REC03630	yieE	N	253	125, 161, 168, 205	P31464	Hypothetical protein yieE	b37013	UNC	0.00
3892281	REC03631	yieP	N	188	27, 31, 59, 103, 133, 182	P31465	Hypothetical protein yieP	b37014	UNC	0.28
3894238	REC06159	yieG	N	445	101, 384	P31466	Hypothetical protein yieG	b37015	UNC	0.66
3894403	REC03633	yieH	N	221	125, 197, 214	P31467	Hypothetical protein yieH	b37016	UNC	0.81
3895135	REC03634	yieI	N	155	21, 52, 74, 85, 108, 122	P31468	Hypothetical protein yieI	b37017	UNC	0.00
3895651	REC03635	yieJ	N	195	22, 29, 72, 108	P31469	Hypothetical protein yieJ	b37018	UNC	0.06
3896952	REC06160	yieK	N	213	28, 195	P31470	Hypothetical protein yieK	b37019	UNC	0.34
3898238	REC06161	yieL	E	400	-	P31471	Hypothetical protein yieL	b37020	UNC	0.00
3899848	REC06162	yieC	N	538	377	P26218	Putative outer membrane protein yieC precursor	b37021	UNC	0.00
3901329	REC06551	bgIB	X	470	-	P11988	6-phospho-beta-glucosidase bgIB (EC 3.2.1.86)	b37221	CHM	0.31
3903225	REC06164	bgIP	N	625	9, 31, 204, 240, 262, 327, 381, 387, 449, 482, 565, 589, 605	P08722	PTS system, beta-glucosidase-specific IIBC component (EC 2.7.1.69)	b37222	MTR	0.47

3904195	REC06165	<i>bglG</i>	N	278	115, 132	P11989	Cryptic beta-glucoside <i>bgl</i> operon antiterminator	b3723	RCD	0.19
3905206	REC06166	<i>phoU</i>	?	241	-	P07656	Phosphate transport system protein <i>phoU</i>	b3724	UNC	0.66
3905994	REC06167	<i>pstB</i>	N	257	60, 181, 254	P07655	Phosphate transport ATP-binding protein <i>pstB</i>	b3725	MTR	0.78
3907067	REC06168	<i>pstA</i>	N	296	202, 294	P07654	Phosphate transport system permease protein <i>pstA</i>	b3726	MTR	0.75
3908026	REC06169	<i>pstC</i>	N	319	253	P07653	Phosphate transport system permease protein <i>pstC</i>	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>gImS</i>	E	609	-	P17169	Glucosamine-fructose-6-phosphate aminotransferase [isomerizing] (I)	b3729	CHM	0.91
3912828	REC06172	<i>gImU</i>	E	456	-	P17114	Bifunctional <i>gImU</i> 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 <i>mioC</i>	b3742	UNC	0.09
3924631	REC06185	<i>asnC</i>	N	152	59, 63, 141, 152	P03809	Regulatory protein <i>asnC</i>	b3743	RCD	0.16
3924783	REC03662	<i>asna</i>	N	330	89, 99, 115, 120, 161, 193, 196, 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 <i>yjeM</i>	b3745	UNC	0.03
3928744	REC06556	<i>yjeN</i>	N	506	92, 169, 391, 485	P31473	Hypothetical protein <i>yjeN</i>	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	P00016	Kup system potassium uptake protein	b3747	MTR	0.31
3930941	REC03667	<i>rbsD</i>	N	151	40, 63	P04982	High affinity ribose transport protein <i>rbsD</i>	b3748	MTR	0.19
3931404	REC03668	<i>rbsA</i>	N	501	212, 227, 273, 305, 323, 331, 366	P04983	Ribose transport ATP-binding protein <i>rbsA</i>	b3749	MTR	0.66
3932914	REC03669	<i>rbsC</i>	N	321	34, 51, 74, 78, 133, 236, 299, 311	P04984	Ribose transport system permease protein <i>rbsC</i>	b3750	MTR	0.38
3933904	REC03670	<i>rbsB</i>	N	296	136	P02925	D-ribose-binding periplasmic protein precursor	b3751	MTR	0.41
3934920	REC03671	<i>rbsK</i>	N	309	166, 167, 221, 232, 255	P05054	Ribokinase (EC 2.7.1.15)	b3752	CHM	0.59
3935853	REC03672	<i>rbsR</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 <i>yjeO</i>	b3754	UNC	0.41
3938806	REC06190	<i>yjeP</i>	N	181	37	P31475	Hypothetical transcriptional regulator <i>yjeP</i>	b3755	UNC	0.16
3945348	REC06191	<i>ppsR</i>	N	198	41, 187	P27826	Possible regulatory protein <i>ppsR</i>	b3763	UNC	0.72
3945590	REC06192	<i>ppsR</i>	N	133	5, 63, 80, 121	P27827	Protein <i>yjeE</i>	b3764	UNC	0.06
3945709	REC06557	<i>yifE</i>	N	112	18, 31, 83, 99	P22787	Hypothetical protein <i>yifB</i>	b3765	UNC	0.75
3947622	REC06193	<i>yifB</i>	N	516	29, 230, 248, 256, 296, 302, 318, 365, 387, 458, 493	P03060	IlvGEMDA operon leader peptide	b3766	RCD	0.00
3947945	REC03679	<i>ilvL</i>	?	32	-	P00892	Acetolactate synthase isozyme II large subunit (EC 4.1.3.18)	b3767	AAM	0.78
3948183	REC03680	<i>ilvG</i>	N	327	323	P13048	Acetolactate synthase isozyme II small subunit (EC 4.1.3.18)	b3769	AAM	0.00
3948824	REC06194	<i>ilvM</i>	N	87	6, 7, 49, 57	P00510	Branched-chain amino acid aminotransferase (EC 2.6.1.42)	b3770	CHM	0.78
3950107	REC03682	<i>ilvE</i>	N	309	91, 187, 209, 268	P05791	Dihydroxy-acid dehydratase (EC 4.2.1.9)	b3771	AAM	0.78
3951132	REC03683	<i>ilvD</i>	N	605	188, 353, 372, 402, 459, 502, 566, 575	P04968	Threonine dehydratase biosynthetic (EC 4.2.1.16)	b3772	AAM	0.75
3952952	REC03684	<i>ilvA</i>	N	514	15, 32, 49, 121, 161, 244, 298, 508	P05827	Transcriptional activator protein <i>ilvY</i>	b3773	RCD	0.06
3955441	REC06195	<i>ilvY</i>	N	297	174, 266	P05793	Ketol-acid reductoisomerase (EC 1.1.1.86)	b3774	AAM	0.81
3955591	REC03686	<i>ilvC</i>	N	491	7, 28, 44, 75, 82, 122, 158, 164, 208, 232, 290, 298, 310, 441, 464	P39159	Peptidyl-prolyl cis-trans isomerase C (EC 5.2.1.8)	b3775	PMS	0.50
3957431	REC06196	<i>ppic</i>	N	93	15	P56259	Hypothetical protein <i>yifN</i>	b3777	UNC	0.03
3957902	REC06558	<i>yifN</i>	N	91	19, 61	P09980	ATP-dependent DNA helicase rep (EC 3.6.1.-)	b3778	NAM	0.28
3958117	REC06559	-	N	86	26	P25552	Guanosine-5'-triphosphate,3'-diphosphate pyrophosphatase (EC 3.6.1.15)	b3779	MSM	0.25
3958292	REC03688	<i>rep</i>	E	673	8	P24229	Putative ATP-dependent RNA helicase <i>rhlB</i>	b3780	UNC	0.13
3961844	REC06197	<i>gppA</i>	N	494	11, 112, 206, 336, 484	P00274	Thioredoxin 1	b3781	MSM	0.97
3963245	REC06198	<i>rhlB</i>	N	421	41, 46, 72, 99, 107, 122, 155, 157, 172, 353	P37324	Very hypothetical rho operon leader peptide	b3782	UNC	0.00
3963322	REC03691	<i>trxA</i>	N	127	16	P03002	Transcription termination factor rho	b3783	RCD	0.88
3963846	REC03692	<i>rhlO</i>	?	33	-	P24235	Undecaprenyl-phosphate alpha-N-acetylglucosaminyltransferase (EC 3.2.1.11)	b3784	LPC	0.53
3964032	REC03693	<i>rhlO</i>	?	419	15	P25905	Lipopolysaccharide biosynthesis protein <i>wzzE</i>	b3785	LPC	0.03
3965531	REC03694	<i>wecA</i>	N	367	60, 148, 164, 210, 260, 315, 343	P27828	UDP-N-acetylglucosamine 2-epimerase (EC 5.1.3.14)	b3786	CHM	0.41
3966643	REC06569	<i>wzzE</i>	N	349	9, 56, 87, 167, 224, 260, 267	P27829	UDP-N-acetyl-D-mannosamine dehydrogenase (EC 1.1.1.-)	b3787	CHM	0.34
3967706	REC06570	<i>wecB</i>	N	389	54, 113, 236	P27830	dTDP-glucose 4,6-dehydratase (EC 4.2.1.46)	b3788	MSM	0.75
3968872	REC06571	<i>wecC</i>	N	420	8, 193, 203, 281, 303, 385, 398	P27831	Glucose-1-phosphate thymidyllyltransferase (EC 2.7.7.24)	b3789	MSM	0.59
3970134	REC03698	<i>rffG</i>	N	355	9, 10, 40, 120, 131, 216, 277, 317	P27832	Lipopolysaccharide biosynthesis protein <i>rffC</i>	b3790	LPC	0.00
3971220	REC03699	<i>rffH</i>	N	293	4, 207, 255	P27833	Lipopolysaccharide biosynthesis protein <i>rffA</i>	b3791	UNC	0.59
3972208	REC03700	<i>rffC</i>	N	181	91	P27834	Wzx protein	b3792	UNC	0.00
3972758	REC06572	<i>rffA</i>	N	376	182, 221	P56258	4-alpha-L-fucosyltransferase (EC 2.4.1.-)	b4404	LPC	0.00
3973890	REC03702	<i>wzxE</i>	N	416	36, 76, 88, 125, 161, 240, 310	P56258	4-alpha-L-fucosyltransferase (EC 2.4.1.-)	b4405	LPC	0.00
3975137	REC06573	-	N	74	11	P27835	Putative ECA polymerase	b3793	UNC	0.00
3975603	REC06574	<i>wecF</i>	N	204	1, 168	P27836	Probable UDP-N-acetyl-D-mannosaminuronic acid transferase (EC 2.4.1.11)	b3794	UNC	0.44
3976214	REC03703	<i>wzyE</i>	E	450	-	P27837	Probable transport protein <i>yifK</i>	b3795	UNC	0.09
3977569	REC06575	<i>wecG</i>	N	246	14, 31, 54, 107, 193, 223	P25550	Putative arylsulfatase regulatory protein	b3800	UNC	0.09
3978500	REC06576	<i>yifK</i>	N	461	49, 365, 371	P25549	Arylsulfatase (EC 3.1.6.1)	b3801	MSM	0.16
3980571	REC06577	<i>aslB</i>	N	411	7, 83, 132, 214, 353	P09128	HemY protein	b3802	NCM	0.09
3983620	REC06199	<i>aslA</i>	N	551	16, 110, 133, 241, 346, 444, 456, 476	P09127	Putative uroporphyrin-III C-methyltransferase (EC 2.1.1.107)	b3803	UNC	0.16
3985495	REC06200	<i>hemY</i>	N	398	108, 307, 368	P09126	Uroporphyrinogen-III synthase (EC 4.2.1.75)	b3804	NCM	0.13
3986679	REC06201	<i>hemX</i>	N	393	276	P06983	Porphobilinogen deaminase (EC 4.3.1.8)	b3805	NCM	0.81
3987441	REC06202	<i>hemD</i>	E	246	-	P00936	Adenylate cyclase (EC 4.6.1.1)	b3806	SMC	0.09
3988400	REC06578	<i>hemC</i>	E	320	-	P11291	Very hypothetical 17.3 kDa protein in <i>cyaA</i> region	b3808	UNC	0.00
3988766	REC03712	<i>cyaA</i>	N	848	410, 436, 461, 483, 546, 662, 720, 790, 792	P27838	CyaY protein	b3807	UNC	0.16
3991463	REC03714	-	N	161	3, 17, 48, 104, 137	P39166	Hypothetical protein <i>yifL</i>	b3809	UNC	0.00
3991672	REC06204	<i>cyaY</i>	N	106	23, 54, 68	P08885	Diaminopimelate epimerase (EC 5.1.1.7)	b3809	AAM	0.78
3992135	REC06705	<i>yifL</i>	N	67	27	P23305	Hypothetical protein <i>yigA</i>	b3810	UNC	0.13
3992372	REC03715	<i>dapF</i>	E	275	-	P22885	Integrase/recombinase <i>xerC</i>	b3811	NAM	0.34
3993196	REC03716	<i>yigA</i>	N	235	68, 157, 158, 179, 181	P23306	Hypothetical protein <i>yigB</i>	b3812	UNC	0.06
3993900	REC03717	<i>xerC</i>	E	298	-	P03018	DNA helicase II (EC 3.6.1.-)	b3813	NAM	1.00
3994796	REC06579	<i>yigB</i>	N	238	10, 120	P27840	Hypothetical protein <i>yigE</i>	b3814	UNC	0.13
3995596	REC06580	<i>uvrD</i>	N	720	80, 200, 382, 458, 476, 551, 563, 589, 591, 629, 667	P27840	Hypothetical protein <i>yigE</i>	b3814	UNC	0.09
3998204	REC06205	-	N	99	4	P27841	Magnesium and cobalt transport protein <i>corA</i>	b3816	MTR	0.78
3998668	REC06206	<i>yigE</i>	N	161	48, 159	P27842	Hypothetical protein <i>yigF</i>	b3817	UNC	0.00
3999038	REC06581	<i>corA</i>	E	316	-	P27843	Hypothetical protein <i>yigG</i>	b3818	UNC	0.00
4000411	REC06207	<i>yigP</i>	N	126	74, 116	P27844	RarD protein	b3819	UNC	0.41
4000841	REC06208	<i>yigG</i>	N	138	5, 50, 89	P27845	Hypothetical protein <i>yigI</i>	b3820	UNC	0.03
4001802	REC06209	<i>rarD</i>	N	300	5, 93, 141, 193, 241, 265, 285	P00631	Phospholipase A1 precursor (EC 3.1.1.32)	b3821	LPC	0.09
4002326	REC06582	<i>yigI</i>	?	161	16, 146	P15043	ATP-dependent DNA helicase <i>recQ</i> (EC 3.6.1.-)	b3822	NAM	0.63
4002473	REC06583	<i>pIdA</i>	N	289	46	P27846	Threonine efflux protein	b3823	MTR	0.19
4003469	REC06584	<i>recQ</i>	N	610	30, 109, 185, 251, 316, 414, 429, 464, 494, 578, 602	P27847	Homoserine/homoserine lactone efflux protein	b3824	MTR	0.13
4005616	REC06585	<i>rhtC</i>	N	122	27	P07000	Lysophospholipase L2 (EC 3.1.1.5)	b3825	LPC	0.44
4006462	REC06211	<i>rhtB</i>	N	138	72, 134	P27848	Hypothetical protein <i>yigL</i>	b3826	UNC	0.03
4006776	REC06586	<i>pIdB</i>	N	340	103, 126, 149, 199, 243, 296	-	-	-	-	-
4007918	REC03732	<i>yigL</i>	N	171	18, 20, 121	-	-	-	-	-

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, 262, 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 carboxymethylglutaminase (EC 3.1.1.45)	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 2.3.1.18)	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	O65938	Sec-independent protein translocase protein tata	b3836	PMS	0.09
4019665	REC06592	<i>tatA</i>	?	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.-)	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, 200, 242, 327, 333, 356	P21177	Fatty oxidation complex alpha subunit	b3846	LPC	0.34
4028751	REC03752	<i>pepQ</i>	N	443	247, 248, 308, 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>polA</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	P06773	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, 426	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>rhn</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>yidD</i>	N	329	228, 253	P32148	Hypothetical protein yidD	b3888	UNC	0.06
4076844	REC03788	<i>yidE</i>	N	81	68	P32149	Hypothetical protein yidE	b3889	UNC	0.03
4077307	REC03789	<i>yidF</i>	X	80	-	P32150	Hypothetical protein yidF	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 ₂ iron-sulfur subunit	b3893	SMC	0.06
4083402	REC06611	<i>fdoG</i>	N	1016	13, 37, 101, 137, 206, 245, 338, 369, 408, 421, 455, 640, 726, 768, 831, 895	P32176	Formate dehydrogenase-O ₂ major subunit (EC 1.2.1.2)	b3894	SMC	0.09
4083596	REC03794	<i>fhdD</i>	N	277	36, 149, 273	P32177	FdhD protein	b3895	UNC	0.47
4084582	REC03795	<i>yigG</i>	N	351	37, 313	P32151	Hypothetical protein yigG	b3896	UNC	0.00
4087436	REC06235	<i>frvR</i>	X	582	561	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 IIIB 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, 233	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, 67, 106, 131, 149, 168, 177	P16244	Transcriptional regulatory protein cpxR	b3912	SMC	0.81
4103398	REC06614	<i>cpxP</i>	N	49	21	P32158	Periplasmic protein cpxP precursor	b3913	UNC	0.03
4103532	REC03812	<i>cpxP</i>	N	122	29, 42, 61	P32158	Periplasmic protein cpxP 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	251	53	P06282	CDP-diacylglycerol 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, 106, 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, 58, 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>glpP</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 (Ec)	b3929	NCM	0.22

4117929	REC06253	mena	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	hslU	N	443	4, 123, 303	P32168	ATP-dependent hsl protease ATP-binding subunit hslU	b3931	SMC	0.63
4119867	REC06255	hslV	N	176	15, 32, 45, 73, 79	P31059	ATP-dependent protease hslV (EC 3.4.25.-)	b3932	SMC	0.63
4120919	REC06256	ftsN	N	319	189, 248, 261, 300	P29131	Cell division protein ftsN	b3933	RCD	0.09
4122036	REC06257	cytR	N	341	14, 115, 120, 187, 259, 298	P06964	Transcriptional repressor cytR	b3934	RCD	0.59
4124390	REC06258	priA	E	732	725	P17888	Primosomal protein N1	b3935	NAM	0.91
4124593	REC03834	rpmE	?	70	-	P02432	50S ribosomal protein L'31	b3936	PMS	0.63
4125474	REC06259	yjiX	N	202	49, 55, 110	P32167	Hypothetical protein yjiX precursor	b3937	RCD	0.00
4125975	REC06260	metJ	N	105	84	P08338	Met repressor	b3938	UNC	0.06
4126252	REC03837	metB	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	metL	N	810	128, 242, 381, 447, 508, 553, 717, 733, 759, 769	P00562	Bifunctional aspartokinase/homoserine dehydrogenase II	b3940	AAM	0.19
4130196	REC03839	metP	N	296	17, 78, 191	P00394	5,10-methylenetetrahydrofolate reductase (EC 1.7.99.5)	b3941	BEN	0.50
4131415	REC03840	katG	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	yjyE	N	312	20, 39, 136, 149, 223	P32667	Hypothetical transport protein yjyE	b3943	UNC	0.22
4135237	REC06261	yjyF	N	205	4, 149, 154	P32668	Hypothetical protein yjyF precursor	b3944	UNC	0.06
4136654	REC06262	gldA	N	380	5, 65, 338	P32665	Glycerol dehydrogenase (EC 1.1.1.6)	b3945	CHM	0.22
4137288	REC06263	fsaB	N	220	4, 65, 154, 180, 196, 216	P32669	Fructose-6-phosphate aldolase 2 (EC 4.1.2.-)	b3946	CHM	0.28
4139435	REC06264	ptsA	N	711	242, 248, 428, 463, 529, 574, 602, 633, 670	P32670	Phosphoenolpyruvate-protein phosphotransferase ptsA (EC 2.7.3.9)	b3947	MTR	0.75
4139437	REC03846	yjiY	X	109	-	Q9Z3C7	Hypothetical protein YjiY	b3948	UNC	0.00
4140109	REC03847	frwC	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	frwB	N	106	26, 32	P32673	PTS system, fructose-like-2 IIB component 1 (EC 2.7.1.69)	b3950	CHM	0.09
4141574	REC03849	pflD	N	765	353, 588, 639, 698, 764	P32674	Formate acetyltransferase 2 (EC 2.3.1.54)	b3951	CHM	0.22
4143837	REC03850	pflC	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	frwD	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	yjyO	N	283	42, 215	P32677	Hypothetical transcriptional regulator yjyO	b3954	UNC	0.13
4147844	REC06266	yjyP	N	577	53, 82, 83, 104, 122, 135, 147, 156, 191, 199, 327, 450	P32678	Protein yjyP	b3955	UNC	0.06
4150677	REC06267	ppc	N	883	3, 15, 82, 104, 123, 148, 171, 489, 624, 676, 881	P00864	Phosphoenolpyruvate carboxylase (EC 4.1.1.31)	b3956	CHM	0.34
4152426	REC06268	argE	X	383	363	P23908	Acetylornithine deacetylase (EC 3.5.1.16)	b3957	AAM	0.44
4152580	REC03856	argC	E	334	317	P11446	N-acetyl-gamma-glutamyl-phosphate reductase (EC 1.2.1.38)	b3958	AAM	0.72
4153592	REC03857	argB	N	258	12, 53, 74, 98, 154, 190	P11445	Acetylglutamate kinase (EC 2.7.2.8)	b3959	AAM	0.72
4154429	REC03858	argH	N	457	13, 47, 58, 128, 130, 189, 374	P11447	Argininosuccinate lyase (EC 4.3.2.1)	b3960	AAM	0.75
4156069	REC03859	oxyR	N	305	181, 301	P11721	Hydrogen peroxide-inducible genes activator	b3961	RCD	0.50
4158303	REC06269	sthA	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	yjyC	N	234	8, 111, 143, 207	P27307	Hypothetical protein yjyC	b3963	UNC	0.09
4159350	REC03862	yjyD	N	119	92, 102	P27308	Hypothetical protein yjyD	b3964	UNC	0.03
4160849	REC06270	trmA	N	366	101, 115, 130, 177, 288	P32303	tRNA (Uracil-5)-methyltransferase (EC 2.1.1.35)	b3965	NAM	0.16
4161218	REC03864	btuB	N	614	49, 109, 174, 273	P06129	Vitamin B12 receptor precursor	b3966	MTR	0.19
4162995	REC03865	murI	E	289	-	P22634	Glutamate racemase (EC 5.1.1.3)	b3967	AAM	0.84
4169636	REC03866	murB	N	342	7, 138, 298	P08373	UDP-N-acetylenolpyruvylglucosamine reductase (EC 1.1.1.158)	b3972	LPC	0.97
4170661	REC03867	birA	E	321	17	P06709	BirA bifunctional protein	b3973	NCM	0.88
4172605	REC06271	coaA	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	tufB	E	394	-	P02990	Elongation factor Tu	b3980	PMS	1.00
4174937	REC03871	secE	N	127	86	P16920	Preprotein translocase secE subunit	b3981	PMS	0.22
4175322	REC03872	nusG	N	181	6, 57, 69	P16921	Transcription antitermination protein nusG	b3982	RCD	0.97
4176025	REC06615	rplK	X	142	-	P02409	50S ribosomal protein L11	b3983	PMS	1.00
4176457	REC03874	rplA	X	234	-	P02384	50S ribosomal protein L1	b3984	PMS	1.00
4177574	REC03875	rplJ	E	165	-	P02408	50S ribosomal protein L10	b3985	PMS	1.00
4178138	REC03876	rplL	E	121	-	P02392	50S ribosomal protein L7/L12	b3986	PMS	1.00
4178823	REC03877	rpoB	E	1342	-	P00575	DNA-directed RNA polymerase beta chain (EC 2.7.7.6)	b3987	NAM	1.00
4182928	REC06616	rpoC	E	1407	35	P00577	DNA-directed RNA polymerase beta' chain (EC 2.7.7.6)	b3988	NAM	1.00
4187364	REC03879	htrC	N	179	76, 108, 166	P27375	Heat shock protein C	b3989	UNC	0.00
4189446	REC06273	thiH	X	377	-	P30140	Thiazole biosynthesis protein thiH	b3990	NCM	0.16
4190288	REC06274	thiG	X	281	-	P30139	Thiazole biosynthesis protein thiG	b3991	NCM	0.63
4191136	REC06275	thiF	N	245	16, 39	P30138	Adenylyltransferase thiF (EC 2.7.7.-)	b3992	NCM	0.16
4191782	REC06276	thiE	N	211	64, 107, 150, 153	P30137	Thiamine-phosphate pyrophosphorylase (EC 2.5.1.3)	b3993	NCM	0.78
4193677	REC06277	thiC	N	631	43, 290, 429, 508	P30136	Thiamine biosynthesis protein thiC	b3994	NCM	0.63
4194386	REC06278	rsd	E	158	-	P31690	Regulator of sigma D	b3995	RCD	0.06
4194481	REC03886	nudC	N	257	13, 67, 84, 128, 187	P32664	NADH pyrophosphatase (EC 3.6.1.-)	b3996	MSM	0.38
4195294	REC06617	hemE	E	354	-	P29680	Uroporphyrinogen decarboxylase (EC 4.1.1.37)	b3997	NCM	0.72
4196362	REC03888	nfi	N	225	107, 204, 212	P32679	Endonuclease V (EC 3.1.-)	b3998	NAM	1.19
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, 86, 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, 498	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	Isocitrate lyase (EC 4.1.3.1)	b4015	CHM	0.34
4216175	REC03902	aceK	N	578	12, 58, 64, 100, 353, 403, 505	P11071	Isocitrate dehydrogenase kinase/phosphatase (EC 2.7.1.116) (EC 3.4.1.1)	b4016	CHM	0.06
4220066	REC06283	arpa	N	728	126, 172, 196, 221, 244, 293, 346, 420, 510, 548, 554, 599, 580, 607, 639, 6	P23325	Ankyrin-repeat protein A	b4017	RCD	0.00
4221246	REC06284	icLR	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 2.1.1.1)	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	394, 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	0.47
4233485	REC03912	yjbE	N	80	20, 52	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, 80, 140, 259, 439, 488, 526, 572, 595	P32689	Hypothetical lipoprotein yjbH precursor	b4029	UNC	0.00
4237904	REC03916	yjbA	E	136	-	P23896	Hypothetical protein yjbA	b4030	UNC	0.09
4239833	REC06288	xyIE	N	491	34, 54, 72, 168, 190, 198, 219	P09098	D-xylitol-5-phosphate 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, 38, 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	dgkA	X	122	-	P00556	Diacylglycerol kinase (EC 2.7.1.107)	b4042	LPC	0.44
4254694	REC03929	lexA	X	202	-	P03033	LexA repressor (EC 3.4.21.88)	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	a1r	N	359	59, 61, 94, 106, 155, 307	P29743	Alanine racemase, biosynthetic (EC 5.1.1.1)	b4053	UNC	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	UNC	0.00	
4266993	REC03941	aphA	N	237	25, 54, 65, 60	P32697	Class B acid phosphatase precursor (EC 3.1.3.2)	b4055	MSM	0.03
4267817	REC03942	yjbQ	N	138	5, 32	P32698	Hypothetical protein yjbQ	b4056	UNC	0.34
4268237	REC06633	yjbr	N	118	75	P32699	Protein yjbr	b4057	UNC	0.00
4271450	REC06634	uvrA	N	940	106, 146, 245, 339, 372, 525	P07671	Exonuclease ABC subunit A	b4058	NAM	0.97
4271704	REC03945	ssb	X	178	-	P02339	Single-strand binding protein	b4059	NAM	0.91
4272689	REC06296	yjcb	X	116	-	P32700	Hypothetical protein yjcb	b4060	UNC	0.00
4273050	REC03947	yjcc	X	528	-	P32701	Hypothetical protein yjcc	b4061	UNC	0.31
4274962	REC06297	soxS	X	107	-	P22539	Regulatory protein soxS	b4062	RCD	0.06
4275048	REC03949	soxR	X	154	-	P22538	Redox-sensitive transcriptional activator soxR	b4063	RCD	0.16
4276058	REC03950	yjcd	N	449	60, 79, 120, 164, 194, 210, 249, 265, 382, 418	P32702	Hypothetical protein yjcd	b4064	UNC	0.66
4277559	REC03951	yjce	N	549	26, 26, 83, 287, 497	P32703	Putative Na(+)/H(+) exchanger yjce	b4065	UNC	0.44
4280654	REC06298	yjcf	N	430	377, 379	P32704	Hypothetical protein yjcf	b4066	UNC	0.03
4282481	REC06299	yjcg	N	549	-	P32705	Putative symporter yjcg	b4067	UNC	0.22
4282792	REC06300	yjch	X	104	-	P32706	Hypothetical protein yjch	b4068	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)	b4069	BEN	0.63
4285343	REC03956	nrfA	N	478	36, 122, 301, 326, 333, 340, 386, 387	P32050	Cytochrome C552 precursor	b4070	CHM	0.06
4286818	REC03957	nrfB	N	190	48, 65, 87, 127	P32707	Cytochrome c-type protein nrfB precursor	b4071	BEN	0.03
4287387	REC06635	nrfC	N	223	132	P32708	NrfC protein	b4072	UNC	0.06
4288055	REC03959	nrfD	N	318	55, 95, 190, 237	P32709	NrfD protein	b4073	UNC	0.03
4289091	REC03960	nrfE	N	552	132, 355, 439, 503, 504	P32710	Cytochrome c-type biogenesis protein nrfE	b4074	UNC	0.00
4290742	REC03961	nrfF	N	127	9, 31, 120	P32711	Cytochrome c-type biogenesis protein nrfF precursor	b4075	UNC	0.00
4291122	REC03962	nrfG	N	198	36, 88, 119, 127	P32712	NrfG protein	b4076	UNC	0.06
4292060	REC03963	gltP	N	437	3, 83, 104, 277, 378, 405	P21345	Proton glutamate symport protein	b4077	MTR	0.28
4294704	REC06302	yjco	N	229	83, 112	P32713	Hypothetical protein yjco precursor	b4078	UNC	0.00
4296945	REC06636	fdhF	N	715	35, 102, 401, 549	P07658	Formate dehydrogenase H (EC 1.2.1.2)	b4079	SMC	0.53
4298609	REC06637	yjcp	N	488	18, 29, 128, 190, 206, 275, 330	P32714	Hypothetical outer-membrane lipoprotein yjcp precursor	b4080	UNC	0.09
4300516	REC06305	yjcq	N	636	18, 563	P32715	Hypothetical transporter yjcq	b4081	UNC	0.00
4301688	REC06306	yjcr	N	343	112, 139, 247, 320	P32716	Hypothetical protein yjcr	b4082	UNC	0.50
4304188	REC06638	yjcs	N	665	608	P32717	Hypothetical protein yjcs	b4083	UNC	0.16
4305378	REC06308	alsK	N	309	239, 254, 274	P32718	D-allose kinase (EC 2.7.1.55)	b4084	CHM	0.09
4306057	REC06309	alsE	X	231	-	P32719	D-allulose-6-phosphate 3-epimerase (EC 5.1.3.-)	b4085	CHM	0.03
4307048	REC06310	alsC	X	326	-	P32720	D-allose transport system permease protein alsC	b4086	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	b4087	MTR	0.28
4309621	REC06312	alsB	N	311	234, 266	P39265	D-allose-binding periplasmic protein precursor	b4088	MTR	0.00
4310603	REC06313	rp1r	N	307	12, 18	P39266	Protein rp1r	b4089	RCD	0.09
4310929	REC03976	rp1B	N	149	54, 119, 142	P37351	Ribose 5-phosphate isomerase B (EC 5.3.1.6)	b4090	CHM	0.56
4311796	REC06314	phnQ	N	135	84, 90	P16693	Very hypothetical phnQ protein	b4091	UNC	0.00
4312680	REC06315	phnP	N	252	210, 237	P16692	PhnP protein	b4092	UNC	0.28
4313116	REC06316	phnO	X	144	-	P16691	PhnO protein	b4093	UNC	0.06
4313660	REC06317	phnN	X	185	-	P16690	ATP-binding protein phnN	b4094	UNC	0.16
4314796	REC06318	phnM	N	378	11, 111, 224, 266, 285	P16689	PhnM protein	b4095	UNC	0.19
4315473	REC06319	phnL	N	226	25, 53, 114	P16679	Phosphonates transport ATP-binding protein phnL	b4096	MSM	0.16
4316342	REC06320	phnK	X	252	-	P16678	Phosphonates transport ATP-binding protein phnK	b4097	MSM	0.75
4317184	REC06321	phnJ	X	281	-	P16688	PhnJ protein	b4098	UNC	0.16
4318241	REC06322	phnI	N	354	125, 202, 266	P16687	PhnI protein	b4099	UNC	0.16
4318825	REC06323	phnH	N	194	83, 95	P16686	PhnH protein	b4100	UNC	0.16
4319274	REC06324	phnG	N	150	25, 150	P16685	PhnG protein	b4101	UNC	0.16
4320000	REC06325	phnF	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	phnE	N	206	21	P16683	Phosphonates transport system permease protein phnE	MTR	0.25	
4321930	REC06328	phnD	N	338	51, 118, 231, 309	P16682	Phosphonates-binding periplasmic protein precursor	b4105	MTR	0.25
4322743	REC06329	phnC	N	262	155, 203	P16677	Phosphonates transport ATP-binding protein phnC	b4106	MTR	0.34
4323319	REC06330	phnB	X	147	-	P16681	PhnB protein	b4107	UNC	0.22
4324312	REC06331	phnA	N	111	11, 33	P16680	PhnA protein	b4108	UNC	0.47
4324713	REC03995	yjda	N	742	6, 41, 62, 137, 156, 241, 520, 575, 615	P16699	Hypothetical protein yjda	b4109	UNC	0.00
4326971	REC03996	yjcz	N	281	190, 220	P39267	Hypothetical protein yjcz	b4110	UNC	0.00
4328080	REC03997	proP	N	500	14, 103, 132, 177, 245, 375, 499	P30848	Proline/betaine transporter	b4111	MTR	0.38
4330850	REC06332	basS	X	363	353	P30844	Sensor protein basS/pmxB (EC 2.7.3.-)	b4112	SMC	0.03
4331528	REC06333	basR	N	222	43, 60, 120, 166	P30843	Transcriptional regulatory protein basR/pmxA	b4113	SMC	0.00
4333198	REC06334	yjdb	N	557	125, 147, 228, 288, 302, 421	P30845	Hypothetical protein yjdb	b4114	UNC	0.31
4334609	REC06335	yjde	X	445	-	P39269	Hypothetical transport protein yjde	b4115	UNC	0.25
4335507	REC06337	adiY	X	253	-	P33234	Putative regulatory protein adiy	b4116	UNC	0.00
4338102	REC06338	adia	N	756	39	P28629	Biodegradative arginine decarboxylase (EC 4.1.1.19)	b4117	AAM	0.31
4339206	REC06339	melR	N	302	46, 53	P10411	Melibiose operon regulatory protein	b4118	RCD	0.16
4339489	REC04006	me1A	N	451	181, 221, 390	P06720	Alpha-galactosidase (EC 3.2.1.22)	b4119	CHM	0.16
4340959	REC04007	me1B	N	469	110, 124, 126, 139, 168, 199, 223, 245, 292, 314, 319, 348, 384, 416, 436, 4	P02921	Melibiose carrier protein	b4120	MTR	0.00
4343136	REC06340	yjdf	N	209	31, 71, 126	P39270	Hypothetical protein yjdf	b4121	UNC	0.00
4344904	REC06341	fumB	N	548	11, 394	P14407	Fumarate hydratase class I, anaerobic (EC 4.2.1.2)	b4122	CHM	0.03
4346322	REC06342	dcuB	N	446	1, 45, 74, 265, 421, 437	P14409	Anaerobic C4-dicarboxylate transporter dcuB	b4123	MTR	0.16
4347612	REC06343	dcuR	N	239	117	P39271	Transcriptional regulatory protein dcuR	b4124	SMC	0.03
4349240	REC06344	dcuS	N	543	152, 212	P39272	Sensor protein dcuS (EC 2.7.3.-)	b4125	SMC	0.03
4349421	REC04013	yjdI	N	76	35	P39273	Hypothetical protein yjdI	b4126	UNC	0.06
4349663	REC04014	yjdJ	N	90	31	P39274	Hypothetical protein yjdJ	b4127	UNC	0.22
4350162	REC04015	yjdK	N	98	15	P39275	Hypothetical protein yjdK	b4128	UNC	0.00
4350486	REC06711	yjdo	X	57	-	P58038	Hypothetical protein yjdo	UNC	0.00	
4352295	REC06345	lysU	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	yjdl	N	485	71, 206, 317, 340, 405, 433	P39276	Hypothetical transporter yjdl	b4130	UNC	0.31
4356195	REC06347	cadA	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	0.41
4365950	REC06354	<i>aspa</i>	N	493	16, 90, 92, 208		P04422	Aspartate ammonia-lyase (EC 4.3.1.1)	b4139	AAM	0.16
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		UNC	0.00
4374303	REC04034	<i>sugE</i>	N	155	79		P30743	SugE protein	b4148	UNC	0.44
4375300	REC06358	<i>blc</i>	?	177	155		P39281	Outer membrane lipoprotein blc 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>frdD</i>	?	119	105		P03806	Fumarate reductase 13 kDa hydrophobic protein	b4151	BEN	0.06
4377350	REC06361	<i>frdC</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	P03812	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, 82, 178, 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	Oligoribonuclease (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	145	-	< 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 3.5.1.28)	b4169	LPC	0.84
4394990	REC04053	<i>mutL</i>	N	615	335, 337, 384, 407, 433, 494, 540, 547, 598		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	0.43
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>rnr</i>	N	827	78, 288		P21499	Ribonuclease R (EC 3.1.-.-)	b4179	NAM	0.88
4406853	REC04063	<i>yjfH</i>	N	243	8, 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	<i>yjfq</i>	X	251	-		P39299	Hypothetical transcriptional regulator yjfq	b4191	UNC	0.13
4417209	REC06371	<i>yjfr</i>	N	356	69, 87, 260		P39300	Hypothetical protein yjfr	b4192	UNC	0.06
4417501	REC06484	<i>sgaT</i>	N	484	11, 87, 129, 138, 327, 371, 443		P39301	Putative transport protein sgaT	b4193	UNC	0.19
4418971	REC04077	<i>sgaB</i>	X	101	-		P39302	Unknown penitrol phosphotransferase enzyme II, B component (EC 2.6.1.9)	b4194	CHM	0.06
4419286	REC06485	<i>sgaA</i>	N	154	80, 130		P39303	Unknown penitrol phosphotransferase enzyme II, A component (EC 2.6.1.9)	b4195	CHM	0.16
4419764	REC04079	<i>sgaH</i>	N	216	62, 200		P39304	Probable hexulose-6-phosphate synthase (EC 4.1.2.-)	b4196	UNC	0.22
4420424	REC04080	<i>sgaU</i>	N	284	26, 57, 66, 135		P39305	Putative hexulose-6-phosphate isomerase (EC 5.-.-.-)	b4197	UNC	0.19
4421278	REC04081	<i>sgaE</i>	N	228	77, 181		P39306	Probable sugar isomerase sgaE (EC 5.1.-.-)	b4198	UNC	0.28
4422369	REC06372	<i>yjfy</i>	X	91	-		P39307	Hypothetical protein yjfy precursor	b4199	UNC	0.00
4422696	REC04083	<i>rpsP</i>	E	131	-	< 0.2	P02358	30S ribosomal protein S6	b4200	PMS	0.81
4423098	REC04084	<i>prbB</i>	E	104	-	< 0.3	P07013	Primosomal replication protein N	b4201	NAM	0.09
4423417	REC04085	<i>rpsR</i>	?	75	-		P02374	30S ribosomal protein S18	b4202	PMS	1.00
4423686	REC04086	<i>rpII</i>	N	149	67, 132		P02418	50S ribosomal protein L9	b4203	PMS	0.97
4425000	REC06373	<i>yjfZ</i>	N	264	49, 127, 181, 215, 232, 264		P39308	Hypothetical protein yjfZ	b4204	UNC	0.00
4425347	REC04088	<i>ytfa</i>	X	108	-		P39309	Hypothetical protein ytfa	b4205	UNC	0.03
4426331	REC06374	<i>ytfb</i>	X	224	-		P39310	Hypothetical protein ytfb	b4206	UNC	0.06
4426354	REC04090	<i>fkIB</i>	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	<i>cycA</i>	N	470	13, 24, 290		P39312	D-serine/D-alanine/glycine transporter	b4208	MTR	0.22
4429561	REC06375	<i>ytfe</i>	N	220	79, 151, 207		P39313	Hypothetical protein ytfe	b4209	UNC	0.19
4430643	REC06376	<i>ytfF</i>	N	324	70, 105, 150		P39314	Hypothetical protein ytfF	b4210	UNC	0.16
4431601	REC04095	<i>ytfH</i>	N	156	112, 145		P39315	Hypothetical protein ytfH	b4212	UNC	0.53
4431602	REC06377	<i>ytfG</i>	N	286	19, 60		P39316	Hypothetical protein ytfG	b4211	UNC	0.38
4434143	REC06378	<i>cpdB</i>	N	647	3, 51, 55, 88, 143, 185, 219, 520, 643		P08331	2',3'-cyclic-nucleotide 2'-phosphodiesterase precursor (EC 3.1.4.16)	b4213	NCM	0.34
4434333	REC04097	<i>cysQ</i>	N	246	29, 43, 200		P22255	CysQ protein	b4214	UNC	0.56
4435285	REC04098	<i>ytfI</i>	E	166	-	< 0.2	P39317	Hypothetical protein ytfI	b4215	UNC	0.00
4435692	REC06764	<i>ytfJ</i>	E	176	-	< 0.2	P39317	Hypothetical protein ytfI	b4215	UNC	0.00
4436839	REC06379	<i>ytfJ</i>	N	184	113		P39187	Protein ytfJ precursor	b4216	UNC	0.06
4437125	REC04100	<i>ytfK</i>	N	81	21		P39318	Hypothetical protein ytfK	b4217	UNC	0.03
4438792	REC06380	<i>ytfL</i>	N	447	115, 220, 248, 293, 412		P39319	Hypothetical protein ytfL	b4218	UNC	0.94
4439753	REC06381	<i>msrA</i>	N	212	128, 212		P27110	Peptide methionine sulfoxide reductase msrA (EC 1.8.4.6)	b4219	PMS	0.81
4439959	REC04103	<i>ytfM</i>	N	577	201, 245, 383, 405, 450, 529		P39320	Hypothetical protein ytfM precursor	b4220	UNC	0.69
4441689	REC04104	<i>ytfN</i>	N	1259	112, 392, 414, 534, 644, 817, 871, 934, 973		P39321	Hypothetical protein ytfN	b4221	UNC	0.38
4445471	REC04105	<i>ytfP</i>	N	113	7, 62		P39323	Hypothetical protein ytfP	b4222	UNC	0.03
4446018	REC04107	<i>chpS</i>	E	85	-	0.46	P08365	PemI-like protein 2	b4224	UNC	0.00
4446269	REC04108	<i>chpB</i>	N	116	35		P33647	PemK-like protein 2	b4225	UNC	0.13
4447229	REC06383	<i>ppa</i>	E	176	-	< 0.2	P17288	Inorganic pyrophosphatase (EC 3.6.1.1)	b4226	MSM	0.66
4447539	REC04110	<i>ytfQ</i>	N	318	88, 115, 250		P39325	ABC transporter periplasmic binding protein ytfQ precursor	b4227	MTR	0.13
4448633	REC04111	<i>ytfR</i>	N	417	197, 242		P39326	Hypothetical ABC transporter ATP-binding protein ytfR	b4228	UNC	0.44
4449862	REC04112	<i>ytfS</i>	E	90	-	0.39	P39326	Hypothetical ABC transporter ATP-binding protein ytfR	b4229	UNC	0.00
4450145	REC04113	<i>ytfT</i>	N	341	71, 234, 292		P39328	Hypothetical ABC transporter permease protein ytfT	b4230	UNC	0.06
4451181	REC04114	<i>ytfP</i>	N	323	42, 85, 124, 206, 248		P37772	Hypothetical ABC transporter permease protein ytfP	b4231	UNC	0.09

4453183	REC06384	<i>fbp</i>	N	332	12, 112, 156, 178, 223, 318	P09200	Fructose-1,6-bisphosphatase (EC 3.1.3.11)	b4232	CHM	0.38
4453359	REC04116	<i>mp1</i>	N	457	66, 216, 267, 407	P37773	UDP-N-acetylmuramate-L-alanyl-gamma-D-glutamyl-meso-diaminopip	b4233	LPC	0.22
4454539	REC06385	<i>yjgA</i>	N	183	25	P26650	Hypothetical protein yjgA	b4234	UNC	0.19
4455533	REC04118	<i>pmbA</i>	N	450	9, 43, 66, 193, 277, 316	P24231	PmbA protein	b4235	UNC	0.53
4457127	REC04119	<i>cybc</i>	?	100	92	P00192	Soluble cytochrome b562 precursor	b4236	BEN	0.00
4457938	REC06386	<i>nrpG</i>	N	154	10, 10, 71	P39329	Anaerobic ribonucleoside-triphosphate reductase activating protein (E	b4237	NCM	0.28
4460234	REC06387	<i>nrpD</i>	N	712	50, 134, 273, 488, 532, 608, 656	P28903	Anaerobic ribonucleoside-triphosphate reductase (EC 1.17.4.2)	b4238	NCM	0.31
4462283	REC06388	<i>treC</i>	N	551	32, 74, 400, 527	P28904	Trehalose-6-phosphate hydrolase (EC 3.2.1.93)	b4239	CHM	0.44
4463754	REC06494	<i>treB</i>	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	<i>treR</i>	N	315	14, 94, 204	P36673	Trehalose operon repressor	b4241	RCD	0.06
4465199	REC06495	<i>mgtA</i>	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
4465262	REC06391	<i>yjgP</i>	E	141	-	P39330	Protein yjgP	b4243	UNC	0.84
4469021	REC06392	<i>pyrI</i>	N	153	78, 78, 104	P00478	Aspartate carbamoyltransferase regulatory chain	b4244	RCD	0.13
4469969	REC06496	<i>pyrB</i>	N	311	105, 150, 206, 263	P00479	Aspartate carbamoyltransferase catalytic chain (EC 2.1.3.2)	b4245	NCM	0.81
4470087	REC04130	<i>yjgG</i>	N	110	75	P76807	HYPOTHETICAL 12.8 kDa PROTEIN IN PYRL-ARGI INTERGENIC R	b4247	UNC	0.00
4470107	REC06394	<i>pyrL</i>	?	44	-	P09150	PyrBI operon leader peptide	b4246	UNC	0.00
4470783	REC06395	<i>yjgH</i>	N	131	47	P39332	Hypothetical protein yjgH	b4248	UNC	0.19
4471627	REC06497	<i>yjgI</i>	N	237	30	P39333	Hypothetical oxidoreductase yjgI (EC 1.-.-.-)	b4249	UNC	0.13
4471801	REC04133		N	54	8, 37	P76808	FROM BASES 4471356 TO 4483288 (SECTION 386 OF 400) OF TH	b4250	UNC	0.00
4472037	REC04134	<i>yjgJ</i>	E	84	82	P39334	Hypothetical protein yjgJ	b4251	UNC	0.00
4472427	REC04135	<i>yjgK</i>	N	153	13, 73, 98	P39335	Protein yjgK	b4252	UNC	0.16
4472975	REC04136	<i>yjgL</i>	N	616	3, 166, 482	P39336	Hypothetical protein yjgL	b4253	UNC	0.00
4475874	REC06397	<i>argI</i>	X	334	-	P04391	Ornithine carbamoyltransferase chain I (EC 2.1.3.3)	b4254	AAM	0.84
4476036	REC04138	<i>yjgD</i>	X	138	-	P37163	Hypothetical protein yjgD	b4255	UNC	0.06
4476890	REC06398	<i>yjgM</i>	X	97	-	P39337	Hypothetical acetyltransferase yjgM (EC 2.3.1.-)	b4256	UNC	0.06
4477310	REC06500	<i>yjgN</i>	N	393	338, 360, 365	P39338	Hypothetical protein yjgN	b4257	UNC	0.13
4481405	REC06399	<i>valS</i>	E	951	-	P07118	Valyl-tRNA synthetase (EC 6.1.1.9)	b4258	PMS	1.00
4481848	REC06400	<i>holC</i>	E	147	-	P28905	DNA polymerase III, chi subunit (EC 2.7.7.7)	b4259	NAM	0.13
4483519	REC06401	<i>pepA</i>	N	503	80, 106, 192, 227, 267, 342, 370, 399, 446, 449, 469, 497	P11648	Cytosol aminopeptidase (EC 3.4.11.1)	b4260	PMS	0.81
4483786	REC04145	<i>yjgP</i>	E	366	-	P39340	Hypothetical protein yjgP	b4261	UNC	0.41
4484883	REC04146	<i>yjgQ</i>	E	361	-	P39341	Hypothetical protein yjgQ	b4262	UNC	0.44
4487631	REC06402	<i>yjgR</i>	N	500	43, 88, 122	P39342	Hypothetical protein yjgR	b4263	UNC	0.25
4488707	REC06403	<i>idnR</i>	N	332	43, 69, 93, 112, 114, 125, 235	P39343	L-Idonate regulatory protein	b4264	RCD	0.06
4490093	REC06404	<i>idnT</i>	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	<i>idnO</i>	N	254	4, 49, 150	P39345	Gluconate 5-dehydrogenase (EC 1.1.1.69)	b4266	CHM	0.44
4491974	REC06406	<i>idnD</i>	X	343	-	P39346	L-Idonate 5-dehydrogenase (EC 1.1.1.264)	b4267	CHM	0.09
4492191	REC04152	<i>idnK</i>	N	187	32, 63, 125	P39208	Thermosensitive gluconokinase (EC 2.7.1.12)	b4268	CHM	0.31
4493819	REC06407	<i>yjgB</i>	N	353	104, 157, 203, 240, 261, 342	P27250	Hypothetical zinc-type alcohol dehydrogenase-like protein yjgB	b4269	UNC	0.06
4494318	REC04154	<i>intB</i>	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	<i>yjgW</i>	N	111	15, 110	Q923A0	Hypothetical protein YJGW	b4274	UNC	0.00
4498057	REC06408	<i>yjgX</i>	X	148	-	P39349	Hypothetical protein yjgX precursor	b4275	UNC	0.00
4498449	REC06409	<i>yjgY</i>	X	149	-	P39350		b4276	UNC	0.00
4498828	REC04160	<i>yjgZ</i>	N	109	1, 109	P39351	Hypothetical protein yjgZ	b4277	UNC	0.00
4500999	REC06410	<i>insG</i>	N	442	241, 369	P03835	Transposase insG for insertion sequence element IS4	b4278	PHT	0.00
4501566	REC04162	<i>yjhB</i>	N	425	1, 285, 308, 388, 409	P39352	Hypothetical metabolite transport protein yjhB	b4279	UNC	0.22
4502840	REC04163	<i>yjhC</i>	N	377	137, 237, 257, 306, 316, 338	P39353	Hypothetical oxidoreductase yjhC (EC 1.-.-.-)	b4280	UNC	0.44
4504568	REC06411	<i>yjhD</i>	N	124	4, 60	P39354	Hypothetical protein yjhD	b4281	UNC	0.00
4504729	REC04166	<i>insN2</i>	N	100	17, 43	P39212	Transposase insN for insertion sequence element IS911B	b4282	PHT	0.56
4506185	REC01364	<i>insI3</i>	N	383	147, 209, 287, 307, 326	P37246	Transposase insI for insertion sequence element IS30B/C/D	b4284	PHT	0.22
4506526	REC04168	<i>insM</i>	N	198	29, 33, 142	Q47718	Transposase insM for insertion sequence element IS600	b4285	PHT	0.56
4507288	REC04169		E	137	-	Q47719	Very hypothetical 15.1 kDa protein in intB-fecE intergenic region	b4286	UNC	0.03
4509025	REC06413	<i>fecE</i>	N	255	84	P15031	Iron(III) dicitrate transport ATP-binding protein fecE	b4287	MTR	0.09
4509982	REC06414	<i>fecD</i>	N	318	29, 279	P15029	Iron(III) dicitrate transport system permease protein fecD	b4288	MTR	0.13
4510977	REC06415	<i>fecC</i>	N	332	44, 117, 234, 309	P15030	Iron(III) dicitrate transport system permease protein fecC	b4289	MTR	0.69
4511882	REC06416	<i>fecB</i>	X	302	-	P15028	Iron(III) dicitrate-binding periplasmic protein precursor	b4290	RCD	0.31
4514245	REC06417	<i>fecA</i>	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	<i>fecR</i>	N	317	174	P23485	Protein fecR	b4292	SMC	0.16
4515803	REC06419	<i>fecI</i>	X	173	-	P23484	Probable RNA polymerase sigma factor fecI	b4293	UNC	0.16
4516095	REC04177	<i>insA7</i>	X	91	-	P19767	Insertion element IS1 7.00 protein insA	b4294	PHT	0.00
4517706	REC06420	<i>yjhU</i>	X	266	-	P39356	Hypothetical transcriptional regulator yjhU	b4295	UNC	0.25
4519588	REC06508	<i>yjhF</i>	N	449	13, 64, 118, 156, 168, 184, 231, 263, 292	P39357	Hypothetical permease yjhF	b4296	UNC	0.31
4521662	REC06509	<i>yjhG</i>	N	655	622, 604, 624	P39358	Hypothetical protein yjhG	b4297	UNC	0.78
4522632	REC06423	<i>yjhH</i>	N	319	75	P39359	Hypothetical protein yjhH	b4298	UNC	0.84
4523371	REC06424	<i>yjhI</i>	N	262	19, 53, 89, 99, 122, 175, 202	P39360	Hypothetical transcriptional regulator yjhI	b4299	UNC	0.00
4524456	REC06425	<i>sgcR</i>	X	260	258	P39361	Putative sgc region transcriptional regulator	b4300	UNC	0.00
4525105	REC06426	<i>sgcE</i>	X	210	-	P39362	Protein sgcE (EC 5.1.3.-)	b4301	UNC	0.94
4525548	REC06427	<i>sgcA</i>	E	143	-	P39363	Putative phosphotransferase enzyme II, A component sgcA (EC 2.7.1.	b4302	UNC	0.03
4526485	REC06428	<i>sgcQ</i>	N	268	62, 96	P39364	Putative sgc region protein sgcQ	b4303	UNC	0.13
4527811	REC06429	<i>sgcC</i>	N	437	11, 65, 170, 258, 349, 373, 430	P39365	Putative phosphotransferase enzyme II, C component sgcC	b4304	UNC	0.09
4528104	REC06714	<i>sgcB</i>	E	93	-	P58035	Putative phosphotransferase enzyme II, B component sgcB (EC 2.7.1.69)	b4305	UNC	0.06
4529249	REC06510	<i>sgcX</i>	N	383	38, 64, 118	P39366	Putative sgc region protein sgcX	b4306	UNC	0.06
4530751	REC06431	<i>yjhP</i>	N	248	32, 66, 73, 167, 187	P39367	Hypothetical protein yjhP	b4307	UNC	0.34
4531352	REC06432	<i>yjhQ</i>	N	181	132, 155	P39368	Hypothetical acetyltransferase yjhQ (EC 2.3.1.-)	b4308	UNC	0.31
4532583	REC04191	<i>yjhr</i>	N	338	22, 49, 83, 97, 188, 207, 321, 335	P39369	Hypothetical protein yjhr	b4308	UNC	0.03
4535162	REC06433	<i>yjhs</i>	N	326	50, 287	P39370	Hypothetical protein yjhs precursor	b4309	UNC	0.00
4536441	REC06434	<i>yjht</i>	N	404	68, 84, 151, 172, 215, 225	P39371	Hypothetical protein yjht precursor	b4310	UNC	0.13
4537078	REC06435	<i>yjha</i>	N	241	21, 26, 108, 134, 208	P39372	Hypothetical protein yjha precursor	b4311	UNC	0.00
4538525	REC04195	<i>fimB</i>	X	200	-	P04742	Type 1 fimbriae regulatory protein fimB	b4312	SMC	0.00
4539605	REC04196	<i>fimE</i>	X	198	-	P04741	Type 1 fimbriae regulatory protein fimE	b4313	RCD	0.00
4540683	REC04197	<i>fimA</i>	X	182	-	P04128	Type-1 fimbrial protein, A chain precursor	b4314	SMC	0.00
4541188	REC04198	<i>fimI</i>	X	215	-	P39264	Fimbrin-like protein fimI precursor	b4315	SMC	0.00
4541872	REC04199	<i>fimC</i>	X	241	-	P31697	Chaperone protein fimC precursor	b4316	SMC	0.00
4542665	REC04200	<i>fimD</i>	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	<i>fimF</i>	X	176	-	P08189	FimF protein precursor	b4318	UNC	0.00
4545854	REC04202	<i>fimG</i>	?	167	144	P08190	FimG protein precursor	b4319	UNC	0.00
4546377	REC04203	<i>fimH</i>	N	300	8, 11, 79, 91, 98, 127, 147, 190, 221, 259	P08191	FimH protein precursor	b4320	UNC	0.00
4548865	REC06436	<i>gntP</i>	N	447	145, 331, 356, 402, 416	P39373	High-affinity gluconate transporter	b4321	MTR	0.31
4549205	REC04205	<i>uxuA</i>	N	394	243, 260, 275	P24215	Mannonate dehydratase (EC 4.2.1.8)	b4322	CHM	0.25
4550470	REC04206	<i>uxuB</i>	N	486	26, 51, 124, 294	P39160	D-mannonate oxidoreductase (EC 1.1.1.157)	b4323	CHM	0.09
4552145	REC04207	<i>uxuR</i>	X	257	-	P39161	Uxu operon transcriptional regulator	b4324	RCD	0.09
4553889	REC06437	<i>yjiC</i>	X	276	-	P39374	Hypothetical protein yjiC	b4325	UNC	0.00
4554553	REC04209	<i>yjiD</i>	X	133	-	P39375	Hypothetical protein yjiD	b4326	UNC	0.00
4555858	REC06438	<i>yjiE</i>	X	303	-	P39376	Hypothetical transcriptional regulator yjiE	b4327	UNC	0.13
4557095	REC06439	<i>iada</i>	N	390	187, 209	P39377	Isoaspartyl dipeptidase (EC 3.4.19.-)	b4328	MSM	0.00

4557569	REC06440	<i>yjiG</i>	N	153	47, 59, 123, 145	P39378	Hypothetical protein yjiG	b4329	UNC	0.03
4558261	REC06441	<i>yjiH</i>	N	231	101	P39379	Hypothetical protein yjiH	b4330	UNC	0.03
4558397	REC04214	<i>kptA</i>	X	218	-	P39380	RNA 2'-phosphotransferase (EC 2.7.-.-)	b4331	NAM	0.13
4560244	REC06442	<i>yjiJ</i>	N	392	52, 67, 114, 153	P39381	Hypothetical protein yjiJ	b4332	UNC	0.19
4561283	REC06443	<i>yjiK</i>	N	323	69, 104, 180, 189, 202, 297, 305	P39382	Hypothetical protein yjiK	b4333	UNC	0.03
4562264	REC06444	<i>yjiL</i>	X	257	-	P39383	Hypothetical protein yjiL	b4334	UNC	0.16
4563440	REC06445	<i>yjiM</i>	N	390	1, 67, 111	P39384	Hypothetical protein yjiM	b4335	UNC	0.00
4564815	REC06446	<i>yjiN</i>	N	426	150, 153, 346	P39385	Hypothetical protein yjiN	b4336	UNC	0.16
4566088	REC06447	<i>yjiO</i>	N	410	226, 296	P39386	Hypothetical transport protein yjiO	b4337	UNC	0.06
4566567	REC04221	<i>yjiP</i>	N	103	13, 21, 38, 89, 96	P39387	Hypothetical protein yjiP	b4338	UNC	0.00
4566927	REC04222	<i>yjiP</i>	N	186	4, 31, 72, 136, 166, 170	P39387	Hypothetical protein yjiP	b4339	UNC	0.00
4569143	REC06448	<i>yjiR</i>	N	470	438, 469	P39389	Hypothetical protein yjiR	b4340	UNC	0.56
4569320	REC04224	<i>yjiS</i>	X	54	-	P39390	Hypothetical protein yjiS	b4341	UNC	0.00
4569935	REC04225	<i>yjiT</i>	N	521	-	P39391	Hypothetical protein yjiT	b4342	UNC	0.00
4571704	REC06527	<i>yjiV</i>	X	513	-	P39393	Hypothetical protein yjiV	b4343	UNC	0.00
4573163	REC04228	<i>mcrD</i>	N	420	74, 115, 158, 251, 317, 401	P27301	McrD protein	b4344	RCD	0.00
4575528	REC06449	<i>mcrC</i>	N	348	6, 76, 335	P15006	Protein mcrC	b4345	UNC	0.09
4576925	REC06450	<i>mcrB</i>	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	<i>yjiW</i>	N	132	8, 15, 130	P39394	Hypothetical protein yjiW	b4347	UNC	0.00
4579032	REC06452	<i>hdsS</i>	N	464	18, 88, 191, 194, 258, 331, 407, 410	P05719	Type I restriction enzyme EcoKI specificity protein	b4348	NAM	0.47
4580618	REC06453	<i>hdsM</i>	N	529	34	P08957	Type I restriction enzyme EcoKI M protein (EC 2.1.1.72)	b4349	NAM	0.50
4584385	REC06454	<i>hdsR</i>	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	<i>mrr</i>	N	304	49, 172, 199	P24202	Mrr restriction system protein	b4351	NAM	0.19
4586333	REC06455	<i>yjiA</i>	N	284	147	P24203	Hypothetical protein yjiA	b4352	UNC	0.34
4586649	REC06456	<i>yjiX</i>	?	67	-	P39395	Hypothetical protein yjiX	b4353	UNC	0.06
4588864	REC06457	<i>yjiY</i>	N	721	21, 93, 182, 211, 396, 458, 514, 516, 580, 562, 683	P39396	Hypothetical protein yjiY	b4354	UNC	0.41
4589227	REC06530	<i>tsr</i>	X	551	-	P02942	Methyl-accepting chemotaxis protein I	b4355	SMC	0.63
4592292	REC06458	<i>yjiL</i>	N	453	46, 81, 163, 256, 363, 440	P39398	Hypothetical transport protein yjiL	b4356	UNC	0.38
4593313	REC06460	<i>yjiM</i>	N	268	201	P39399	Hypothetical protein yjiM	b4357	UNC	0.09
4593544	REC04243	<i>yjiN</i>	N	345	106, 117, 150, 181, 243	P39400	Hypothetical zinc-type alcohol dehydrogenase-like protein yjiN	b4358	UNC	0.56
4596971	REC06461	<i>mcbB</i>	X	750	-	P39401	Phosphoglycerol transferase I (EC 2.7.8.20)	b4359	LPC	0.09
4597761	REC06462	<i>yjiA</i>	N	165	20, 49, 76	P18390	Hypothetical protein yjiA precursor	b4360	UNC	0.00
4598544	REC06463	<i>dnac</i>	E	245	-	P07905	DNA replication protein dnaC	b4361	NAM	0.09
4599086	REC06464	<i>dnat</i>	E	179	-	P07904	Primosomal protein I	b4362	NAM	0.03
4599519	REC06465	<i>yjiB</i>	?	108	84	P18389	Protein yjiB	b4363	UNC	0.34
4600490	REC06466	<i>yjiP</i>	N	277	168	P39402	Hypothetical protein yjiP	b4364	UNC	0.34
4601046	REC04250	<i>yjiQ</i>	N	241	31, 51, 106, 126, 188, 237	P39403	Hypothetical protein yjiQ	b4365	UNC	0.00
4601729	REC04251	<i>bgIJ</i>	N	225	9, 16, 59, 79, 143, 224	P39404	Transcriptional activator protein bgIJ	b4366	RCD	0.00
4603232	REC06467	<i>fhuf</i>	X	262	-	P39405	Ferric iron reductase protein fhuf	b4367	MSM	0.03
4603262	REC06716	<i>yjiZ</i>	X	115	-	P55914	Hypothetical protein yjiZ	UNC	0.00	
4605269	REC06468	<i>rsmC</i>	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	<i>hoLD</i>	E	137	20	P28632	DNA polymerase III, psi subunit (EC 2.7.7.7)	b4372	NAM	0.06
4605754	REC06532	<i>rimI</i>	E	148	-	P09453	Ribosomal-protein-alanine acetyltransferase (EC 2.3.1.128)	b4373	PMS	0.66
4606215	REC04256	<i>yjiG</i>	N	225	174	P39399	Hypothetical protein yjiG	b4374	UNC	0.25
4606983	REC04257	<i>prfC</i>	N	529	14, 252, 281, 298, 367, 407, 445, 494	P39398	Peptide chain release factor 3	b4375	PMS	0.63
4608965	REC04258	<i>osmY</i>	?	201	5	P27291	Osmotically inducible protein Y precursor	b4376	UNC	0.06
4609980	REC04259	<i>yjiU</i>	N	357	69, 215, 350	P39407	Hypothetical protein yjiU	b4377	UNC	0.56
4611194	REC04260	<i>yjiV</i>	E	211	204	P39408	Putative deoxyribonuclease yjiV (EC 3.1.21.-)	b4378	UNC	0.19
4613112	REC06469	<i>yjiW</i>	N	287	33, 74, 249, 250	P39409	Hypothetical protein yjiW	b4379	UNC	0.00
4614634	REC06470	<i>yjiI</i>	N	516	137, 233, 366	P37342	Hypothetical protein yjiI	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>deocA</i>	N	440	43, 87, 265, 286, 359, 374	P07650	Thymidine phosphorylase (EC 2.4.2.4)	b4382	NCM	0.44
4617172	REC04265	<i>deocB</i>	N	407	82, 202, 257, 305, 326, 360	P07651	Phosphopentomutase (EC 5.4.2.7)	b4383	CHM	0.41
4618452	REC04266	<i>deocD</i>	N	239	2, 104, 153, 160, 209	P09743	Purine nucleoside phosphorylase (EC 2.4.2.1)	b4384	NCM	0.41
4619338	REC04267	<i>yjiJ</i>	N	443	111, 192, 314	P39410	Hypothetical protein yjiJ	b4385	UNC	0.00
4621686	REC06471	<i>lplA</i>	E	338	-	P32099	Lipoate-protein ligase A (EC 6.-.-.-)	b4386	NCM	0.31
4622358	REC06472	<i>smf</i>	N	214	24, 64, 74, 170	P18838	Protein smf 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>yjiK</i>	N	555	25, 237	P37797	ABC transporter ATP-binding protein yjiK	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>yjiX</i>	N	173	93	P39411	Hypothetical protein yjiX	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>yjiY</i>	X	46	-	P39412	Hypothetical protein yjiY	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