

Table 1. List of identified proteins.

Spot No.	UniprotKB best hit	Gene Name	Protein Function
[2Fe-2S] cluster assembly			
235	B7I5Q3	<i>iscS</i>	Cysteine desulfurase IscS
318	Q88PK8	<i>iscS</i>	Cysteine desulfurase IscS
5-phosphoribose 1-diphosphate biosynthetic process			
58	Q818Z9	<i>deoB</i>	Phosphopentomutase
128	Q81VZ0	<i>prs</i>	Ribose-phosphate pyrophosphokinase
216	Q88PX6	<i>prs</i>	Ribose-phosphate pyrophosphokinase
Acetyl-CoA biosynthetic process			
98	Q817C0	<i>ackA</i>	Acetate kinase
363	P39646	<i>pta</i>	Phosphate acetyltransferase
Alanine catabolic process			
239	Q8CNW8	<i>ald</i>	Alanine dehydrogenase
682	Q49YD9	<i>ald</i>	Alanine dehydrogenase
Amino-acid biosynthesis			
297	B7IBD1	<i>hisA</i>	1-(5-phosphoribosyl)-5-[(5-phosphoribosylamino)methylideneamino] imidazole-4-carboxamide isomerase
574	Q88R42	<i>hisA</i>	1-(5-phosphoribosyl)-5-[(5-phosphoribosylamino)methylideneamino] imidazole-4-carboxamide isomerase
187	Q819J5	<i>dapH</i>	2,3,4,5-tetrahydropyridine-2,6-dicarboxylate N-acetyltransferase
195	Q5DL43	<i>dapD</i>	2,3,4,5-tetrahydropyridine-2,6-dicarboxylate N-succinyltransferase
421	Q6F9A5	<i>dapD</i>	2,3,4,5-tetrahydropyridine-2,6-dicarboxylate N-succinyltransferase
176	Q88MP1	<i>dapD</i>	2,3,4,5-tetrahydropyridine-2,6-dicarboxylate N-succinyltransferase
446	A5WDV6	<i>dapD</i>	2,3,4,5-tetrahydropyridine-2,6-dicarboxylate N-succinyltransferase

342	Q88DU4	<i>dapB</i>	4-hydroxy-tetrahydrodipicolinate reductase
241	Q812S1	<i>mtnN</i>	5'-methylthioadenosine/S-adenosylhomocysteine nucleosidase
228	Q6FFB2	<i>argH</i>	Argininosuccinate lyase
966	Q1I314	<i>argH</i>	Argininosuccinate lyase
472	Q9JXC1	<i>argG</i>	Argininosuccinate synthase
273	Q1IE03	<i>argG</i>	Argininosuccinate synthase
204	Q8XWC1	<i>argG</i>	Argininosuccinate synthase
355	Q6FCR9	<i>ilvD</i>	Dihydroxy-acid dehydratase 1
734	B7I2C2	<i>ilvD</i>	Dihydroxy-acid dehydratase
726	Q8XAV1	<i>ilvD</i>	Dihydroxy-acid dehydratase
463	B7I5I9	<i>ilvC</i>	Ketol-acid reductoisomerase (NADP(+))
41	Q6F821	<i>ilvC</i>	Ketol-acid reductoisomerase (NADP(+))
126	Q88DZ0	<i>ilvC</i>	Ketol-acid reductoisomerase (NADP(+))
888	Q88Q27	<i>glyA</i>	Serine hydroxymethyltransferase 2
612	Q6FA66	<i>glyA</i>	Serine hydroxymethyltransferase
71	O85718	<i>glyA</i>	Serine hydroxymethyltransferase
746	B3PBD6	<i>glyA</i>	Serine hydroxymethyltransferase
AMP salvage			
210	Q6FD71	<i>adk</i>	Adenylate kinase
259	B7IT40	<i>adk</i>	Adenylate kinase
Antibiotic resistance			
386	P13364	<i>gyrB</i>	DNA gyrase subunit B
Arginine metabolism			
9	Q81II1	<i>arcA</i>	Arginine deiminase
42	P41142	<i>arcA</i>	Arginine deiminase
400	B0V6G5	<i>arcB</i>	Ornithine carbamoyltransferase
453	Q73E86	<i>arcB</i>	Ornithine carbamoyltransferase, catabolic
35	Q81II0	<i>arcB</i>	Ornithine carbamoyltransferase, catabolic
60	Q88P53	<i>arcB</i>	Ornithine carbamoyltransferase, catabolic

ATP binding			
513	Q8X9L0	<i>ftsH</i>	ATP-dependent zinc metalloprotease FtsH
ATP synthesis coupled electron transport			
266	Q88FH2	<i>nuoG</i>	NADH-quinone oxidoreductase subunit G
ATP synthesis coupled proton transport			
276	Q6FFJ9	<i>atpC</i>	ATP synthase epsilon chain
96	B7H295	<i>atpG</i>	ATP synthase gamma chain
85	Q81JZ4	<i>atpG</i>	ATP synthase gamma chain OS=Bacillus anthracis
137	Q88BX3	<i>atpG</i>	ATP synthase gamma chain
242	Q6FFK6	<i>atpB</i>	ATP synthase subunit a
53	B711W2	<i>atpA</i>	ATP synthase subunit alpha
603	Q6FFK2	<i>atpA</i>	ATP synthase subunit alpha
55	Q81JZ3	<i>atpA</i>	ATP synthase subunit alpha
18	B0KRBO	<i>atpA</i>	ATP synthase subunit alpha
108	Q6FFK4	<i>atpF</i>	ATP synthase subunit b
206	Q72XE4	<i>atpF</i>	ATP synthase subunit b
91	B1JFU5	<i>atpF</i>	ATP synthase subunit b
536	Q3SF62	<i>atpF</i>	ATP synthase subunit b
572	Q6LKZ6	<i>atpD</i>	ATP synthase subunit beta 2
45	Q6FFK0	<i>atpD</i>	ATP synthase subunit beta
27	Q814W2	<i>atpD</i>	ATP synthase subunit beta
408	A9VSA3	<i>atpD</i>	ATP synthase subunit beta
1263	C3KYJ3	<i>atpD</i>	ATP synthase subunit beta
461	Q1I2I7	<i>atpD</i>	ATP synthase subunit beta
19	B0KRA8	<i>atpD</i>	ATP synthase subunit beta
462	B1JFU1	<i>atpD</i>	ATP synthase subunit beta
139	B7IQW1	<i>atpH</i>	ATP synthase subunit delta
Biosynthetic process			
385	P56744	<i>dat</i>	Diaminobutyrate--2-oxoglutarate aminotransferase
Branched-chain amino acid catabolic process			

304	P37940	<i>bfmBAA</i>	2-oxoisovalerate dehydrogenase subunit alpha
Calvin cycle			
372	Q8DIS5	<i>cbbL</i>	Ribulose biphosphate carboxylase large chain
Carbohydrate derivative biosynthetic process			
69	Q81VN5	<i>glmS</i>	Glutamine--fructose-6-phosphate aminotransferase [isomerizing]
Carbohydrate metabolic process			
169	Q81K80	<i>ldh</i>	L-lactate dehydrogenase 2
149	Q815X8	<i>ldh</i>	L-lactate dehydrogenase 3
Carbohydrate metabolism			
317	P43753	<i>pflB</i>	Formate acetyltransferase
164	Q8CTX6	<i>pflB</i>	Formate acetyltransferase
390	B2HWU2	<i>fbp</i>	Fructose-1,6-bisphosphatase class 1
Carbon dioxide fixation			
145	Q6F6Q6	<i>ppc</i>	Phosphoenolpyruvate carboxylase
Cell cycle			
154	P0A139	<i>pal</i>	Peptidoglycan-associated lipoprotein
369	Q81VZ2	<i>spoVG</i>	Putative septation protein SpoVG
Cell division			
490	B7I4X8	<i>tig</i>	Trigger factor
338	Q6FEP9	<i>tig</i>	Trigger factor
757	C1DHE8	<i>tig</i>	Trigger factor
140	Q812Q9	<i>tig</i>	Trigger factor
728	Q88KJ1	<i>tig</i>	Trigger factor
86	B0KJG5	<i>tig</i>	Trigger factor
Cell morphogenesis			
362	P32444	<i>mbl</i>	MreB-like protein
Cell redox homeostasis			
370	P35340	<i>ahpF</i>	Alkyl hydroperoxide reductase subunit F
Cellular response to DNA damage stimulus			

598	P39451	<i>adhP</i>	Alcohol dehydrogenase, propanol-preferring
<i>de novo</i> AMP biosynthetic process			
229	Q6FCS7	<i>purA</i>	Adenylosuccinate synthetase
649	Q88DD8	<i>purA</i>	Adenylosuccinate synthetase
482	Q12RX5	<i>purA</i>	Adenylosuccinate synthetase
<i>de novo</i> CTP biosynthetic process			
134	Q6FAT7	<i>pyrG</i>	CTP synthase
300	B7IQZ1	<i>pyrG</i>	CTP synthase
729	Q9CJW9	<i>pyrG</i>	CTP synthase
597	Q1I644	<i>pyrG</i>	CTP synthase
66	Q88MG1	<i>pyrG</i>	CTP synthase
<i>de novo</i> IMP biosynthetic process			
104	B7I289	<i>purC</i>	Phosphoribosylaminoimidazole-succinocarboxamide synthase
467	Q6F6U0	<i>purC</i>	Phosphoribosylaminoimidazole-succinocarboxamide synthase
691	Q88NG9	<i>purC</i>	Phosphoribosylaminoimidazole-succinocarboxamide synthase
<i>de novo</i> UMP biosynthesis			
715	Q8K9Z7	<i>carB</i>	Carbamoyl-phosphate synthase large chain
17	Q88DU6	<i>carB</i>	Carbamoyl-phosphate synthase large chain
884	Q87WP4	<i>carB</i>	Carbamoyl-phosphate synthase large chain
780	Q8XZ83	<i>carB</i>	Carbamoyl-phosphate synthase large chain
302	Q9KPH9	<i>carB</i>	Carbamoyl-phosphate synthase large chain
341	Q6FD29	<i>pyrC</i>	Dihydroorotase
DNA repair			
294	B7IBV9	<i>mutS</i>	DNA mismatch repair protein MutS
344	B7I9U0	<i>recA</i>	Protein RecA
293	Q88ME4	<i>recA</i>	Protein RecA
282	Q81JI3	<i>ssb</i>	Single-stranded DNA-binding protein
320	Q8VMM4	<i>ssb</i>	Single-stranded DNA-binding protein

DNA topological change			
337	P41513	<i>gyrA</i>	DNA gyrase subunit A
510	Q92IZ6	<i>gyrA</i>	DNA gyrase subunit A
72	Q44274	<i>gyrB</i>	DNA gyrase subunit B (Fragment)
1203	Q44273	<i>gyrB</i>	DNA gyrase subunit B (Fragments)
DNA-binding			
346	Q81U72	<i>yhaM</i>	3'-5' exoribonuclease YhaM
Electron transport			
379	Q9HZP7	<i>etfA</i>	Electron transfer flavoprotein subunit alpha
332	Q9HZP6	<i>etfB</i>	Electron transfer flavoprotein subunit beta
275	P94132	<i>etfD</i>	Probable electron transfer flavoprotein-ubiquinone oxidoreductase
74	P85097	<i>narG</i>	Respiratory nitrate reductase alpha chain (Fragments)
Fatty acid biosynthesis			
305	B7I6A3	<i>accA</i>	Acetyl-coenzyme A carboxylase carboxyl transferase subunit alpha
301	Q81WI7	<i>acpP</i>	Acyl carrier protein
296	Q81GI3	<i>fabI</i>	Enoyl-[acyl-carrier-protein] reductase [NADH] FabI
Gamma-aminobutyric acid metabolic process			
57	Q88RB9	<i>davT</i>	5-aminovalerate aminotransferase DavT
209	Q88RC0	<i>davD</i>	Glutarate-semialdehyde dehydrogenase DavD
Gluconeogenesis			
256	B0KI05	<i>pckA</i>	Phosphoenolpyruvate carboxykinase (ATP)
483	B1JET1	<i>pckA</i>	Phosphoenolpyruvate carboxykinase (ATP)
350	B7I624	<i>pckG</i>	Phosphoenolpyruvate carboxykinase [GTP]
61	Q6F8P2	<i>pckG</i>	Phosphoenolpyruvate carboxykinase [GTP]
163	Q02KR1	<i>ppsA</i>	Phosphoenolpyruvate synthase
Glutamine biosynthetic process			
295	P19064	<i>glnA</i>	Glutamine synthetase
339	Q3V5W6	<i>glnA</i>	Glutamine synthetase
374	Q9KNJ2	<i>glnAv</i>	Glutamine synthetase

Glycine decarboxylation via glycine cleavage system			
303	Q81XK8	<i>gcvH</i>	Glycine cleavage system H protein
248	Q81M08	<i>gcvPB</i>	Probable glycine dehydrogenase (decarboxylating) subunit 2
Glycolysis			
202	P20707	<i>sucA</i>	2-oxoglutarate dehydrogenase E1 component
56	Q81KZ0	<i>pfkA</i>	ATP-dependent 6-phosphofructokinase
52	P31052	<i>lpdG</i>	Dihydrolipoyl dehydrogenase
255	P21883	<i>pdhC</i>	Dihydrolipoyllysine-residue acetyltransferase component of pyruvate dehydrogenase complex
718	Q8K9T8	<i>aceF</i>	Dihydrolipoyllysine-residue acetyltransferase component of pyruvate dehydrogenase complex
1264	Q8NX76	<i>pdhC</i>	Dihydrolipoyllysine-residue acetyltransferase component of pyruvate dehydrogenase complex
151	Q6FAT9	<i>eno</i>	Enolase
16	B7IP20	<i>eno</i>	Enolase
1092	B0KSB9	<i>eno</i>	Enolase
267	B1JB38	<i>eno</i>	Enolase
443	Q4FR74	<i>eno</i>	Enolase
347	Q9I5Y1	<i>fba</i>	Fructose-bisphosphate aldolase
136	Q816G0	<i>pgi</i>	Glucose-6-phosphate isomerase
59	Q4MQ58	<i>gap</i>	Glyceraldehyde-3-phosphate dehydrogenase 1
699	P00362	<i>gap</i>	Glyceraldehyde-3-phosphate dehydrogenase
772	Q81X75	<i>pgk</i>	Phosphoglycerate kinase
24	B7HED5	<i>pgk</i>	Phosphoglycerate kinase
124	Q4MTG0	<i>pdhA</i>	Pyruvate dehydrogenase E1 component subunit alpha
1068	P21881	<i>pdhA</i>	Pyruvate dehydrogenase E1 component subunit alpha
198	P21882	<i>pdhB</i>	Pyruvate dehydrogenase E1 component subunit beta
481	P21874	<i>pdhB</i>	Pyruvate dehydrogenase E1 component subunit beta
31	Q6HBF1	<i>tpiA</i>	Triosephosphate isomerase
196	Q81X77	<i>gpml</i>	2,3-bisphosphoglycerate-independent phosphoglycerate mutase

Glycosyltransferase			
529	Q6FF51	<i>ppnP</i>	Pyrimidine/purine nucleoside phosphorylase
1265	P77836	<i>pdp</i>	Pyrimidine-nucleoside phosphorylase
334	Q8CNH8	<i>pdp</i>	Pyrimidine-nucleoside phosphorylase
Glyoxylate cycle			
292	P16100	<i>icd</i>	Isocitrate dehydrogenase [NADP]
494	Q8RQL9	<i>icd</i>	Isocitrate dehydrogenase [NADP]
578	Q9I0K4	<i>PA</i>	Isocitrate lyase
GMP biosynthesis			
87	Q6FFN2	<i>guaA</i>	GMP synthase [glutamine-hydrolyzing]
287	Q886X5	<i>guaA</i>	GMP synthase [glutamine-hydrolyzing]
438	P31002	<i>guaB</i>	Inosine-5'-monophosphate dehydrogenase
285	Q49UU8	<i>guaB</i>	Inosine-5'-monophosphate dehydrogenase
Hydrolase activity			
331	B7IM63	<i>BCG9842_B</i>	Putative phosphoesterase
IMP salvage			
330	P0A9M4	<i>hpt</i>	Hypoxanthine phosphoribosyltransferase
Ion transport			
257	P22263	<i>oprF</i>	Outer membrane porin F
218	Q6RYW5	<i>omp</i>	Outer membrane protein Omp38
413	Q81HQ0	<i>kdpB</i>	Potassium-transporting ATPase ATP-binding subunit
Iron storage			
249	Q8RPQ1	<i>dps</i>	DNA protection during starvation protein 1
264	Q8RPQ2	<i>dps</i>	DNA protection during starvation protein 2
Lactate metabolic process			
306	Q6FFS1	<i>lldD</i>	L-lactate dehydrogenase
L-alanine catabolic process			
759	Q8NW54	<i>ald</i>	Alanine dehydrogenase 2
Leucine catabolic process			
44	P0A393	<i>ldh</i>	Leucine dehydrogenase

Lipid biosynthesis/Lipid metabolism			
364	Q814Y7	<i>fabZ</i>	3-hydroxyacyl-[acyl-carrier-protein] dehydratase FabZ
252	Q88MG9	<i>fabZ</i>	3-hydroxyacyl-[acyl-carrier-protein] dehydratase FabZ
271	B7IP83	<i>gpsA</i>	Glycerol-3-phosphate dehydrogenase [NAD(P)+]
Lipopolysaccharide biosynthesis			
333	A8GN21	<i>capD</i>	UDP-glucose 4-epimerase
L-serine biosynthetic process			
381	B2HWW3	<i>serC</i>	Phosphoserine aminotransferase
Malate metabolic process			
336	P43837	<i>maeB</i>	NADP-dependent malic enzyme
Menaquinone biosynthesis			
299	Q49WG8	<i>menB</i>	1,4-dihydroxy-2-naphthoyl-CoA synthase
Metabolic process			
367	Q87LK8	<i>tkt</i>	Transketolase 1
mRNA catabolic process			
937	B7I3U1	<i>pnp</i>	Polyribonucleotide nucleotidyltransferase
43	Q6FF12	<i>pnp</i>	Polyribonucleotide nucleotidyltransferase
190	B7IUG5	<i>pnp</i>	Polyribonucleotide nucleotidyltransferase
67	B0KHX3	<i>pnp</i>	Polyribonucleotide nucleotidyltransferase
422	Q81WQ4	<i>rny</i>	Ribonuclease Y
Nitrate assimilation			
234	P42175	<i>narG</i>	Nitrate reductase alpha chain
Nucleobase-containing compound metabolic process			
265	P57072	<i>NMA</i>	Uncharacterized protein NMA0194
Nucleoside metabolic process			
263	Q81T09	<i>deoD</i>	Purine nucleoside phosphorylase DeoD-type
Nucleotide metabolism			
175	Q6FE29	<i>dcd</i>	dCTP deaminase
88	Q81FQ4	<i>ndk</i>	Nucleoside diphosphate kinase
168	Q3K7B2	<i>ndk</i>	Nucleoside diphosphate kinase

One-carbon metabolism			
365	Q6FA43	<i>ahcY</i>	Adenosylhomocysteinase
868	B0KM00	<i>ahcY</i>	Adenosylhomocysteinase
147	B1J2Y8	<i>ahcY</i>	Adenosylhomocysteinase
366	Q81SW2	<i>folE</i>	GTP cyclohydrolase 1
291	B2HYY9	<i>metK</i>	S-adenosylmethionine synthase
441	Q4L7C7	<i>metK</i>	S-adenosylmethionine synthase
Oxidoreductase			
321	Q8CQ56	<i>adh</i>	Alcohol dehydrogenase
Pentose shunt			
83	Q81V33	<i>tal</i>	Probable transaldolase 1
Phosphorus metabolic process			
279	Q81PH9	<i>ppaC</i>	Probable manganese-dependent inorganic pyrophosphatase
Phosphotransferase system			
193	Q81JY0	<i>crr</i>	PTS system glucose-specific EIIA component
Protein biosynthesis			
76	B2HWK7	<i>alaS</i>	Alanine--tRNA ligase
214	Q817Z0	<i>alaS</i>	Alanine--tRNA ligase 1
211	Q88E18	<i>alaS</i>	Alanine--tRNA ligase
340	B711U9	<i>argS</i>	Arginine--tRNA ligase
138	Q6FEH6	<i>aspS</i>	Aspartate--tRNA(Asp/Asn) ligase
571	C1DRG2	<i>aspS</i>	Aspartate--tRNA(Asp/Asn) ligase
877	A1U1C2	<i>aspS</i>	Aspartate--tRNA(Asp/Asn) ligase
829	Q4K7D5	<i>aspS</i>	Aspartate--tRNA(Asp/Asn) ligase
238	Q4FSF4	<i>aspS</i>	Aspartate--tRNA(Asp/Asn) ligase
289	Q6FDY4	<i>gatB</i>	Aspartyl/glutamyl-tRNA(Asn/Gln) amidotransferase subunit B
395	B7I580	<i>lepA</i>	Elongation factor 4
22	Q88QN8	<i>fusA</i>	Elongation factor G 1
965	Q9I244	<i>fusB</i>	Elongation factor G 2

310	B7I7S1	<i>fusA</i>	Elongation factor G
12	Q6FDS6	<i>fusA</i>	Elongation factor G
473	Q0ABH8	<i>fusA</i>	Elongation factor G
6	B7IT16	<i>fusA</i>	Elongation factor G
1202	P80868	<i>fusA</i>	Elongation factor G
478	P59451	<i>fusA</i>	Elongation factor G
468	Q7NQF0	<i>fusA</i>	Elongation factor G
716	Q1ISC5	<i>fusA</i>	Elongation factor G
562	A6Q1M7	<i>fusA</i>	Elongation factor G
470	C5CP58	<i>fusA</i>	Elongation factor G
499	A5CXN7	<i>fusA</i>	Elongation factor G
710	Q8PNS6	<i>fusA</i>	Elongation factor G
308	Q3K918	<i>efp</i>	Elongation factor P
720	C3K6L0	<i>efp</i>	Elongation factor P
839	B7I3K0	<i>tsf</i>	Elongation factor Ts
38	Q6FA54	<i>tsf</i>	Elongation factor Ts
75	B7IUI5	<i>tsf</i>	Elongation factor Ts
683	Q6AP40	<i>tsf</i>	Elongation factor Ts
28	A5W849	<i>tsf</i>	Elongation factor Ts
475	A5WCX3	<i>tsf</i>	Elongation factor Ts
1159	A1WCN6	<i>tuf</i>	Elongation factor Tu 2
39	B7H1K5	<i>tuf</i>	Elongation factor Tu
460	Q6FF97	<i>tuf</i>	Elongation factor Tu
14	B7IT17	<i>tuf</i>	Elongation factor Tu
751	A7ZCN0	<i>tuf</i>	Elongation factor Tu
442	B8I5N8	<i>tuf</i>	Elongation factor Tu
736	P33168	<i>tuf</i>	Elongation factor Tu
1091	B8DLL9	<i>tuf</i>	Elongation factor Tu
471	Q9ZK19	<i>tuf</i>	Elongation factor Tu
750	Q18CE4	<i>tuf</i>	Elongation factor Tu

20	Q3K5X4	<i>tuf</i>	Elongation factor Tu
1260	Q88QP8	<i>tufA</i>	Elongation factor Tu-A
311	Q88QN7	<i>tufB</i>	Elongation factor Tu-B
351	Q81VV3	<i>gltX</i>	Glutamate--tRNA ligase
286	Q6F7L8	<i>glyS</i>	Glycine--tRNA ligase beta subunit
32	Q819R4	<i>ileS</i>	Isoleucine--tRNA ligase 1
278	Q6FG02	<i>ileS</i>	Isoleucine--tRNA ligase
474	Q9HVM4	<i>ileS</i>	Isoleucine--tRNA ligase
79	B1JF83	<i>ileS</i>	Isoleucine--tRNA ligase
40	B7I5I5	<i>leuS</i>	Leucine--tRNA ligase
312	Q6F817	<i>leuS</i>	Leucine--tRNA ligase
162	Q88DN1	<i>leuS</i>	Leucine--tRNA ligase
492	Q8ZDF8	<i>leuS</i>	Leucine--tRNA ligase
389	B1JD39	<i>lysS</i>	Lysine--tRNA ligase
225	Q81JA8	<i>metG</i>	Methionine--tRNA ligase 1
281	Q6FE36	<i>metG</i>	Methionine--tRNA ligase
182	B0VV85	<i>pheS</i>	Phenylalanine--tRNA ligase alpha subunit
181	Q81L31	<i>pheT</i>	Phenylalanine--tRNA ligase beta subunit
220	B7H005	<i>thrS</i>	Threonine--tRNA ligase
588	Q6F860	<i>thrS</i>	Threonine--tRNA ligase
1161	B7I3R9	<i>infB</i>	Translation initiation factor IF-2
102	Q6FF40	<i>infB</i>	Translation initiation factor IF-2
455	B4RXT8	<i>infB</i>	Translation initiation factor IF-2
143	A9VT50	<i>infB</i>	Translation initiation factor IF-2
192	Q88DV7	<i>infB</i>	Translation initiation factor IF-2
246	Q812P6	<i>infC</i>	Translation initiation factor IF-3
82	Q6F8F0	<i>valS</i>	Valine--tRNA ligase
94	Q81LD3	<i>valS</i>	Valine--tRNA ligase
821	Q7VN93	<i>valS</i>	Valine--tRNA ligase
383	Q88P76	<i>valS</i>	Valine--tRNA ligase

Protein catabolic process to glutamate			
118	Q81IP0	<i>rocA</i>	1-pyrroline-5-carboxylate dehydrogenase
Protein folding			
290	B7I619	<i>groS</i>	10 kDa chaperonin
416	Q1I5E1	<i>groS</i>	10 kDa chaperonin
280		<i>clpX</i>	ATP-dependent Clp protease ATP-binding subunit ClpX
Protein homotetramerization			
288		<i>ald</i>	Long-chain-aldehyde dehydrogenase
Protein refolding			
21	Q6F8P6	<i>groL</i>	60 kDa chaperonin
25	B7IUT0	<i>groL</i>	60 kDa chaperonin
1262	B4EXE2	<i>groL</i>	60 kDa chaperonin
360	Q88N55	<i>groL</i>	60 kDa chaperonin
15	B0KFQ2	<i>groL</i>	60 kDa chaperonin
608	Q87X14	<i>groL</i>	60 kDa chaperonin
479	Q8Y1P8	<i>groL</i>	60 kDa chaperonin
Protein secretion			
258	Q81GY5	<i>prsA</i>	Foldase protein PrsA 1
Protein transport			
221	A3M8M4	<i>secA</i>	Protein translocase subunit SecA
26	B7IPV1	<i>secA</i>	Protein translocase subunit SecA
730	P0CAW7	<i>secA</i>	Protein translocase subunit SecA
1094	A3DF88	<i>secA</i>	Protein translocase subunit SecA
990	B9EAE8	<i>secA</i>	Protein translocase subunit SecA
599	Q9HWF5	<i>secY</i>	Protein translocase subunit SecY
272	B7I5H3	<i>secB</i>	Protein-export protein SecB
Purine salvage			
378	Q88CB6	<i>xpt</i>	Xanthine phosphoribosyltransferase
Pyrimidine biosynthesis			
161	A3M9Y5	<i>pyrE</i>	Orotate phosphoribosyltransferase

792	Q6F6Z6	<i>pyrE</i>	Orotate phosphoribosyltransferase
388	A3M658	<i>pyrH</i>	Uridylate kinase
324	Q819Y0	<i>pyrH</i>	Uridylate kinase
Pyridoxal phosphate biosynthetic process			
109	Q73FJ5	<i>pdxS</i>	Pyridoxal 5'-phosphate synthase subunit PdxS
322	Q81W26	<i>pdxT</i>	Pyridoxal 5'-phosphate synthase subunit PdxT
Removal of superoxide radicals			
240	Q88PD5	<i>sodB</i>	Superoxide dismutase [Fe]
133	Q81LW0	<i>sodA</i>	Superoxide dismutase [Mn] 1
Response to organic substance			
283	B0KJ96	<i>lptD</i>	LPS-assembly protein LptD
Riboflavin biosynthesis			
115	Q88QH6	<i>ribH</i>	6,7-dimethyl-8-ribityllumazine synthase
Ribosome biogenesis/Translation			
357	B7I358	<i>rplJ</i>	50S ribosomal protein L10
224	B7IT08	<i>rplJ</i>	50S ribosomal protein L10
685	Q1IFX5	<i>rplJ</i>	50S ribosomal protein L10 =3 SV=1
148	Q88QP3	<i>rplJ</i>	50S ribosomal protein L10
rRNA processing			
325	Q6FFX5	<i>rph</i>	Ribonuclease PH
326	Q6FF39	<i>rbfA</i>	Ribosome-binding factor A
Stress response			
208	Q81TT4	<i>clpB</i>	Chaperone protein ClpB
620	Q6MIV0	<i>clpB</i>	Chaperone protein ClpB
445	P17422	<i>clpB</i>	Chaperone protein ClpB
92	Q88Q71	<i>clpB</i>	Chaperone protein ClpB
885	Q6N1H2	<i>clpB</i>	Chaperone protein ClpB
236	Q8EBE6	<i>clpB</i>	Chaperone protein ClpB
915	Q7UBW5	<i>clpB</i>	Chaperone protein ClpB
930	Q99VB5	<i>clpB</i>	Chaperone protein ClpB

951	Q8PHQ4	<i>clpB</i>	Chaperone protein ClpB
11	B2HZZ7	<i>dnaK</i>	Chaperone protein DnaK
690	Q6F6N3	<i>dnaK</i>	Chaperone protein DnaK
952	A1K4C5	<i>dnaK</i>	Chaperone protein DnaK
30	Q81LS2	<i>dnaK</i>	Chaperone protein DnaK
487	B1XRU1	<i>dnaK</i>	Chaperone protein DnaK
277	B0KIS5	<i>dnaK</i>	Chaperone protein DnaK
36	B1J254	<i>dnaK</i>	Chaperone protein DnaK
1051	A5WI20	<i>dnaK</i>	Chaperone protein DnaK
121	Q6FF82	<i>htpG</i>	Chaperone protein HtpG
661	Q4KFX8	<i>htpG</i>	Chaperone protein HtpG
106	Q88FB9	<i>htpG</i>	Chaperone protein HtpG
489	Q21SJ8	<i>htpG</i>	Chaperone protein HtpG
1128	Q31GE9	<i>lon</i>	Lon protease 1
49	B7GXS7	<i>lon</i>	Lon protease
579	A0RJ87	<i>lon</i>	Lon protease
480	Q32JJ5	<i>lon</i>	Lon protease
392	B7IBK6	<i>grpE</i>	Protein GrpE
207	Q2SBC2	<i>hfq</i>	RNA-binding protein Hfq
Tetrahydrofolate interconversion			
245	A3M846	<i>fold</i>	Bifunctional protein FOLD
425	Q818R5	<i>fold</i>	Bifunctional protein FOLD
95	Q81RE1	<i>fhs</i>	Formate--tetrahydrofolate ligase
Transcription			
29	Q6F7T7	<i>rpoA</i>	DNA-directed RNA polymerase subunit alpha
223	Q81VQ4	<i>rpoA</i>	DNA-directed RNA polymerase subunit alpha
112	Q88QL1	<i>rpoA</i>	DNA-directed RNA polymerase subunit alpha
10	B7I360	<i>rpoB</i>	DNA-directed RNA polymerase subunit beta
90	B21I22	<i>rpoC</i>	DNA-directed RNA polymerase subunit beta'
212	Q6FF90	<i>rpoB</i>	DNA-directed RNA polymerase subunit beta

1	Q6FF89	<i>rpoC</i>	DNA-directed RNA polymerase subunit beta'
23	Q81J48	<i>rpoB</i>	DNA-directed RNA polymerase subunit beta
862	Q81J47	<i>rpoC</i>	DNA-directed RNA polymerase subunit beta'
13	A9VP70	<i>rpoC</i>	DNA-directed RNA polymerase subunit beta'
773	Q47UV9	<i>rpoB</i>	DNA-directed RNA polymerase subunit beta
464	A6W398	<i>rpoC</i>	DNA-directed RNA polymerase subunit beta'
1127	A1ALT4	<i>rpoB</i>	DNA-directed RNA polymerase subunit beta
1201	Q1IFX3	<i>rpoB</i>	DNA-directed RNA polymerase subunit beta
1126	Q3K5Y2	<i>rpoC</i>	DNA-directed RNA polymerase subunit beta'
2	Q88QP2	<i>rpoB</i>	DNA-directed RNA polymerase subunit beta
459	B0KK60	<i>rpoB</i>	DNA-directed RNA polymerase subunit beta
5	B0KK61	<i>rpoC</i>	DNA-directed RNA polymerase subunit beta'
349	Q1Q8P9	<i>rpoB</i>	DNA-directed RNA polymerase subunit beta
1261	Q160X8	<i>rpoC</i>	DNA-directed RNA polymerase subunit beta'
465	Q8Z320	<i>rpoB</i>	DNA-directed RNA polymerase subunit beta
329	Q52083	<i>fur</i>	Ferric uptake regulation protein
205	Q819X8	<i>codY</i>	GTP-sensing transcriptional pleiotropic repressor CodY
231	P52327	<i>rpoD</i>	RNA polymerase sigma factor RpoD
Transcription regulation			
274	B0VSL8	<i>greA</i>	Transcription elongation factor GreA
420	A5WDP3	<i>greA</i>	Transcription elongation factor GreA
244	P52152	<i>rho</i>	Transcription termination factor Rho
433	P57652	<i>rho</i>	Transcription termination factor Rho
732	Q9FC33	<i>rho</i>	Transcription termination factor Rho
Translation			
78	O06000	<i>BCE</i>	30S ribosomal protein S1 homolog
373	P57395	<i>rpsA</i>	30S ribosomal protein S1
68	Q9HZ71	<i>rpsA</i>	30S ribosomal protein S1
107	Q6F7R1	<i>rpsJ</i>	30S ribosomal protein S10
203	B7IT18	<i>rpsJ</i>	30S ribosomal protein S10

232	Q88QN6	<i>rpsJ</i>	30S ribosomal protein S10
125	Q6F7T5	<i>rpsK</i>	30S ribosomal protein S11
268	B7IT45	<i>rpsK</i>	30S ribosomal protein S11
213	Q1IFU3	<i>rpsK</i>	30S ribosomal protein S11
377	Q6FDS8	<i>rpsL</i>	30S ribosomal protein S12
201	Q81VT5	<i>rpsL</i>	30S ribosomal protein S12
247	Q9HWD0	<i>rpsL</i>	30S ribosomal protein S12
219	B7IA17	<i>rpsM</i>	30S ribosomal protein S13
179	B7IT44	<i>rpsM</i>	30S ribosomal protein S13
89	Q88QL3	<i>rpsM</i>	30S ribosomal protein S13
189	B7IA26	<i>rpsN</i>	30S ribosomal protein S14
368	Q6F7H9	<i>rpsP</i>	30S ribosomal protein S16
328	Q6F7S1	<i>rpsQ</i>	30S ribosomal protein S17
262	Q81VS1	<i>rpsQ</i>	30S ribosomal protein S17
260	Q814G7	<i>rpsR</i>	30S ribosomal protein S18
237	Q6F7R6	<i>rpsS</i>	30S ribosomal protein S19
172	Q81J38	<i>rpsS</i>	30S ribosomal protein S19
173	Q88QN1	<i>rpsS</i>	30S ribosomal protein S19
103	Q6FA53	<i>rpsB</i>	30S ribosomal protein S2
46	Q9XBK3	<i>rpsB</i>	30S ribosomal protein S2
111	B1JBR0	<i>rpsB</i>	30S ribosomal protein S2
359	Q6FCL0	<i>rpsU</i>	30S ribosomal protein S21
84	B7IA33	<i>rpsC</i>	30S ribosomal protein S3
97	Q81VS4	<i>rpsC</i>	30S ribosomal protein S3
1160	A7GK26	<i>rpsC</i>	30S ribosomal protein S3
123	Q88QM9	<i>rpsC</i>	30S ribosomal protein S3
484	Q4FUF0	<i>rpsC</i>	30S ribosomal protein S3
54	Q6F7T6	<i>rpsD</i>	30S ribosomal protein S4
794	Q81KT2	<i>rpsD</i>	30S ribosomal protein S4
62	B7IKS0	<i>rpsD</i>	30S ribosomal protein S4

48	Q88QL2	<i>rpsD</i>	30S ribosomal protein S4
171	Q6F7S9	<i>rpsE</i>	30S ribosomal protein S5
116	Q81VR3	<i>rpsE</i>	30S ribosomal protein S5
81	Q88QL8	<i>rpsE</i>	30S ribosomal protein S5
188	Q6F9R0	<i>rpsF</i>	30S ribosomal protein S6
185	Q88DE8	<i>rpsF</i>	30S ribosomal protein S6
64	B7I7S0	<i>rpsG</i>	30S ribosomal protein S7
73	B7IT15	<i>rpsG</i>	30S ribosomal protein S7
678	Q9HWD1	<i>rpsG</i>	30S ribosomal protein S7
132	Q88QN9	<i>rpsG</i>	30S ribosomal protein S7
184	Q6F7S6	<i>rpsH</i>	30S ribosomal protein S8
146	Q81VR6	<i>rpsH</i>	30S ribosomal protein S8
119	Q88QM1	<i>rpsH</i>	30S ribosomal protein S8
323	Q81VP8	<i>rpsI</i>	30S ribosomal protein S9
1093	Q4QKG9	<i>rpsI</i>	30S ribosomal protein S9
153	Q1I597	<i>rpsI</i>	30S ribosomal protein S9
101	B7I356	<i>rplK</i>	50S ribosomal protein L11
110	Q81VU3	<i>rplK</i>	50S ribosomal protein L11
488	A2SLG9	<i>rplK</i>	50S ribosomal protein L11
170	Q88QP5	<i>rplK</i>	50S ribosomal protein L11
486	B7I9B0	<i>rplM</i>	50S ribosomal protein L13
269	Q6F898	<i>rplM</i>	50S ribosomal protein L13
158	B7IT52	<i>rplM</i>	50S ribosomal protein L13
99	Q88N97	<i>rplM</i>	50S ribosomal protein L13
681	Q5PJS5	<i>rplM</i>	50S ribosomal protein L13
70	Q6F7S2	<i>rplN</i>	50S ribosomal protein L14
114	Q81VS0	<i>rplN</i>	50S ribosomal protein L14
938	Q7VKE3	<i>rplN</i>	50S ribosomal protein L14
251	Q88QM5	<i>rplN</i>	50S ribosomal protein L14
117	B7IA20	<i>rplO</i>	50S ribosomal protein L15

183	B7IT38	<i>rplO</i>	50S ribosomal protein L15
100	Q88QL6	<i>rplO</i>	50S ribosomal protein L15
233	Q73F89	<i>rplP</i>	50S ribosomal protein L16
491	A6W385	<i>rplP</i>	50S ribosomal protein L16
177	Q88QM8	<i>rplP</i>	50S ribosomal protein L16
343	Q6F7T8	<i>rplQ</i>	50S ribosomal protein L17
200	Q81VQ3	<i>rplQ</i>	50S ribosomal protein L17
144	Q88QL0	<i>rplQ</i>	50S ribosomal protein L17
270	B7IA23	<i>rplR</i>	50S ribosomal protein L18
122	Q88QL9	<i>rplR</i>	50S ribosomal protein L18
167	Q81WJ6	<i>rplS</i>	50S ribosomal protein L19
1266	C4L604	<i>rplS</i>	50S ribosomal protein L19
778	Q6LMW0	<i>rplS</i>	50S ribosomal protein L19
93	Q88MV3	<i>rplS</i>	50S ribosomal protein L19
968	Q88MV3	<i>rplS</i>	50S ribosomal protein L19
495	A9NED6	<i>rplB</i>	50S ribosomal protein L2
314	B7IA36	<i>rplB</i>	50S ribosomal protein L2
166	Q6F7R5	<i>rplB</i>	50S ribosomal protein L2
77	Q81J39	<i>rplB</i>	50S ribosomal protein L2
37	B0KK70	<i>rplB</i>	50S ribosomal protein L2
230	Q6F868	<i>rplT</i>	50S ribosomal protein L20
752	B4RSL5	<i>rplT</i>	50S ribosomal protein L20
454	Q8RPZ9	<i>rplT</i>	50S ribosomal protein L20
335	Q81L17	<i>rplT</i>	50S ribosomal protein L20
222	Q6F8G1	<i>rplU</i>	50S ribosomal protein L21
160	Q81LE6	<i>rplU</i>	50S ribosomal protein L21
127	Q88Q10	<i>rplU</i>	50S ribosomal protein L21
120	B2HZL7	<i>rplV</i>	50S ribosomal protein L22
156	Q81J37	<i>rplV</i>	50S ribosomal protein L22
180	Q9HWE0	<i>rplV</i>	50S ribosomal protein L22

307	Q6F7R4	<i>rplW</i>	50S ribosomal protein L23
226	Q81VS8	<i>rplW</i>	50S ribosomal protein L23
186	Q88QN3	<i>rplW</i>	50S ribosomal protein L23
217	Q6F7S3	<i>rplX</i>	50S ribosomal protein L24
152	Q81VR9	<i>rplX</i>	50S ribosomal protein L24
191	Q88QM4	<i>rplX</i>	50S ribosomal protein L24
129	A5VYF9	<i>rplY</i>	50S ribosomal protein L25
469	B0KND5	<i>rplY</i>	50S ribosomal protein L25
316	B1JEQ2	<i>rplY</i>	50S ribosomal protein L25
643	Q6F8G2	<i>rpmA</i>	50S ribosomal protein L27
250	Q81LE8	<i>rpmA</i>	50S ribosomal protein L27
431	Q6FES9	<i>rpmB</i>	50S ribosomal protein L28
261	Q88C99	<i>rpmB</i>	50S ribosomal protein L28
243	Q6F7R2	<i>rplC</i>	50S ribosomal protein L3
150	B7IT19	<i>rplC</i>	50S ribosomal protein L3
105	Q88QN5	<i>rplC</i>	50S ribosomal protein L3
531	Q6F867	<i>rpmI</i>	50S ribosomal protein L35
165	Q6F7R3	<i>rplD</i>	50S ribosomal protein L4
174	Q81VS9	<i>rplD</i>	50S ribosomal protein L4
253	Q88QN4	<i>rplD</i>	50S ribosomal protein L4
624	B7IA27	<i>rplE</i>	50S ribosomal protein L5
135	Q6F7S4	<i>rplE</i>	50S ribosomal protein L5
80	B7IT31	<i>rplE</i>	50S ribosomal protein L5
878	B3PK49	<i>rplE</i>	50S ribosomal protein L5
774	A4G9S6	<i>rplE</i>	50S ribosomal protein L5
567	B1XSR3	<i>rplE</i>	50S ribosomal protein L5
50	Q88QM3	<i>rplE</i>	50S ribosomal protein L5
315	B7IA24	<i>rplF</i>	50S ribosomal protein L6
141	Q6F7S7	<i>rplF</i>	50S ribosomal protein L6
194	Q81VR5	<i>rplF</i>	50S ribosomal protein L6

142	Q88QM0	<i>rplF</i>	50S ribosomal protein L6
130	Q6FF91	<i>rplL</i>	50S ribosomal protein L7/L12
197	Q81VU0	<i>rplL</i>	50S ribosomal protein L7/L12
254	Q3K5Y0	<i>rplL</i>	50S ribosomal protein L7/L12
284	Q6F9Q8	<i>rplI</i>	50S ribosomal protein L9
157	Q88DF1	<i>rplI</i>	50S ribosomal protein L9
581	A4VQM7	<i>rplI</i>	50S ribosomal protein L9
131	Q81WL1	<i>frr</i>	Ribosome-recycling factor
Translation regulation			
589	B7I357	<i>rplA</i>	50S ribosomal protein L1
298	Q6FF93	<i>rplA</i>	50S ribosomal protein L1
601	B7IT07	<i>rplA</i>	50S ribosomal protein L1
155	A9VNB1	<i>rplA</i>	50S ribosomal protein L1
51	B0KK57	<i>rplA</i>	50S ribosomal protein L1
466	Q889Y1	<i>rplA</i>	50S ribosomal protein L1
Transport			
178	B7I740	<i>nuoB</i>	NADH-quinone oxidoreductase subunit B
159	B7I741	<i>nuoC</i>	NADH-quinone oxidoreductase subunit C/D
375	B1J6N2	<i>nuoC</i>	NADH-quinone oxidoreductase subunit C/D
215	B2HU48	<i>nuoI</i>	NADH-quinone oxidoreductase subunit I
380	P80866	<i>sufC</i>	Vegetative protein 296
Tricarboxylic acid cycle			
352	Q8CPC2	<i>acnA</i>	Aconitate hydratase A
47	Q9I2V5	<i>acnB</i>	Aconitate hydratase B
967	Q8ZRS8	<i>acnB</i>	Aconitate hydratase B
477	P74582	<i>acnB</i>	Aconitate hydratase B
476	P20901	<i>aarA</i>	Citrate synthase
113	P20902	<i>gltA</i>	Citrate synthase
387	Q9I3D2	<i>sucB</i>	Dihydrolipoyllysine-residue succinyltransferase component of 2-oxoglutarate dehydrogenase complex

34	Q6F7X1	<i>mdh</i>	Malate dehydrogenase
1005	A1K5Q9	<i>mdh</i>	Malate dehydrogenase
313	A9IIS3	<i>mdh</i>	Malate dehydrogenase
573	A9IIS3	<i>mdh</i>	Malate dehydrogenase
319	Q8ZQU3	<i>sdhA</i>	Succinate dehydrogenase flavoprotein subunit
371	P08066	<i>sdhB</i>	Succinate dehydrogenase iron-sulfur subunit
65	Q51567	<i>sucD</i>	Succinate--CoA ligase [ADP-forming] subunit alpha
227	B7I6T2	<i>sucC</i>	Succinate--CoA ligase [ADP-forming] subunit beta
63	Q819X0	<i>sucC</i>	Succinate--CoA ligase [ADP-forming] subunit beta
1162	Q5QU21	<i>sucC</i>	Succinate--CoA ligase [ADP-forming] subunit beta
33	B0KNW8	<i>sucC</i>	Succinate--CoA ligase [ADP-forming] subunit beta
485	Q1QEK5	<i>sucC</i>	Succinate--CoA ligase [ADP-forming] subunit beta
UMP salvage			
309	Q81JY5	<i>upp</i>	Uracil phosphoribosyltransferase