Supplemental Table S1. All *B. anthracis* proteins identified

N	Uniprot accession	Gene name	Function	Dor[a]	Germ[b]
1	B9ZSG0	*truB*	tRNA pseudouridine synthase B	+	+
2	P62176	*rpsM*	30S ribosomal protein S13	+	+
3	P77819	*rpoC*	DNA-directed RNA polymerase subunit beta'	+	+
4	P94217	*eag*	S-layer protein EA1	+	+
5	Q6HR05	*BAS4994*	Lipoprotein, putative	+	+
6	Q6HRE6	*csd*	Cysteine desulfurase	-	+
7	Q6HSS4	*BAS4367*	Lon protease	-	+
8	Q6HSW8	*BAS4323*	Forespore-specific protein, putative	+	+
9	Q6HTK0	*BAS4088*	Acetyl-CoA carboxylase, biotin carboxylase	-	+
10	Q6HU42	*BAS3896*	Putative uncharacterized protein	-	+
11	Q6HUJ4	*ylyB*	Pseudouridine synthase	+	+
12	Q6HW55	*BAS3176*	Putative uncharacterized protein	-	+
13	Q6HZK6	*BAS1969*	Metallo-beta-lactamase family protein	-	+
14	Q6I0U2	*BAS1522*	Metallo-beta-lactamase family protein	+	+
15	Q6I180	*rluB*	Pseudouridine synthase	+	+
16	Q6I2F1	*NA (WP_000554487.1)*	Putative uncharacterized protein	+	+
17	Q6I447	*GBAA_0367*	Amino acid ABC transporter, solute binding protein	+	-
18	Q6I460	*NA (WP_000051541.1)*	Putative uncharacterized protein	+	+
19	Q6I4E9	*tsaD*	Probable tRNA threonylcarbamoyladenosine biosynthesis protein Gcp	+	+
20	Q6I4F4	*BAS0241*	S1 RNA binding domain protein	-	+
21	Q81JD9	*mnmE*	tRNA modification GTPase MnmE	+	+
22	Q81JE0	*fabZ*	3-hydroxyacyl-[acyl-carrier-protein] dehydratase FabZ	+	+
23	Q81JE1	*GBAA_4943*	Putative tRNA binding domain protein	+	-
24	Q81JF3	*GBAA_2171*	PBS lyase HEAT-like repeat domain protein	+	+
25	Q81JF8	*fabI*	Enoyl-[acyl-carrier-protein] reductase [NADH]	+	+
26	Q81JF9	*fabF*	3-oxoacyl-[acyl-carrier-protein] synthase 2	+	+
27	Q81JG0	*fabH1*	3-oxoacyl-[acyl-carrier-protein] synthase 3 protein 1	+	+
28	Q81JG6	*fabG*	3-oxoacyl-(Acyl-carrier-protein) reductase	+	+
29	Q81JH1	*yidC2*	Membrane protein insertase YidC 2	+	+
30	Q81JH3	*mnmG*	tRNA uridine 5-carboxymethylaminomethyl modification enzyme MnmG	+	+
31	Q81JH4	*rsmG*	Ribosomal RNA small subunit methyltransferase G	-	+
32	Q81JI1	*ychF*	GTP-binding protein YchF	+	+
33	Q81JI3	*ssb*	Single-stranded DNA-binding protein	+	+
34	Q81JI9	*purA*	Adenylosuccinate synthetase	+	+
35	Q81JJ0	*yycF*	DNA-binding response regulator YycF	-	+
36	Q81JJ5	*GBAA_5710*	Serine protease	+	-
37	Q81JL7	*msrAB*	Peptide methionine sulfoxide reductase	+	+
38	Q81JM0	*GBAA_5684*	Glycosyl transferase, group 2 family protein	+	+
39	Q81JM8	*GBAA_5675*	Cytosolic long-chain acyl-CoA thioester hydrolase family protein	-	+
40	Q81JN3	*GBAA_5670*	Glycosyl transferase, group 1 family protein	+	+
41	Q81JP0	*thiD2*	Phosphomethylpyrimidine kinase	+	+
42	Q81JR0	*gerQ*	Spore coat protein GerQ	+	+
43	Q81JR1	*cwlJ2*	Cell wall hydrolase	+	+
44	Q81JR3	*BA_5637*	UPF0447 protein BA_5637/GBAA_5637/BAS5239	+	+
45	Q81JR4	*pta*	Phosphate acetyltransferase	+	+
46	Q81JT0	*speE1*	Spermidine synthase 1	+	+
47	Q81JT1	*speB*	Agmatinase	+	+
48	Q81JT7	*argS1*	Arginine--tRNA ligase 1	+	+

49	Q81JU4	*maP3*	Methionine aminopeptidase	-	+
50	Q81JV5	*GBAA_5589*	Acetyl-CoA acetyltransferase	+	+
51	Q81JV6	*GBAA_5588*	3-hydroxyacyl-CoA dehydrogenase	+	+
52	Q81JV7	*GBAA_5587*	Acyl-CoA dehydrogenase	-	+
53	Q81JV8	*GBAA_5586*	Acyl-CoA dehydrogenase	+	+
54	Q81JW0	*rpoE*	Probable DNA-directed RNA polymerase subunit delta	+	+
55	Q81JW1	*pyrG*	CTP synthase	+	+
56	Q81JW4	*fba2*	Fructose-bisphosphate aldolase, class II	+	+
57	Q81JW5	*murA2*	UDP-N-acetylglucosamine 1-carboxyvinyltransferase 2	+	-
58	Q81JW8	*rho*	Transcription termination factor Rho	+	+
59	Q81JX1	*prfA*	Peptide chain release factor 1	+	+
60	Q81JX8	*GBAA_5565*	Putative uncharacterized protein	+	-
61	Q81JY0	*crr*	Glucose-specific phosphotransferase enzyme IIA component	+	+
62	Q81JY4	*glyA*	Serine hydroxymethyltransferase	+	+
63	Q81JY5	*upp*	Uracil phosphoribosyltransferase	+	+
64	Q81JZ1	*atpF*	ATP synthase subunit b	+	+
65	Q81JZ2	*atpH*	ATP synthase subunit delta	+	+
66	Q81JZ3	*atpA*	ATP synthase subunit alpha	+	+
67	Q81JZ4	*atpG*	ATP synthase gamma chain	+	+
68	Q81JZ5	*atpD*	ATP synthase subunit beta	+	+
69	Q81K13	*murA1*	UDP-N-acetylglucosamine 1-carboxyvinyltransferase 1	+	+
70	Q81K21	*mbl*	Mbl protein	+	+
71	Q81K33	*tagU*	Transcriptional regulator LytR	+	-
72	Q81K34	*galE1*	UDP-glucose 4-epimerase	+	+
73	Q81K66	*sodC*	Superoxide dismutase [Cu-Zn]	+	+
74	Q81K67	*GBAA_5138*	Aminotransferase, class I/II	+	+
75	Q81K71	*yugG*	Transcriptional regulator, AsnC family	-	+
76	Q81K75	*pgi*	Glucose-6-phosphate isomerase	+	+
77	Q81K89	*BA_5116*	Putative uncharacterized protein	+	+
78	Q81K96	*menB*	Naphthoate synthase	+	+
79	Q81KB4	*GBAA_5087*	DNA-binding response regulator	-	+
80	Q81KC7	*hpt2*	Hypoxanthine phosphoribosyltransferase	+	+
81	Q81KD9	*GBAA_5061*	Putative uncharacterized protein	+	-
82	Q81KE1	*GBAA_5059*	Putative uncharacterized protein	+	-
83	Q81KI0	*metK*	S-adenosylmethionine synthase	+	+
84	Q81KK6	*leuS*	Leucine--tRNA ligase	+	+
85	Q81KM8	*gdH*	Glucose 1-dehydrogenase	+	+
86	Q81KN9	*GBAA_4955*	2'-5' RNA ligase family protein, putative	-	+
87	Q81KP6	*GBAA_4947*	Peptidase, M42 family	+	+
88	Q81KQ1	*GBAA_4939*	Putative uncharacterized protein	+	+
89	Q81KQ2	*murC*	UDP-N-acetylmuramate--L-alanine ligase	+	+
90	Q81KQ3	*GBAA_4937*	Putative ribosomal-protein-serine acetyltransferase	-	+
91	Q81KQ7	*GBAA_4933*	Aminopeptidase, putative	+	+
92	Q81KR1	*ccpA*	Catabolite control protein A	+	+
93	Q81KS9	*tyrS1*	Tyrosine--tRNA ligase 1	+	+
94	Q81KT2	*rpsD*	30S ribosomal protein S4	+	+
95	Q81KU0	*thiI*	Probable tRNA sulfurtransferase	+	+
96	Q81KU4	*GBAA_4894*	Putative uncharacterized protein	+	-
97	Q81KU5	*nadK2*	Probable inorganic polyphosphate/ATP-NAD kinase 2	+	+
98	Q81KU7	*GBAA_4891*	Putative uncharacterized protein	+	+
99	Q81KU8	*tpx*	Probable thiol peroxidase	+	+
100	Q81KV0	*ackA*	Acetate kinase	+	+
101	Q81KV3	*GBAA_4885*	Putative uncharacterized protein	+	+

102	Q81KW2	*BA_4875*	Universal stress family protein	+	+
103	Q81KX5	*ykvY*	Proline dipeptidase	+	+
104	Q81KX6	*BA_4860*	UPF0173 metal-dependent hydrolase BA_4860/GBAA_4860/BAS4507	-	+
105	Q81KX8	*GBAA_4858*	Thioesterase family protein	-	+
106	Q81KY2	*GBAA_4852*	DHH subfamily 1 protein	+	+
107	Q81KY6	*BA_4848*	Malate dehydrogenase, putative	-	+
108	Q81KY8	*accD*	Acetyl-coenzyme A carboxylase carboxyl transferase subunit beta	-	+
109	Q81KZ0	*pfkA*	6-phosphofructokinase	+	+
110	Q81KZ1	*pyk*	Pyruvate kinase	+	+
111	Q81KZ6	*citC*	Isocitrate dehydrogenase [NADP]	+	+
112	Q81L03	*polA*	DNA polymerase	+	+
113	Q81L14	*thrS2*	Threonine--tRNA ligase	+	+
114	Q81L15	*infC*	Translation initiation factor IF-3	+	+
115	Q81L16	*rpmI*	50S ribosomal protein L35	+	+
116	Q81L17	*rplT*	50S ribosomal protein L20	+	+
117	Q81L18	*GBAA_4816*	Putative uncharacterized protein	+	+
118	Q81L19	*BA_4815*	Peptidase, M42 family	+	+
119	Q81L29	*BA_4805*	RNA methyltransferase, TrmH family	+	+
120	Q81L30	*pheS*	Phenylalanine--tRNA ligase alpha subunit	+	+
121	Q81L31	*pheT*	Phenylalanine--tRNA ligase beta subunit	+	+
122	Q81L32	*asnS*	Asparagine--tRNA ligase	+	+
123	Q81L39	*GBAA_4795*	PHP domain protein	+	+
124	Q81L40	*mutS2*	MutS2 protein	+	+
125	Q81L52	*GBAA_4780*	Putative uncharacterized protein	+	-
126	Q81L65	*fpuA*	Iron compound ABC transporter, iron compound-binding protein	+	-
127	Q81L70	*GBAA_4761*	Enoyl-CoA hydratase/isomerase family protein	+	+
128	Q81L77	*sdhA*	Succinate dehydrogenase, flavoprotein subunit	+	-
129	Q81L79	*GBAA_4751*	4-hydroxybenzoyl-CoA thioesterase, putative	-	+
130	Q81L82	*GBAA_4746*	5'-nucleotidase, lipoprotein e(P4) family	+	-
131	Q81LA9	*rph*	Ribonuclease PH	+	+
132	Q81LB0	*BA_4714*	Non-canonical purine NTP pyrophosphatase	+	+
133	Q81LB1	*GBAA_4713*	Phosphoesterase, putative	+	+
134	Q81LB4	*GBAA_4710*	Putative uncharacterized protein	+	+
135	Q81LB9	*clpX*	ATP-dependent Clp protease ATP-binding subunit ClpX	+	+
136	Q81LC1	*loN*	Lon protease	+	+
137	Q81LC3	*GBAA_4700*	Organic hydroperoxide resistance protein	+	-
138	Q81LC9	*hemB*	Delta-aminolevulinic acid dehydratase	+	+
139	Q81LD0	*hemL2*	Glutamate-1-semialdehyde 2,1-aminomutase 2	+	+
140	Q81LD3	*valS*	Valine--tRNA ligase	+	+
141	Q81LD6	*maf*	Septum formation protein Maf	-	+
142	Q81LD8	*mreB*	Rod shape-determining protein MreB	+	+
143	Q81LE6	*rplU*	50S ribosomal protein L21	+	+
144	Q81LE8	*rpmA*	50S ribosomal protein L27	+	+
145	Q81LF0	*obg*	GTPase obg	+	+
146	Q81LH2	*tgt*	Queuine tRNA-ribosyltransferase	+	+
147	Q81LH8	*secDF*	Protein-export membrane protein SecDF	+	-
148	Q81LI1	*apt*	Adenine phosphoribosyltransferase	+	+
149	Q81LI2	*relA*	GTP diphosphokinase	+	+
150	Q81LI6	*hisS-2*	Histidine--tRNA ligase 2	+	+
151	Q81LI7	*aspS*	Aspartate--tRNA ligase	+	+
152	Q81LI8	*GBAA_4630*	HesA/moeB/thiF family protein	+	+
153	Q81LJ2	*GBAA_4626*	Aminotransferase, class V	+	+

154	Q81LK0	*alaS*	Alanine--tRNA ligase	+	+
155	Q81LL4	*mtnN*	5'-methylthioadenosine/S-adenosylhomocysteine nucleosidase	+	+
156	Q81LL6	*GBAA_4600*	Cys/Met metabolism PLP-dependent enzyme	+	+
157	Q81LM6	*GBAA_4590*	DNA-binding protein	-	+
158	Q81LP7	*psd*	Phosphatidylserine decarboxylase proenzyme	+	+
159	Q81LP9	*GBAA_4563*	Hydrolase, HAD subfamily IIIA	-	+
160	Q81LQ0	*GBAA_4562*	GTPase family protein	+	+
161	Q81LQ6	*rsfS*	Iojap-like ribosome-associated protein	+	+
162	Q81LR5	*gpr*	Germination protease	+	+
163	Q81LR7	*lepA*	Elongation factor 4	+	+
164	Q81LS2	*dnaK*	Chaperone protein DnaK	+	+
165	Q81LS3	*dnaJ*	Chaperone protein DnaJ	+	+
166	Q81LS4	*prmA*	Ribosomal protein L11 methyltransferase	+	+
167	Q81LS5	*rsmE*	Ribosomal RNA small subunit methyltransferase E	-	+
168	Q81LT6	*cdd2*	Cytidine deaminase	+	+
169	Q81LT7	*era*	GTPase Era	+	+
170	Q81LU0	*GBAA_4521*	CBS domain protein	-	+
171	Q81LU1	*BA_4520*	Putative pyruvate, phosphate dikinase regulatory protein	+	+
172	Q81LU5	*sigA*	RNA polymerase sigma factor	+	+
173	Q81LU6	*cccA*	Cytochrome c-550	+	+
174	Q81LV0	*cshB*	ATP-dependent RNA helicase, DEAD/DEAH box family	+	+
175	Q81LV1	*nfo*	Probable endonuclease 4	-	+
176	Q81LW0	*sodA1*	Superoxide dismutase [Mn] 1	+	+
177	Q81LX2	*glcK*	Glucokinase	+	+
178	Q81M04	*GBAA_4451*	Putative uncharacterized protein	+	-
179	Q81M06	*gcvT*	Aminomethyltransferase	-	+
180	Q81M07	*gcvPA*	Probable glycine dehydrogenase [decarboxylating] subunit 1	+	+
181	Q81M08	*gcvPB*	Probable glycine dehydrogenase [decarboxylating] subunit 2	+	+
182	Q81M21	*BA_4434*	Transcriptional regulator, TetR family	-	+
183	Q81M23	*GBAA_4432*	Rhodanese-like domain protein	+	+
184	Q81M33	*pepQ1*	Proline dipeptidase	+	+
185	Q81M50	*folD*	Bifunctional protein FolD	+	-
186	Q81M65	*yqiS*	Phosphate butyryltransferase	+	+
187	Q81M66	*GBAA_4387*	Leucine dehydrogenase	+	+
188	Q81M68	*bfmbC*	Dihydrolipoyl dehydrogenase	+	+
189	Q81M69	*bfmbAa*	3-methyl-2-oxobutanoate dehydrogenase, alpha subunit	+	+
190	Q81M70	*bfmbAb*	3-methyl-2-oxobutanoate dehydrogenase, beta subunit	+	+
191	Q81M71	*bfmbB*	Dihydrolipoamide acetyltransferase	+	+
192	Q81M74	*BA_4378*	UPF0403 protein BA_4378/GBAA_4378/BAS4061	+	+
193	Q81M84	*GBAA_4368*	Peptidase T	+	+
194	Q81MB5	*ribH*	6,7-dimethyl-8-ribityllumazine synthase	-	+
195	Q81MD3	*GBAA_4316*	MutT/nudix family protein	-	+
196	Q81MD4	*GBAA_4315*	Acetyltransferase, GNAT family	+	+
197	Q81MD8	*xerD*	Integrase/recombinase XerD	-	+
198	Q81MD9	*BA_4310*	Putative lipoprotein	+	+
199	Q81ME0	*deoB*	Phosphopentomutase	+	+
200	Q81ME1	*GBAA_4308*	Purine nucleoside phosphorylase	+	+
201	Q81ME2	*pyn2*	Pyrimidine-nucleoside phosphorylase	+	+
202	Q81MF3	*spoIIAA*	Anti-sigma F factor antagonist	+	+
203	Q81MG1	*GBAA_4288*	Stage V sporulation protein AD	+	+
204	Q81MG2	*spoVAF*	Stage V sporulation protein AF	+	-
205	Q81MG5	*GBAA_4283*	Peptidyl-prolyl cis-trans isomerase	-	+
206	Q81MH4	*nagA*	N-acetylglucosamine-6-phosphate deacetylase	+	+

207	Q81MH5	*nagB*	Glucosamine-6-phosphate deaminase	-	+
208	Q81MH6	*phnF*	Transcriptional regulator, GntR family	+	-
209	Q81MH9	*ptsG*	PTS system, glucose-specific IIABC component	+	-
210	Q81MI1	*ptsI*	Phosphoenolpyruvate-protein phosphotransferase	+	+
211	Q81MI2	*cot*	Spore coat protein alphaha	+	+
212	Q81MJ8	*GBAA_4249*	Oxidoreductase, short-chain dehydrogenase/reductase family	+	-
213	Q81MK7	*GBAA_4240*	Acetyl-CoA acetyltransferase	+	+
214	Q81ML7	*GBAA_4230*	Alpha-amylase	+	+
215	Q81ML8	*GBAA_4229*	Maltosaccharide ABC transporter, maltosaccharide-binding protein	+	+
216	Q81MM2	*GBAA_4225*	Aminotransferase, class I/II	-	+
217	Q81MN8	*GBAA_4209*	Ppx/GppA phosphatase family protein	-	+
218	Q81MP2	*GBAA_4204*	Oxidoreductase, short chain dehydrogenase/reductase family	+	+
219	Q81MQ2	*dapH*	2,3,4,5-tetrahydropyridine-2,6-dicarboxylate N-acetyltransferase	+	+
220	Q81MQ5	*GBAA_4191*	Potassium uptake protein, TrkA family	+	+
221	Q81MQ6	*rnj*	RNA-metabolising metallo-beta-lactamase family protein	+	+
222	Q81MQ8	*GBAA_4188*	Hydrolase, haloacid dehalogenase-like family	-	+
223	Q81MR1	*pdhA*	Pyruvate dehydrogenase complex E1 component, alpha subunit	+	+
224	Q81MR2	*pdhB*	Pyruvate dehydrogenase complex E1 component, beta subunit	+	+
225	Q81MR3	*pdhC*	Pyruvate dehydrogenase complex E2 component, dihydrolipoamide acetyltransferase	+	+
226	Q81MR4	*pdhD*	Dihydrolipoyl dehydrogenase	+	+
227	Q81MS8	*typA*	GTP-binding protein TypA	+	+
228	Q81MT6	*pyc*	Pyruvate carboxylase	+	+
229	Q81MT9	*ctaC*	Cytochrome c oxidase subunit 2	+	-
230	Q81MX0	*GBAA_3450*	Glyoxalase family protein	-	+
231	Q81MX4	*GBAA_3446*	Oxidoreductase, aldo/keto reductase family	+	+
232	Q81MY6	*zwf*	Glucose-6-phosphate 1-dehydrogenase	+	+
233	Q81MY7	*tkt1*	Transketolase	+	+
234	Q81MY8	*GBAA_3431*	6-phosphogluconate dehydrogenase, decarboxylating	+	+
235	Q81MY9	*tal2*	Probable transaldolase 2	+	+
236	Q81MZ1	*gntK*	Gluconate kinase	-	+
237	Q81MZ2	*GBAA_3427*	Putative uncharacterized protein	+	+
238	Q81N35	*pykA1*	Pyruvate kinase	+	+
239	Q81N37	*GBAA_3380*	NAD(P)H-flavin oxidoreductase	+	+
240	Q81N95	*GBAA_3320*	D-3-phosphoglycerate dehydrogenase, putative	+	+
241	Q81NH4	*cypD*	Bifunctional P-450:NADPH-P450 reductase 1	+	+
242	Q81NM4	*GBAA_3164*	Catalase	+	+
243	Q81NP6	*GBAA_3134*	Catalase, Mn-containing	+	+
244	Q81NP8	*GBAA_3131*	Alcohol dehydrogenase, zinc-containing	+	+
245	Q81NQ0	*GBAA_3129*	Putative uncharacterized protein	+	+
246	Q81NQ1	*GBAA_3128*	Putative uncharacterized protein	+	-
247	Q81NX4	*GBAA_3048*	ABC transporter, ATP-binding protein	+	+
248	Q81P56	*GBAA_2961*	Putative uncharacterized protein	+	+
249	Q81P59	*GBAA_2958*	Chorismate mutase/phospho-2-dehydro-3-deoxyheptonate aldolase	+	+
250	Q81P64	*aroA*	3-phosphoshikimate 1-carboxyvinyltransferase	+	+
251	Q81P66	*GBAA_2951*	Transcriptional regulator, TetR family	-	+
252	Q81P74	*GBAA_2942*	Lipoprotein, putative	+	-
253	Q81PC5	*BA_2886*	Putative uncharacterized protein	-	+
254	Q81PC7	*GBAA_2883*	Lipoprotein, putative	+	-

255	Q81PG5	*GBAA_2841*	Putative uncharacterized protein	+	-
256	Q81PH9	*ppaC*	Probable manganese-dependent inorganic pyrophosphatase	+	+
257	Q81PL5	*GBAA_2787*	Glycine betaine/L-proline ABC transporter, glycine betaine/L-proline-binding protein, putative	+	+
258	Q81PL6	*proV2*	Glycine betaine/L-proline ABC transporter, ATP-binding protein	+	+
259	Q81PQ3	*sleB*	Spore cortex-lytic enzyme prepeptide	+	+
260	Q81PQ4	*ypeB*	Germination protein YpeB	+	-
261	Q81PQ5	*GBAA_2746*	Lipoprotein, putative	+	-
262	Q81PU1	*GBAA_2705*	Endo/excinuclease amino terminal domain protein	+	+
263	Q81QC9	*pepD*	Aminoacyl-histidine dipeptidase	-	+
264	Q81QF0	*GBAA_2475*	ATP-dependent RNA helicase, DEAD/DEAH box family	+	+
265	Q81QF6	*tdcB*	Threonine ammonia-lyase, catabolic	+	-
266	Q81QR5	*iolA1*	Methylmalonate semialdehyde dehydrogenase [acylating] 1	+	+
267	Q81QR8	*prpB*	Carboxyvinyl-carboxyphosphonate phosphorylmutase	+	+
268	Q81QS3	*GBAA_2345*	Penicillin-binding protein 1A	+	-
269	Q81QT5	*GBAA_2332*	Putative uncharacterized protein	+	+
270	Q81QW5	*kamA*	L-lysine 2,3-aminomutase	+	+
271	Q81QW7	*GBAA_2298*	Acetyltransferase, GNAT family	+	+
272	Q81QW8	*GBAA_2297*	Peptidase, M20/M25/M40 family	+	-
273	Q81QX6	*GBAA_2289*	Aldehyde dehydrogenase family protein	+	+
274	Q81R09	*asnO3*	Asparagine synthetase	+	+
275	Q81R11	*GBAA_2249*	SCO1/SenC family lipoprotein	+	-
276	Q81R22	*dfrA*	Dihydrofolate reductase	-	+
277	Q81R75	*ileS2*	Isoleucine--tRNA ligase 2	+	+
278	Q81R83	*BA_2173*	UPF0403 protein BA_2173/GBAA_2173/BAS2019	-	+
279	Q81RD2	*GBAA_2117*	Metallo-beta-lactamase family protein	+	+
280	Q81RE0	*GBAA_2109*	ATP-dependent RNA helicase, DEAD/DEAH box family	+	+
281	Q81RE7	*GBAA_2101*	Putative uncharacterized protein	+	+
282	Q81RG8	*dal2*	Alanine racemase	-	+
283	Q81RK9	*GBAA_2035*	Adhesion lipoprotein	+	-
284	Q81RM3	*GBAA_2019*	Acetyltransferase, GNAT family	+	+
285	Q81RP3	*nadE*	NH(3)-dependent NAD(+) synthetase	+	+
286	Q81RT0	*yoxD*	Oxidoreductase, short-chain dehydrogenase/reductase family	-	+
287	Q81RT6	*BA_1951*	Putative uncharacterized protein	+	+
288	Q81RW4	*ldh1*	L-lactate dehydrogenase 1	+	+
289	Q81RX7	*azoR2*	FMN-dependent NADH-azoreductase 2	+	+
290	Q81S64	*asnA*	Aspartate--ammonia ligase	-	+
291	Q81SK8	*rnj*	Metallo-beta-lactamase family protein	-	+
292	Q81SM2	*GBAA_1626*	Conserved domain protein	-	+
293	Q81SR2	*GBAA_1584*	Putative uncharacterized protein	+	+
294	Q81SS7	*aspB*	Aspartate aminotransferase	+	+
295	Q81ST0	*dinG*	DnaQ family exonuclease/DinG family helicase, putative	-	+
296	Q81ST5	*birA*	Biotin operon repressor/biotin--[acetyl-CoA-carboxylase] ligase	-	+
297	Q81ST6	*cca*	CCA-adding enzyme	-	+
298	Q81ST7	*bshA*	Glycosyl transferase, group 1 family protein	-	+
299	Q81SU0	*dapB*	Dihydrodipicolinate reductase	+	+
300	Q81SV0	*qcrB*	Menaquinol-cytochrome c reductase, cytochrome b subunit	+	-
301	Q81SV1	*qcrA*	Menaquinol-cytochrome c reductase, iron-sulfur subunit	+	+
302	Q81SV8	*ndk*	Nucleoside diphosphate kinase	+	+
303	Q81SW2	*folE*	GTP cyclohydrolase 1	+	+
304	Q81SW9	*der*	GTPase Der	+	+

305	Q81SX1	*GBAA_1523*	Putative uncharacterized protein	+	+
306	Q81SX5	*rpsA*	Ribosomal protein S1	-	+
307	Q81SX8	*ansA*	L-asparaginase	+	+
308	Q81SY3	*gudB*	Glutamate dehydrogenase	+	+
309	Q81SZ0	*fer*	Ferredoxin	+	+
310	Q81SZ6	*resD*	DNA-binding response regulator ResD	+	+
311	Q81SZ9	*resA*	Thiol-disulfide oxidoreductase ResA	+	-
312	Q81T03	*GBAA_1489*	Superoxide dismutase	+	+
313	Q81T09	*deoD*	Purine nucleoside phosphorylase DeoD-type	+	+
314	Q81T17	*GBAA_1474*	Penicillin-binding protein	+	-
315	Q81T18	*GBAA_1472*	Putative uncharacterized protein	+	+
316	Q81T23	*hmp*	Flavohemoprotein	+	+
317	Q81T61	*hisB*	Imidazoleglycerol-phosphate dehydratase	-	+
318	Q81T67	*leuB*	3-isopropylmalate dehydrogenase	-	+
319	Q81T77	*BA_1410*	Putative uncharacterized protein	+	+
320	Q81T97	*dltA*	D-alanine--poly(phosphoribitol) ligase subunit 1	+	+
321	Q81TB4	*nrdF*	Ribonucleoside-diphosphate reductase subunit beta	+	+
322	Q81TB6	*nrdE*	Ribonucleoside-diphosphate reductase	+	+
323	Q81TD1	*GBAA_1353*	Oligoendopeptidase F, putative	+	+
324	Q81TD2	*GBAA_1352*	Transcriptional regulator, MarR family	-	+
325	Q81TH5	*potD*	Spermidine/putrescine ABC transporter, spermidine/putrescine-binding protein	+	+
326	Q81TH8	*potA*	Spermidine/putrescine import ATP-binding protein PotA	+	-
327	Q81TK1	*odhA*	2-oxoglutarate dehydrogenase E1 component	-	+
328	Q81TK2	*odhB*	2-oxoglutarate dehydrogenase, E2 component, dihydrolipoamide succinyltransferase	+	+
329	Q81TK8	*GBAA_1263*	Pyridine nucleotide-disulfide oxidoreductase, class I	+	+
330	Q81TN0	*BA_1241*	UPF0477 protein BA_1241/GBAA_1241/BAS1148	+	+
331	Q81TN4	*bxpB*	Exosporium protein F	+	+
332	Q81TN7	*cotZ1*	Exosporium protein Y	+	+
333	Q81TQ0	*prpE*	Bis(5'-nucleosyl)-tetraphosphatase PrpE [asymmetrical]	+	+
334	Q81TR0	*pepF1*	Oligoendopeptidase F	+	+
335	Q81TS0	*GBAA_1195*	Oligopeptide ABC transporter, ATP-binding protein	+	+
336	Q81TS1	*GBAA_1194*	Oligopeptide ABC transporter, ATP-binding protein	+	-
337	Q81TS2	*GBAA_1193*	Oligopeptide ABC transporter, permease protein	+	-
338	Q81TS3	*GBAA_1192*	Oligopeptide ABC transporter, permease protein	+	-
339	Q81TT4	*clpB*	Chaperone protein ClpB	+	+
340	Q81TU3	*GBAA_1167*	Putative uncharacterized protein	+	+
341	Q81TV3	*rocD*	Ornithine aminotransferase	-	+
342	Q81U05	*GBAA_1089*	Lipoate-protein ligase A, putative	+	+
343	Q81U14	*GBAA_1080*	Transcriptional regulator, TetR family	-	+
344	Q81U40	*ecsA*	ABC transporter, ATP-binding protein EcsA	+	-
345	Q81U45	*prsA1*	Foldase protein PrsA 1	+	+
346	Q81U46	*GBAA_1040*	Helicase, UvrD/Rep family	+	+
347	Q81U58	*glpK*	Glycerol kinase	+	+
348	Q81U68	*GBAA_1016*	Glyoxylase family protein	+	+
349	Q81U69	*GBAA_1015*	Glyoxalase family protein	+	+
350	Q81U72	*yhaM*	3'-5' exoribonuclease YhaM	+	+
351	Q81UH5	*GBAA_0897*	Peptidase, family M20/M25/M40 protein	+	+
352	Q81UL3	*GBAA_0855*	Amino acid ABC transporter, amino acid-binding protein	+	+
353	Q81UP1	*murQ*	N-acetylmuramic acid 6-phosphate etherase	+	+
354	Q81UQ5	*ku*	Probable DNA repair protein BA_0808	+	+
355	Q81UV8	*GBAA_0748*	Oxidoreductase, short chain dehydrogenase/reductase family	+	+
356	Q81V33	*tal1*	Probable transaldolase 1	+	+

357	Q81V34	*rbsB*	Ribose ABC transporter, ribose-binding protein	+	-
358	Q81V38	*rbsK*	Ribokinase	+	+
359	Q81V45	*GBAA_0656*	Oligopeptide ABC transporter, oligopeptide-binding protein	+	+
360	Q81V68	*treC*	Alpha,alpha-phosphotrehalase	+	+
361	Q81V80	*BA_0620*	Putative pyridoxal phosphate-dependent acyltransferase	+	-
362	Q81V85	*GBAA_0615*	Iron compound ABC transporter, iron compound-binding protein	+	+
363	Q81V90	*aspA1*	Fumarate hydratase class II	+	+
364	Q81V91	*GBAA_0608*	CBS domain protein	+	+
365	Q81V97	*GBAA_0602*	Putative lipoprotein	+	+
366	Q81VA2	*GBAA_0596*	Nicotinate phosphoribosyltransferase	+	+
367	Q81VA3	*GBAA_0595*	Heavy metal-transporting ATPase	+	-
368	Q81VB4	*GBAA_0583*	Acetyltransferase, GNAT family	+	+
369	Q81VE0	*guaA*	GMP synthase [glutamine-hydrolyzing]	+	+
370	Q81VE1	*groL*	60 kDa chaperonin	+	+
371	Q81VE5	*rex*	Redox-sensing transcriptional repressor rex	+	-
372	Q81VE9	*GBAA_0259*	Putative uncharacterized protein	+	+
373	Q81VF0	*GBAA_0258*	ATPase, YjeE family	-	+
374	Q81VF3	*GBAA_0255*	S1 RNA binding domain protein	+	+
375	Q81VF6	*dal1*	Alanine racemase	+	+
376	Q81VG0	*cshA*	DEAD-box ATP-dependent RNA helicase CshA	+	+
377	Q81VK1	*GBAA_0196*	Oxidoreductase, aldo/keto reductase family	+	+
378	Q81VK7	*GBAA_0190*	Lipoprotein, putative	+	+
379	Q81VN1	*yqjI*	6-phosphogluconate dehydrogenase, decarboxylating	+	+
380	Q81VN5	*glmS*	Glutamine--fructose-6-phosphate aminotransferase [isomerizing]	+	+
381	Q81VN7	*glmM*	Phosphoglucosamine mutase	+	+
382	Q81VP0	*rocF*	Arginase	+	+
383	Q81VP4	*gerD*	Spore germination protein GerD	+	-
384	Q81VP8	*rpsI*	30S ribosomal protein S9	+	+
385	Q81VP9	*rplM*	50S ribosomal protein L13	+	+
386	Q81VQ3	*rplQ*	50S ribosomal protein L17	+	+
387	Q81VQ4	*rpoA*	DNA-directed RNA polymerase subunit alpha	+	+
388	Q81VQ5	*rpsK*	30S ribosomal protein S11	+	+
389	Q81VQ9	*adk*	Adenylate kinase	-	+
390	Q81VR0	*secY1*	Protein translocase subunit SecY	+	-
391	Q81VR1	*rplO*	50S ribosomal protein L15	+	+
392	Q81VR3	*rpsE*	30S ribosomal protein S5	+	+
393	Q81VR4	*rplR*	50S ribosomal protein L18	+	+
394	Q81VR5	*rplF*	50S ribosomal protein L6	+	+
395	Q81VR6	*rpsH*	30S ribosomal protein S8	+	+
396	Q81VR8	*rplE*	50S ribosomal protein L5	+	+
397	Q81VR9	*rplX*	50S ribosomal protein L24	+	+
398	Q81VS0	*rplN*	50S ribosomal protein L14	+	+
399	Q81VS1	*rpsQ*	30S ribosomal protein S17	+	+
400	Q81VS3	*rplP*	50S ribosomal protein L16	+	+
401	Q81VS4	*rpsC*	30S ribosomal protein S3	+	+
402	Q81VS5	*rplV*	50S ribosomal protein L22	+	+
403	Q81VS7	*rplB*	50S ribosomal protein L2	+	+
404	Q81VS9	*rplD*	50S ribosomal protein L4	+	+
405	Q81VT0	*rplC*	50S ribosomal protein L3	+	+
406	Q81VT2	*tuf*	Elongation factor Tu	+	+
407	Q81VT3	*fusA*	Elongation factor G	+	+
408	Q81VT4	*rpsG*	30S ribosomal protein S7	+	+

409	Q81VT5	*rpsL*	30S ribosomal protein S12	+	+
410	Q81VT8	*rpoB*	DNA-directed RNA polymerase subunit beta	+	+
411	Q81VT9	*GBAA_0101*	YbxB protein	+	+
412	Q81VU1	*rplJ*	50S ribosomal protein L10	+	+
413	Q81VU2	*rplA*	50S ribosomal protein L1	+	+
414	Q81VU3	*rplK*	50S ribosomal protein L11	+	+
415	Q81VU9	*GBAA_0091*	RNA methyltransferase, TrmH family, group 3	+	+
416	Q81VV1	*cysS*	Cysteine--tRNA ligase	+	+
417	Q81VV3	*gltX*	Glutamate--tRNA ligase	+	+
418	Q81VV5	*ispD*	2-C-methyl-D-erythritol 4-phosphate cytidylyltransferase	-	+
419	Q81VV7	*disA*	DNA integrity scanning protein DisA	+	+
420	Q81VV8	*radA*	DNA repair protein radA	-	+
421	Q81VV9	*GBAA_0080*	Negative regulator of genetic competence ClpC/MecB	+	+
422	Q81VW0	*mcsB*	Putative ATP:guanido phosphotransferase	+	+
423	Q81VW3	*lysS*	Lysine--tRNA ligase	+	+
424	Q81VX2	*cysK1*	Cysteine synthase	+	+
425	Q81VX3	*hslO*	33 kDa chaperonin	+	+
426	Q81VX4	*coaX*	Type III pantothenate kinase	-	+
427	Q81VX5	*ftsH*	ATP-dependent zinc metalloprotease FtsH	+	+
428	Q81VX6	*hpt*	Hypoxanthine phosphoribosyltransferase	+	+
429	Q81VY4	*GBAA_0055*	Tetrapyrrole methylase family protein/MazG family protein	+	+
430	Q81VY6	*spoVT*	Stage V sporulation protein T	+	+
431	Q81VY7	*mfd*	Transcription-repair coupling factor	+	+
432	Q81VY9	*pth*	Peptidyl-tRNA hydrolase	+	+
433	Q81VZ0	*prs*	Ribose-phosphate pyrophosphokinase	+	+
434	Q81VZ1	*glmU*	Bifunctional protein GlmU	-	+
435	Q81VZ5	*purR*	Pur operon repressor	+	+
436	Q81VZ6	*ispE*	4-diphosphocytidyl-2-C-methyl-D-erythritol kinase	-	+
437	Q81VZ8	*GBAA_0041*	Veg protein	+	+
438	Q81W00	*rsmA*	Ribosomal RNA small subunit methyltransferase A	+	+
439	Q81W03	*metG1*	Methionine--tRNA ligase 1	+	+
440	Q81W11	*tmk*	Thymidylate kinase	+	+
441	Q81W23	*GBAA_0014*	Deoxynucleoside kinase family protein	-	+
442	Q81W24	*GBAA_0013*	Putative uncharacterized protein	-	+
443	Q81W25	*serS*	Serine--tRNA ligase	+	+
444	Q81W27	*pdxS*	Pyridoxal biosynthesis lyase PdxS	+	+
445	Q81W29	*guaB*	Inosine-5'-monophosphate dehydrogenase	+	+
446	Q81W30	*gyrA*	DNA gyrase subunit A	+	+
447	Q81W34	*dnaN1*	DNA polymerase III subunit beta	+	+
448	Q81W35	*dnaA*	Chromosomal replication initiator protein DnaA	+	+
449	Q81W42	*GBAA_4140*	Methyltransferase, putative	-	+
450	Q81W43	*coaD*	Phosphopantetheine adenylyltransferase	-	+
451	Q81W46	*GBAA_4136*	PDZ domain protein	+	-
452	Q81W47	*BA_4135*	UPF0348 protein BA_4135/GBAA_4135/BAS3837	+	+
453	Q81WB7	*GBAA_4063*	Putative uncharacterized protein	+	-
454	Q81WC2	*bshC*	UPF0747 protein BA_4058/GBAA_4058/BAS3770	+	+
455	Q81WC3	*rsmH*	Ribosomal RNA small subunit methyltransferase H	+	+
456	Q81WC7	*murE*	UDP-N-acetylmuramoyl-L-alanyl-D-glutamate--2,6-diaminopimelate ligase	+	+
457	Q81WD3	*ftsA*	Cell division protein ftsA	+	-
458	Q81WD6	*sigG*	RNA polymerase sigma factor	+	-
459	Q81WE4	*ileS1*	Isoleucine--tRNA ligase 1	+	+
460	Q81WE7	*pyrR*	Bifunctional protein PyrR	+	+
461	Q81WG3	*GBAA_4013*	Fibronectin/fibrinogen-binding protein, putative	+	+

462	Q81WG7	*gmk*	Guanylate kinase	+	+
463	Q81WH2	*fmt*	Methionyl-tRNA formyltransferase	+	+
464	Q81WH3	*sun*	Ribosomal RNA small subunit methyltransferase B	-	+
465	Q81WH4	*rlmN*	Probable dual-specificity RNA methyltransferase RlmN	+	+
466	Q81WH7	*rsgA*	Putative ribosome biogenesis GTPase RsgA	+	+
467	Q81WH8	*rpe*	Ribulose-phosphate 3-epimerase	-	+
468	Q81WI2	*GBAA_3994*	Phosphatase, putative	+	+
469	Q81WI5	*plsX*	Phosphate acyltransferase	+	+
470	Q81WI7	*acpP*	Acyl carrier protein	-	+
471	Q81WI8	*rnc*	Ribonuclease 3	-	+
472	Q81WJ2	*ffH*	Signal recognition particle protein	+	-
473	Q81WJ5	*rimM*	Ribosome maturation factor RimM	-	+
474	Q81WJ6	*rplS*	50S ribosomal protein L19	+	+
475	Q81WJ7	*sipS2*	Signal peptidase I	+	-
476	Q81WK0	*sucC*	Succinyl-CoA ligase [ADP-forming] subunit beta	+	+
477	Q81WK1	*sucD*	Succinyl-CoA ligase [ADP-forming] subunit alpha	+	-
478	Q81WK2	*topA*	DNA topoisomerase	+	+
479	Q81WK3	*trmFO*	Methylenetetrahydrofolate--tRNA-(uracil-5-)-methyltransferase TrmFO	+	+
480	Q81WK5	*hslV*	ATP-dependent protease subunit HslV	+	+
481	Q81WK6	*hslU*	ATP-dependent protease ATPase subunit HslU	+	+
482	Q81WK7	*codY*	GTP-sensing transcriptional pleiotropic repressor CodY	+	+
483	Q81WK8	*rpsB*	30S ribosomal protein S2	+	+
484	Q81WK9	*tsf*	Elongation factor Ts	+	+
485	Q81WL0	*pyrH*	Uridylate kinase	+	+
486	Q81WL4	*dxr2*	1-deoxy-D-xylulose 5-phosphate reductoisomerase 2	+	+
487	Q81WL5	*rasP*	Membrane-associated zinc metalloprotease, putative	+	-
488	Q81WL6	*proS1*	Proline--tRNA ligase 1	+	+
489	Q81WL9	*rimP*	Ribosome maturation factor RimP	-	+
490	Q81WM0	*nusA*	N utilization substance protein A	+	+
491	Q81WM3	*infB*	Translation initiation factor IF-2	+	+
492	Q81WM8	*pnp*	Polyribonucleotide nucleotidyltransferase	+	+
493	Q81WN0	*GBAA_3942*	Zinc protease, insulinase family	+	+
494	Q81WN5	*asd2*	Aspartate-semialdehyde dehydrogenase	+	+
495	Q81WN9	*rnj*	Metallo-beta-lactamase family protein	+	+
496	Q81WP0	*clpP*	Clp protease	+	+
497	Q81WP4	*GBAA_3927*	Lipoprotein, Bmp family	+	+
498	Q81WP6	*GBAA_3923*	Putative uncharacterized protein	+	+
499	Q81WP7	*GBAA_3922*	Zinc protease, insulinase family	+	+
500	Q81WQ1	*GBAA_3918*	Putative uncharacterized protein	+	+
501	Q81WQ4	*rny*	Ribonuclease Y	+	+
502	Q81WQ5	*GBAA_3913*	Metallophosphoesterase, MG_246/BB_0505 family	+	+
503	Q81WQ7	*GBAA_3911*	Renal dipeptidase family protein	-	+
504	Q81WQ8	*GBAA_3910*	Putative pyruvate ferredoxin oxidoreductase, alpha subunit	+	+
505	Q81WQ9	*GBAA_3909*	Putative pyruvate ferredoxin oxidoreductase, beta subunit	+	+
506	Q81WR2	*cotE*	Spore coat protein E	+	+
507	Q81WR3	*mutS*	DNA mismatch repair protein MutS	-	+
508	Q81WU4	*pepT*	Peptidase T	-	+
509	Q81WX8	*GBAA_3835*	Aluminum resistance protein	+	-
510	Q81WZ0	*cydA3*	Cytochrome d ubiquinol oxidase, subunit I	+	+
511	Q81X16	*GBAA_5433*	UDP-N-acetylglucosamine 2-epimerase	+	+
512	Q81X26	*secA1*	Protein translocase subunit SecA 1	+	+
513	Q81X47	*uvrB*	UvrABC system protein B	-	+
514	Q81X48	*uvrA*	UvrABC system protein A	+	+

515	Q81X56	*trxB*	Thioredoxin reductase	+	+
516	Q81X58	*GBAA_5385*	MutT/nudix family protein	+	+
517	Q81X59	*BA_5384*	UPF0042 nucleotide-binding protein BA_5384/GBAA_5384/BAS5004	+	+
518	Q81X63	*clpP2*	ATP-dependent Clp protease proteolytic subunit 2	+	+
519	Q81X64	*GBAA_5379*	Putative uncharacterized protein	+	+
520	Q81X67	*GBAA_5376*	Stage V sporulation protein AD	+	+
521	Q81X68	*GBAA_5375*	SpoVA family protein	+	-
522	Q81X69	*GBAA_5374*	Putative lipoprotein	-	+
523	Q81X74	*gap2*	Glyceraldehyde 3-phosphate dehydrogenase	+	+
524	Q81X75	*pgk*	Phosphoglycerate kinase	+	+
525	Q81X76	*tpiA*	Triosephosphate isomerase	+	+
526	Q81X77	*gpmI*	2,3-bisphosphoglycerate-independent phosphoglycerate mutase	+	+
527	Q81X78	*eno*	Enolase	+	+
528	Q81XA5	*estA*	Carboxylesterase	+	+
529	Q81XA6	*vacB*	Ribonuclease R	+	+
530	Q81XB0	*GBAA_5330*	Iron compound ABC transporter, iron compound-binding protein	+	-
531	Q81XC6	*tyrS2*	Tyrosine--tRNA ligase 2	+	+
532	Q81XC7	*GBAA_5313*	Pyridine nucleotide-disulphide oxidoreductase	+	+
533	Q81XD1	*GBAA_5308*	Oxidoreductase, aldo/keto reductase family	-	+
534	Q81XK0	*GBAA_5237*	Lipoprotein, putative	+	-
535	Q81XL5	*GBAA_5220*	Lipoprotein	+	-
536	Q81XL7	*sufC*	ABC transporter, ATP-binding protein	+	+
537	Q81XL8	*sufD*	FeS assembly protein SufD	+	+
538	Q81XL9	*sufS*	Cysteine desulfurase	+	+
539	Q81XM1	*sufB*	FeS assembly protein SufB	+	+
540	Q81XM8	*lipA*	Lipoyl synthase	-	+
541	Q81XN4	*GBAA_5199*	Lipoprotein, putative	+	-
542	Q81XP1	*GBAA_5192*	Phosphatase,haloacid dehalogenase family	+	-
543	Q81XS0	*BA_5160*	Ferredoxin--NADP reductase 2	+	+
544	Q81XS1	*GBAA_5159*	Pyridine nucleotide-disulphide oxidoreductase	+	+
545	Q81XS5	*pepA*	Probable cytosol aminopeptidase	+	-
546	Q81XS6	*dacB*	Putative uncharacterized protein	-	+
547	Q81XS7	*GBAA_5153*	Phosphoglucomutase/phosphomannomutase family protein	+	+
548	Q81XS8	*gtaB*	UTP--glucose-1-phosphate uridylyltransferase	+	+
549	Q81XT3	*glyQS*	Glycine--tRNA ligase	+	+
550	Q81XT6	*glnA*	Glutamine synthetase	+	+
551	Q81XW2	*GBAA_3805*	Prophage LambdaBa01, acyltransferase, putative	-	+
552	Q81Y15	*tkt2*	Transketolase	+	+
553	Q81Y17	*BA_3742*	UPF0154 protein BA_3742/GBAA_3742/BAS3468	+	+
554	Q81Y80	*acnA*	Aconitate hydratase 1	-	+
555	Q81Y89	*GBAA_3668*	Glycosyl hydrolase, family 18	+	+
556	Q81Y92	*plsY3*	Glycerol-3-phosphate acyltransferase 3	+	-
557	Q81Y99	*parC*	DNA topoisomerase IV, A subunit	-	+
558	Q81YA0	*GBAA_3655*	Oxidoreductase, Gfo/Idh/MocA family	+	+
559	Q81YI0	*BA_3567*	UPF0061 protein BA_3567/GBAA_3567/BAS3307	+	+
560	Q81YK3	*GBAA_3539*	Putative uncharacterized protein	+	+
561	Q81YL7	*GBAA_3524*	Putative uncharacterized protein	-	+
562	Q81YT5	*GBAA_0547*	Putative tRNA (cytidine(34)-2'-O)-methyltransferase	+	+
563	Q81YT8	*bdbD*	Probable disulfide bond formation protein D	+	-
564	Q81YU4	*GBAA_0537*	Transcriptional regulator, Fur family	-	+
565	Q81YV0	*hemL1*	Glutamate-1-semialdehyde 2,1-aminomutase 1	+	+
566	Q81YX6	*GBAA_0503*	Putative uncharacterized protein	-	+

567	Q81Z48	*BA_0426*	Uncharacterized RNA methyltransferase BA_0426/GBAA_0426/BAS0414	+	-
568	Q81Z55	*GBAA_0418*	General stress protein 26	+	+
569	Q81Z71	*GBAA_0401*	Tellurium resistance protein	+	+
570	Q81Z72	*GBAA_0400*	Tellurium resistance protein	+	+
571	Q81Z90	*GBAA_0382*	ABC transporter, substrate-binding protein, putative	+	-
572	Q81Z98	*GBAA_0374*	Conserved domain protein	+	-
573	Q81ZA6	*GBAA_0365*	Putative Rieske 2Fe-2S iron-sulfur protein	+	+
574	Q81ZB0	*GBAA_0361*	Putative cyclase	-	+
575	Q81ZB8	*GBAA_0351*	Iron compound ABC transporter, iron compound-binding protein	+	-
576	Q81ZC2	*mtnA1*	Methylthioribose-1-phosphate isomerase 1	-	+
577	Q81ZC4	*ahpC*	Alkyl hydroperoxide reductase, subunit C	+	+
578	Q81ZC5	*ahpF*	Alkyl hydroperoxide reductase, F subunit	+	+
579	Q81ZE0	*ampS*	Aminopeptidase AmpS	+	-
580	Q81ZE6	*GBAA_0323*	Putative uncharacterized protein	+	+
581	Q81ZE7	*gatB*	Aspartyl/glutamyl-tRNA(Asn/Gln) amidotransferase subunit B	+	+
582	Q81ZE8	*gatA*	Glutamyl-tRNA(Gln) amidotransferase subunit A	+	+
583	Q81ZF8	*rocA*	1-pyrroline-5-carboxylate dehydrogenase	+	+
584	Q81ZG1	*ligA*	DNA ligase	+	+
585	Q81ZG2	*pcrA*	ATP-dependent DNA helicase PcrA	+	+
586	Q81ZG4	*GBAA_0302*	Putative uncharacterized protein	+	+
587	Q81ZH6	*purB*	Adenylosuccinate lyase	+	+
588	Q8RPQ1	*dps1*	DNA protection during starvation protein 1	+	+
589	Q8RPQ2	*dps2*	DNA protection during starvation protein 2	+	+
590	Q9APZ2	*recA*	Protein RecA	+	+
591	Q9X315	*repX*	Plasmid replication protein RepX	+	+
592	Q9X388	*GBAA_pXO1_0199*	PXO1-131O1_0199	+	+
593	Q9X3Y6	*gyrB*	DNA gyrase subunit B	+	+

[a] Sample was detected in dormant spores.

[b] Sample was detected in germinated spores

Supplemental Table S2. All *B. subtilis* proteins identified

N	Uniprot accession	Gene name	Function	Dor[a]	Germ[b]
1	C0SP90	*ythA*	Cytochrome d ubiquinol oxidase subunit 1-like protein	+	+
2	C0SP93	*accD*	Acetyl-coenzyme A carboxylase carboxyl transferase subunit beta	-	+
3	C0SP94	*yhfQ*	Putative ABC transporter substrate-binding lipoprotein	+	+
4	C0SPB0	*ytcI*	Uncharacterized acyl--CoA ligase YtcI	+	+
5	O05235	*yugF*	Uncharacterized hydrolase yugF	-	+
6	O05239	*yugJ*	Probable NADH-dependent butanol dehydrogenase 1	+	+
7	O05240	*yugK*	Probable NADH-dependent butanol dehydrogenase 2	+	+
8	O05241	*yugS*	UPF0053 protein yugS	+	+
9	O05248	*yugP*	Putative membrane protease yugP	+	+
10	O05267	*yumB*	NADH dehydrogenase-like protein yumB	+	+
11	O05268	*yumC*	Ferredoxin--NADP reductase 2	+	+
12	O05495	*ydhD*	Putative sporulation-specific glycosylase ydhD	-	+
13	O05508	*gmuD*	6-phospho-beta-glucosidase gmuD	+	+
14	O05516	*tsaB*	Uncharacterized protein YdiC	+	+
15	O05521	*rex*	Redox-sensing transcriptional repressor rex	+	+
16	O06012	*adhB*	Uncharacterized zinc-type alcohol dehydrogenase-like protein	+	+
17	O06478	*yfmT*	Putative aldehyde dehydrogenase yfmT	+	+
18	O06491	*gatA*	Glutamyl-tRNA(Gln) amidotransferase subunit A	+	+
19	O06741	*yitF*	Putative isomerase yitF	+	+
20	O06747	*yitL*	Uncharacterized protein yitL	-	+
21	O06965	*yvcA*	Putative lipoprotein yvcA	+	-
22	O06973	*yvcJ*	UPF0042 nucleotide-binding protein yvcJ	+	+
23	O06975	*whiA*	Putative sporulation transcription regulator whiA	-	+
24	O06986	*yvdD*	LOG family protein yvdD	+	-
25	O06988	*bbmA*	Intracellular maltogenic amylase	-	+
26	O06993	*mdxK*	Uncharacterized glycosyl hydrolase yvdK	+	+
27	O06994	*malL*	Oligo-1,6-glucosidase 1	+	+
28	O07001	*yvdT*	Uncharacterized HTH-type transcriptional regulator yvdT	+	+
29	O07002	*yveA*	Aspartate-proton symporter	+	+
30	O07513	*hit*	Protein hit	+	+
31	O07533	*yhaR*	Putative enoyl-CoA hydratase/isomerase yhaR	+	+
32	O07543	*yheB*	UPF0754 membrane protein yheB	+	+
33	O07581	*yhdL*	Probable anti-sigma-M factor yhdL	+	-
34	O07584	*plsC*	1-acyl-sn-glycerol-3-phosphate acyltransferase	+	+
35	O07595	*cobB*	NAD-dependent deacetylase	+	+
36	O07603	*yhfE*	Putative aminopeptidase yhfE	+	+
37	O07607	*yhfI*	Uncharacterized protein yhfI	+	-
38	O07608	*lplJ*	Lipoate-protein ligase LplJ	+	+
39	O07609	*yhfK*	Uncharacterized sugar epimerase yhfK	+	-
40	O07615	*yhfP*	Putative quinone oxidoreductase YhfP	+	+
41	O07622	*yhfW*	Putative Rieske 2Fe-2S iron-sulfur protein yhfW	+	+
42	O07631	*typA*	GTP-binding protein TypA/BipA homolog	+	+
43	O07634	*ylaJ*	Uncharacterized lipoprotein ylaJ	+	+
44	O08394	*cypD*	Probable bifunctional P-450/NADPH-P450 reductase 1	+	+
45	O30509	*gatB*	Aspartyl/glutamyl-tRNA(Asn/Gln) amidotransferase subunit B	+	+
46	O31473	*ycgI*	Uncharacterized protein ycgI	+	+
47	O31489	*ydcI*	Uncharacterized protein ydcI	+	+
48	O31498	*ligA*	DNA ligase	+	-
49	O31502	*dagK*	Diacylglycerol kinase	-	+
50	O31533	*yetF*	UPF0702 transmembrane protein yetF	+	+

51	O31545	*yfjO*	Uncharacterized RNA methyltransferase yfjO	+	+
52	O31581	*yfhM*	AB hydrolase superfamily protein yfhM	+	+
53	O31593	*yhbJ*	Putative efflux system component yhbJ	+	-
54	O31601	*yjbC*	Putative acetyltransferase YjbC	+	-
55	O31605	*yjbG*	Oligoendopeptidase F homolog	+	+
56	O31612	*ppnKA*	Probable inorganic polyphosphate/ATP-NAD kinase 1	-	+
57	O31614	*prpE*	Bis(5'-nucleosyl)-tetraphosphatase prpE [asymmetrical]	+	+
58	O31615	*yjbQ*	Putative Na(+)/H(+) antiporter yjbQ	+	-
59	O31629	*yjcG*	UPF0477 protein yjc	+	+
60	O31630	*yjcH*	Uncharacterized protein yjcH	+	+
61	O31649	*yjdH*	Uncharacterized protein yjdH	+	-
62	O31656	*ykrK*	Uncharacterized protein ykrK	+	-
63	O31657	*htpX*	Protease HtpX homolog	+	-
64	O31689	*ykvY*	Putative dipeptidase ykvY	+	+
65	O31714	*fruK*	1-phosphofructokinase	+	+
66	O31716	*ykpA*	Uncharacterized ABC transporter ATP-binding protein YkpA	+	+
67	O31741	*trmD*	tRNA (guanine-N(1)-)-methyltransferase	-	+
68	O31742	*rplS*	50S ribosomal protein L19	+	+
69	O31743	*rbgA*	Ribosome biogenesis GTPase A	+	+
70	O31749	*pyrH*	Uridylate kinase	+	+
71	O31753	*dxr*	1-deoxy-D-xylulose 5-phosphate reductoisomerase	-	+
72	O31755	*proS*	Proline--tRNA ligase	+	+
73	O31760	*rnjB*	Ribonuclease J 2	+	+
74	O31764	*ymfF*	Probable inactive metalloprotease ymfF	+	+
75	O31766	*ymfH*	Uncharacterized zinc protease ymfH	+	+
76	O31771	*ymfM*	Uncharacterized membrane protein ymfM	+	-
77	O31774	*rny*	Ribonuclease Y	+	+
78	O31777	*kbl*	Putative 8-amino-7-oxononanoate synthase/2-amino-3-ketobutyrate coenzyme A ligase	+	+
79	O31782	*pksN*	Polyketide synthase PksN	+	-
80	O31788	*aprX*	Serine protease AprX	+	-
81	O31816	*yndM*	Uncharacterized membrane protein yndM	+	-
82	O31824	*nrnB*	Oligoribonuclease nrn	+	+
83	O31853	*yojK*	Uncharacterized UDP-glucosyltransferase yojK	+	+
84	O31854	*cdaS*	Uncharacterized protein yojJ	+	+
85	O32028	*mtnN*	5'-methylthioadenosine/S-adenosylhomocysteine nucleosidase	-	+
86	O32037	*tcdA*	Uncharacterized protein yrvM	+	+
87	O32038	*aspS*	Aspartate--tRNA ligase	+	+
88	O32039	*hisS*	Histidine--tRNA ligase	+	+
89	O32045	*yrvD*	Uncharacterized protein yrvD	+	+
90	O32047	*secDF*	Protein translocase subunit SecDF	+	+
91	O32050	*yrbG*	UPF0702 transmembrane protein yrbG	+	-
92	O32052	*yrbF*	UPF0092 membrane protein yrbF	+	+
93	O32053	*tgt*	Queuine tRNA-ribosyltransferase	+	+
94	O32054	*queA*	S-adenosylmethionine:tRNA ribosyltransferase-isomerase	+	+
95	O32076	*yuaG*	Uncharacterized protein yuaG	+	-
96	O32090	*pncB*	Nicotinate phosphoribosyltransferase	+	+
97	O32106	*pepA*	Probable cytosol aminopeptidase	+	+
98	O32117	*yutJ*	NADH dehydrogenase-like protein yutJ	+	+
99	O32125	*yutF*	Uncharacterized hydrolase yutF	+	+
100	O32128	*yutC*	Uncharacterized lipoprotein yutC	+	-
101	O32158	*yurQ*	Uncharacterized protein yurQ	+	+
102	O32162	*sufB*	FeS cluster assembly protein sufB	+	+
103	O32164	*sufS*	Probable cysteine desulfurase	+	+

104	O32165	*sufD*	FeS cluster assembly protein sufD	+	+
105	O32167	*metQ*	Methionine-binding lipoprotein metQ	+	+
106	O32169	*metN*	Methionine import ATP-binding protein MetN	-	+
107	O32210	*yvgN*	Glyoxal reductase	-	+
108	O32213	*cysI*	Sulfite reductase [NADPH] hemoprotein beta-component	+	-
109	O32218	*bdbD*	Disulfide bond formation protein D	+	-
110	O32223	*iolW*	Uncharacterized oxidoreductase yvaA	+	+
111	O32224	*azoR2*	FMN-dependent NADH-azoreductase 2	+	+
112	O32229	*yvaG*	Uncharacterized oxidoreductase yvaG	-	+
113	O32231	*rnr*	Ribonuclease R	+	+
114	O32232	*est*	Carboxylesterase	+	+
115	O32254	*yvbT*	Uncharacterized protein yvbT	+	-
116	O32268	*tuaG*	Putative teichuronic acid biosynthesis glycosyltransferase tuaG	+	+
117	O34334	*yjoA*	Uncharacterized protein yjoA	-	+
118	O34340	*fabF*	3-oxoacyl-[acyl-carrier-protein] synthase 2	+	+
119	O34348	*yfmC*	Fe(3+)-citrate-binding protein yfmC	+	+
120	O34355	*ytcJ*	Putative amidohydrolase ytcJ	+	+
121	O34389	*malS*	Probable NAD-dependent malic enzyme 3	+	+
122	O34409	*yflN*	Uncharacterized protein yflN	+	+
123	O34423	*yjqC*	Uncharacterized protein YjqC	-	+
124	O34433	*yobO*	Putative phage-related protein yobO	-	+
125	O34443	*apt*	Adenine phosphoribosyltransferase	-	+
126	O34454	*ykaA*	UPF0111 protein ykaA	+	+
127	O34470	*ylbL*	Uncharacterized protein ylbL	+	-
128	O34475	*yfkO*	Putative NAD(P)H nitroreductase yfkO	+	+
129	O34493	*ytmA*	Uncharacterized peptidase ytmA	+	-
130	O34497	*ykgA*	Uncharacterized protein ykgA	+	+
131	O34499	*pgl*	Uncharacterized protein YkgB	+	+
132	O34507	*prkC*	Serine/threonine-protein kinase PrkC	+	-
133	O34521	*nagP*	PTS system N-acetylglucosamine-specific EIICB component	+	-
134	O34525	*sppA*	Putative signal peptide peptidase sppA	+	-
135	O34526	*alaS*	Alanine--tRNA ligase	+	+
136	O34529	*pfkA*	6-phosphofructokinase	+	+
137	O34543	*mhqE*	Putative ring-cleaving dioxygenase mhqE	+	+
138	O34558	*yopR*	SPBc2 prophage-derived uncharacterized protein yopR	+	+
139	O34564	*ykuU*	Thioredoxin-like protein ykuU	+	+
140	O34570	*ytlP*	UPF0097 protein ytlP	+	-
141	O34580	*pcrA*	ATP-dependent DNA helicase pcrA	+	+
142	O34586	*ylbC*	Uncharacterized membrane protein ylbC	+	-
143	O34595	*thiI*	Probable tRNA sulfurtransferase	-	+
144	O34599	*iscS1*	Putative cysteine desulfurase IscS 1	+	+
145	O34600	*nrnA*	Bifunctional oligoribonuclease and PAP phosphatase nrnA	+	+
146	O34617	*rlmN*	Ribosomal RNA large subunit methyltransferase N	+	-
147	O34628	*yvlB*	Uncharacterized protein yvlB	+	-
148	O34629	*yerH*	Uncharacterized lipoprotein yerH	+	-
149	O34645	*melA*	Alpha-galactosidase	-	+
150	O34654	*yodI*	Uncharacterized protein yodI	+	+
151	O34666	*ctpA*	Carboxy-terminal processing protease CtpA	+	-
152	O34689	*mhqA*	Putative ring-cleaving dioxygenase mhqA	+	+
153	O34717	*fadH*	Probable 2,4-dienoyl-CoA reductase	+	-
154	O34726	*yflS*	Putative malate transporter yflS	+	+
155	O34746	*fabHA*	3-oxoacyl-[acyl-carrier-protein] synthase 3 protein 1	+	+
156	O34750	*yfmL*	Putative ATP-dependent RNA helicase yfmL	+	+
157	O34752	*lgt*	Prolipoprotein diacylglyceryl transferase	+	-

158	O34782	*yvrD*	Uncharacterized oxidoreductase yvrD	+	+
159	O34788	*bdhA*	(R,R)-butanediol dehydrogenase	+	+
160	O34806	*ytfJ*	Uncharacterized spore protein ytfJ	+	+
161	O34812	*yfmJ*	Putative NADP-dependent oxidoreductase yfmJ	+	+
162	O34824	*glmM*	Phosphoglucosamine mutase	+	+
163	O34827	*ykuM*	Uncharacterized HTH-type transcriptional regulator ykuM	-	+
164	O34840	*chaA*	Putative cation exchanger chaA	+	-
165	O34842	*mhqD*	Putative hydrolase MhqD	+	+
166	O34847	*accA*	Acetyl-coenzyme A carboxylase carboxyl transferase subunit alph	+	+
167	O34859	*ku*	Probable DNA repair protein ykoV	+	+
168	O34860	*rsbRB*	RsbT co-antagonist protein rsbRB	-	+
169	O34863	*uvrA*	UvrABC system protein A	+	+
170	O34885	*ydiS*	Type-2 restriction enzyme BsuMI component ydiS	+	+
171	O34894	*ezrA*	Septation ring formation regulator EzrA	+	-
172	O34915	*yobE*	UPF0361 protein yobE	-	+
173	O34924	*ytoP*	Putative aminopeptidase ytoP	+	+
174	O34925	*deoD*	Purine nucleoside phosphorylase deoD-type	+	+
175	O34934	*nadK2*	Probable inorganic polyphosphate/ATP-NAD kinase 2	+	+
176	O34940	*yvrE*	Uncharacterized protein yvrE	+	+
177	O34944	*ytjP*	Putative dipeptidase ytjP	+	+
178	O34962	*ytsJ*	Probable NAD-dependent malic enzyme 4	+	+
179	O34966	*znuA*	Zinc transport system zinc-binding lipoprotein ZnuA	+	+
180	O34968	*yerB*	Putative lipoprotein yerB	+	-
181	O34987	*pbuG*	Guanine/hypoxanthine permease pbuG	+	-
182	O34996	*polA*	DNA polymerase I	+	+
183	O35020	*mnmA*	tRNA-specific 2-thiouridylase mnmA	-	+
184	O35023	*sodF*	Probable superoxide dismutase [Fe]	-	+
185	O35028	*yfkR*	Putative spore germination protein yfkR	+	-
186	O54408	*relA*	GTP pyrophosphokinase	+	+
187	P04969	*rpsK*	30S ribosomal protein S11	+	+
188	P05648	*dnaA*	Chromosomal replication initiator protein DnaA	+	+
189	P05649	*dnaN*	DNA polymerase III subunit beta	+	+
190	P05651	*recF*	DNA replication and repair protein recF	+	+
191	P05652	*gyrB*	DNA gyrase subunit B	+	+
192	P05653	*gyrA*	DNA gyrase subunit A	+	+
193	P06224	*sigA*	RNA polymerase sigma factor rpoD	+	+
194	P07343	*fumC*	Fumarate hydratase class II	+	+
195	P07870	*gerAC*	Spore germination protein A3	+	+
196	P08065	*sdhA*	Succinate dehydrogenase flavoprotein subunit	+	+
197	P08066	*sdhB*	Succinate dehydrogenase iron-sulfur subunit	-	+
198	P08164	*nadE*	NH(3)-dependent NAD(+) synthetase	+	+
199	P08750	*dacA*	D-alanyl-D-alanine carboxypeptidase dacA	+	+
200	P08838	*ptsI*	Phosphoenolpyruvate-protein phosphotransferase	+	+
201	P09124	*gapA*	Glyceraldehyde-3-phosphate dehydrogenase 1	+	+
202	P09339	*citB*	Aconitate hydratase	+	+
203	P0CI73	*glmS*	Glucosamine--fructose-6-phosphate aminotransferase	+	-
204	P10944	*hutH*	Histidine ammonia-lyase	+	+
205	P11998	*ribH*	6,7-dimethyl-8-ribityllumazine synthase	+	+
206	P12011	*gntK*	Gluconokinase	+	-
207	P12013	*gntZ*	6-phosphogluconate dehydrogenase, decarboxylating	+	+
208	P12047	*purB*	Adenylosuccinate lyase	+	+
209	P12310	*gdh*	Glucose 1-dehydrogenase	+	+
210	P12425	*glnA*	Glutamine synthetase	+	+
211	P12877	*rplE*	50S ribosomal protein L5	+	+

212	P13242	*pyrG*	CTP synthase	+	+
213	P13243	*fbaA*	Probable fructose-bisphosphate aldolase	+	+
214	P13792	*phoP*	Alkaline phosphatase synthesis transcriptional regulatory protein	+	-
215	P14016	*cotE*	Spore coat protein E	+	+
216	P14193	*prs*	Ribose-phosphate pyrophosphokinase	+	+
217	P14577	*rplP*	50S ribosomal protein L16	+	+
218	P14802	*yoxD*	Uncharacterized oxidoreductase yoxD	+	-
219	P16263	*odhB*	Dihydrolipoyllysine-residue succinyltransferase component of 2-oxoglutarate dehydrogenase complex	+	-
220	P16304	*adk*	Adenylate kinase	-	+
221	P16336	*secY*	Protein translocase subunit SecY	+	-
222	P16440	*ribE*	Riboflavin synthase alpha chain	-	+
223	P16450	*gerD*	Spore germination protein gerD	+	+
224	P16524	*dapX*	Putative aminotransferase A	-	+
225	P16616	*hemC*	Porphobilinogen deaminase	+	+
226	P17620	*ribBA*	Riboflavin biosynthesis protein ribBA	+	+
227	P17631	*dnaJ*	Chaperone protein DnaJ	-	+
228	P17820	*dnaK*	Chaperone protein DnaK	+	+
229	P17889	*infB*	Translation initiation factor IF-2	+	+
230	P17921	*pheS*	Phenylalanine--tRNA ligase alpha chain	+	+
231	P17922	*pheT*	Phenylalanine--tRNA ligase beta chain	+	+
232	P18157	*glpK*	Glycerol kinase	+	+
233	P18158	*glpD*	Aerobic glycerol-3-phosphate dehydrogenase	+	+
234	P18255	*thrS*	Threonine--tRNA ligase 1	+	+
235	P18579	*murB*	UDP-N-acetylenolpyruvoylglucosamine reductase	-	+
236	P19465	*folE*	GTP cyclohydrolase 1	+	-
237	P19582	*hom*	Homoserine dehydrogenase	+	+
238	P19669	*tal*	Transaldolase	+	+
239	P19670	*murAB*	UDP-N-acetylglucosamine 1-carboxyvinyltransferase 2	+	+
240	P20166	*ptsG*	PTS system glucose-specific EIICBA component	+	+
241	P20277	*rplQ*	50S ribosomal protein L17	+	+
242	P20282	*rpsM*	30S ribosomal protein S13	+	+
243	P20429	*rpoA*	DNA-directed RNA polymerase subunit alpha	+	+
244	P20964	*obg*	GTPase obgE	+	+
245	P21464	*rpsB*	30S ribosomal protein S2	+	+
246	P21465	*rpsC*	30S ribosomal protein S3	+	+
247	P21466	*rpsD*	30S ribosomal protein S4	+	+
248	P21467	*rpsE*	30S ribosomal protein S5	+	+
249	P21469	*rpsG*	30S ribosomal protein S7	+	+
250	P21470	*rpsI*	30S ribosomal protein S9	-	+
251	P21472	*rpsL*	30S ribosomal protein S12	+	-
252	P21656	*trpS*	Tryptophan--tRNA ligase	+	+
253	P21879	*guaB*	Inosine-5'-monophosphate dehydrogenase	+	+
254	P21880	*pdhD*	Dihydrolipoyl dehydrogenase	+	+
255	P21881	*pdhA*	Pyruvate dehydrogenase E1 component subunit alpha	+	+
256	P21882	*pdhB*	Pyruvate dehydrogenase E1 component subunit beta	+	+
257	P21883	*pdhC*	Dihydrolipoyllysine-residue acetyltransferase component of pyruvate dehydrogenase complex	+	+
258	P21885	*speA*	Arginine decarboxylase	+	+
259	P22250	*gltX*	Glutamate--tRNA ligase	+	+
260	P22322	*gpr*	Germination protease	+	+
261	P22326	*tyrS1*	Tyrosine--tRNA ligase 1	+	+
262	P23129	*odhA*	2-oxoglutarate dehydrogenase E1 component	+	+
263	P23261	*cotF*	Spore coat protein F	+	+

264	P23545	*phoR*	Alkaline phosphatase synthesis sensor protein phoR	+	-
265	P23630	*lysA*	Diaminopimelate decarboxylase	+	+
266	P23966	*menB*	1,4-Dihydroxy-2-naphthoyl-CoA synthase	+	+
267	P24136	*oppD*	Oligopeptide transport ATP-binding protein OppD	+	+
268	P24137	*oppF*	Oligopeptide transport ATP-binding protein OppF	+	+
269	P24138	*oppB*	Oligopeptide transport system permease protein OppB	+	-
270	P24139	*oppC*	Oligopeptide transport system permease protein OppC	+	+
271	P24141	*oppA*	Oligopeptide-binding protein OppA	+	+
272	P24327	*prsA*	Foldase protein prsA	+	+
273	P25144	*ccpA*	Catabolite control protein A	+	+
274	P25972	*pyrE*	Orotate phosphoribosyltransferase	+	-
275	P26899	*ansB*	Aspartate ammonia-lyase	+	+
276	P26900	*ansA*	L-asparaginase 1	+	+
277	P26902	*dppA*	D-aminopeptidase	+	+
278	P27876	*tpiA*	Triosephosphate isomerase,	+	+
279	P28366	*secA*	Protein translocase subunit SecA	+	+
280	P28598	*groL*	60 kDa chaperonin	+	+
281	P28619	*rph*	Ribonuclease PH	+	+
282	P28628	*sipS*	Signal peptidase I S	+	-
283	P29726	*purA*	Adenylosuccinate synthetase	+	+
284	P29727	*guaA*	GMP synthase [glutamine-hydrolyzing]	+	+
285	P30300	*glpP*	Glycerol uptake operon antiterminator regulatory protein	+	-
286	P30949	*hemL*	Glutamate-1-semialdehyde 2,1-aminomutase	+	+
287	P30950	*hemB*	Delta-aminolevulinic acid dehydratase	+	+
288	P31102	*aroB*	3-dehydroquinate synthase	+	+
289	P31103	*ndk*	Nucleoside diphosphate kinase	-	+
290	P31104	*aroC*	Chorismate synthase	+	+
291	P31845	*spoVAF*	Stage V sporulation protein AF	+	+
292	P32395	*hemE*	Uroporphyrinogen decarboxylase	+	+
293	P32396	*hemH*	Ferrochelatase	+	+
294	P32397	*hemY*	Protoporphyrinogen oxidase	+	+
295	P32727	*nusA*	Transcription elongation protein nusA	-	+
296	P32731	*rbfA*	Ribosome-binding factor A	+	+
297	P33166	*tuf*	Elongation factor Tu	+	+
298	P34957	*qoxA*	Quinol oxidase subunit 2	+	+
299	P35136	*serA*	D-3-phosphoglycerate dehydrogenase	+	+
300	P35137	*ppiB*	Peptidyl-prolyl cis-trans isomerase B	-	+
301	P35149	*spoIVA*	Stage IV sporulation protein A	-	+
302	P35159	*rluB*	Ribosomal large subunit pseudouridine synthase B	+	+
303	P35160	*resA*	Thiol-disulfide oxidoreductase resA	+	-
304	P35163	*resD*	Transcriptional regulatory protein resD	+	+
305	P36430	*leuS*	Leucine--tRNA ligase	+	+
306	P36945	*rbsK*	Ribokinase	+	+
307	P36947	*rbsA*	Ribose import ATP-binding protein RbsA	+	+
308	P36949	*rbsB*	D-ribose-binding protein	+	-
309	P37105	*ffh*	Signal recognition particle protein	+	+
310	P37455	*ssbA*	Single-stranded DNA-binding protein ssb	-	+
311	P37464	*serS*	Serine--tRNA ligase	+	+
312	P37465	*metG*	Methionine--tRNA ligase	+	+
313	P37470	*spoVC*	Peptidyl-tRNA hydrolase	-	+
314	P37472	*hprT*	Hypoxanthine-guanine phosphoribosyltransferase	+	+
315	P37474	*mfd*	Transcription-repair-coupling factor	+	+
316	P37476	*ftsH*	ATP-dependent zinc metalloprotease FtsH	+	+
317	P37477	*lysS*	Lysine--tRNA ligase	+	+

318	P37487	*ppaC*	Manganese-dependent inorganic pyrophosphatase	+	+
319	P37518	*ychF*	GTP-dependent nucleic acid-binding protein engD	+	+
320	P37526	*yaaC*	Uncharacterized protein yaaC	+	+
321	P37527	*pdxS*	Pyridoxal biosynthesis lyase pdxS	+	+
322	P37528	*pdxT*	Glutamine amidotransferase subunit pdxT	+	+
323	P37531	*sleL*	Spore germination protein yaaH	+	+
324	P37545	*yabD*	Uncharacterized deoxyribonuclease YabD	-	+
325	P37550	*ispE*	4-diphosphocytidyl-2-C-methyl-D-erythritol kinase	-	+
326	P37551	*purR*	Pur operon repressor	-	+
327	P37554	*spoVT*	Stage V sporulation protein T	+	+
328	P37556	*yabN*	Uncharacterized protein yabN	+	+
329	P37565	*hslO*	33 kDa chaperonin	-	+
330	P37566	*yacD*	Putative peptidyl-prolyl cis-trans isomerase YacD	+	-
331	P37569	*mcsA*	Uncharacterized protein yacH	-	+
332	P37570	*mcsB*	Putative ATP:guanido phosphotransferase yacI	+	+
333	P37571	*clpC*	Negative regulator of genetic competence ClpC/MecB	+	+
334	P37580	*fhuD*	Iron(3+)-hydroxamate-binding protein fhuD	+	+
335	P37585	*murG*	UDP-N-acetylglucosamine--N-acetylmuramyl-(pentapeptide) pyrophosphoryl-undecaprenol N-acetylglucosamine transferase	+	+
336	P37808	*atpA*	ATP synthase subunit alpha	+	+
337	P37809	*atpD*	ATP synthase subunit beta	+	+
338	P37810	*atpG*	ATP synthase gamma chain	+	+
339	P37811	*atpH*	ATP synthase subunit delta	-	+
340	P37813	*atpB*	ATP synthase subunit a	+	-
341	P37814	*atpF*	ATP synthase subunit b	+	+
342	P37869	*eno*	Enolase	+	+
343	P37870	*rpoB*	DNA-directed RNA polymerase subunit beta	+	+
344	P37871	*rpoC*	DNA-directed RNA polymerase subunit beta'	+	+
345	P37876	*ytxK*	Uncharacterized protein ytxK	+	+
346	P37877	*ackA*	Acetate kinase	+	+
347	P37887	*cysK*	Cysteine synthase	+	+
348	P37940	*bfmBAA*	2-oxoisovalerate dehydrogenase subunit alpha	+	-
349	P37941	*bfmBAB*	2-oxoisovalerate dehydrogenase subunit beta	+	+
350	P37942	*bfmBB*	Lipoamide acyltransferase component of branched-chain alpha-keto acid dehydrogenase complex	+	+
351	P37945	*lon1*	Lon protease 1	+	+
352	P37949	*lepA*	Elongation factor 4	+	+
353	P37954	*uvrB*	UvrABC system protein B	+	+
354	P37956	*splB*	Spore photoproduct lyase	+	+
355	P37967	*pnbA*	Para-nitrobenzyl esterase	-	+
356	P38050	*pbpF*	Penicillin-binding protein 1F	+	-
357	P38424	*engB*	Probable GTP-binding protein EngB	-	+
358	P38490	*ypeB*	Sporulation protein ypeB	+	+
359	P38494	*ypfD*	30S ribosomal protein S1 homolog	-	+
360	P39071	*dhbA*	2,3-dihydro-2,3-dihydroxybenzoate dehydrogenase	+	+
361	P39074	*bmrU*	Putative lipid kinase BmrU	+	+
362	P39126	*icd*	Isocitrate dehydrogenase [NADP]	+	+
363	P39131	*mnaA*	UDP-N-acetylglucosamine 2-epimerase	-	+
364	P39138	*rocF*	Arginase	+	+
365	P39142	*pdp*	Pyrimidine-nucleoside phosphorylase	+	+
366	P39148	*glyA*	Pyridoxal-phosphate-dependent serine hydroxymethyltransferase	+	+
367	P39149	*upp*	Uracil phosphoribosyltransferase	+	+
368	P39571	*gerBC*	Spore germination protein B3	+	+
369	P39574	*galK*	Galactokinase	+	+

370	P39575	*galT*	Galactose-1-phosphate uridylyltransferase	+	-
371	P39577	*dltE*	Uncharacterized oxidoreductase dltE	+	+
372	P39578	*dltD*	Protein dltD	+	-
373	P39587	*ywbD*	Putative ribosomal RNA large subunit methyltransferase YwbD	-	+
374	P39605	*nfrA1*	FMN reductase (NADPH)	+	+
375	P39634	*rocA*	1-pyrroline-5-carboxylate dehydrogenase	+	+
376	P39644	*bacG*	Bacilysin biosynthesis oxidoreductase ywfH	-	+
377	P39645	*ywfI*	UPF0447 protein ywfI	-	+
378	P39646	*pta*	Phosphate acetyltransferase	+	+
379	P39668	*yyxA*	Uncharacterized serine protease yyxA	+	+
380	P39751	*mbl*	MreB-like protein	+	+
381	P39762	*ampS*	Aminopeptidase AmpS	+	+
382	P39765	*pyrR*	Bifunctional protein pyrR	+	+
383	P39772	*asnS*	Asparagine--tRNA ligase	+	+
384	P39773	*gpmI*	2,3-bisphosphoglycerate-independent phosphoglycerate mutase	+	+
385	P39778	*clpY*	ATP-dependent protease ATPase subunit ClpY	+	+
386	P39779	*codY*	GTP-sensing transcriptional pleiotropic repressor CodY	+	+
387	P39793	*ponA*	Penicillin-binding protein 1A/1B	+	-
388	P39814	*topA*	DNA topoisomerase 1	+	+
389	P39815	*trmFO*	Methylenetetrahydrofolate--tRNA-(uracil-5-)-methyltransferase	-	+
390	P39839	*yuxL*	Uncharacterized peptidase yuxL	+	+
391	P39840	*galM*	Aldose 1-epimerase	+	+
392	P40397	*yhxC*	Uncharacterized oxidoreductase yhxC	+	+
393	P40740	*bglH*	Aryl-phospho-beta-D-glucosidase BglH	+	+
394	P40778	*murC*	UDP-N-acetylmuramate--L-alanine ligase	+	+
395	P40779	*ytxG*	UPF0478 protein ytxG	+	-
396	P40780	*ytxH*	Uncharacterized protein ytxH	+	+
397	P40868	*spoVAC*	Stage V sporulation protein AC	+	-
398	P40869	*spoVAD*	Stage V sporulation protein AD	+	+
399	P40870	*spoVAEA*	Stage V sporulation protein AE	+	-
400	P40924	*pgk*	Phosphoglycerate kinase	+	+
401	P42060	*rplV*	50S ribosomal protein L22	+	+
402	P42068	*hutG*	Formimidoylglutamase	+	+
403	P42084	*hutI*	Imidazolonepropionase	+	+
404	P42182	*era*	GTPase Era	+	+
405	P42199	*tcyA*	L-cystine-binding protein tcyA	+	+
406	P42305	*dbpA*	ATP-dependent RNA helicase dbpA	+	+
407	P42400	*yckB*	Probable ABC transporter extracellular-binding protein yckB	+	-
408	P42403	*bglC*	Aryl-phospho-beta-D-glucosidase BglC	+	+
409	P42412	*iolA*	Methylmalonate semialdehyde dehydrogenase [acylating]	+	+
410	P42413	*iolB*	5-deoxy-glucuronate isomerase	+	-
411	P42414	*iolC*	5-dehydro-2-deoxygluconokinase	+	+
412	P42415	*iolD*	3D-(3,5/4)-trihydroxycyclohexane-1,2-dione hydrolase	+	+
413	P42418	*iolH*	Protein iolH	+	+
414	P42419	*iolI*	Inosose isomerase	+	+
415	P42919	*rplB*	50S ribosomal protein L2	+	+
416	P42920	*rplC*	50S ribosomal protein L3	+	+
417	P42921	*rplD*	50S ribosomal protein L4	+	+
418	P42923	*rplJ*	50S ribosomal protein L10	+	+
419	P42953	*tagG*	Teichoic acid translocation permease protein tagG	+	-
420	P42958	*ycsA*	Probable tartrate dehydrogenase/decarboxylase	+	+
421	P42972	*ycsN*	Uncharacterized oxidoreductase YcsN	-	+
422	P42973	*bglA*	Aryl-phospho-beta-D-glucosidase BglA	+	+
423	P42974	*ahpF*	NADH dehydrogenase	+	+

424	P45694	*tkt*	Transketolase	+	+
425	P45864	*uvsE*	UV DNA damage endonuclease	+	+
426	P45865	*clsB*	Uncharacterized protein YwjE	+	-
427	P45872	*prfA*	Peptide chain release factor 1	+	+
428	P45914	*yqaR*	Uncharacterized protein yqaR	+	-
429	P46323	*cinA*	Putative competence-damage inducible protein	+	+
430	P46336	*iolS*	Protein IolS	+	+
431	P46337	*iolR*	HTH-type transcriptional regulator iolR	-	+
432	P46343	*phoH*	PhoH-like protein	+	+
433	P46353	*drm*	Phosphopentomutase	+	+
434	P46354	*punA*	Purine nucleoside phosphorylase 1	+	+
435	P46898	*rplF*	50S ribosomal protein L6	+	+
436	P46899	*rplR*	50S ribosomal protein L18	+	+
437	P46905	*yccK*	Uncharacterized oxidoreductase YccK	+	+
438	P46906	*argS*	Arginine--tRNA ligase	+	+
439	P46911	*qcrA*	Menaquinol-cytochrome c reductase iron-sulfur subunit	+	+
440	P46912	*qcrB*	Menaquinol-cytochrome c reductase cytochrome b subunit	+	+
441	P46919	*gpsA*	Glycerol-3-phosphate dehydrogenase [NAD(P)+]	+	+
442	P46920	*opuAA*	Glycine betaine transport ATP-binding protein OpuAA	+	+
443	P46921	*opuAB*	Glycine betaine transport system permease protein opuAB	+	+
444	P46922	*opuAC*	Glycine betaine-binding protein	+	-
445	P49787	*accC1*	Biotin carboxylase 1	+	+
446	P49852	*hmp*	Flavohemoprotein	+	+
447	P49941	*gerKC*	Spore germination protein KC	+	+
448	P50736	*ypdA*	Uncharacterized protein ypdA	+	+
449	P50739	*sleB*	Spore cortex-lytic enzyme	+	+
450	P50743	*der*	GTPase Der	+	+
451	P50840	*ypsC*	Putative RNA methyltransferase YpsC	+	+
452	P50843	*kduI*	4-deoxy-L-threo-5-hexosulose-uronate ketol-isomerase	+	+
453	P50848	*ypwA*	Putative metalloprotease ypwA	+	+
454	P50849	*pnp*	Polyribonucleotide nucleotidyltransferase	+	+
455	P50866	*clpX*	ATP-dependent Clp protease ATP-binding subunit ClpX	+	+
456	P51831	*fabG*	3-oxoacyl-[acyl-carrier-protein] reductase FabG	+	-
457	P51835	*ftsY*	Cell division protein FtsY homolog	+	+
458	P52996	*panB*	3-methyl-2-oxobutanoate hydroxymethyltransferase	-	+
459	P52998	*panC*	Pantothenate synthetase	-	+
460	P53001	*aspB*	Aspartate aminotransferase	+	+
461	P53555	*bioK*	L-Lysine-8-amino-7-oxononanoate aminotransferase	+	+
462	P54154	*msrA*	Peptide methionine sulfoxide reductase MsrA	+	+
463	P54157	*bcsA*	Putative chalcone synthase	+	+
464	P54164	*ypeP*	Uncharacterized protein ypeP	-	+
465	P54169	*ypgR*	Uncharacterized protein ypgR	+	-
466	P54178	*ypmQ*	SCO1 protein homolog	+	+
467	P54375	*sodA*	Superoxide dismutase [Mn]	+	+
468	P54376	*gcvPA*	Probable glycine dehydrogenase [decarboxylating] subunit 1	+	+
469	P54377	*gcvPB*	Probable glycine dehydrogenase [decarboxylating] subunit 2	+	+
470	P54378	*gcvT*	Aminomethyltransferase	+	+
471	P54380	*glyQ*	Glycine--tRNA ligase alpha subunit	+	+
472	P54381	*glyS*	Glycine--tRNA ligase beta subunit	-	+
473	P54382	*folD*	Bifunctional protein FolD	+	+
474	P54394	*dinG*	Probable ATP-dependent helicase dinG homolog	-	+
475	P54418	*pckA*	Phosphoenolpyruvate carboxykinase [ATP]	+	-
476	P54419	*metK*	S-adenosylmethionine synthase	+	+
477	P54430	*yrkC*	Uncharacterized protein yrkC	-	+

478	P54448	*yqeC*	Putative 6-phosphogluconate dehydrogenase YqeC	+	+
479	P54452	*yqeG*	Uncharacterized protein yqeG	+	-
480	P54453	*yqeH*	Uncharacterized protein yqeH	+	+
481	P54456	*yqeK*	Uncharacterized protein yqeK	+	+
482	P54466	*yqfA*	UPF0365 protein yqfA	+	+
483	P54472	*yqfO*	UPF0135 protein yqfO	+	+
484	P54475	*cshB*	DEAD-box ATP-dependent RNA helicase CshB	+	+
485	P54481	*yqfX*	Uncharacterized protein yqfX	+	+
486	P54488	*yqgF*	Uncharacterized protein yqgF	+	-
487	P54495	*glcK*	Glucokinase	+	+
488	P54509	*yqhH*	Uncharacterized ATP-dependent helicase yqhH	+	+
489	P54510	*yqhL*	Uncharacterized protein yqhL	+	+
490	P54511	*lipM*	Octanoyltransferase LipM	-	+
491	P54518	*yqhT*	Uncharacterized peptidase yqhT	+	+
492	P54524	*yqiG*	Probable NADH-dependent flavin oxidoreductase yqiG	+	+
493	P54531	*yqiT*	Leucine dehydrogenase	+	+
494	P54532	*buk*	Probable butyrate kinase	+	-
495	P54535	*artP*	Arginine-binding extracellular protein ArtP	+	+
496	P54536	*artQ*	Arginine transport system permease protein ArtQ	+	-
497	P54542	*yqjE*	Uncharacterized protein yqjE	+	-
498	P54543	*yqjF*	Uncharacterized protein yqjF	-	+
499	P54547	*zwf*	Glucose-6-phosphate 1-dehydrogenase	+	+
500	P54550	*namA*	NADPH dehydrogenase	+	+
501	P54569	*yqkF*	Uncharacterized oxidoreductase YqkF	+	-
502	P54586	*yhcB*	Uncharacterized protein yhcB	+	-
503	P54587	*yhcC*	Uncharacterized protein yhcC	+	-
504	P54597	*yhcM*	Uncharacterized protein yhcM	+	+
505	P54598	*yhcN*	Lipoprotein yhcN	+	+
506	P54601	*yhcQ*	Spore coat protein F-like protein YhcQ	+	+
507	P54607	*yhcW*	Uncharacterized protein YhcW	+	+
508	P54608	*yhcX*	UPF0012 hydrolase yhcX	+	+
509	P54616	*fabI*	Enoyl-[acyl-carrier-protein] reductase [NADH] FabI	+	+
510	P54721	*catE*	Catechol-2,3-dioxygenase	-	+
511	P54944	*yxeE*	Uncharacterized protein yxeE	-	+
512	P54947	*yxeH*	Uncharacterized protein YxeH	+	-
513	P55179	*pepT*	Peptidase T	+	+
514	P55180	*galE*	UDP-glucose 4-epimerase	+	+
515	P55342	*bshC*	UPF0747 protein yllA	+	+
516	P55872	*infC*	Translation initiation factor IF-3	+	+
517	P55874	*rpmI*	50S ribosomal protein L35	-	+
518	P68569	*bdbA*	SPBc2 prophage-derived disulfide bond formation protein A	+	-
519	P70945	*yitS*	DegV domain-containing protein yitS	-	+
520	P70974	*rplM*	50S ribosomal protein L13	+	+
521	P70998	*speE*	Spermidine synthase	+	+
522	P70999	*speB*	Agmatinase	-	+
523	P71009	*albC*	Putative ABC transporter ATP-binding protein AlbC	-	+
524	P71012	*fruA*	PTS system fructose-specific EIIABC component	+	+
525	P71013	*sipT*	Signal peptidase I T	+	-
526	P71014	*bslA*	Uncharacterized protein yuaB	+	-
527	P71018	*plsX*	Phosphate acyltransferase	+	+
528	P71079	*fabL*	Enoyl-[acyl-carrier-protein] reductase [NADPH] FabL	+	+
529	P71084	*gsaB*	Glutamate-1-semialdehyde 2,1-aminomutase 2	+	+
530	P71088	*spo0M*	Sporulation-control protein spo0M	+	+
531	P80239	*ahpC*	Alkyl hydroperoxide reductase subunit C	+	+

532	P80244	*clpP*	ATP-dependent Clp protease proteolytic subunit	+	+
533	P80700	*tsf*	Elongation factor Ts	+	+
534	P80859	*gndA*	6-phosphogluconate dehydrogenase, decarboxylating 2	+	+
535	P80860	*pgi*	Glucose-6-phosphate isomerase	+	+
536	P80862	*serC*	Phosphoserine aminotransferase	+	-
537	P80864	*tpx*	Probable thiol peroxidase	-	+
538	P80865	*sucD*	Succinyl-CoA ligase [ADP-forming] subunit alpha	-	+
539	P80866	*sufC*	Vegetative protein 296	+	-
540	P80868	*fusA*	Elongation factor G	+	+
541	P80879	*dps*	General stress protein 20U	+	+
542	P80880	*trxB*	Thioredoxin reductase	+	+
543	P80885	*pyk*	Pyruvate kinase	+	+
544	P80886	*sucC*	Succinyl-CoA ligase [ADP-forming] subunit beta	+	+
545	P94358	*aldY*	Uncharacterized aldehyde dehydrogenase AldY	+	+
546	P94360	*msmX*	Maltodextrin import ATP-binding protein MsmX	+	-
547	P94377	*katX*	Catalase X	+	+
548	P94391	*putC*	1-pyrroline-5-carboxylate dehydrogenase 2	+	+
549	P94434	*ycnL*	Uncharacterized protein ycnL	+	-
550	P94446	*coxA*	Sporulation cortex protein CoxA	+	-
551	P94464	*rsmB*	Ribosomal RNA small subunit methyltransferase B	+	+
552	P94478	*hflX*	GTPase HflX	+	+
553	P94479	*ynbB*	Uncharacterized protein ynbB	+	-
554	P94494	*alr2*	Alanine racemase 2	+	-
555	P94512	*ysaA*	Putative uncharacterized hydrolase ysaA	-	+
556	P94520	*ysdB*	Sigma-w pathway protein ysdB	+	-
557	P94521	*ysdC*	Putative aminopeptidase ysdC	+	+
558	P94531	*abfA*	Alpha-N-arabinofuranosidase 1	-	+
559	P94544	*polX*	DNA polymerase/3'-5' exonuclease PolX	+	-
560	P94545	*mutSB*	MutS2 protein	+	+
561	P94552	*abf2*	Alpha-N-arabinofuranosidase 2	+	-
562	P94559	*ysnB*	Putative metallophosphoesterase ysnB	-	+
563	P94573	*ywoC*	Uncharacterized isochorismatase family protein ywoC	+	+
564	P94584	*fabZ*	(3R)-hydroxymyristoyl-[acyl-carrier-protein] dehydratase	+	+
565	P96583	*topB*	DNA topoisomerase 3	+	-
566	P96612	*ddl*	D-alanine--D-alanine ligase	+	+
567	P96614	*cshA*	DEAD-box ATP-dependent RNA helicase CshA	+	+
568	P97032	*yhbD*	Uncharacterized protein yhbD	+	-
569	Q01464	*minD*	Septum site-determining protein MinD	-	+
570	Q01465	*mreB*	Rod shape-determining protein MreB	+	+
571	Q01466	*mreC*	Rod shape-determining protein mreC	+	-
572	Q01625	*misCA*	Membrane protein insertase MisCA	+	-
573	Q03222	*rho*	Transcription termination factor Rho	+	+
574	Q03522	*murD*	UDP-N-acetylmuramoylalanine--D-glutamate ligase	+	+
575	Q03523	*murE*	UDP-N-acetylmuramoyl-L-alanyl-D-glutamate--2,6-diaminopimelate ligase	+	-
576	Q04796	*dapA*	Dihydrodipicolinate synthase	+	+
577	Q04797	*asd*	Aspartate-semialdehyde dehydrogenase	-	+
578	Q04805	*ymxG*	Uncharacterized zinc protease ymxG	+	+
579	Q05852	*gtaB*	UTP--glucose-1-phosphate uridylyltransferase	+	+
580	Q05873	*valS*	Valine--tRNA ligase	+	+
581	Q06752	*cysS*	Cysteine--tRNA ligase	+	+
582	Q06797	*rplA*	50S ribosomal protein L1	+	+
583	Q07876	*rsmH*	Ribosomal RNA small subunit methyltransferase H	+	+
584	Q08311	*cotY*	Spore coat protein Y	+	+

585	Q08313	*cotX*	Spore coat protein X	+	+
586	Q08352	*ald*	Alanine dehydrogenase	+	+
587	Q08432	*patB*	Cystathionine beta-lyase PatB	+	+
588	Q45064	*plsY*	Glycerol-3-phosphate acyltransferase	+	-
589	Q45066	*parC*	DNA topoisomerase 4 subunit A	+	-
590	Q45477	*ileS*	Isoleucine--tRNA ligase	+	+
591	Q45480	*ylyB*	Uncharacterized RNA pseudouridine synthase ylyB	-	+
592	Q45493	*rnjA*	Ribonuclease J 1	+	+
593	Q45494	*ykrA*	Putative phosphatase YkrA	-	+
594	Q45498	*yktB*	UPF0637 protein yktB	+	+
595	Q45499	*suhB*	Inositol-1-monophosphatase	+	+
596	Q45538	*cotJC*	Protein CotJC	-	+
597	Q45604	*yycR*	Uncharacterized zinc-type alcohol dehydrogenase-like protein	+	+
598	Q795M6	*yugH*	Putative aminotransferase YugH	+	-
599	Q795R8	*ytfP*	Uncharacterized protein ytfP	+	+
600	Q795U4	*ytkL*	UPF0173 metal-dependent hydrolase ytkL	-	+
601	Q796Q1	*yitG*	Uncharacterized MFS-type transporter yitG	+	+
602	Q99171	*tepA*	Translocation-enhancing protein TepA	+	+
603	Q9KWU4	*pyc*	Pyruvate carboxylase	+	+

[a] Sample was detected in dormant spores.

[b] Sample was detected in germinated spores

Table S3: *B. subtilis* and *B. anthracis* spore membrane-associated proteins identified by mass spectrometry.

Gene[a]	**COG Functional category**	***B. subtilis* Uniprot number**	***B. anthracis* Uniprot number**	**Membrane prediction[b]**	**Previous ID[c]**		**Regulon[d]**
					Spore Proteome	**Vegetative Proteome**	
ythA/*cydA3*	Energy production	C0SP90	Q81WZ0	Integral	B C		σ^G
yhfQ	Ion transport & metab.[e].	C0SP94		Lipoprotein	B C	F H I	
yugS/ *GBAA_0608*	Unknown	O05241	Q81V91	Integral	B C		
yugP	Posttranslational modification	O05248		Integral	B C	G I	
yvcA	Colony structure	O06965		Lipoprotein	C	G I	
yveA	Amino acid transport & metab.	O07002		Integral	B C		σ^G
yheB	Unknown	O07543		Integral	B C	F I	
ylaJ/ *GBAA_2746*	Unknown	O07634	Q81PQ5	Lipoprotein	A B C E	E I	σ^G
yetF/BAS4999	Unknown	O31533	Q81X64	Integral	B C		σ^F
yhbJ	Defense mechanisms	O31593		Integral	B C	G I	σ^G
yjbQ	Ion transport & metab.	O31615		Integral	C	I	
ykrK/ *GBAA_2841*	Unknown	O31656	Q81PG5	Peripheral	C		
htpX	Posttranslational modification	O31657		Integral	B C	H I	
yndM/BAS2909	Unknown	O31816	Q6HWX1	Integral	B C		
yrvD	Unknown	O32045		Integral	C	G I	
secDF	Intracellular trafficking	O32047	Q81LH8	Integral	B C	F H I J	
yrbG	Unknown	O32050		Integral	B C		σ^G
yrbF	Intracellular trafficking	O32052		Integral	B C	H I	
yuaG	Unknown	O32076		Integral	B C	G H I	
yutC/ *GBAA_5199*	Unknown	O32128	Q81XN4	Lipoprotein	B C		σ^G
metQ/ *GBAA_5220*	Amino acid transport & metab.	O32167	Q81XL5	Lipoprotein	B C	H I	
bdbD	Posttranslational modification	O32218	Q81YT8	Integral	B C	F H I	σ^E
yfmC/*fpuA*	Ion transport & metab.	O34348	Q81L65	Lipoprotein	B C	F H I J	
ylbL	Signal transduction	O34470		Integral	B C	F H	

prkC	Germination	O34507		Integral	B C	G H I	
sppA	Intracellular trafficking	O34525		Integral	B C	G H I	
ylbC	Unknown	O34586		Integral	B C	G I	σ^F
yerH	Unknown	O34629		Lipoprotein	B C	F H I	
yodI	Unknown	O34654		Integral	A B C		σ^K
yflS	Ion transport & metab.	O34726		Integral	B C		
lgt	Posttranslational modification	O34752		Integral	B C	G I	
chaA	Ion transport & metab.	O34840		Integral	B C	I	
ezrA	Cell cycle control	O34894		Integral	B C	G H I	
znuA/GBAA_2035	Ion transport & metab.	O34966	Q81RK9	Lipoprotein	B C	H	
yerB	Unknown	O34968		Lipoprotein			
pbuG	General transporter	O34987		Integral	C	F I	
yfkR	Germination	O35028		Lipoprotein	B C		σ^G
gerAC	Germination	P07870		Lipoprotein	B		σ^G
dacA	Cell wall biogenesis	P08750		Integral	B C	F H I	
secY/secY1	Intracellular trafficking	P16336	Q81VR0	Integral	B C	F H I	
gerD	Germination	P16450	Q81VP4	Lipoprotein	B C		σ^G
ptsG/ptsG	Carbohydrate transp. & metab.	P20166	Q81MH9	Integral	B C	F H I	
phoR	Signal transduction	P23545		Integral	B C	H I	σ^E
oppD/GBAA_1194	General Transporter	P24136	Q81TS1	Peripheral	B C	G H I J	
oppF/GBAA_1195	Amino acid transport & metab.	P24137	Q81TS0	Peripheral	B C	G H I	
oppB/GBAA_1192	General Transporter	P24138	Q81TS3	Integral	B C	G H I J	
oppC/GBAA_1193	General Transporter	P24139	Q81TS2	Integral	B C	G H I	
oppA/GBAA_0656	Amino acid transport & metab.	P24141	Q81V45	Lipoprotein	B C	F H I J	
prsA/prsA1	Posttranslational modification	P24327	Q81U45	Lipoprotein	B C	F H I	
sipS	Intracellular trafficking	P28628		Integral	B C	G I	σ^E
spoVAF	DPA transport	P31845	Q81MG2	Integral	B C		σ^G
qoxA/ctaC	Energy production	P34957	Q81MT9	Integral	B C	F H I	

resA	Posttranslational modification	P35160	Q81SZ9	Integral	C	G I	
rbsA	Carbohydrate transp. & metab.	P36947		Peripheral		F	
ftsH	Posttranslational modification	P37476	Q81VX5	Integral	B C	F H I J	
yacD	Posttranslational modification	P37566		Integral	C	F I	
fhuD/GBAA_0351	Ion transport & metab.	P37580	Q81ZB8	Integral	B C	F H I J	
murG	Cell wall biogenesis	P37585		Peripheral	B C	I	σ^E
atpD	Energy production	P37809	Q81JZ5	Peripheral	B C D	F H I	
atpG	Energy production	P37810	Q81JZ4	Peripheral	B C	F H I	
atpB	Energy production	P37813		Integral	C	F I	
atpF	Energy production	P37814	Q81JZ1	Integral	B C	F H I	
pbpF/GBAA_1474	Cell wall biogenesis	P38050	Q81T17	Integral	B C	G J	
ypeB	Germination	P38490	Q81PQ4	Integral	B C		σ^G
gerBC	Germination	P39571		Lipoprotein	B		σ^G
dltD	Cell wall biogenesis	P39578		Integral	C	F H I	
yyxA/GBAA_5710	Posttranslational modification	P39668	Q81JJ5	Integral	B C		
ponA/GBAA_2345	Cell wall biogenesis	P39793	Q81QS3	Integral	B C	F H I	
ytxG	Unknown	P40779		Integral	B C	G H I	
ytxH	Unknown	P40780		Integral	B C	G H I	
spoVAC	DPA transport	P40868	Q81X68	Integral	B C	H	σ^G
spoVAD	DPA transport	P40869	Q81X67	Peripheral	B C	H	σ^G
era	Unknown	P42182	Q81LT7	Peripheral	B C E	H I	
tcyA/GBAA_0855	Amino acid transport & metab.	P42199	Q81UL3	Lipoprotein	B C E	H I	
yckB	Amino acid transport & metab.	P42400		Lipoprotein		F H I	
tagG	Cell wall biogenesis	P42953		Integral	B	G	
ahpF	Posttranslational modification	P42974	Q81ZC5	Peripheral	B C	G H I	
clsB	Lipid metabolism	P45865		Integral	B C		σ^G
yqaR	Unknown	P45914		Integral		I	
qcrA	Energy production	P46911	Q81SV1	Integral	B C	G H I	

qcrB	Energy production	P46912	Q81SV0	Integral	B C	G H I	
opuAB	Amino acid transport & metab.	P46921		Integral	B C	G H I	
opuAC	Amino acid transport & metab.	P46922		Lipoprotein	B C	F H I	
gerKC	Germination	P49941		Lipoprotein	B C		σ^G
ftsY	Intracellular trafficking	P51835		Peripheral	B C	G H I	σ^K
ypmQ/GBAA_2249	Energy production	P54178	Q81R11	Lipoprotein			
yqfA	Unknown	P54466		Integral	B C	F H I	
yqfX/BA_1410	Unknown	P54481	Q81T77	Integral	B C E	H	σ^G
yqgF	Cell wall biogenesis	P54488		Integral	C	I	
artP/GBAA_0367	Amino acid transport & metab.	P54535	Q6I447	Lipoprotein	B C	H I	
artQ	Amino acid transport & metab.	P54536		Integral	B C	H I	
yhcC	Unknown	P54587		Integral	B C		σ^G
yhcM	Unknown	P54597		Integral	A B C		σ^F
yhcN	Germination	P54598		Lipoprotein	B C	G	σ^F & σ^G
fruA	Carbohydrate transp. & metab.	P71012		Integral	B C	F H I	
sipT	Intracellular trafficking	P71013		Integral	B C	G I	
yuaB	Colony structure	P71014		Integral			
msmX/potA	Amino acid transport & metab.	P94360	Q81TH8	Peripheral	B C	G H I J	
ycnL	Ion transport & metab.	P94434		Integral	B C		
ysdB	Transcription	P94520		Integral	C	G I	
misCA/yidC2	Intracellular trafficking	Q01625	Q81JH1	Integral	B C	H I	
lytR	Transcription	Q02115	Q81K33	Integral	B C	F H I	
plsY/plsY3	Lipid metabolism	Q45064	Q81Y92	Integral	B C	I	
yitG	General transporter	Q796Q1		Integral	B C		σ^G
BAS4994	Unknown		Q6HR05	Lipoprotein			
GBAA_5330	Ion transport & metab.		Q81XB0	Lipoprotein			
BAS4323	Unknown		Q6HSW8	Lipoprotein	E		
BAS0569	Unknown		Q6I3I4	Lipoprotein			

fabF	Lipid metabolism		Q81JF9	Peripheral			
GBAA_5684	Cell wall biogenesis		Q81JM0	Integral			
GBAA_5061	Unknown		Q81KD9	Peripheral	D		
GBAA_4746	Unknown		Q81L82	Lipoprotein			
psd	Lipid metabolism		Q81LP7	Peripheral			
cccA	Energy production		Q81LU6	Integral			
BA_4310	Unknown		Q81MD9	Lipoprotein			
GBAA_4229	Carbohydrate transp. & metab.		Q81ML8	Lipoprotein	E		
typA	Signal transduction		Q81MS8	Peripheral			
GBAA_3380	Energy production		Q81N37	Peripheral			
GBAA_3129	Unknown		Q81NQ0	Peripheral	D		
GBAA_3048	Defense mechanisms		Q81NX4	Peripheral		J	
GBAA_2961	Unknown		Q81P56	Integral			
GBAA_2942	Unknown		Q81P74	Lipoprotein	E		
GBAA_2883	Unknown		Q81PC7	Lipoprotein			
proV2	Amino acid transport & metab.		Q81PL6	Peripheral			
GBAA_1523	Unknown		Q81SX1	Integral			
potD	Amino acid transport & metab.		Q81TH5	Lipoprotein			
ecsA	Defense mechanisms		Q81U40	Peripheral			
GBAA_0615	Ion transport & metab.		Q81V85	Lipoprotein		J	
GBAA_0595	Ion transport & metab.		Q81VA3	Integral			
GBAA_0190	Unknown		Q81VK7	Lipoprotein	E		
ftsY	Intracellular trafficking		Q81WJ0	Peripheral			
ffh	Intracellular trafficking		Q81WJ2	Peripheral			
rasP	Cell envelope biogenesis		Q81WL5	Integral			
GBAA_3927	Unknown		Q81WP4	Lipoprotein			
GBAA_5313	Energy production		Q81XC7	Peripheral			
GBAA_5237	Unknown		Q81XK0	Lipoprotein			

GBAA_5173	Energy production		Q81XR0	Peripheral			
BA_5160	Posttranslational modification		Q81XS0	Peripheral			
GBAA_5159	Energy production		Q81XS1	Peripheral			
BA_3742	Unknown		Q81Y17	Integral			
GBAA_0418	Unknown		Q81Z55	Peripheral	E		
GBAA_0382	Ion transport & metab.		Q81Z90	Lipoprotein			
GBAA_0374	Unknown		Q81Z98	Integral			
GBAA_0365	Energy production		Q81ZA6	Peripheral			

[a] If a protein doesn't have an annotated gene name, the ordered locus name is listed.

[b] Mechanism of membrane association predicted as described in Materials and Methods.

[c] Previous identification of the protein in a proteomic analysis: A=(1); B=(2); C=(3); D=(4); E=(5); F=(6); G=(7); H=(2); I=(3); J=(8).

[d] Sigma factor dependence was drawn from references: (1, 9-11).

[e] metabolism

Table S4. Spore membrane proteins that were no longer detected following germination.

Gene	*B. subtilis* Uniprot number	*B. anthracis* Uniprot number
artQ	P54536	
atpB	P37813	
bdbD	O32218	Q81YT8
clsB	P45865	
dltD	P39578	
ezrA	O34894	
htpX	O31657	
lgt	O34752	
lytR	Q02115	Q81K33
misCA	Q01625	
msmX/potA	P94360	Q81TH8
oppB/GBAA_1192	P24138	Q81TS3
opuAC	P46922	
pbpF/GBAA_1474	P38050	Q81T17
pbuG	O34987	
phoR	P23545	
plsY/plsY3	Q45064	Q81Y92
ponA/GBAA_2345	P39793	Q81QS3
qcrA	P46911	
rbsB	P36949	
resA	P35160	Q81SZ9
secY	P16336	Q81VR0
sipS	P28628	
sipT	P71013	
sppA	O34525	
tagG	P42953	
yacD	P37566	
ybC	O34586	
yckB	P42400	
ycnL	P94434	
yerB	O34968	
yerH	O34629	
chaA	O34840	
yfkR	O35028	
yhbJ	O31593	
yhcC	P54587	
yjbQ	O31615	
ylbL	O34470	
yndM	O31816	
yqaR	P45914	
yqgF	P54488	

yrbG	O32050	
ysdB	P94520	
ytxG	P40779	
yuaB	P71014	
yuaG	O32076	
yutC	O32128	
yvcA	O06965	
GBAA_0351		Q81ZB8
GBAA_0367		Q6I447
GBAA_0374		Q81Z98
GBAA_0382		Q81Z90
GBAA_0595		Q81VA3
GBAA_1193		Q81TS2
GBAA_1194		Q81TS1
GBAA_2035		Q81RK9
GBAA_2249		Q81R11
GBAA_2746		Q81PQ5
GBAA_2841		Q81PG5
GBAA_2883		Q81PC7
GBAA_2942		Q81P74
BAS2909		Q6HWX1
BA_4310		Q81MD9
GBAA_4746		Q81L82
fpuA		Q81L65
GBAA_5061		Q81KD9
GBAA_5173		Q81XR0
GBAA_5199		Q81XN4
GBAA_5220		Q81XL5
GBAA_5237		Q81XK0
GBAA_5330		Q81XB0
BAS4994		Q6HR05
GBAA_5710		Q81JJ5
ctaC		Q81MT9
ecsA		Q81U40
ffH		Q81WJ2
gerD		Q81VP4
ptsG		Q81MH9
qcrB		Q81SV0
rasP		Q81WL5
secDF		Q81LH8
spoVAC		Q81X68
spoVAF		Q81MG2
ypeB		Q81PQ4

Table S5. Oligonucleotides used in this work.

Name	Sequence (5’-3’)	Use
DLP668	AGTAGCCCGGCATTTTTAGC	PCR verification of Δ*znuA*
DLP669	TAGCGGCCTGACTGAACAAG	PCR verification of Δ*znuA*
DLP670	CCGAACCTTGCGCTGATGTC	PCR verification of Δ*ycnL*
DLP671	GCCGCCTTGCTGCTGTTCTT	PCR verification of Δ*ycnL*
DLP672	TCAAGCGGGTGCGGGTAAAT	PCR verification of Δ*yflS*
DLP673	TGTATGCTGAACGGCTAACG	PCR verification of Δ*yflS*
DLP676	GTTCGCTTGGATTTTCATAA	PCR verification of Δ*yloB*
DLP677	CACCCAATTCTTCCCTGTTC	PCR verification of Δ*yloB*
DLP687	GATCCGACTGCCATTCCTGC	Construction of Δ*chaA::spec*
DLP688	CAATAAACCCTTGCCCTCGCTACGCAGAAAGCGGAACACCGGCC	Construction of Δ*chaA::spec*
DLP689	CGTTACGTTATTAGCGAGCCAGTCATGTCATTATGGCGATCGGC	Construction of Δ*chaA::spec*
DLP690	CCAGCCTTGCAGTAAGACGG	Construction of Δ*chaA::spec*
DLP683	ATCGGTACGCAGCTGGCGGC	Construction of Δ*yugS::mls*
DLP684	CGATTATGTCTTTTGCGCAGTCGGCACCATAAATGGTAAGGGGCC	Construction of Δ*yugS::mls*
DLP685	GAGGGTTGCCAGAGTTAAAGGATCCCTCGACGCCGAAGATCACC	Construction of Δ*yugS::mls*
DLP686	GCTTCTTTTGCAGCGACGCC	Construction of Δ*yugS::mls*
DLP675	CTGCTTTTTCGCGTGGATGG	PCR verification of Δ*chaA::spec*
DLP677	CGTAGCGAGGGCAAGGGTTTATTGTTTTCTAAAATCTG	PCR verification of Δ*chaA::spec*
DLP679	CTACGGCTTCCTTCCACCAA	PCR verification of Δ*yugS::mls*
DLP565	GCCGACTGCGCAAAAGACATAATCG	PCR verification of Δ*yugS::mls*

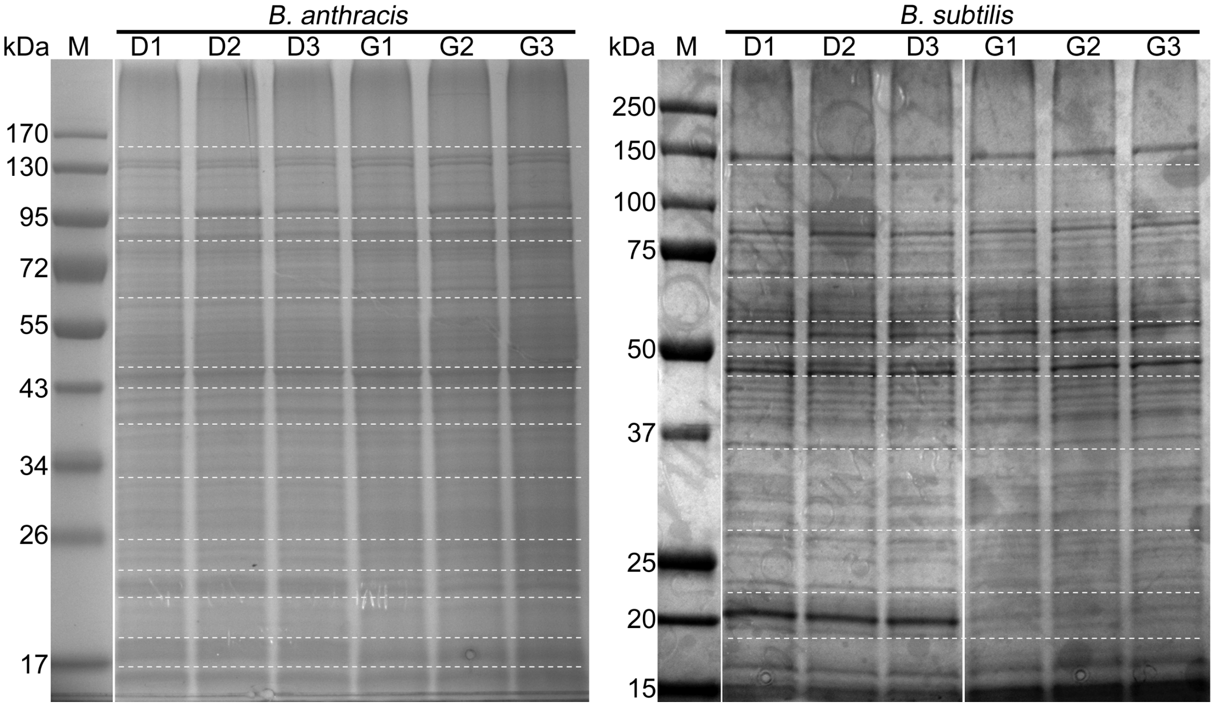

Figure S1. SDS-PAGE separation of *B. anthracis* and *B. subtilis* spore membrane preparations. Samples from three independent dormant (D1, D2, D3) and germinated (G1, G2, G3) spore preparations were prepared and broken, and membrane fractions were purified as described in Materials and Methods. Protein concentrations were determined by amino acid analysis, and equal amounts of protein from each preparation were loaded on gels. Gels were stained with Coomassie blue. The positions at which each lane was cut into slices are indicated by dashed lines. The masses of standard protein markers (M) are shown to the left of each gel.

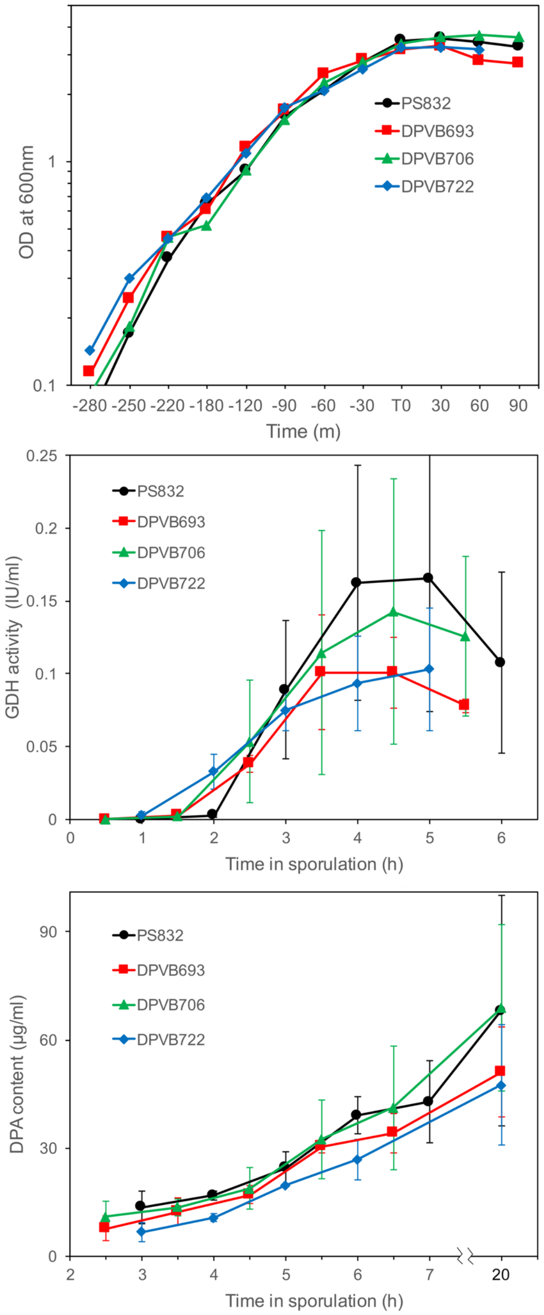

Figure S2. Growth and sporulation of putative ion transporter mutant strains of *B. subtilis.* A) Strains were grown with shaking in 2xSG medium at 37^{0}C and O.D.$_{600}$ was measured. Time 0 was the estimated time of initiation of sporulation (T$_0$) for each strain. B) Samples were collected for measuring GDH activity as previously described (12). Values are averages of three assays and error bars are standard deviations. C) Samples were removed starting at T$_3$ for measurement of DPA accumulation. DPA was quantified using a colorimetric assay as previously described (12). Values are averages of three assays and error bars are standard deviations.

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