

Bacillus Genetic Stock Center Catalog of Strains, Seventh Edition,
Volume 1: *Bacillus subtilis* 168

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Disclaimer: The information in this catalog is believed to be correct. Due to the dynamic nature of the scientific process and to normal human limitations in dealing with such a large amount of data, however, some undetected errors may persist. Users bear the responsibility of verifying any important data before making a significant investment of time or other physical or financial resources.

Cover: Portions of the *Bacillus subtilis* 168 genomic sequence serve as a backdrop to a common lab scene. The cover symbolizes the transition of *B. subtilis* research into the genomics age. The images were edited with Microsoft Image Composer and combined with Macromedia Freehand.

Links: This document contains many internal hyperlinks. Clicking on a text in color opens a link to another page with more information about that strain, reference, or gene.

THIS CATALOG IS UNDER CONSTRUCTION. Look for regular updates and additional technical material to be added during the coming year.

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(Note: Additional Sections are In Preparation)

What is the *Bacillus* Genetic Stock Center?

The primary mission of the *Bacillus* Genetic Stock Center (BGSC) is to maintain genetically characterized strains, cloning vectors, and bacteriophage for the genus *Bacillus* and related organisms and to distribute these materials without prejudice to qualified scientists and educators throughout the world. Since 1978, the National Science Foundation has funded the activities of the BGSC. The Department of Biochemistry in the College of Biological Sciences at the Ohio State University provides facilities and administrative support. The Director of the BGSC, Dr. Daniel R. Zeigler, is assisted by two part-time technicians and data entry specialists.

What kinds of cultures are available from the BGSC?

- The nomenclatural type strains for 34 species;
- 1291 mutant or plasmid bearing strains derived from *Bacillus subtilis* 168, including a collection of 115 genetically characterized sporulation mutants;
- 158 strains of round spore formers, comprised of 136 strains of *B. sphaericus*, 17 of *B. fusiformis*, and five of *Rommeliibacillus pycnus*;
- 191 wild type strains of *B. thuringiensis*, along with 10 cloned *B. thuringiensis cry* genes;
- 239 genetically characterized wild-type, mutant, and plasmid-bearing strains of *B. megaterium*;
- 96 lytic or lysogenic *Bacillus* bacteriophages;
- 42 wild-type and mutant strains from the thermophilic genus *Geobacillus*
- 41 wild-type, mutant, and lysogenic strains of *Bacillus licheniformis*;
- 55 other wild-type, mutant, and plasmid-bearing *B. subtilis* isolates, including 12 from *B. subtilis* subsp. *spizizenii* and 43 from other *B. subtilis* backgrounds;
- 104 wild-type strains from the *Bacillus cereus* group, also including *B. mycoides* and *B. weihenstephanensis*;
- 18 wild-type isolates from the genus *Brevibacillus*, including *B. brevis*, *B. borstelensis*, *B. centrosporus*, and *B. laterosporus*;
- 18 wild-type and mutant strains from *B. amyloliquefaciens*;
- 30 wild-type isolates from the genus *Paenibacillus*, including *P. alvei*, *P. dendritiformus*, *P. macerans*, *P. polymyxa*, *P. popilliae*, *P. thiaminolyticus*, and *P. vorticalis*;
- 42 isolates from 22 other related species, including *Aneurinibacillus aneurinilyticus*, *A. migulanus*, *B. atrophaeus*, *B. badius*, *B. carboniphilus*, *B. circulans*, *B. clausii*, *B. coagulans*, *B. firmus*, *B. lentus*, *B. mojavensis*, 'B. natto,' *B. oleronius*, *B. pumilus*, *B. shackletonii*, *Marinibacillus marinus*, *Sporosarcina ureae*, and *Virgibacillus marismortui*
- 204 *Escherichia coli* strains bearing shuttle plasmids or cloned *Bacillus* DNA;
- Warehoused *Bacillus* strain collections of Joshua Lederberg, Eugene Nester, Bernard Reilly, Patricia Vary, Allan Yousten, Stanley Zahler, and the late Ernst W. Freese.

Please note that the BGSC has never carried *B. anthracis* or products derived from it.

The collections maintained in the BGSC Warehouse are available to the scientific community upon request. They do not receive the same level of curation, quality control, or data publication as the strains in the main collection. However, they are maintained because of their high level of historical importance as a service to the *Bacillus* research community.

All stocks are made available via the BGSC web site, www.bgsc.org.

Please inquire about any of these strains that might be of interest to you.

What you can do to help the BGSC

Our NSF grant partially subsidizes many services we offer. User fees are vitally important if we are to close the funding gap and continue operations. We greatly appreciate your understanding! Additionally, we would be grateful for the following kinds of help:

- *Strain contributions:* Although we have obtained a few cultures from other strain repositories, the vast majority of our holdings were contributed by individual researchers. Please take a moment to look over our collection and consider: are there strains, vectors, phage, or clones that you have developed or acquired that we do not have? Would these materials be of some potential use to others in the research community? If so, please take the time to deposit the material in the BGSC. There is no charge whatsoever to you. There is also no compensation--except for the knowledge that you have made the fruits of your labor more accessible for the benefit of others. Generally, all we would require would be a culture (or lysate) with appropriate reprints or other helpful information. Please contact us (see below) if you have any questions.
- *Financial Contributions:* The BGSC relies on corporate strain sales and contributions to purchase equipment and undertake special projects not covered by the NSF grant. The Ohio State University Development Fund has a separate account for the BGSC. Contributions are tax deductible to the full extent of the law. Please contact us if you wish to make such a contribution.

How to order cultures

There are several ways to place orders with or request information from the BGSC:

- E-mail: zeigler.1@osu.edu
- Internet: www.bgsc.org
- Phone: 614-292-5550
- FAX: 614-292-3206
- Mail: Daniel R. Zeigler, Ph.D.
Department of Biochemistry
The Ohio State University
484 West Twelfth Avenue
Columbus, OH 43210 / USA

All users will be invoiced for strain, plasmid, or phage requests. Payment must be in US dollars via check, bank transfer, or procurement card (Visa, MasterCard, and American Express accepted). Orders can be placed via any of the five methods above with an institutional purchase order. Credit card orders should be made via phone or fax.

Pricing information

- *Academic, Government, and Non-Profit Users*—Not-for-profit users are requested to pay a \$195 yearly subscription fee. This subscription entitles the user to receive up to 20 strains over a twelve-month period. Alternatively, a user may purchase individual strains at \$35 each. If you are lacking in research support, please contact us to inquire about a fee waiver for a particular order.
- *For-profit Corporate Users*--Users may purchase cultures as needed at \$135 per item. Shipping via UPS is included for all domestic orders and for international orders of two or more items. A pre-paid service plan is available for \$1950. It entitles the user to receive up to 50 cultures within the next twelve calendar months at no additional cost. UPS delivery service is included (to a maximum of five express deliveries per year on overseas shipments).

Important Notice

Please read this notice before ordering materials from this catalog!

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- (1) All warranties, express or implied, in respect of Materials, including warranties of merchantability and of fitness for any particular purpose, are disclaimed by The Ohio State University (OSU).
- (2) The Materials are provided for research use only and are not to be used for commercial purposes which include, but are not limited to, the sale, lease, license, or other transfer of the Materials or modifications to a for-profit organization **without the express permission of the owners of the Materials.**
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BACILLUS SUBTILIS 168 STRAINS INDEXED BY BGSC ACCESSION NUMBER

BGSC	ORIGINAL CODE	DESCRIPTION	SOURCE	DONOR	REF
1A1	168	<i>trpC2</i>	Giles N	Shapiro JA	30
1A2	SB491	prototrophic	Lederberg J	Lederberg J	155
1A3	QB944 KIT-1	<i>cysE14 purA26 trpC2</i>	Dedonder RA	Dedonder RA	60
1A4	QB928 KIT-2	<i>aroI906 dal-1 purE1 trpC2</i>	Dedonder RA	Dedonder RA	60
1A5	QB934 KIT-3	<i>glyB133 metC3 treA12 trpC2</i>	Dedonder RA	Dedonder RA	60
1A6	QB943 KIT-4	<i>ilvA1 pyrD1 thyA1 thyB1 trpC2</i>	Dedonder RA	Dedonder RA	60
1A7	QB922 KIT-5	<i>glrA292 trpC2</i>	Dedonder RA	Dedonder RA	60
1A8	QB935 KIT-6	<i>aroD120 lys-1 trpC2</i>	Dedonder RA	Dedonder RA	60
1A9	QB936 KIT-7	<i>ald-1 aroA932 leuB8 trpC2</i>	Dedonder RA	Dedonder RA	60
1A10	QB917 KIT-8	<i>hisA1 thr-5 trpC2</i>	Dedonder RA	Dedonder RA	60
1A11	QB123 KIT-9	<i>ctrA1 sacA321 trpC2</i>	Dedonder RA	Dedonder RA	60
1A12	Mu8u5u6	<i>leuB8 metB5 purF6</i>	Seuoka N	Shapiro JA	292
1A13	Mu8u5u6u41	<i>car-41 leuB8 metB5 purF6</i>	Sueoka N	Shapiro JA	150
1A14	SU+III 168SU* γ	<i>-(metB5)+ -(thr-5)+ leuB8 trnS-Lys3</i>	(Georgopoulos C	Sonenshein AL	96
1A15	BR63	<i>pheA2 trpC2</i>	Reilly BE	Sonenshein AL	216
1A16	JH404	<i>citG4 trpC2</i>	Hoch JA	Hoch JA	225
1A17	CU403,TS-134	<i>dnaB134 ilvA1 thyA1 thyB1</i>	Mendelson NH	Mendelson NH	176
1A18	TSDNA-A13	<i>dnaA13 ilvA1 metB5</i>	Karamata D	Brown NC	146
1A19	TSDNA-B19	<i>dnaB19 ilvA1 metB5</i>	Karamata D	Brown NC	146
1A20	TSDNA-C30	<i>dnaC30 ilvA1 metB5</i>	Karamata D	Brown NC	146
1A21	TSDNA-D23	<i>dnaD23 ilvA1 metB5</i>	Karamata D	Brown NC	146
1A22	TSDNA-E20	<i>dnaE20 ilvA1 metB5</i>	Karamata D	Brown NC	146
1A23	TSDNA-F133	<i>ilvA1 metB5 polC133</i>	Karamata D	Brown NC	146
1A24	TSDNA-G34	<i>dnaN34 ilvA1 metB5</i>	Karamata D	Brown NC	146
1A25	TSDNA-H151	<i>dnaA151 ilvA1 metB5</i>	Karamata D	Brown NC	146
1A26	TSDNA-I102	<i>dnaI102 ilvA1 metB5</i>	Karamata D	Brown NC	146
1A27	BD97	<i>pyrA26</i>	Dubnau D	Karamata D	65
1A28	C-4 SB1 BC38	<i>argF4 hisA1 trpC2</i>	Marmur J	Copeland JC	166
1A29	BC50	<i>leuB8 metB5 nic-38 purA16</i>	Copeland JC	Copeland JC	45
1A30	BC53	<i>ilvA64 leuB8 metB5 purA16</i>	Copeland JC	Copeland JC	44
1A31	SB3 (BD92)	<i>cysB3 hisA1 trpC2</i>	Nester EW	Copeland JC	159
1A32	JH406	<i>citC6 trpC2</i>	Hoch JA	Hoch JA	225
1A33	JH402	<i>sdhA2 trpC2</i>	Hoch JA	Hoch JA	225
1A34	CU635	<i>furC1 trpC2</i>	Zahler SA	Zahler SA	300
1A35	RUB814	<i>tagE lys-3 metB10 trpC2</i>	Young FE	Yasbin RE	293
1A36	RUB834	<i>aroB2 hisH2 metB10 trpC2 tyrA1</i>	Young FE	Yasbin RE	293
1A37	RUB836	<i>hisA metB10 trpC2</i>	Young FE	Yasbin RE	293
1A38	RUB2112	<i>metB10 purF6 trpC2</i>	Young FE	Young FE	293
1A39	BR85	<i>argF4 trpC2</i>	Reilly BE	Young FE	294
1A40	BR151	<i>lys-3 metB10 trpC2</i>	Reilly BE	Young FE	294
1A41	DNA-1	<i>dnaB1 thyA1 thyB1 trpC2</i>	Sueoka N	Sueoka N	261
1A42	BD170	<i>thr-5 trpC2</i>	Dubnau DA	Dubnau DA	64
1A43	BD194	<i>recA1 trpC2</i>	Dubnau DA	Garro AJ	64
1A44	BD191	<i>recB2 thr-5 trpC2</i>	Dubnau DA	Garro AJ	64
1A45	BD193	<i>recB3 thr-5 trpC2</i>	Dubnau DA	Garro AJ	64
1A46	BD224	<i>recA4 thr-5 trpC2</i>	Dubnau DA	Garro AJ	64
1A47	BD241	<i>recL16 thr-5 trpC2</i>	Dubnau DA	Garro AJ	64
1A48	BD246	<i>reCm13 thr-5 trpC2</i>	Dubnau DA	Garro AJ	64
1A49	QB2,PUR(+)	<i>sacA321</i>	Dedonder RA	Dedonder RA	59, 158
1A50	QB42	<i>sac(XY)46 trpC2</i>	Dedonder RA	Dedonder RA	158
1A51	QB58	<i>purA16 sac(XY)46</i>	Dedonder RA	Dedonder RA	59
1A52	QB687	<i>sacA321 treA12 trpC2</i>	Dedonder RA	Dedonder RA	159
1A53	QB698	<i>ald-1 degQ36 trpC2</i>	Dedonder RA	Dedonder RA	159
1A54	QB819	<i>mtID1 nasC1 sacA321</i>	Dedonder RA	Dedonder RA	159
1A55	QB820	<i>aroI906 dal-1 metB5 sacA321</i>	Dedonder RA	Dedonder RA	159
1A56	QB821	<i>aroA932 trpC2</i>	Dedonder RA	Dedonder RA	59
1A57	BR95	<i>ilvC1 pheA1 trpC2</i>	Reilly BE	Garro AJ	216
1A58	SB25	<i>hisH2 trpC2</i>	Lederberg J	Mahler I	191
1A59	SB1	<i>hisA1 trpC2</i>	Lederberg J	Mahler I	190
1A60	GB64/219	<i>metC3 pyrA xin-1</i>	Garro AJ	Garro AJ	92
1A61	JH715	<i>furF5 spo</i>	Hoch JA	Hoch JA	123

B. subtilis 168 Strains Indexed by BGSC Accession Number

BGSC	ORIGINAL CODE	DESCRIPTION	SOURCE	DONOR	REF
1A62	GB153 (ICR 7)	<i>trpA5</i>	Carlton BC	Garro AJ	285
1A63	GB151 (NG 14)	<i>trpB4</i>	Carlton BC	Garro AJ	285
1A64	GB152 (NA 3)	<i>trpD2</i>	Carlton BC	Garro AJ	285
1A65	BS166	<i>trpE26</i>	Yanofsky C	Spizizen J	30
1A66	SCR500	<i>pheA12 tolA6 trpC2</i>	Ito J	Ito J	135
1A67	SCR506	<i>pheA12 tolA6 trpC2</i> ϕ 29 ^R	Ito J	Ito J	136
1A68	MB500	<i>leuB8 metB5 tsi-23</i>	Hoch JA	Mahler I	246
1A69	SB120	<i>aroD120 trpC2</i>	Nester EW	Lepesant J-A	127
1A70	JH422	<i>citL22 trpC2</i>	Hoch JA	Hoch JA	125
1A71	GSY292	<i>gltA1 trpC2</i>	Anagnostopoulos C	Lepesant J-A	9, 61
1A72	GSY264	<i>mtr-264</i>	Anagnostopoulos C	Hoch JA	128
1A73	GSY1025	<i>metB4 recA1 trpC2</i>	Anagnostopoulos C	Lepesant JA	124
1A74	NH5	<i>dnaX8132 hisA1 thr-5</i>	Harford N	Lepesant J-A	109
1A75	MU8U5U1 (BD54)	<i>ilvA1 leuB8 metB5</i>	Dubnau DA	Brown NC	292
1A76	BD54, spcB	<i>ilvA1 metB5 spcB1</i>	Brown NC	Brown NC	164
1A77	BD54, strB	<i>ilvA1 metB5 strB3</i>	Brown NC	Brown NC	164
1A78	MB251	<i>metC3 pyrA xtl-1</i>	Garro AJ	Garro AJ	93
1A79	JH158	<i>cysC1 trpC2</i>	Hoch JA	Brown NC	123, 126
1A80	SB26	<i>metC7 trpC2</i>	Lederberg J	Brown NC	155
1A81	BD54, spcB, azp	<i>ilvA1 leuB8 metB5 polC12 spcB1</i>	Brown NC	Brown NC	164
1A82	BD54, azp	<i>ilvA1 leuB8 metB5 polC12</i>	Brown NC	Brown NC	164
1A83	SB137	<i>aroB2 hisH2</i>	Lederberg J	Lederberg J	191
1A84	QB858	<i>glyB133 metD1</i>	Lepesant J-A	Lepesant J-A	156
1A85	PB3046 (BD96)	<i>furA1</i>	Dubnau DA	Brown NC	209
1A86	1443	<i>ilvA1 leu leuB8 metB5 polA1443</i>	Gross J	Brown NC	21, 117
1A87	SB68	<i>hisH2 trpC2 tyrA1</i>	Lederberg J	Lederberg J	155
1A88	QB19	<i>rplV1 sac(XY)32 trpC2</i>	Lepesant JA	Lepesant JA	158
1A89	QB99	<i>hisH2 leuB8</i>	Lepesant JA	Lepesant JA	60
1A90	QB666	<i>hisA1 sacA321 trpC2</i>	Lepesant JA	Lepesant JA	60
1A91	QB712	<i>fruB138 sacA321 trpC2</i>	Lepesant JA	Lepesant JA	156
1A92	QB889	<i>arg(GH)2 aroA932 bioB141 sacA321</i>	Lepesant JA	Lepesant JA	156
1A93	QB1506	<i>dnaX8132 hisA1 sacA321 thr-5</i>	Lepesant JA	Lepesant JA	156
1A94	CU495	<i>narA1 trpC2</i>	Zahler SA	Zahler SA	302
1A95	QB136	<i>leuB8 deg(H)32 trpC2</i>	Lepesant J-A	Lepesant J-A	152
1A96	JH642	<i>pheA1 trpC2</i>	Hoch JA	Hoch JA	58
1A97	CU135	<i>cysE14 trpC2</i>	Zahler SA	Zahler SA	300
1A98	CU968	<i>ilv 1 kauA1 metB5</i>	Zahler SA	Zahler SA	302
1A99	CU173	<i>citM1 ilvA3 trpC2</i>	Zahler SA	Zahler SA	80, 300
1A100	CU1065	<i>SPB⁻ trpC2</i>	Zahler SA	Zahler SA	303
1A101	SB19SEM BC110	<i>rplC1 rplV1 str-2</i>	Nester EW	Copeland JC	66
1A102	GSY1307	<i>trpC2 trpS1</i>	Anagnostopoulos C	Copeland JC	258
1A103	PB1640	<i>aroB2 hisH2 recG40 trpC2 tyrA1</i>	Mazza PG	Mazza PG	172
1A104	SB164	<i>aroB2</i>	Lederberg J	Lederberg J	155
1A105	BR290	<i>gtaB290 trpC2</i>	Young FE	Streips UN	294
1A106	C33	<i>gtaC33 trpC2</i>	Young FE	Streips UN	293
1A107	C10	<i>gtaC10 trpC2</i>	Young FE	Streips UN	293
1A108	SB69	<i>hisA1 tyrA1</i>	Lederberg J	Lederberg J	155
1A109	CU229	<i>ilvB2 trpC2</i>	Zahler SA	Zahler SA	281
1A110	CU219	<i>ilvD15 trpC2</i>	Zahler SA	Zahler SA	300
1A111	CU456	<i>arg(GH)2 aziB101 trpC2</i>	Zahler SA	Zahler SA	300
1A112	CU457	<i>aziA102 trpC2</i>	Zahler SA	Zahler SA	282
1A113	CU626	<i>furB1 trpC2</i>	Zahler SA	Zahler SA	300
1A114	CU134 (JAS8)	<i>leuB6 trpC2</i>	Zahler SA	Shapiro JA	300
1A115	SB5	<i>hisA1 pyrA5 trpC2</i>	Potvin B	Zahler SA	127
1A116	BR54 (JAS9)	<i>leuB7 trpC2</i>	Reilly BE	Shapiro JA	216
1A117	CU776	<i>aroH1 cotA73</i>	Zahler SA	Zahler SA	300
1A118	CU785	<i>arg(ABCDE)1 metA8 trpC2</i>	Zahler SA	Zahler SA	300
1A119	CU810	<i>arg(GH)2 leuA164 pheA2 trpC2</i>	Zahler SA	Zahler SA	300
1A120	CU872	<i>citB75 trpC2</i>	Zahler SA	Zahler SA	300
1A121	CU893	<i>arg(GH)2 pheA2 sdhC109 trpC2</i>	Freese E	Zahler SA	300
1A122	QB870	<i>glpK21 glyB133 thiA78 treA12</i>	Lepesant J-A	Zahler SA	156
1A123	CU973	<i>furE1 trpC2</i>	Zahler SA	Zahler SA	300
1A125	QB879	<i>argF4 metA29 thiB4</i>	Lepesant J-A	Zahler SA	156
1A126	QB890	<i>hisH2 leuB8 sacA321 thiC5</i>	Lepesant J-A	Zahler SA	156

B. subtilis 168 Strains Indexed by BGSC Accession Number

BGSC	ORIGINAL CODE	DESCRIPTION	SOURCE	DONOR	REF
1A127	CU1002	<i>novB75 trpC2</i>	Zahler SA	Zahler SA	300
1A128	CU1021	<i>serR1 trpC2</i>	Lepesant J-A	Zahler SA	156
1A129	CU1018	<i>ser-22 trpC2</i>	Zahler SA	Zahler SA	300
1A130	WB2281B	<i>aroA6</i>	Nester EW	Nester EW	300
1A131	SB136	<i>aroB4 hisH2</i>	Lederberg J	Lederberg J	191
1A132	SB121	<i>aroC7 trpC2</i>	Lederberg J	Nester EW	127
1A133	SB130	<i>aroE1 hisH2</i>	Lederberg J	Nester EW	192
1A134	WB888	<i>aroF5</i>	Nester EW	Nester EW	127
1A135	WB428	<i>suh-428</i>	Nester EW	Nester EW	189
1A136	G10	<i>argF4 tagE hag-2</i>	Simon MI	Ordal GW	99
1A137	G22	<i>hag-3 hisA1 ura</i>	Simon MI	Ordal GW	99
1A138	BR85	<i>argF4 hag-1 smo-1 trpC2</i>	Reilly BE	Ordal GW	294
1A139	fla-TS4	<i>flaA4 hag-1 lys trpC2</i>	Simon MI	Ordal GW	99
1A140	G26/3	<i>hag-2 hisA1 ifm-1 ura uvrB1</i>	Simon MI	Ordal GW	99
1A141	PS9	<i>hisA1 hsrM1 leuB8 lys-21 metB5 nonA1 SP10^S thr-5 trpC2 φNR2^S</i>	Saito H	Mandel M	229
1A142	ED43	<i>ilvA1 sacA78 thyA112</i>	Neuhard J	Neuhard J	193
1A143	ED54	<i>citB17 ilvA1 sacA78 thyB204</i>	Neuhard J	Neuhard J	193
1A144	ED53	<i>ilvA1 sacA78 thyA112 thyB204</i>	Neuhard J	Neuhard J	193
1A145	MU8U5U16 BC100	<i>leuB8 metB5 purA16</i>	Sueoka N	Copeland JC	196
1A146	BC101	<i>leuB8 metB5 purA16 divIB12</i>	Copeland JC	Copeland JC	45
1A147	CU532	<i>ccpA1 alsR1 ilvBΔ1 trpC2</i>	Zahler SA	Zahler SA	302
1A148	120	<i>arg(ABCDE)</i>	Kelley MS	Dedonder RA	149
1A149	VUB192	<i>pycA19 recA1 trpC2</i>	Harford N	Dedonder RA	109
1A150	QB804	<i>hpr hisA1 pha-1</i>	Dedonder RA	Dedonder RA	159
1A151	QB832	<i>argF4 hpr hisA1 pha-1</i>	Dedonder RA	Dedonder RA	59
1A152	JH417	<i>citB17 trpC2</i>	Hoch JA	Dedonder RA	123
1A153	TS2	<i>sigD2 lys trpC2</i>	Simon MI	Dedonder RA	99
1A154	QB813	<i>furB gutR met purF6 trpC2</i>	Dedonder RA	Dedonder RA	59
1A155	BR95,GLPD6	<i>glpD6 trpC2</i>	Rutberg B	Dedonder RA	161
1A156	QB861	<i>glpK21 purE1 sacA321</i>	Dedonder RA	Dedonder RA	59
1A157	BR95,GLPP	<i>glpP18 ilvC1 trpC2</i>	Rutberg B	Rutberg B	161
1A158	VUB79	<i>metA4</i>	Harford N	Dedonder RA	109
1A159	QB694	<i>narA1 deg(H)25</i>	Dedonder RA	Dedonder RA	59
1A160	NH3 QB552	<i>gyrB1 sacA321</i>	Harford N	Dedonder RA	109
1A161	Dedonder RA	<i>sac(XY)43</i>	Dedonder RA	Dedonder RA	59
1A162	VUB333	<i>ilvA1 novB thyA1</i>	Harford N	Dedonder RA	109
1A163	VUB221	<i>gyrB1 recF15 thr-5 trpC2</i>	Harford N	Dedonder RA	109
1A164	QB642	<i>sacR47</i>	Dedonder RA	Dedonder RA	59
1A165	QB13	<i>deg(H)32 trpC2</i>	Dedonder RA	Dedonder RA	202
1A166	QB39	<i>sacT3 trpC2</i>	Dedonder RA	Dedonder RA	157
1A167	QB689	<i>treA12 trpC2</i>	Dedonder RA	Dedonder RA	59
1A168	GSY1059	<i>hisA1 metB5 uvrB1</i>	Anagnostoupoulos C	Dedonder RA	9
1A169	QB562	<i>hisA1 sacB182 trpC2</i>	Dedonder RA	Dedonder RA	59
1A170	QB200	<i>sacP1 trpC2</i>	Dedonder RA	Dedonder RA	59
1A171	QB952	<i>hisH leuB8 sacP1 sac(XY)189</i>	Dedonder RA	Dedonder RA	59
1A172	CU371	<i>ilvB 1 trpC2</i>	Zahler SA	Zahler SA	302
1A173	SB70	<i>hisH2 tyrA1</i>	Lederberg J	Lederberg J	191
1A174	DRD-2	<i>glnA100 ilvC1 pheA1 trpC2</i>	Dean DR	Aronson AI	58
1A175	DRD-2A	<i>dnaA13 glnA100 pheA1 trpC2</i>	Dean DR	Aronson AI	57
1A176	DRD-4	<i>glnA103 pheA1 trpC2</i>	Dean DR	Aronson AI	58
1A177	JH818	<i>guaB1 rplV1</i>	Hoch JA	Hoch JA	123
1A178	HPR10	<i>hpr-10 trpC2</i>	Higerd TB	Streips UN	119
1A179	HPR12	<i>hpr-12 trpC2</i>	Higerd TB	Streips UN	119
1A180	HPR16	<i>hpr-16</i>	Higerd TB	Streips UN	119
1A181	HPR18	<i>hpr-18</i>	Higerd TB	Streips UN	119
1A182	YN9	<i>amyE(+M) amyR1 metB5 pro(L) purF6 deg-9 str trpB3</i>	Yoneda YS	Yoneda YS	290
1A183	PIG18TB	<i>cotA8 trpC2</i>	Schaeffer P	Rogolsky M	235
1A184	PIGY1	<i>cotA1 trpC2</i>	Schaeffer P	Rogolsky M	235
1A185	168,Ksg ^S ,Thy 168TT	<i>thyA1 thyB1 trpC2</i>	Rothman F	Kobayashi Y	77
1A187	KSG618	<i>ksgA618 thyA1 thyB1 trpC2</i>	Kobayashi Y	Kobayashi Y	272

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BGSC	ORIGINAL CODE	DESCRIPTION	SOURCE	DONOR	REF
1A188	KSG619	<i>ksgA619 thyA1 thyB1 trpC2</i>	Kobayashi Y	Kobayashi Y	272
1A189	168BLT	<i>blt-2 trpC2</i>	Rogolsky M	Rogolsky M	219
1A190	IS115	<i>cysE14 Spo⁻ tuf-7</i>	Smith I	Smith I	250
1A191	IS116	<i>rpsL1 thr-5 trpC2 tuf-2</i>	Smith I	Smith I	250
1A192	IS126	<i>cysE14 fus-1 Spo⁻</i>	Smith I	Smith I	98
1A193	IS153 CYS ⁺	<i>kan-2 Spo⁻</i>	Smith I	Smith I	97
1A194	IS154	<i>cysE14 nea-1 Spo⁻</i>	Smith I	Smith I	97
1A195	IS155	<i>cysE14 ole-2 Spo⁻</i>	Smith I	Smith I	97
1A196	CU403,DIVIVA	<i>divIVA1 ilvD thyA1 thyB1</i>	Reeve JN	Reeve JN	215
1A197	CU403,DIVIVB,SPO ⁻	<i>minD1 metB5 Spo⁻ thyA1 thyB1</i>	Reeve JN	Reeve JN	215
1A198	ST-3	<i>strB3</i>	Hoch JA	Hoch JA	123
1A199	QB127	<i>leuB8 deg(H)200 trpC2</i>	Dedonder RA	Dedonder RA	152
1A200	QB157	<i>leuB8 deg(H)100 trpC2</i>	Dedonder RA	Dedonder RA	59
1A201	QB254	<i>hisA1 sacA321 deg-42 trpC2</i>	Dedonder RA	Dedonder RA	158
1A202	WB1097	<i>leuB8 deg trpC2</i>	Dedonder RA	Dedonder RA	259
1A203	JAS11	<i>ilvB3 trpC2</i>	Shapiro JA	Shapiro JA	243
1A204	JAS12	<i>ilvA3 trpC2</i>	Shapiro JA	Shapiro JA	243
1A205	QB8087	<i>narA1 trpC2 ura-1</i>	Dedonder RA	Dedonder RA	59
1A206	SB29	<i>trpC2 tyrA1</i>	Lederberg J	Lederberg J	191
1A207	SB193	<i>aroE1 hisA1</i>	Lederberg J	Lederberg J	155
1A208	SB32	<i>hisH2</i>	Lederberg J	Lederberg J	190
1A209	TAG-1	<i>tag-1 thyA1 thyB1 trpC2</i>	Mendelson NH	Mendelson NH	176
1A210	BD35	<i>rib-2</i>	Greer S	Dubnau DA	65
1A211	BD40	<i>arg(GH)3 pheA12 rpIV1</i>	Dubnau DA	Dubnau DA	65
1A212	BD108	<i>arg(GH)3 lys-21 metB5 pheA12 purA16 rpIV1</i>	Dubnau DA	Dubnau DA	63
1A213	BD237	<i>recA8 thr-5 trpC2</i>	Dubnau DA	Dubnau DA	64
1A214	BD274	<i>polA59 thr-5 trpC2</i>	Dubnau DA	Dubnau DA	63
1A215	BD291	<i>polA5 thr-5 trpC2</i>	Dubnau DA	Dubnau DA	63
1A216	BD332	<i>polC12 pyrA26 spcB3 strB3</i>	Dubnau DA	Dubnau DA	63
1A217	BD336	<i>polC133 thr-5 trpC2</i>	Dubnau DA	Dubnau DA	63
1A218	IS121	<i>rpIV1</i>	Smith I	Smith I	250
1A219	IS158	<i>rpsE2</i>	Smith I	Smith I	97
1A220	IS164	<i>rplC1</i>	Smith I	Smith I	97
1A221	IS165	<i>lmrA2</i>	Smith I	Smith I	97
1A222	IS166	<i>cysE14 rpIV1 Spo⁻</i>	Smith I	Smith I	97
1A223	170-1	<i>rpsL1 tmsB853</i>	Smith I	Smith I	252
1A224	SB1058	<i>hisH2 pheA1 trpC2</i>	Lederberg J	Lederberg J	155
1A225	SB1059	<i>pheA1 polA5 trpC2</i>	Lederberg J	Lederberg J	155
1A226	SB1060	<i>hisH2 pheA1 polA5 trpC2</i>	Lederberg J	Lederberg J	155
1A227	SB112	<i>pheA1 trpC2</i>	Lederberg J	Lederberg J	191
1A228	CU373 SB1115	<i>ilvB 5 trpC2</i>	Zahler SA	Lederberg J	300
1A229	SB135	<i>aroE1</i>	Lederberg J	Lederberg J	155
1A230	GSY483 SB1141	<i>ilvD6 thyA1 trpC2</i>	Anagnostopoulos C	Lederberg J	155
1A231	GSY277 SB1142	<i>ilvA2 trpC2</i>	Lederberg J	Lederberg J	19
1A232	GSY276 SB1143	<i>ilvD4 trpC2</i>	Lederberg J	Lederberg J	19
1A233	GSY260 SB1144	<i>ilvD2 trpC2</i>	Lederberg J	Lederberg J	19
1A234	GSY226 SB1145	<i>metB2 trpC2</i>	Lederberg J	Lederberg J	19
1A235	GSY227 SB1146	<i>metB3 trpC2</i>	Lederberg J	Lederberg J	19
1A236	PG522	<i>fruA20 ura-3</i>	Gay P	Gay P	95
1A237	PG524	<i>fruB22 ura-3</i>	Gay P	Gay P	95
1A238	TS3	<i>fus-3 str</i>	Ron EZ	Ron EZ	3
1A239	BR95,GLPD8	<i>glpD8 ilvC1 trpC2</i>	Rutberg B	Rutberg B	161
1A240	BR95,GLPK	<i>glpK21 pheA1 trpC2</i>	Rutberg B	Rutberg B	161
1A241	JAS1	<i>cysE14 rpsE2</i>	Shapiro JA	Shapiro JA	243
1A242	BD99	<i>hisA1 thr-5 trpC2</i>	Dubnau DA	Mahler I	63
1A243	168TT	<i>thyA1 thyB1 trpC2</i>	Rothman F	Marmur J	77
1A246	SB168 168	<i>trpC2</i>	Lederberg J	Lederberg J	30
1A248	LS11	<i>rpoB500 trpC2</i>	Sonenshein AL	Sonenshein AL	255
1A249	JH825	<i>ilvC1 pheA1 strC23</i>	Hoch JA	Hoch JA	123
1A250	CU466	<i>alsR1 ilvB 1 trpC2</i>	Zahler SA	Zahler SA	302
1A251	CU869	<i>purM1 trpC2</i>	Zahler SA	Zahler SA	301
1A253	RM125	<i>arg(GH)15 leuB8 hsd_RRM SP10^S</i>	Uozumi T	Uozumi T	277
1A254	PHOP,PHEA	<i>pheA phoP</i>	Cozzarelli NR	Mahler I	46

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1A255	PHOP12	<i>phoP12</i>	Hoch JA	Mahler I	123
1A256	NP22.1	<i>phoP22</i>	Grant W	Mahler I	100
1A257	NP4.1	<i>phoP4</i>	Grant W	Mahler I	100
1A258	103	<i>ile leu metB5 thyA1 thyB1</i>	Farmer JL	Arnaud M	76
1A259	RC220 103SU+3	<i>-(met)+ ile leu trnS-Lys3 thyA1 thyB1</i>	Halvorson HO	Arnaud M	107
1A260	RC221 103SU+44	<i>-(met)+ ile leu sup-44 thyA1 thyB1</i>	Halvorson HO	Arnaud M	107
1A261	VUB212	<i>metB4 gyrB1 recD27 trpC2</i>	Harford N	Dedonder RA	109
1A262	VUB234	<i>gyrB2 recF15 thr-5 trpC2</i>	Harford N	Dedonder RA	109
1A263	QB752	<i>metC pfk ptsI1</i>	Dedonder RA	Dedonder RA	59
1A264	QB1180	<i>-(hisA1)+ sup-44 thr-5</i>	Dedonder RA	Dedonder RA	59
1A267	168BRY	<i>bry</i>	Sonenshein AL	Sonenshein AL	253
1A268	TS-151	<i>thyA1 thyB1 tmsA151 trpC2</i>	Mendelson NH	Mendelson NH	176
1A269	TS-355	<i>spo⁻ thyA1 thyB1 trpC2 ts-355</i>	Mendelson NH	Mendelson NH	176
1A270	SH	prototroph <i>str sul</i>	Magasanik B	Magasanik B	37
1A271	SH-5	<i>hutP1 str sul</i>	Magasanik B	Magasanik B	37
1A272	SH-3	<i>hutH1 str sul</i>	Magasanik B	Magasanik B	37
1A273	SH-2	<i>hutCR1 str sul</i>	Magasanik B	Magasanik B	37
1A274	512	<i>npr</i>	Millet J	Streips UN	179
1A275	SB133	<i>pheA1</i>	Lederberg J	Lederberg J	191
1A276	2355	<i>ilvA1 metB5 polA1443 polC1</i>	Gross J	Brown NC	102
1A277	BC37,PUR ⁺	<i>arg(GH)3 lys-21 metB5 pheA12</i>	Copeland JC	Copeland JC	43
1A278	CU296	<i>citD 1 trpC2</i>	Zahler SA	Zahler SA	302
1A279	CU79	<i>-(hisA1)+ -(metC3)+ sup-22 trpC2</i>	Zahler SA	Zahler SA	300
1A280	QUA2	<i>asaA 2 leu-2 trpC2</i>	Adams, A.	Adams, A.	2
1A281	QUA4	<i>asaA4 leu-2 trpC2</i>	Adams, A.	Adams, A.	2
1A282	QUA184	<i>asaA 2 asaB1 leu-2 trpC2</i>	Adams, A.	Adams, A.	1
1A283	QUA188	<i>asaA4 asaB4 leu-2 trpC2</i>	Adams, A.	Adams, A.	1
1A284	GB78	<i>metC3 pyrA xhd-1</i>	Garro, AJ	Garro, AJ	92
1A285	SB419	<i>inh-1</i>	Lederberg, J	Lederberg, J	192
1A286	SB443	<i>inh-491</i>	Lederberg, J	Lederberg, J	191
1A287	168S ^R	<i>rpsL tmsA1 trpC2</i>	McDonald WC	McDonald WC	173
1A288	QB1130	<i>amyE dal-1 metB5 sacA321</i>	Dedonder RA	Dedonder RA	259
1A289	QB1133	<i>amyE aroI906 metB5 sacA321</i>	Dedonder RA	Dedonder RA	259
1A290	TS-134	<i>dnaB134 thyA1 thyB1 trpC2</i>	Mendelson NH	Mendelson NH	176
1A291	BC102	<i>leuB8 metB5 purA16 gcaD26</i>	Copeland JC	Copeland JC	45
1A292	CU403,DIVIVB	<i>minD1 metB5 thyA1 thyB1</i>	Mendelson NH	Mendelson NH	215
1A293	61676	<i>guaB3 metC7 purH1 trpC2</i>	Heinz J	Freese E	113
1A294	61677	<i>guaA2 metC7 purH1 trpC2</i>	Heinz J	Freese E	113
1A295	C66	<i>aspB66 trpC2</i>	Hoch JA	Freese E	123
1A296	61501	<i>aspH1 trpC2</i>	Diesterhaft M	Freese E	131
1A297	60348	<i>amyE aspT1 trpC2</i>	Freese E	Freese E	284
1A298	PB1728	<i>aroB2 azpB80 hisH2 trpC2 tyrA1</i>	Mazza PG	Mazza PG	34
1A299	PB1782	<i>aroB2 hisH2 gyrA trpC2 tyrA1</i>	Mazza PG	Mazza PG	34
1A300	PB3292	<i>glyA thyA1 thyB1 trpC2</i>	Mazza PG	Mazza PG	34
1A301	PB1663	<i>hisH2 recH342 trpC2</i>	Prozorov AA	Mazza PG	213
1A302	GSY908	<i>argF4 hisA1 recA4</i>	Anagnostopoulos C	Anagnostopoulos C	9
1A303	1604	<i>trpC2</i>	Smith DA	Moir A	181
1A304	YB886	<i>metB5 SPβ⁻ trpC2 xin-1</i>	Yasbin R	Yasbin R	288
1A305	CU1459	<i>trpC2 urs-77</i>	Zahler SA	Zahler SA	300
1A306	SL330	<i>metC3 phoR2 tal-1</i>	Piggot PJ	Piggot PJ	204
1A307	305.7	<i>leuB8 phoS5 tal-1</i>	Piggot PJ	Piggot PJ	207
1A308	W168,RIF-18 DB31	<i>rpoB18</i>	Sueoka N	Doi RH	261
1A309	NP40	prototrophic	Jensen RA	Jensen RA	141
1A311	YY88	<i>amyE^(+M) amyR2 metB5 pro(L) purF6</i> <i>deg-9 str</i>	Yondea YS	Zalkin H	290
1A312	tmsB1	<i>argF4 flaC51 hag-1 hisA1 ura</i>	Simon MI	Ordal GW	247
1A313	BR77	<i>thr-5 trpC2</i>	Reilly BE	Ordal GW	294
1A314	VA321	<i>divV32 thr-5 trpC2</i>	Simon MI	Ordal GW	278
1A315	VA71,THR(+)	<i>divV71 trpC2</i>	Simon MI	Ordal GW	278
1A316	VA55	<i>divII55 thr-5 trpC2</i>	Simon MI	Ordal GW	278
1A317	VA61	<i>divII61 thr-5 trpC2</i>	Simon MI	Ordal GW	278
1A318	VA322,THR(+)	<i>divI32 trpC2</i>	Simon MI	Ordal GW	278
1A319	SB22	<i>argF4 hisA1 purH4 trpC2</i>	Lederberg J	Lederberg J	155
1A320	SB58A	<i>purE6 trpC2</i>	Lederberg J	Lederberg J	155

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1A321	SB270A	<i>pyrE270</i>	Lederberg J	Lederberg J	155
1A322	SB305	<i>met pyrE305</i>	Lederberg J	Lederberg J	155
1A323	SB319	<i>met pyrD319</i>	Lederberg J	Lederberg J	155
1A325	CU641	<i>furB1 pyrR1 trpC2</i>	Zahler SA	Zahler SA	300
1A326	CU806	<i>citB1 gltA2 ilvA8 thyB1</i>	Zahler SA	Zahler SA	302
1A327	CU809	<i>gltA2 ilvA8 thyA1 thyB1</i>	Zahler SA	Zahler SA	302
1A329	168M	<i>trpC2</i>	Zahler SA	Zahler SA	302
1A330	JKB3141	<i>aroA932 bioB141</i>	Pai CH	Zahler SA	201
1A331	CU281	<i>citB1 trpC2</i>	Zahler SA	Zahler SA	300
1A332	CU927	<i>citD 1 ilvA8 thyA1 thyB1</i>	Zahler SA	Zahler SA	300
1A333	WB577	<i>pyrD</i>	Nester EW	Nester EW	189
1A334	GSY2258	<i>addA5 hisH2 metB5</i>	Anagnostopoulos C	Anagnostopoulos C	9
1A335	GSY1028	<i>metB4 recB2 trpC2</i>	Anagnostopoulos C	Saito H	124
1A336	BD77	<i>amm-35 leuB8 metB5 purA16</i>	Dubnau D	Dubnau D	63
1A337	PB1429	<i>amt</i>	Polsinelli M	Polsinelli M	209
1A338	6160	<i>amyE^(+M) amyR1^(+M) metB5 pro^L purF6</i>	Ikeda Y	Yoneda YS	132
1A339	YN21	<i>trpB3</i> <i>amyE^(+M) amyR21^{(+M)(H)} metB5 pro^L purF6</i>	Yoneda YS	Yoneda YS	289
1A340	YN118	<i>str trpB3</i> <i>amyE^(+M) amyR1 aroI116 metB5 pro^L deg-118 str trpB3</i>	Yoneda YS	Yamane K	290
1A341	NP58	<i>amyE^(+M) amyR1^(+M) metB5 pro^H purF6 str trpB3</i>	Uehara H	Yoneda YS	276
1A342	168EBR	<i>ebr-2 hisH2 thyA1 thyB1</i>	Munakata N	Munakata N	185
1A343	UVS80	<i>hisH2 rec-80 thyA1 thyB1</i>	Munakata N	Munakata N	185
1A344	UVS1	<i>met-14 sul thyA1 thyB1 trpC2 uvrB10</i>	Munakata N	Munakata N	185
1A345	UVS42	<i>met-14 sul thyA1 thyB1 trpC2 uvrB42</i>	Munakata N	Munakata N	185
1A346	UVS109	<i>hisH2 thyA1 thyB1 uvrC109</i>	Munakata N	Munakata N	185
1A347	UVS114	<i>hisH2 thyA1 thyB1 uvrC114</i>	Munakata N	Munakata N	185
1A348	VB104	<i>lys-1 lysS2</i>	Steinberg W	Zuber PA	214
1A349	VB106	<i>lysS2 metB3</i>	Steinberg W	Zuber PA	214
1A350	VB107A	<i>lysS1 trpC2</i>	Steinberg W	Zuber PA	257
1A351	VB122A	<i>lys-1 lysS1</i>	Steinberg W	Zuber PA	257
1A352	VB126	<i>trpC2 trpS1</i>	Steinberg W	Zuber PA	257
1A353	VB127	<i>trpS1</i>	Steinberg W	Zuber PA	257
1A354	VB157	<i>sul trpC2</i>	Steinberg W	Zuber PA	257
1A355	VB158	<i>hisH2 pabB trpC2</i>	Steinberg W	Zuber PA	257
1A356	VB293	<i>aec hom-1 trpC2</i>	Steinberg W	Zuber PA	257
1A357	VB355B	<i>aecB lys-1 sul trpC2</i>	Steinberg W	Zuber PA	257
1A358	VB336F	<i>aecA lys-1 sul trpC2</i>	Steinberg W	Zuber PA	257
1A360	GSY293	<i>hom-1 trpC2</i>	Anagnostopoulos C	Anagnostopoulos C	9
1A361	GSY505	<i>ilvA6</i>	Anagnostopoulos C	Anagnostopoulos C	9
1A363	RM125,MIT	<i>arg(GH)15 leuB8 hsd_RR^M rplV</i>	Mahler I	Mahler I	165
1A364	HS1A21	<i>citH</i>	Hanson RS	Hanson RS	108
1A365	N1G17	<i>arg(GH)15 trpB3</i>	Kada T	Kada T	143
1A366	N1G45	<i>arg(GH)15 recA45 trpB3</i>	Kada T	Kada T	143
1A367	CU812	<i>leuA169 suf-1 trpC2</i>	Zahler SA	Zahler SA	300
1A368	CU850	<i>leuD117 sup-67 trpC2</i>	Zahler SA	Zahler SA	300
1A369	HCR-9	<i>trpC2 uvrB9</i>	Okubo S	Matsumoto K	198
1A372	YB886TNR	<i>gyrB1 recF15 SPb^S trpC2 xin</i>	Dean DH	Perkins JB	54
1A373	N1G43	<i>arg(GH)15 recD43 trpB3</i>	Kada T	Kada T	143
1A374	S19TI	<i>thyA1 thyB1 trpC2 uvrB19</i>	Matsumoto K	Matsumoto K	170
1A375	S80TI	<i>rec-80 thyA1 thyB1 trpC2</i>	Matsumoto K	Matsumoto K	170
1A376	PG602	<i>fruC1 metC3 trpC2</i>	Gay P	Gay P	95
1A377	PG599	<i>fruB22 fruC1 metC3 trpC2</i>	Gay P	Gay P	95
1A378	PB1641	<i>aroB2 hisH2 recD41 trpC2 tyrA1</i>	Mazza GP	Mazza GP	172
1A379	PB1693	<i>aroB2 hisH2 recG39 trpC2 tyrA1</i>	Mazza GP	Mazza GP	14
1A380	PB1633	<i>aroB2 hisH2 recF33 trpC2 tyrA1</i>	Mazza GP	Mazza GP	172
1A381	PB1775	<i>cafA1 metB10 trpC2</i>	Mazza PG	Mazza PG	33
1A382	PB1440	<i>hisH2 pur-60 trpC2</i>	Mazza PG	Mazza PG	163
1A383	PB1439	<i>hisH2 purE7 trpC2</i>	Mazza PG	Mazza PG	163
1A384	PB2417	<i>pur-67 thyA1 thyB1</i>	Mazza PG	Mazza PG	163
1A385	PB3197	<i>hisH2 purE8 trpC2</i>	Mazza PG	Mazza PG	163
1A386	PB3233	<i>hisH2 purH5 thr trpC2</i>	Mazza PG	Mazza PG	163

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BGSC	ORIGINAL CODE	DESCRIPTION	SOURCE	DONOR	REF
1A387	Mu5u26	<i>metB5 purB26</i>	Chilton MD	Mazza PG	38
1A388	Mu5u12	<i>metB5 purE4</i>	Chilton MD	Mazza PG	38
1A389	Mu5u11	<i>metB5 purE5</i>	Chilton MD	Mazza PG	38
1A390	PB1673	<i>hisA53 rna-53</i>	Riva S	Mazza PG	218
1A391	H-37	<i>arg(S) pyrA</i>	Jensen R	Potvin BW	140,210
1A392	168MIU8	<i>pyrB trpC2</i>	Potvin BW	Potvin BW	211
1A393	168MIU16	<i>pyrB trpC3</i>	Potvin BW	Potvin BW	211
1A394	168MIU7	<i>pyrC trpC2</i>	Potvin BW	Potvin BW	211
1A395	168MIU17	<i>pyrC trpC2</i>	Potvin BW	Potvin BW	211
1A396	168MIU18	<i>pyrD trpC2</i>	Potvin BW	Potvin BW	211
1A397	SB491U6	<i>pyrD</i>	Potvin BW	Potvin BW	211
1A398	17A-42	<i>pyrCD</i>	Greer SB	Potvin BW	101
1A399	168MIU1	<i>pyrDF trpC2</i>	Potvin BW	Potvin BW	211
1A400	168MIU9	<i>pyrF trpC2</i>	Potvin BW	Potvin BW	211
1A401	168SU7	<i>pyrF trpC2</i>	Potvin BW	Potvin BW	211
1A402	168TUT	<i>pyrABC thyA1 thyB1 trpC2</i>	Romig W	Potvin BW	221
1A403	SB491U5	<i>pyrACD</i>	Potvin BW	Potvin BW	211
1A404	PB1653	<i>aroB2 hisA53 hisH2 rna-53 trpC2 tyrA1</i>	Riva S	Sonenshein AL	218
1A405	DR10	<i>rpoC10</i>	Rothstein D	Sonenshein AL	224
1A408	KE2	<i>aroD120 recA4 trpC2</i>	Epstein K	Sonenshein AL	69
1A409	RM22	<i>arg(GH)15 leuB8 hsd_RR^M recA4</i>	Sonenshein AL	Sonenshein AL	253
1A410	BS122	<i>nic</i>	Yanofsky C	Spizizen J	30
1A411	BS168NT	<i>his trpC2</i>	Young F	Spizizen J	293
1A412	NA64	<i>amyE^(+M) amyR2 metB5 purF6</i>	Yoneda Y	Yamane K	290
1A413	NA20-22	<i>amyE^(+N) amyR1 metB5</i>	Yoneda Y	Yamane K	291
1A414	NA20	<i>amyE^(+N) amyR2 metB5 purF6</i>	Yoneda Y	Yamane K	291
1A415	2M(I)S(I)	prototrophic	Cocito C	Cocito C	40
1A416	XVM(R)S(I)	<i>virM</i>	Cocito C	Cocito C	40
1A417	9M(I)S(R)	<i>virS</i>	Cocito C	Cocito C	39
1A418	91M(R)S(R)	<i>virM virS</i>	Cocito C	Cocito C	39
1A419	RB1479	<i>thyA thyB trpC2 xhi-1479 xki-1479</i>	Buxton RS	Buxton RS	31
1A420	RB1952	<i>ilvA1 metB5 purA16 xhi-1479 xki-1479</i>	Buxton RS	Buxton RS	31
1A421	RB1034	(ϕ 105) <i>ilvA1 metB5 purA16 xhi-1479 xki-1479</i>	Buxton RS	Buxton RS	31
1A422	MI120	<i>leuB6 hsd_RR^M recA4</i>	Tanaka T	Tanaka T	269
1A423	MI112	<i>arg(GH)15 leuB8 recA4 thr-5 hsd_RR^M</i>	Tanaka T	Tanaka T	269
1A424	FB7	<i>fnd-7</i>	Bazzicalupo M	Bazzicalupo M	22
1A425	FB8	<i>fnd-8</i>	Bazzicalupo M	Bazzicalupo M	22
1A426	PB3315	<i>fnd-15</i>	Bazzicalupo M	Bazzicalupo M	22
1A427	FB21	<i>ftr-21</i>	Bazzicalupo M	Bazzicalupo M	22
1A428	KA3	<i>met trpC2 ts-39-2</i>	Lindgren V	Lindgren V	160
1A429	KA10	<i>aroI906 glpT6 trpC2</i>	Lindgren V	Lindgren V	160
1A430	FB6	<i>azc-1</i>	Polsinelli M	Polsinelli M	91
1A431	FB56	<i>aec-56</i>	Polsinelli M	Polsinelli M	171
1A432	FB59	<i>aec-59</i>	Polsinelli M	Polsinelli M	171
1A433	PB3242	<i>ptm-42</i>	Polsinelli M	Polsinelli M	208
1A434	FB74	<i>ala-1 leuB8 metB pur thr-5 trpC</i>	Polsinelli M	Polsinelli M	208
1A435	FB12	<i>pro-1</i>	Polsinelli M	Polsinelli M	208
1A436	IG-20	<i>hsd_RR^M trpC2</i>	Bron S	Bron S	27
1A437	8G-5	<i>ade his hsd_RR^M met nic rib trp tyr ura</i>	Bron S	Bron S	27
1A438	6G-R	<i>hsd_RR^M met nic rib trp tyr ura</i>	Bron S	Bron S	27
1A439	RB403	<i>leuB8 menC315 trpC2</i>	Taber HW	Taber HW	265
1A440	RB308	<i>arg(GH)2 hema1</i>	Ivanovics G	Taber HW	137
1A441	PG650	<i>gutR1 ura-3</i>	Gay P	Gay P	94
1A442	PG662	<i>gutA2 leuB8 trpC2</i>	Gay P	Gay P	36
1A443	PG668	<i>gutB2 leuB8 trpC2</i>	Gay P	Gay P	36
1A445	HLL3g	<i>hisA1 leuB8 lys-21 metB5 nonA1 purF6 SP10(R) thr-5 trpC2</i>	Saito H	Witmer HJ	229
1A446	PRA2	<i>hisA1 leuB8 lys-21 metB5 nonA1 SP10(R) trpC2</i>	Saito H	Witmer HJ	228
1A447	1019	<i>hsrM1 leuB8 metB5 SP10(R)</i>	Saito H	Witmer HJ	229
1A448	PS9W7	<i>hisA1 hsrM1 leuB8 nonA1 rpoB SP10(S) thr-5</i>	Saito H	Witmer HJ	229
1A449	LS105	<i>car-41 leuB8 metB5 purF6 rpoC105</i>	Sonenshein AL	Sonenshein AL	254

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BGSC	ORIGINAL CODE	DESCRIPTION	SOURCE	DONOR	REF
1A450	LS121	<i>rpoC121</i>	Sonenshein AL	Sonenshein AL	253
1A451	IAM1247	<i>hsd_BR⁺M⁺ hsd_CR⁺M⁺</i>	Saito H	Witmer HJ	229
1A452	GB7044	<i>ilvB2 leuA169</i>	Garro AJ	Garro AJ	92
1A453	GB7018,CU229	<i>ilvB2 trpC2</i>	Zahler SA	Garro AJ	281
1A454	GB7037,CU614	<i>leuA169 trpC2</i>	Zahler SA	Garro AJ	281
1A455	GB7075	<i>trpC2 uvrB9</i>	Garro AJ	Garro AJ	92
1A456	GB7068	<i>ilvD6 thyA thyB1</i>	Garro AJ	Garro AJ	92
1A457	CU1428	<i>ilvA2 ilvD15 SPβ^S thyA5 thyB5 trpC2</i>	Zahler SA	Zahler SA	79
1A458	CU1430	<i>ilvA2 SPβ^S thyA5 thyB5 trpC2</i>	Zahler SA	Zahler SA	79
1A459	SU+III	<i>leuB8 metB5 SPβ^S trnS-Lys3 thr-5</i>	Hemphill HE	Zahler SA	283
1A460	CU403	<i>ilvA8 metB5 thyA1 thyB1</i>	Zahler SA	Zahler SA	300
1A461	SB19E,ts2pyrG1	<i>ctrA1 ts-2</i>	Takahashi I	Takahashi I	266
1A462	6TR1	<i>leuB8 metB5 tem-1</i>	Siegel E	Siegel E	245
1A463	RB1949	<i>ddlA1475 ilvA1 metB5 purA16</i>	Buxton RS	Buxton RS	32
1A464	MS320	<i>dapE320 thyA1 thyB1 trpC2</i>	Buxton RS	Buxton RS	32
1A465	61656	<i>fbp-1 hisA1 leuB8 metB5 trpC2</i>	Iijima T	Freese E	85
1A466	MY2011	<i>lys-1 pyrD1 rpoB sas-1</i>	Yudkin MD	Yudkin MD	299
1A467	MY2013	<i>lys-1 pyrD1 rpoB sas-2</i>	Yudkin MD	Yudkin MD	299
1A468	60984	<i>glms2 metC7 trpC2</i>	Freese EB	Freese E	84
1A471	61494	<i>aceA1 bfmB metC7 trpC2</i>	Willecke K	Freese E	25
1A472	61539	<i>bfmB1 iur trpC2</i>	Iijima T	Freese E	25
1A473	61571	<i>bfmB1 strC2 trpC2</i>	Iijima T	Freese E	25
1A474	TIBS 57	<i>amyE3 aroI10</i>	Trenk HL	Turner HR	274
1A475	IS169	<i>rplK6 thr-5 trpC2</i>	Smith I	Smith I	251
1A476	HA101	<i>hisA1 metB5</i>	Okuba S	Steward C	199
1A477	HA101B	<i>-(hisA1)+ -(metB5)+ sup-1</i>	Okuba S	Steward C	199
1A478	M5	<i>lys-3 metB10 spc spcD trpC2</i>	Chambliss G	Chambliss G	118
1A479	22-4	<i>cdd-1 crk-1 dck-3</i>	Takahashi I	Takahashi I	266
1A480	ddd-3	<i>cdd-1 ddd-3</i>	Takahashi I	Takahashi I	266
1A481	PB3242	<i>ptm-42</i>	Galizzi A	Galizzi A	89
1A482	PB2328	<i>hisH2 metD4 outA7 trpC2</i>	Galizzi A	Galizzi A	89
1A483	FJ3	<i>lyt-1 metC3</i>	Rogers HJ	Buxton RS	78
1A484	FJ6	<i>lyt-2 metC3</i>	Rogers HJ	Buxton RS	78
1A485	ROD104	<i>leuB8 mreD1</i>	Rogers HJ	Buxton RS	147
1A486	ROD113	<i>leuB8 tagF1</i>	Rogers HJ	Buxton RS	147
1A487	TKJ6901	<i>thyA1 thyB1 urg-1</i>	Munakata N	Munakata N	167
1A488	SSP	<i>met-14 splB1 sul thyA1 thyB1 trpC2</i>	Munakata N	Munakata N	187
1A489	UVSP-42-1	<i>met-14 splB1 sul thyA1 thyB1 trpC2 uvrB42</i>	Munakata N	Munakata N	186
1A490	UTB600	<i>gltB1 leuB8 metB10</i>	Kane J	Kane J	144
1A491	TTK24	<i>dfrA24 pabA7</i>	Kane J	Kane J	144
1A492	HA101-2-9	<i>citC met pheA trpC2</i>	Peebles C	Hadden C	203
1A493	HA101-2-10	<i>citC met polA10 trpC2</i>	Peebles C	Hadden C	203
1A494	HA106	<i>hisH2 leu met recF7</i>	Strauss B	Hadden C	110, 260
1A495	GSY1619	<i>metB4 recB19 trpC2</i>	Harford N	Hadden C	110
1A496	GSY1615	<i>metB4 recF15 trpC2</i>	Harford N	Hadden C	110
1A497	PB1625	<i>hisH2 rec-25 trpC2</i>	Mazza G	Hadden C	172
1A498	PB1629	<i>hisH2 rec-29 trpC2</i>	Mazza G	Hadden C	172
1A499	PB1630	<i>hisH2 rec-30 trpC2</i>	Mazza G	Hadden C	172
1A500	MB23	<i>cym-1 rpoB1</i>	Piggot PJ	Piggot PJ	205
1A501	EE1	<i>amy-3 aro-10 lmrA2</i>	Eng E	Dean DH	54
1A502	Nil (oxr-1)	<i>oxr-1 thyA thyB</i>	Mandelstam J	Mandelstam J	280
1A503	Nil (oxr-2)	<i>oxr-2 thyA thyB trpC2</i>	Mandelstam J	Mandelstam J	280
1A504	NI15	<i>lyt-15 thyA thyB trpC2 xin-15</i>	Karamata D	Karamata D	145
1A505	MCB	<i>MC^S trpC2 UC^S</i>	Trautner TA	Trautner TA	273
1A506	222	<i>arg trp</i>	Hiroka H	Hiroka H	122, 236
1A507	FUS426	<i>fus Spo(Ts)</i>	Kobayashi T	Kobayashi T	121
1A508	FUS429	<i>fus Spo(Con)</i>	Kobayashi T	Kobayashi T	121
1A509	UOTO277	<i>hisA1 hsd_RR⁺M⁺ metB5 recA4</i>	Shimotsu H	Shimotsu H	244
1A510	PSL1	<i>arg(GH)15 leuB8 hsd_RR⁺M⁺ recA4 stp thr</i>	Pene J	Pene J	200
1A511	BD393	<i>lys-3 thyA thyB trpC2</i>	Dubnau D	Dubnau D	63

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1A512	RB541	<i>ahrC2</i>	Baumberg S	Baumberg S	20
1A513	CU403, DIVIVB1	<i>minD1 metB5 tag-1 thyA thyB1</i>	Mendelson NH	Mendelson NH	176
1A514	TKJ3422	<i>hisH101 lys-21 recA4 spiB1 thyA thyB uvrB10</i>	Munakata N	Munakata N	184
1A516	trpE1 (ICR 1)	<i>trpE1</i>	Carlton BC	Carlton BC	285
1A517	trpE2 (ICR 6)	<i>trpE2</i>	Carlton BC	Carlton BC	285
1A518	trpE3 (ICR 14)	<i>trpE3</i>	Carlton BC	Carlton BC	285
1A519	trpE4 (ICR 16)	<i>trpE4</i>	Carlton BC	Carlton BC	285
1A520	trpE5 (UV 17)	<i>trpE5</i>	Carlton BC	Carlton BC	285
1A521	trpE194 (SB194)	<i>trpE194</i>	Carlton BC	Carlton BC	285
1A522	trpD1 (NA 1)	<i>trpD1</i>	Carlton BC	Carlton BC	285
1A523	trpD2 (NA 3)	<i>trpD3</i>	Carlton BC	Carlton BC	285
1A524	trpD4 (NG 61)	<i>trpD4</i>	Carlton BC	Carlton BC	285
1A525	trpD5 (NG 62)	<i>trpD5</i>	Carlton BC	Carlton BC	285
1A526	trpD6 (NG 120)	<i>trpD6</i>	Carlton BC	Carlton BC	285
1A527	trpD7 (ICR 10)	<i>trpD7</i>	Carlton BC	Carlton BC	285
1A528	trpD8 (ICR 11)	<i>trpD8</i>	Carlton BC	Carlton BC	285
1A529	trpD9 (ICR 19)	<i>trpD9</i>	Carlton BC	Carlton BC	285
1A530	trpD10 (ICR 22)	<i>trpD10</i>	Carlton BC	Carlton BC	285
1A531	trpF1 (NA 2)	<i>trpF1</i>	Carlton BC	Carlton BC	285
1A532	trpF2 (NA 4)	<i>trpF2</i>	Carlton BC	Carlton BC	285
1A533	trpF3 (NA 6)	<i>trpF3</i>	Carlton BC	Carlton BC	285
1A534	trpF4 (NA 7)	<i>trpF4</i>	Carlton BC	Carlton BC	285
1A535	trpF5 (NA 10)	<i>trpF5</i>	Carlton BC	Carlton BC	285
1A536	trpF6 (NA 11)	<i>trpF6</i>	Carlton BC	Carlton BC	285
1A537	trpF8 (HA2)	<i>trpF8</i>	Carlton BC	Carlton BC	285
1A538	trpF9 (PH 1)	<i>trpF9</i>	Carlton BC	Carlton BC	285
1A539	trpF10 (ICR 12)	<i>trpF10</i>	Carlton BC	Carlton BC	285
1A540	trpF11 (SB 11)	<i>trpF11</i>	Carlton BC	Carlton BC	285
1A541	trpF12 (NA 5)	<i>trpF12</i>	Carlton BC	Carlton BC	285
1A542	trpF13 (HA 1)	<i>trpF13</i>	Carlton BC	Carlton BC	285
1A543	trpC1 (NG 1)	<i>trpC1</i>	Carlton BC	Carlton BC	285
1A544	trpC3 (NG 3)	<i>trpC3</i>	Carlton BC	Carlton BC	285
1A545	trpC4 (NG 5)	<i>trpC4</i>	Carlton BC	Carlton BC	285
1A546	trpC5 (NG 24)	<i>trpC5</i>	Carlton BC	Carlton BC	285
1A547	trpC6 (UV 15)	<i>trpC6</i>	Carlton BC	Carlton BC	285
1A548	trpC7 (UV 16)	<i>trpC7</i>	Carlton BC	Carlton BC	285
1A549	trpC8 (UV 18)	<i>trpC8</i>	Carlton BC	Carlton BC	285
1A550	trpC9 (EMS 1)	<i>trpC9</i>	Carlton BC	Carlton BC	285
1A551	trpC10 (EMS 2)	<i>trpC10</i>	Carlton BC	Carlton BC	285
1A552	trpC11 (NG 2)	<i>trpC11</i>	Carlton BC	Carlton BC	285
1A553	trpA1 (NG 63)	<i>trpA1</i>	Carlton BC	Carlton BC	285
1A554	trpA2 (NA 9)	<i>trpA2</i>	Carlton BC	Carlton BC	285
1A555	trpA3 (T 50)	<i>trpA3</i>	Carlton BC	Carlton BC	285
1A556	trpA4 (T 51)	<i>trpA4</i>	Carlton BC	Carlton BC	285
1A557	trpA6 (ICR 17)	<i>trpA6</i>	Carlton BC	Carlton BC	285
1A558	trpA7 (ICR 21)	<i>trpA7</i>	Carlton BC	Carlton BC	285
1A559	trpB1 (NG 4)	<i>trpB1</i>	Carlton BC	Carlton BC	285
1A560	trpB2 (NG 6)	<i>trpB2</i>	Carlton BC	Carlton BC	285
1A561	trpB5 (NG 14)	<i>trpB5</i>	Carlton BC	Carlton BC	285
1A562	trpB6 (NG 57)	<i>trpB6</i>	Carlton BC	Carlton BC	285
1A563	trpB7 (NG 58)	<i>trpB7</i>	Carlton BC	Carlton BC	285
1A564	trpB8 (NG 59)	<i>trpB8</i>	Carlton BC	Carlton BC	285
1A565	trpB9 (NG 60)	<i>trpB9</i>	Carlton BC	Carlton BC	285
1A566	trpB10 (ICR 8)	<i>trpB10</i>	Carlton BC	Carlton BC	285
1A567	trpB11 (ICR 9)	<i>trpB11</i>	Carlton BC	Carlton BC	285
1A568	trpB12 (ICR 13)	<i>trpB12</i>	Carlton BC	Carlton BC	285
1A569	trpB13 (ICR 15)	<i>trpB13</i>	Carlton BC	Carlton BC	285
1A570	trpB14 (ICR 18)	<i>trpB14</i>	Carlton BC	Carlton BC	285

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1A571	trpB15 (ICR 20)	<i>trpB15</i>	Carlton BC	Carlton BC	285
1A572	trpB16 (NG 7)	<i>trpB16</i>	Carlton BC	Carlton BC	285
1A573	OBS2	<i>cer-2 trpC2</i>	Zeigler DR	Zeigler DR	304
1A574	GSY1127	<i>hisH2 ilvC1/ilvC(+)</i>	Anagnostopoulos C	Anagnostopoulos C	237
1A575	CU3497	<i>ilvA2 recA4 spcB1 trpC2</i>	Zahler SA	Zahler SA	300
1A576	OBS14	<i>cer-14 trpC2</i>	Zeigler D	Zeigler D	304
1A577	OBS20	<i>cer-20 trpC2</i>	Zeigler D	Zeigler D	304
1A578	168 cam2	<i>cam-2 trpC2</i>	Bott KF	Bott KF	10
1A579	GLU-1	<i>sigA1</i>	Takahashi I	Takahashi I	267
1A580	FRU-4	<i>sigA4</i>	Takahashi I	Takahashi I	267
1A581	GLU-47	<i>sigA47</i>	Takahashi I	Takahashi I	267
1A582	GLU-40	<i>crsB40</i>	Takahashi I	Takahashi I	267
1A583	RIB-2	<i>crsC1</i>	Takahashi I	Takahashi I	267
1A584	GLN-2	<i>crsC2</i>	Takahashi I	Takahashi I	267
1A585	MAN-A1 (CS25)	<i>crsD1</i>	Takahashi I	Takahashi I	263
1A586	MAN-B1 (CS26)	<i>crsE1</i>	Takahashi I	Takahashi I	263
1A587	MAL-4	<i>crsF4</i>	Takahashi I	Takahashi I	267
1A588	Sz 3 (R15)	<i>hemA1 trpC2</i>	Miczák A	Miczák A	11
1A589	Sz 15 (I/1)	<i>hemB1 trpC2</i>	Miczák A	Miczák A	23
1A590	Sz 16 (II/33)	<i>hemC33 trpC2</i>	Miczák A	Miczák A	23
1A591	Sz 34	<i>hemD11 trpC2</i>	Miczák A	Miczák A	178
1A592	Sz 26 (V/64)	<i>hemE64 trpC2</i>	Miczák A	Miczák A	23
1A593	Sz 27 (VI/180)	<i>hemH180 trpC2</i>	Miczák A	Miczák A	23
1A594	Sz 28 (III/321)	<i>hemY321 trpC2</i>	Miczák A	Miczák A	23
1A595	PB2321	<i>arg thyA thyB tscA1</i>	Galizzi A	Galizzi A	90
1A596	PB2338	<i>arg thyA thyB tscA23</i>	Galizzi A	Galizzi A	90
1A597	PB2355	<i>arg thyA thyB nadE49</i>	Galizzi A	Galizzi A	90
1A598	PB2330	<i>arg thyA thyB tscC11</i>	Galizzi A	Galizzi A	90
1A599	PB2336	<i>arg thyA thyB tscD14</i>	Galizzi A	Galizzi A	90
1A600	CU4120	(SPβc2) <i>cym-84::Tn917 trpC2</i>	Zahler SA	Zahler SA	279
1A601	CU4121	(SPβc2) <i>purM::Tn917 trpC2</i>	Zahler SA	Zahler SA	279
1A602	CU4122	(SPβc2) <i>ath-83::Tn917 trpC2</i>	Zahler SA	Zahler SA	279
1A603	CU4123	(SPβc2) <i>thiA84::Tn917 trpC2</i>	Zahler SA	Zahler SA	279
1A604	CU4124	(SPβc2) <i>metD83::Tn917 trpC2</i>	Zahler SA	Zahler SA	279
1A605	CU4125	(SPβc2) <i>argF83::Tn917 trpC2</i>	Zahler SA	Zahler SA	279
1A606	CU4126	(SPβc2) <i>argF82::Tn917 trpC2</i>	Zahler SA	Zahler SA	279
1A607	CU4127	(SPβc2) <i>metC85::Tn917 trpC2</i>	Zahler SA	Zahler SA	279
1A608	CU4128	(SPβc2) <i>arg342::Tn917 trpC2</i>	Zahler SA	Zahler SA	279
1A609	CU4129	(SPβc2) <i>pyr-82::Tn917 trpC2</i>	Zahler SA	Zahler SA	279
1A610	CU4130	(SPβc2) <i>pyr-83::Tn917 trpC2</i>	Zahler SA	Zahler SA	279
1A611	CU4131	(SPβc2) <i>trpC2 urc-83::Tn917</i>	Zahler SA	Zahler SA	279
1A612	CU4132	(SPβc2) <i>gltAB81::Tn917 trpC2</i>	Zahler SA	Zahler SA	279
1A613	CU4133	(SPβc2) <i>aroBC84::Tn917 trpC2</i>	Zahler SA	Zahler SA	279
1A614	CU4134	(SPβc2) <i>serA84::Tn917 trpC2</i>	Zahler SA	Zahler SA	279
1A615	CU4135	(SPβc2) <i>lys-82::Tn917 trpC2</i>	Zahler SA	Zahler SA	279
1A616	CU4136	(SPβc2) <i>nic-82::Tn917 trpC2</i>	Zahler SA	Zahler SA	279
1A617	CU4137	(SPβc2) <i>pheA82::Tn917 trpC2</i>	Zahler SA	Zahler SA	279
1A618	CU4138	(SPβc2) <i>leuB84::Tn917 trpC2</i>	Zahler SA	Zahler SA	279
1A619	CU4139	(SPβc2) <i>liv1-82::Tn917 trpC2</i>	Zahler SA	Zahler SA	279
1A620	CU4140	(SPβc2) <i>liv3-83::Tn917 trpC2</i>	Zahler SA	Zahler SA	279
1A621	CU4141	(SPβc2) <i>serC82::Tn917 trpC2</i>	Zahler SA	Zahler SA	279
1A622	CU4142	(SPβc2) <i>arg(GH)85::Tn917 trpC2</i>	Zahler SA	Zahler SA	279
1A623	CU4143	(SPβc2) <i>alaA84::Tn917 trpC2</i>	Zahler SA	Zahler SA	279
1A624	CU4144	(SPβc2) <i>mth-83::Tn917 trpC2</i>	Zahler SA	Zahler SA	279
1A625	CU4145	(SPβc2) <i>mth-84::Tn917 trpC2</i>	Zahler SA	Zahler SA	279
1A626	CU4146	(SPβc2) <i>hisA82::Tn917 trpC2</i>	Zahler SA	Zahler SA	279
1A627	CU4147	(SPβc2) <i>trpC2 zaa-84::Tn917</i>	Zahler SA	Zahler SA	279
1A628	CU4148	(SPβc2) <i>trpC2 zbj-82::Tn917</i>	Zahler SA	Zahler SA	82, 279
1A629	CU4149	(SPβc2) <i>trpC2 zca-82::Tn917</i>	Zahler SA	Zahler SA	279
1A630	CU4150	(SPβc2) <i>trpC2 zce-82::Tn917</i>	Zahler SA	Zahler SA	82, 279
1A631	CU4151	(SPβc2) <i>trpC2 motA::Tn917</i>	Zahler SA	Zahler SA	82, 279
1A632	CU4152	(SPβc2) <i>trpC2 kinC::Tn917</i>	Zahler SA	Zahler SA	82, 279

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BGSC	ORIGINAL CODE	DESCRIPTION	SOURCE	DONOR	REF
1A633	CU4153	(SP β c2) <i>trpC2 zdi-82::Tn917</i>	Zahler SA	Zahler SA	82, 279
1A634	CU4154	(SP β c2) <i>trpC2 zci-82::Tn917</i>	Zahler SA	Zahler SA	82, 279
1A635	CU4155	(SP β c2) <i>trpC2 proJ::Tn917</i>	Zahler SA	Zahler SA	82, 279
1A636	CU4156	(SP β c2) <i>trpC2 cgeE::Tn917</i>	Zahler SA	Zahler SA	82, 279
1A637	CU4157	(SP β c2) <i>trpC2 yokH::Tn917</i>	Zahler SA	Zahler SA	82, 279
1A638	CU4158	(SP β c2) <i>trpC2 zfg-83::Tn917</i>	Zahler SA	Zahler SA	82, 279
1A639	CU4159	(SP β c2) <i>trpC2 spoVID::Tn917</i>	Zahler SA	Zahler SA	82, 279
1A640	CU4160	(SP β c2) <i>trpC2 zhb-83::Tn917</i>	Zahler SA	Zahler SA	279
1A641	CU4161	(SP β c2) <i>trpC2 zhc-85::Tn917</i>	Zahler SA	Zahler SA	82, 279
1A642	CU4162	(SP β c2) <i>trpC2 yufR::Tn917</i>	Zahler SA	Zahler SA	82, 279
1A643	CU4163	(SP β c2) <i>trpC2 yvaC::Tn917</i>	Zahler SA	Zahler SA	82, 279
1A644	CU4164	(SP β c2) <i>trpC2 zii-83::Tn917</i>	Zahler SA	Zahler SA	279
1A645	CU4165	(SP β c2) <i>trpC2 zjf-85::Tn917</i>	Zahler SA	Zahler SA	279
1A646	CU2111	(SP β c2 <i>zfd-81::Tn917</i>) <i>trpC2</i>	Zahler SA	Zahler SA	279
1A647	PB2353	<i>arg thyA thyB nadE47</i>	Galizzi A	Galizzi A	90
1A648	PB2354	<i>arg thyA thyB nadE48</i>	Galizzi A	Galizzi A	90
1A649	PB2333	<i>arg thyA thyB tscD14</i>	Galizzi A	Galizzi A	90
1A650	R11	<i>lys-3 xynB7</i>	Roncero MIG	Roncero MIG	222
1A651	R21	<i>lys-3 xynA8</i>	Roncero MIG	Roncero MIG	222
1A652	146	<i>pro(AB)</i>	Harwood CR	Harwood CR	111
1A653	HJS30	<i>glnA200</i>	Schreier HJ	Schreier HJ	239
1A654	BG314	<i>aroD120 bgIS33 trpC2</i>	Borriss R	Borriss R	24
1A655	OBS30	<i>aroI906 cdr-1 trpC2</i>	Zeigler D	Zeigler D	304
1A656	KR10	<i>rpsI2</i>	Dabbs ER	Dabbs ER	51
1A657	DA9	<i>rplE1</i>	Dabbs ER	Dabbs ER	49
1A658	DA65	<i>rplK2 rpsH2</i>	Dabbs ER	Dabbs ER	49
1A659	DA63	<i>rpmD2</i>	Dabbs ER	Dabbs ER	48
1A660	DA14	<i>rplV1</i>	Dabbs ER	Dabbs ER	48
1A661	DA49	<i>rpsG3</i>	Dabbs ER	Dabbs ER	48
1A662	DB65	<i>cysE14 purA16 rpmA1 trpC2</i>	Dabbs ER	Dabbs ER	51
1A663	DB14	<i>cysE14 purA16 rpsK2 trpC2</i>	Dabbs ER	Dabbs ER	48
1A664	DA36	<i>rpsF1</i>	Dabbs ER	Dabbs ER	50
1A665	DA463	<i>rplA1 rplJ1 rplL1</i>	Dabbs ER	Dabbs ER	52
1A666	DA73	<i>rplE3</i>	Dabbs ER	Dabbs ER	48
1A667	DA46	<i>rplL1</i>	Dabbs ER	Dabbs ER	49
1A668	CA302	<i>rpsE302</i>	Dabbs ER	Dabbs ER	53
1A669	DA47	<i>rplX2</i>	Dabbs ER	Dabbs ER	48
1A670	DA32	<i>rplU1</i>	Dabbs ER	Dabbs ER	53
1A671	DA34	<i>rpsH3</i>	Dabbs ER	Dabbs ER	48
1A672	KA31805	<i>citK5 trpC2</i>	Rutberg L	Rutberg L	225
1A673	KA32817	<i>citM17 trpC2</i>	Hederstedt L	Hederstedt L	35
1A674	KA97103	<i>leu-2 sdhB103 trpC2</i>	Hederstedt L	Hederstedt L	112
1A675	PB73	<i>furB1 sigB::cat trpC2</i>	Price CW	Price CW	67
1A676	PB70	<i>rpoA::cat trpC2</i>	Price CW	Price CW	262
1A677	PB106	<i>gerD97::Tn917 rpoA::cat</i>	Price CW	Price CW	212
1A678	RB413	<i>leuB8 menB325 trpC2</i>	Taber HW	Taber HW	265
1A679	RB397	<i>ald-1 leuB8 menE312 trpC2</i>	Taber HW	Taber HW	265
1A680	SG64	<i>lacA1 lacR1</i>	Errington J	Errington J	73
1A681	ED179	<i>apt-6 ilvA1 pbuG3 pupA3 sacA78 upp</i>	Saxild HH	Saxild HH	234
1A682	ED193	<i>ilvA1 pbuG1 sacA78 upp xpt</i>	Saxild HH	Saxild HH	234
1A683	ED249	<i>his</i>	Saxild HH	Saxild HH	234
1A684	BM1	<i>met</i>	Alonso JC	Alonso JC	7
1A685	6GM	<i>hsd_RRM* rib trpC2 tyr-1 ura</i>	Bron S	Bron S	105
1A686	CU4617	SP β ⁻ <i>trpC2 zae86::Tn917</i>	Zahler SA	Zahler SA	300
1A687	CU4619	(SP β c2) <i>trpC2 zba89::Tn917</i>	Zahler SA	Zahler SA	300
1A688	CU4620	(SP β c2) <i>trpC2 ydaO::Tn917</i>	Zahler SA	Zahler SA	82, 300
1A689	CU4621	(SP β c2) <i>trpC2 zdf88::Tn917</i>	Zahler SA	Zahler SA	300
1A690	CU4624	(SP β c2) <i>trpC2 zec88::Tn917</i>	Zahler SA	Zahler SA	300
1A691	CU4626	(SP β c2) <i>trpC2 zfe86::Tn917</i>	Zahler SA	Zahler SA	300
1A692	CU4627	(SP β c2) <i>trpC2 zhf86::Tn917</i>	Zahler SA	Zahler SA	300

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1A693	CU4628	(SPβc2) <i>trpC2 zhg86::Tn917</i>	Zahler SA	Zahler SA	300
1A694	CU4553	SPβ ⁻ <i>recA4 trpC2 zef87::Tn917</i>	Zahler SA	Zahler SA	300
1A695	NHO3	<i>hisH2 sul ten trpC2</i>	Zahler SA	Zahler SA	300
1A698	OKB105	<i>pheA1 sfp</i>	Zuber P	Zuber P	188
1A699	OKB120	<i>pheA1 sfp srfA::Tn917</i>	Zuber P	Zuber P	188
1A700	168	<i>trpC2</i>	Anagnostopoulos	Anagnostopoulos	30
1A701	BG126	<i>addB72 amyE attSPβ metB5 sigB trpC2 xin-1</i>	Alonso JC	Alonso JC	8
1A702	BG124	<i>addB71 amyE attSPβ metB5 sigB xin-1</i>	Alonso JC	Alonso JC	6
1A703	BG101	<i>amyE attSPβ metB5 recP149 sigB trpC2 xin-1</i>	Alonso JC	Alonso JC	8
1A704	60173	<i>purD1</i>	Saxild HH	Saxild HH	234
1A706	FB91	<i>com-9 hisA1 leu-8 lys-21 metB5 thr-5 trpC2</i>	Mastromei G	Mastromei G	75
1A707	FB92	<i>com-71 hisA1 leu-8 metB5 purB6 thr-5 trpC2</i>	Mastromei G	Mastromei G	75
1A708	FB93	<i>com-30 hisA1 leu-8 lys-21 metB5 thr-5 trpC2</i>	Mastromei G	Mastromei G	75
1A709	FB94	<i>com-104 hisA1 leu-8 lys-21 metB5 thr-5 trpC2</i>	Mastromei G	Mastromei G	75
1A710	FB108	<i>com-31 hisA1 leu-8 lys-21 metB5 thr-5 trpC2</i>	Mastromei G	Mastromei G	75
1A711	FBT14	<i>com-14::Tn917 hisA1 leu-8 lys-21 metB5 purB6 thr-5 trpC2</i>	Mastromei G	Mastromei G	75
1A712	FBT18	<i>com-18::Tn917 hisA1 leu-8 lys-21 metB5 purB6 thr-5 trpC2</i>	Mastromei G	Mastromei G	75
1A713	FBT44	<i>com-44::Tn917 hisA1 leu-8 lys-21 metB5 purB6 thr-5 trpC2</i>	Mastromei G	Mastromei G	75
1A715	HJS31	<i>glnR57</i>	Schreier HJ	Schreier HJ	238
1A716	CB100	<i>Cm sigD::pLM5 trpC2</i>	Marquez-Magaña LM	Marquez-Magaña LM	114
1A717	MO1099	<i>amyE::erm Em</i>	Stragier P	Stragier P	104
1A718	6GM15	<i>his Km lacZ- M15 met hsd_{RI}R^M rib trpC2 tyr ura</i>	Bron S	Bron S	106
1A719	WH152	<i>metB10 trpC2 xylAB 1</i>	Hillen W	Hillen W	227
1A720	YB965	<i>hisB leuA8 metB5 polA5 SPβ⁻ xin-1</i>	Yasbin R	Bol D	287
1A721	CU4834	(SPβc2) <i>arol86::Tn917 trpC2</i>	Zahler SA	Zahler SA	300
1A722	CU4199	(SPβc2) <i>bfmB84::Tn917 trpC2</i>	Zahler SA	Zahler SA	300
1A724	CU4836	(SPβc2) <i>trpC2 zba-88::Tn917</i>	Zahler SA	Zahler SA	300
1A727	CU3574	(SPβc2) <i>trpC2 zeh-82::Tn917</i>	Zahler SA	Zahler SA	300
1A728	CU3737	(SPβc2) <i>trpC2 zjf-83::Tn917</i>	Zahler SA	Zahler SA	300
1A730	CU3757	(SPβc2) <i>trpC2 zhf-83::Tn917</i>	Zahler SA	Zahler SA	300
1A731	CU3522	(SPβc2) <i>trpC2 zib-82::Tn917</i>	Zahler SA	Zahler SA	300
1A732	CU4665	(SPβc2) <i>trpC2 zjd-89::Tn917</i>	Zahler SA	Zahler SA	300
1A733	CU4845	(SPβc2) <i>trpC2 zjj-85::Tn917</i>	Zahler SA	Zahler SA	300
1A734	MB61	<i>rapA::cat</i>	Mueller JP	Mueller JP	182
1A735	MP82	<i>gsiB::neo</i>	Mueller JP	Mueller JP	182
1A736	MB170	<i>kinA82</i>	Mueller JP	Mueller JP	183
1A737	MB307	<i>dppE132::neo pheA1 trpC2</i>	Mueller JP	Mueller JP	169
1A738	61668	<i>iolG6 metC7 trpC2</i>	Fujita Y	Fujita Y	87
1A739	YF127	<i>gntK4 metC7 trpC2</i>	Fujita Y	Fujita Y	86
1A740	YF171	<i>gntP9 metC7 trpC2</i>	Fujita Y	Fujita Y	86
1A741	YF176	<i>gntR1 metC7 trpC2</i>	Fujita Y	Fujita Y	88
1A742	JT175	<i>dacA::cat+ trpC2</i>	Buchanan CE	Buchanan CE	271
1A743	JT2000	<i>dacA+::cat+ trpC2</i>	Buchanan CE	Buchanan CE	271
1A744	CB11	<i>dacB⁺::cat⁺ trpC2</i>	Buchanan CE	Buchanan CE	28
1A745	CB36	<i>dacB::cat⁺ trpC2</i>	Buchanan CE	Buchanan CE	28
1A746	recA260	<i>Em metB5 recA260 SPβ⁻ trpC2 xin-1</i>	Yasbin R	Yasbin R	287
1A747	PY79	prototroph SPβ-	Youngman P	Youngman P	298
1A748	1012M15	<i>glgB::lacZ M15 Km leu met hsd_{RI}R^M</i>	Bron S	Bron S	26
1A749	5:7	<i>::Tn917lac MLS^R</i>	Mendelson NH	Salhi B	231
1A751	MW10	<i>bglC 102 bglS EV npr apr his</i>	Borris R	Borris R	286
1A752	MW10	<i>bglC 102 bglS EV npr apr his glgB::lacZ M15</i>	Borris R	Borris R	286
1A753	1R4	<i>thr-5 trpC2 bmr^R</i>	Neyfakh AA	Neyfakh AA	195
1A754	BD170/bmr::cat	<i>thr-5 trpC2 bmr::cat Cm</i>	Neyfakh AA	Neyfakh AA	194
1A755	BD170/bmrR::cat	<i>thr-5 trpC2 bmrR::cat Cm</i>	Neyfakh AA	Neyfakh AA	194
1A756	BD170/bfMB::cat	<i>thr-5 trpC2 bfMB::cat Cm</i>	Neyfakh AA	Neyfakh AA	194
1A757	PS832	prototrophic	Setlow P	Setlow P	242
1A758	ng 79	<i>bac-1</i>	Demain A	Demain A	120

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1A759	MH18	::Tn917 MLS ^R	Demain A	Demain A	120
1A760	MH20	::Tn917::pTV20 Cm MLS ^R	Demain A	Demain A	120
1A761	MH21	::Tn917::pTV21 2 Cm	Demain A	Demain A	120
1A762	MH22	::Tn917::pTV20 <i>bac-1</i> Cm MLS ^R	Demain A	Demain A	120
1A763	CB138	<i>trpC2 fla/che::pLM19</i> Cm	Chamberlin MJ	Ordal G	168
1A764	CB149	<i>trpC2 pheA1 flgM 80</i>	Chamberlin MJ	Ordal GW	180
1A765	BR16	<i>trpC2 lys</i>	Strauch M	Strauch M	264
1A766	BR17	<i>trpC2 lys relA</i>	Strauch M	Strauch M	264
1A767	MH3402	<i>trpC2 pheA1 phoA::pCE413 phoB::Tn917</i> Cm MLS	Hulett FM	Hulett FM	130
1A771	MO1099	<i>trpC2 pheA1 amyE::ery</i> MLS	Stragier P	Stragier P	104
1A772	MO1813	<i>trpC2 pheA1 amy::cat</i> Cm	Stragier P	Stragier P	104
1A773	MO649	<i>trpC2 pheA1 thrC::cat</i> Cm	Stragier P	Stragier P	104
1A774	JH642PolHis	<i>trpC2 pheA1 rpoC::His₆-tag</i> Sp	Moran CP	Moran CP	253
1A775	SMY	prototrophic	Sonenshein LS	Henkin T	103
1G1	PB2442	<i>hisH2 outF4 trpC2</i>	Galizzi A	Galizzi A	4
1G2	PB2427	<i>hisH2 nadE81 trpC2</i>	Galizzi A	Galizzi A	5
1G3	PB2439	<i>hisH2 outE42 trpC2</i>	Galizzi A	Galizzi A	4
1G4	PB2398	<i>hisH2 metD4 outD1 trpC2</i>	Galizzi A	Galizzi A	5
1G5	PB2430	<i>hisH2 outC25 trpC2</i>	Galizzi A	Galizzi A	4
1G6	PB2443	<i>gsp-10 hisH2 metD4 trpC2</i>	Galizzi A	Galizzi A	4
1G7	4744	<i>gerA(ABC)11 thr-5 trpC2</i>	Smith DA	Moir A	248
1G8	4592	<i>gerB(ABC)18 trpC2</i>	Smith DA	Moir A	181
1G9	4593	<i>gerD19 trpC2</i>	Smith DA	Moir A	181
1G10	4728	<i>gerF45 trpC2</i>	Smith DA	Moir A	181
1G11	1558	<i>gerCC58 trpC2 tzm wrd</i>	Smith DA	Moir A	181
1G12	4751	<i>gerE36 leu-2</i>	Smith DA	Moir A	248
1G13	61111	<i>gerG47 met pgk trpC2</i>	Freese E	Smith D	83
1G14	PB2328	<i>hisH2 metD4 outA7 trpC2</i>	Galizzi A	Galizzi A	89
1L1	CU1065(φ3T)	(φ3T) SPβ ⁻ <i>trpC2</i>	Zahler SA	Hemphill HE	300
1L2	CU1065(Z)	(Zeta) SPβ ⁻	Zahler SA	Hemphill HE	300
1L4	SU+III(SPβ)	(SPβ) <i>leuB8 metB5 thr-5</i>	Hemphill HE	Hemphill HE	283
1L5	CU1147	(SPβc2) <i>trpC2</i>	Zahler SA	Zahler SA	223
1L6	168(SPO2)	(SPO2) <i>trpC2</i>	Okubo S	Sonenshein AL	197
1L7	GB1061	(SPO2 <i>ind-1</i>) <i>hisA1 thr-5 trpC2</i>	Garro AJ	Garro AJ	92
1L8	168(SP16)	(SP16) <i>trpC2</i>	Thorne CB	Thorne CB	174, 270
1L9	168(ρ6)	(ρ6) <i>trpC2</i>	Dean DH	Dean DH	55
1L10	168(ρ10)	(ρ10) <i>trpC2</i>	Dean DH	Dean DH	55
1L11	168(φ105)	(φ105) <i>trpC2</i>	Rutberg L	Rutberg L	226
1L12	GB1064 BD99	(φ105 <i>ind-1</i>) <i>hisA1 thr-5 trpC2</i>	Garro AJ	Garro AJ	92
1L13	JAS50	(φ105 <i>d50</i>) <i>ilv leuB7 trpC2</i>	Shapiro JA	Shapiro JA	243
1L15	168(ρ14)	(ρ14) <i>trpC2</i>	Dean DH	Dean DH	55
1L16	168(φDO7)	(φDO7) <i>trpC2</i>	Kroyer JM	Dean DH	151
1L17	GB113	(φ105K <i>sus7</i>) <i>-(met)+ -(thr-5)+ leuB8 sup-3</i>	Garro AJ	Garro AJ	12
1L18	GB114	(φ105L <i>sus9</i>) <i>-(met)+ -(thr-5)+ leuB8 trnS-Lys3</i>	Garro AJ	Garro AJ	12
1L19	GB1115	(φ105J <i>sus11</i>) <i>-(met)+ -(thr-5)+ leuB8 sup-3</i>	Garro AJ	Garro AJ	12
1L20	GB1116	(φ105F <i>sus12</i>) <i>-(met)+ -(thr-5)+ leuB8 sup-3</i>	Garro AJ	Garro AJ	12
1L21	GB1117	(φ105B <i>sus14</i>) <i>-(met)+ -(thr-5)+ leuB8 sup-3</i>	Garro AJ	Garro AJ	12
1L22	GB1118	(φ105B <i>sus14</i>) <i>-(met)+ -(thr-5)+ leuB8 sup-3</i>	Garro AJ	Garro AJ	12
1L23	GB1119	(φ105C <i>sus19</i>) <i>-(met)+ -(thr-5)+ leuB8 sup-3</i>	Garro AJ	Garro AJ	12
1L24	GB1120	(φ105E <i>tsN9</i>) <i>-(met)+ -(thr-5)+ leuB8 sup-3</i>	Garro AJ	Garro AJ	12
1L25	GB1121	(φ105H <i>tsN34</i>) <i>-(met)+ -(thr-5)+ leuB8 sup-3</i>	Garro AJ	Garro AJ	12
1L26	3610(φ3T)	(φ3T)	Tucker R	Thorne CB	54, 56
1L27	DBS-15(ρ11)	(ρ11) <i>pheA2 trpC2</i>	Perkins JB	Dean DH	54, 56
1L28	φ105 DI:29t	(φ105DI:29t) <i>trpC2</i>	Flock JI	Flock JI	81
1L29	φ105 DI:1t	(φ105DI:1t) <i>trpC2</i>	Flock JI	Flock JI	81
1L30	CU2058	(SPβc2 <i>int-5::sup3-1</i>) (SPβc2) <i>-(metB5)+ dal-1</i>	Zahler SA	Zahler SA	162
1L31	CU2059	(SPβc2 <i>int-5::sup44-1</i>) (SPβc2) <i>-(metB5)+ dal-1</i>	Zahler SA	Zahler SA	162
1L32	1A304(φ105)	(φ105) <i>metB10 SPβ- trpC2 xin-1</i>	Ellis DM	Ellis DM	68
1L33	CU1160(Z)	(Zeta) <i>thyA thyB trpC2</i>	Hemphill HE	Hemphill HE	115

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BGSC	ORIGINAL CODE	DESCRIPTION	SOURCE	DONOR	REF
1L34	φ105 DI:1t	(φ105DI:1t) <i>metB10</i> SPβ- <i>trpC2 xin-1</i>	Lampel J	Lampel J	116
1L35	168(φ105J9)	(φ105J9) <i>trpC2</i>	Errington J	Errington J	71
1L36	UOT-0994	(φCM) Cm <i>hisA1 metB51</i>	Kawamura H	Kawamura H	240
1L37	UOT-0756	(φCL) Cm <i>hisA1 leuB8 metB51 nonB1 trpC2</i>	Kawamura H	Kawamura H	240
1L38	UOT-0531	(φPA14) <i>leuB8 metB51 nonB1 trpC2</i>	Kawamura H	Kawamura H	241
1L39	CU267(φ105J23)	(φ105J23) <i>ilvB2 leuB16 trpC2</i>	Errington J	Errington J	142
1L40	CU267(φ105J27)	(φ105J27) <i>ilvB2 leuB16 trpC2</i>	Errington J	Errington J	142
1L41	UOT-0533	(φ105spo0F+) <i>leuB8 metB51 nonB1 spo0F77 trpC2</i>	Kawamura F	Kawamura F	148
1L42	CU267(φ105J106)	(φ105J106) <i>ilvB2 leuB16 trpC2</i>	Errington J	Errington J	70
1L43	566(φ105DS1)	(φ105DS1) <i>-(spoIIAA562)+ -(sigF561)+</i>	Mandelstam J	Mandelstam J	233
1L44	MB75(φ105J13)	(φ105J13) <i>-(lys-1)+ metC3 tal-1</i>	Errington J	Errington J	71
1L45	522(φ105J45)	(φ105J45) <i>-(gerE36)+ trpC2</i>	Mandelstam J	Mandelstam J	138
1L46	CU448(φ105J38)	(φ105J38) <i>-(arg(GH)2)+ ilvA1 pheA2 trpC2</i>	Errington J	Errington J	72
1L47	488.1(φ105J39)	(φ105J39) <i>-(spo0B136)+ lys-1</i>	Errington J	Errington J	72
1L48	221.1 (φ105J40)	(φ105J40) <i>-(spo0F221)+ trpC2</i>	Errington J	Errington J	72
1L49	SG5(φ105J65)	(φ105J65) <i>-(thr-5)+ pheA12</i>	Errington J	Errington J	70
1L50	23.1(φ105J78)	(φ105J78) <i>-(spoIVC)+ trpC2</i>	Errington J	Errington J	72
1L51	17.2(φ105J80)	(φ105J80) <i>-(sigH)+ metC3 tal-1</i>	Errington J	Errington J	72
1L52	517(φ105J81)	(φ105J81) <i>-(spoVK517)+ trpC2</i>	Errington J	Errington J	72
1L53	298.2(φ105J85)	(φ105J85) <i>-(spoIID298)+ pheA12</i>	Errington J	Errington J	72
1L54	43.6(φ105J94)	(φ105J94) <i>-(spo0A43)+ trpC2</i>	Errington J	Errington J	72
1L55	55.2(φ105J114)	(φ105J114) <i>-(spoIIIG55)+ rpoB2 trpC2</i>	Errington J	Errington J	70
1L56	87.2	(φ105J93) <i>leuA8 spoIIJ87 tal-1</i>	Errington J	Errington J	72
1S1	3NA	<i>spo0A3</i>	Schaeffer P	Schaeffer P	177
1S2	184	<i>metB5 spo0A3 thr-5</i>	Salas M	Arnaud M	230
1S3	FR24	<i>-(metB5)+ spo0A3 sup-44 thr-5</i>	Salas M	Arnaud M	175
1S4	FR32	<i>-(metB5)+ -(thr-5)+ spo0A3 trnS-Lys3</i>	Salas M	Arnaud M	175
1S5	PB3A	<i>spo0A3 trpC2</i>	Spizizen J	Rogolsky M	256
1S6	5NA	<i>spo0A5</i>	Schaeffer P	Schaeffer P	133
1S7	6U	<i>metB4 spo0A6 trpC2</i>	Schaeffer P	Schaeffer P	133
1S8	9V	<i>spo0A9 trpC2</i>	Schaeffer P	Schaeffer P	133
1S9	JH646	<i>pheA1 spo0A12 trpC2</i>	Hoch JA	Hoch JA	275
1S10	SR22	<i>spo0A12 trpC2</i>	Ito J	Ito J	135
1S11	SCR584	<i>spo0A12 tolB24 trpC2</i>	Ito J	Ito J	135
1S12	JH82	<i>spo0A12 trpF7</i>	Hoch JA	Hoch JA	123
1S13	13V	<i>spo0A13 trpC2</i>	Schaeffer P	Schaeffer P	133
1S14	170-2	<i>spo0A170 tyr</i>	Takahashi I	Takahashi I	268
1S15	B332H	<i>spo0A332 trpC2</i>	Rogolsky M	Rogolsky M	220
1S16	JH648	<i>pheA1 spo0B136 trpC2</i>	Hoch JA	Hoch JA	123
1S17	JH647	<i>pheA1 spo0E11 trpC2</i>	Hoch JA	Hoch JA	123
1S19	JH649	<i>pheA1 spo0F221 trpC2</i>	Hoch JA	Hoch JA	123
1S20	B4NA	<i>sigH4 str trpC2</i>	Rogolsky M	Rogolsky M	220
1S21	B14NG	<i>sigH14 trpC2</i>	Rogolsky M	Rogolsky M	220
1S22	E22	<i>rpoB2 sigH17 trpC2</i>	Piggot PJ	Young M	206
1S23	B37NA	<i>sigH37 trpC2</i>	Rogolsky M	Rogolsky M	220
1S24	JH651	<i>pheA1 sigH81 trpC2</i>	Hoch JA	Hoch JA	123
1S25	B116NG	<i>sigH116 trpC2</i>	Rogolsky M	Rogolsky M	220
1S26	JH696	<i>pheA1 spoIIJ87 trpC2</i>	Hoch JA	Hoch JA	123
1S27	87	<i>metC3 spoIIJ87 tal-1</i>	Hranueli D	Young M	129
1S28	Z31	<i>opp(ABCDEF)(ABCDEF)141 trpC2</i>	Coote JG	Mandelstam J	42
1S29	N2-2	<i>ser spoIIA2</i>	Takahashi I	Takahashi I	268
1S30	12U	<i>spoIIA12</i>	Schaeffer P	Schaeffer P	133
1S31	26U	<i>ade met spoIIA26 trpC2</i>	Schaeffer P	Schaeffer P	133
1S32	NG18.6	<i>rpoB2 spoIIA69 trpC2</i>	Piggot PJ	Young M	206
1S33	NG17.22	<i>rpoB2 spoIID66 trpC2</i>	Piggot PJ	Young M	206
1S34	NG15.4	<i>spoIIE61 trpC2</i>	Piggot PJ	Young M	206
1S35	NG17.15	<i>rpoB2 spoIIE64 trpC2</i>	Piggot PJ	Young M	206
1S36	7Z	<i>ilvC1 spoIIIA(A-H)7 trpC2</i>	Schaeffer P	Schaeffer P	133
1S37	NG12.5	<i>rpoB2 spoIIIA(A-H)53 trpC2</i>	Piggot PJ	Young M	206
1S38	94U	<i>spoIIIC94 trpC2</i>	Schaeffer P	Schaeffer P	133

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1S39	83U	<i>spolIID83 trpC2</i>	Schaeffer P	Schaeffer P	133
1S40	11T	<i>spolIIC11</i>	Schaeffer P	Schaeffer P	133
1S41	168DPA(-)	<i>spoVF trpC2</i>	Halvorson HO	Arnaud M	306
1S42	NG1.13	<i>metC3 spolIIA(A-H)35 tal-1</i>	Piggot PJ	Young M	206
1S43	P9	<i>spolIID298 trpC2</i>	Coote JG	Mandelstam J	42
1S44	91	<i>argF4 hisA1 metB5 pheA12 purA16 pyrA26 spoVB91 trpC2</i>	Hranueli D	Young M	129
1S45	SL931	<i>rpoB2 spoVD156 trpC2</i>	Piggot PJ	Piggot PJ	204
1S46	P20	<i>pheA12 spoIVA178</i>	Coote JG	Mandelstam J	42
1S47	Z7	<i>spoIVC133 trpC2</i>	Coote JG	Coote JG	41
1S48	A3	<i>spolIIB2 trpC2</i>	Piggot PJ	Young M	206
1S49	Z3	<i>spolIB131 trpC2</i>	Coote JG	Mandelstam J	42
1S50	89	<i>spoVA89 trpC2</i>	Hranueli D	Young M	129
1S51	85	<i>spoVE85 trpC2</i>	Hranueli D	Young M	129
1S52	SL824	<i>spoVF224 trpC2</i>	Piggot PJ	Piggot PJ	204
1S53	667	<i>spoOA 677</i>	Ito J	Ito J	135
1S54	SCR690	<i>spoOB12</i>	Ito J	Ito J	135
1S55	306.1	<i>rpoB2 sapA6 spollA69</i>	Piggot PJ	Piggot PJ	207
1S56	300.1	<i>rpoB2 sapB2 spollA69</i>	Piggot PJ	Piggot PJ	207
1S57	P7	<i>spoIVB165 trp</i>	Coote JG	Mandelstam J	42
1S58	X8	<i>spoIVF152 trpC2</i>	Coote JG	Mandelstam J	42
1S59	96	<i>kinA96 trpC2</i>	Hranueli D	Young M	129
1S60	41.1	<i>leuB8 spollG41 tal-1</i>	Young M	Young M	297
1S61	NG12.12	<i>rpoB2 sigE55 trpC2</i>	Piggot PJ	Young M	206
1S63	NG1.67	<i>spolIIE36 trpC2</i>	Piggot PJ	Young M	206
1S64	92	<i>leuB8 rpoB2 spollIC92 tal-1</i>	Hranueli D	Young M	129
1S65	88	<i>metC3 spoIVF88 tal-1</i>	Hranueli D	Young M	129
1S66	285	<i>metC3 rpoB2 spoVC285</i>	Young, M	Young, M	296
1S67	279.6	<i>cysC7 furA2 spollG279</i>	Young, M	Young, M	297
1S68	R15-13	<i>abrB23 pheA1 spo0A12 trpC2</i>	Hoch JA	Mahler I	123
1S69	SCR354	<i>abrB6 spo0A12 trpC2</i>	Ito J	Ito J	136
1S70	SCR372	<i>abrB24 spo0A12 trpC2</i>	Ito J	Ito J	136
1S71	4Z	<i>spollA4 trpC2</i>	Schaeffer P	Schaeffer P	133
1S72	4Z	<i>spollA4 trpC2</i>	Schaeffer P	Schaeffer P	133
1S73	16U ATM16 SPIIB	<i>ade met Sm spo0A16 trpC2</i>	Schaeffer P	Schaeffer P	235
1S74	4SA2 OIIB	<i>spollA5</i>	Schaeffer P	Schaeffer P	235
1S75	RUB331	<i>spo-331 thyA1 thyB1 trpC2</i>	Wilson GA	Wilson GA	295
1S76	ASB298	<i>citD 29 dal-1 spo0A 677 str- 76 thyA thyB uvr-1</i>	Burke WF	Burke WF	29
1S77	SL613 50.2	<i>metB5 spollA50 thr-5</i>	Piggot PJ	Piggot PJ	204
1S78	SL631 63.2	<i>metC3 rpoB2 sigF63 tal-1</i>	Piggot PJ	Piggot PJ	204
1S79	NG1.82	<i>spollA37 trpC2</i>	Piggot PJ	Mandelstam J	206
1S80	NG6.13	<i>spollA42 trpC2</i>	Piggot PJ	Mandelstam J	206
1S81	P18	<i>spollA176 trpC2</i>	Coote JG	Mandelstam J	42
1S82	DB16	<i>pyrA1 spoL1 trpC2</i>	Balassa G	Pasteur Institute	17
1S83	AB12	<i>pheA1 spoVF1 trpC2</i>	Balassa G	Pasteur Institute	18
1S84	EV15	<i>argF4 cotA leu-2 pyrA26 scoA1</i>	Balassa G	Pasteur Institute	16
1S85	EC21	<i>argF4 leu-2 pyrA26 kinA2</i>	Balassa G	Pasteur Institute	16
1S86	SL401	<i>sigF1 trpC2</i>	Piggot PJ	Piggot PJ	204
1S87	SL55-7	<i>metC3 spoIVG-25 tal-1</i>	Piggot PJ	Jenkinson HF	204
1S88	513	<i>spoVIA513 trpC2</i>	Jenkinson HF	Jenkinson HF	139
1S89	181	<i>spoIVF(TS) trpC2</i>	Mandelstam J	Mandelstam J	154
1S90	580	<i>lys-1 spoOB(TS)</i>	Mandelstam J	Mandelstam J	154
1S91	581	<i>lys-1 spoOB(TS)</i>	Mandelstam J	Mandelstam J	154
1S92	587	<i>lys-1 spoIVF(TS)</i>	Mandelstam J	Mandelstam J	154
1S93	590	<i>lys-1 spoVB</i>	Mandelstam J	Mandelstam J	153
1S94	93.2	<i>spo0J93 trpC2</i>	Errington J	Errington J	70
1S95	517	<i>spoVK517 trpC2</i>	Errington J	Errington J	70
1S96	KI224	<i>bofA::Tn917lac pheA1 trpC2</i>	Grossman AD	Grossman AD	134
1S97	IS720	<i>hisA1 leuA8 metB5 sinR::phl</i>	Smith I	Smith I	15, 249

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1S98	IS875	<i>hisA1 leuA8 metB5 sinI::kan-50</i> Spo ⁻	Smith I	Smith I	249
1S99	RL673	MLS ^R <i>spoVK::Tn917HU8</i> SPβ ⁻	Losick R	Cutting S	74
1S100	RL774	<i>bofA::cat</i> Cm SPβ ⁻	Losick R	Cutting S	217
1S101	RL50	Cm <i>cotA::cat trpC2</i>	Losick R	Driks A	62
1S102	RL51	<i>cotB::cat trpC2</i>	Losick R	Driks A	62
1S103	RL52	<i>cotC::cat trpC2</i>	Losick R	Driks A	62
1S104	RL53	<i>cotD::cat trpC2</i>	Losick R	Driks A	62
1S105	RL48	<i>cotE::cat trpC2</i>	Losick R	Losick R	305
1S106	RL653	<i>cotF::cat trpC2</i>	Losick R	Cutting S	47
1S107	RL654	<i>cotF::cat trpC2</i>	Losick R	Cutting S	47
1S108	DB200	Cm <i>cotT::pDE194 pheA1 trpC2</i>	Aronson I	Aronson I	13
1S109	PS273	<i>sspA</i>	Setlow P	Setlow P	242
1S110	PS339	<i>sspB</i>	Setlow P	Setlow P	242
1S111	PS356	<i>sspA sspB</i>	Setlow P	Setlow P	242
1S112	PS481	<i>sspA sspE</i> Cm	Setlow P	Setlow P	242
1S113	PS482	<i>sspA sspB sspE</i> Cm	Setlow P	Setlow P	242
1S114	PS499	<i>sspE</i>	Setlow P	Setlow P	242
1S115	PY179	<i>spoIID::Tn917 HU8</i>	Youngman P	Youngman P	232
1S116	PY180	<i>spoIIE::Tn917 HU7</i>	Youngman P	Youngman P	232
1S117	KS8	<i>spoVK::Tn917 HU8</i>	Sandman K	Youngman P	232
1S118	KS10	<i>spoIVD::Tn917 HU10</i>	Sandman K	Youngman P	232
1S119	KS13	<i>spoIIIA(A-H)::Tn917 HU13</i>	Sandman K	Youngman P	232
1S120	KS19	<i>kinA::Tn917 HU19</i>	Sandman K	Youngman P	232
1S121	KS25	<i>spoIIIB::Tn917 HU25</i>	Sandman K	Youngman P	232
1S122	KS178	<i>spoVK::Tn917 HU178</i>	Sandman K	Youngman P	232
1S123	KS179	<i>spoIVFA::Tn917 HU179</i>	Sandman K	Youngman P	232
1S124	KS181	<i>spoIIE::Tn917 HU181</i>	Sandman K	Youngman P	232
1S125	KS188	<i>spoIIM::Tn917 HU188</i>	Sandman K	Youngman P	232
1S126	KS194	<i>spoIVA::Tn917 HU194</i>	Sandman K	Youngman P	232
1S127	KS195	<i>spoVA::Tn917 HU195</i>	Sandman K	Youngman P	232
1S128	KS215	<i>spoIVC::Tn917 HU215</i>	Sandman K	Youngman P	232
1S129	KS261	<i>spo0J::Tn917 HU261</i>	Sandman K	Youngman P	232
1S130	KS265	<i>spoVG::Tn917 HU265</i>	Sandman K	Youngman P	232
1S131	KS276	<i>spoVA::Tn917 HU276</i>	Sandman K	Youngman P	232
1S132	KS287	<i>spoIIM::Tn917 HU287</i>	Sandman K	Youngman P	232
1S133	KS289	<i>spo0A::Tn917 HU289</i>	Sandman K	Youngman P	232
1S134	KS297	<i>ald::Tn917 HU297</i>	Sandman K	Youngman P	232
1S135	KS298	<i>spoIID::Tn917 HU298</i>	Sandman K	Youngman P	232
1S136	KS306	<i>cotA::Tn917 HU306</i>	Sandman K	Youngman P	232
1S137	KS324	<i>spoVM::Tn917 HU324</i>	Sandman K	Youngman P	232
1S138	KS325	<i>spoIIG::Tn917 HU325</i>	Sandman K	Youngman P	232

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B. SUBTILIS 168 STRAINS BY ORIGINAL CODE

ORIGINAL CODE	BGSC	ORIGINAL CODE	BGSC	ORIGINAL CODE	BGSC
1012M15	1A748	4593	1G9	9M(I)S ^K	1A417
1019	1A447	4702	1G13	9V	1S8
103	1A258	4728	1G10	A3	1S48
103SU+3	1A259	4744	1G7	AB12	1S83
103SU+44	1A260	4751	1G12	ASB298	1S76
11T	1S40	4SA2	1S74	ATCC 31578	1S75
120	1A148	4Z	1S71	B116NG	1S25
12U	1S30	4Z	1S72	B14NG	1S21
13V	1S13	5:7	1A749	B332H	1S15
141	1S28	50.2	1S77	B37NA	1S23
1443	1A86	512	1A274	B4NA	1S20
146	1A652	513	1S88	BC100	1A145
152	1S58	517	1S95	BC101	1A146
1558	1G11	53.1	1S37	BC102	1A291
1604	1A303	5-5	1A316	BC110	1A102
165.1	1S57	5-5	1A316	BC31	1A101
168	1A1	55.2	1S61	BC37,PUR ⁺	1A277
168	1A700	580	1S90	BC38	1A28
168 cam2	1A578	581	1S91	BC50	1A29
168 ts-3	1A238	587	1S92	BC53	1A30
168,Ksg ^S ,Thy	1A185	590	1S93	BC67	1A31
168BLT	1A189	5NA	1S6	BD108	1A212
168DPA(-)	1S41	60173	1A704	BD170	1A42
168EBR	1A342	60348	1A297	BD170/bfmB::cat	1A756
168M	1A329	60984	1A468	BD170/bmr::cat	1A754
168MIU1	1A399	6-1	1A317	BD170/bmrR::cat	1A755
168MIU16	1A393	61.1	1S34	BD170-1	1A223
168MIU17	1A395	61111	1G13	BD191	1A44
168MIU18	1A396	61494	1A471	BD193	1A45
168MIU7	1A394	61501	1A296	BD194	1A43
168MIU8	1A392	61539	1A472	BD224	1A46
168S ^R	1A287	61571	1A473	BD237	1A213
168SU7	1A401	6160	1A338	BD241	1A47
168TT	1A185	61656	1A465	BD246	1A48
168TT	1A243	61668	1A738	BD274	1A214
168TUT	1A402	61676	1A293	BD291	1A215
16U	1S73	61677	1A294	BD332	1A216
17.1	1S22	63.2	1S78	BD336	1A217
170-2	1S14	64.1	1S35	BD35	1A210
17A-42	1A398	66.2	1S33	BD393	1A511
181	1S89	667	1S53	BD40	1A211
184	1S2	69.1	1S32	BD54,azp	1A82
1R4	1A753	6GM	1A685	BD54,spcB,Leu ⁺	1A76
222	1A506	6GM15	1A718	BD54,spcB,T	1A81
22-4	1A479	6G-R	1A438	BD54,strB,Leu ⁺	1A77
2355	1A276	6TR1	1A462	BD77	1A336
26U	1S31	6TR23	1A68	BD97	1A27
279.6	1S67	6U	1S7	BD99	1A242
285	1S66	7Z	1S36	BG101	1A703
2M(I)S(I)	1A415	83U	1S39	BG124	1A702
300.1	1S56	85	1S51	BG126	1A701
302.7	1A306	87	1S27	BG314	1A654
305.7	1A307	88	1S65	BM1	1A684
306.1	1S55	89	1S50	BR151	1A40
32-12	1A314	8G-5	1A437	BR16	1A765
32-24	1A318	91	1S44	BR17	1A766
35.2	1S42	91'M ^R S ^R	1A418	BR290	1A105
36	1S63	92	1S64	BR54 (JAS9)	1A116
3NA	1S1	93.2	1S94	BR63	1A15
41.1	1S60	94U	1S38	BR77	1A313
4592	1G8	96	1S59	BR85	1A39

B. subtilis 168 Strains Indexed Original Code

ORIGINAL CODE	BGSC	ORIGINAL CODE	BGSC	ORIGINAL CODE	BGSC
BR85	1A138	CU972	1A122	CU4199	1A722
BR95	1A57	CU973	1A123	CU4553	1A694
BR95, GLPD6	1A155	CU978	1A125	CU4617	1A686
BR95, GLPD8	1A239	CU1002	1A127	CU4619	1A687
BR95, GLPK	1A240	CU1018	1A129	CU4620	1A688
BR95, GLPP	1A157	CU1021	1A128	CU4621	1A689
BS122	1A410	CU1021	1A126	CU4624	1A690
BS166	1A65	CU1050	1A459	CU4626	1A691
BS168NT	1A411	CU1065	1A100	CU4627	1A692
C10	1A107	CU1428	1A457	CU4628	1A693
C33	1A106	CU1430	1A458	CU4665	1A732
C66	1A295	CU1459	1A305	CU4834	1A721
CA302	1A668	CU2111	1A646	CU4836	1A724
CB100	1A716	CU3497	1A575	CU4845	1A733
CB11	1A744	CU3522	1A731	DA14	1A660
CB138	1A763	CU3574	1A727	DA32	1A670
CB149	1A764	CU3737	1A728	DA34	1A671
CB36	1A745	CU3757	1A730	DA36	1A664
CB-66	1A476	CU4120	1A600	DA46	1A667
CB-67	1A477	CU4121	1A601	DA463	1A665
CIP7627	1S82	CU4122	1A602	DA47	1A669
CIP7635	1S83	CU4123	1A603	DA49	1A661
CIP7669	1S85	CU4124	1A604	DA63	1A659
CIP7670	1S84	CU4125	1A605	DA65	1A658
CU79	1A279	CU4126	1A606	DA73	1A666
CU134	1A114	CU4127	1A607	DA9	1A657
CU135	1A97	CU4128	1A608	DB14	1A663
CU173	1A99	CU4129	1A609	DB16	1S82
CU219	1A110	CU4130	1A610	DB200	1S108
CU229	1A109	CU4131	1A611	DB31	1A308
CU229	1A453	CU4132	1A612	DB65	1A662
CU281	1A331	CU4133	1A613	ddd-3	1A480
CU296	1A278	CU4134	1A614	DG47	1S52
CU371	1A172	CU4135	1A615	DNA-1	1A41
CU373	1A228	CU4136	1A616	DR10	1A405
CU403	1A460	CU4137	1A617	DRD-2	1A174
CU403, DIVIVA	1A196	CU4138	1A618	DRD-2A	1A175
CU403, DIVIVB	1A197	CU4139	1A619	DRD-4	1A176
CU403, DIVIVB	1A292	CU4140	1A620	E22	1S22
CU403, DIVIVB1		CU4141	1A621	EC21	1S85
CU403, TS-134	1A17	CU4142	1A622	ED179	1A681
CU456	1A111	CU4143	1A623	ED193	1A682
CU457	1A112	CU4144	1A624	ED249	1A683
CU466	1A250	CU4145	1A625	ED43	1A142
CU495	1A94	CU4146	1A626	ED53	1A144
CU532	1A147	CU4147	1A627	ED54	1A143
CU614	1A454	CU4148	1A628	EE1	1A501
CU626	1A113	CU4149	1A629	EV15	1S84
CU635	1A34	CU4150	1A630	FB108	1A710
CU641	1A325	CU4151	1A631	FB12	1A435
CU661	1A115	CU4152	1A632	FB21	1A427
CU706	1A330	CU4153	1A633	FB56	1A431
CU776	1A117	CU4154	1A634	FB59	1A432
CU785	1A118	CU4155	1A635	FB6	1A430
CU806	1A326	CU4156	1A636	FB7	1A424
CU809	1A327	CU4157	1A637	FB74	1A434
CU810	1A119	CU4158	1A638	FB8	1A425
CU812	1A367	CU4159	1A639	FB91	1A706
CU850	1A368	CU4160	1A640	FB92	1A707
CU869	1A251	CU4161	1A641	FB93	1A708
CU872	1A120	CU4162	1A642	FB94	1A709
CU893	1A121	CU4163	1A643	FBT14	1A711
CU927	1A332	CU4164	1A644	FBT18	1A712
CU968	1A98	CU4165	1A645	FBT44	1A713

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ORIGINAL CODE	BGSC	ORIGINAL CODE	BGSC	ORIGINAL CODE	BGSC
FJ3	1A483	IS126	1A192	KS298	1S135
FJ6	1A484	IS153, CYS ⁺	1A193	KS306	1S136
fla-TS2	1A153	IS154	1A194	KS324	1S137
fla-TS4	1A139	IS155	1A195	KS325	1S138
FR24	1S3	IS158	1A219	KS8	1S117
FR32	1S4	IS164	1A220	KSG618	1A187
FRU-4	1A580	IS165	1A221	KSG619	1A188
FUS426	1A507	IS166	1A222	KUS429	1A508
G10	1A136	IS169	1A475	LS105	1A449
G22	1A137	IS720	1S97	LS11	1A248
G26/3	1A140	IS875	1S98	LS121	1A450
GB151 (NG 14)	1A63	JAS1	1A241	M5	1A478
GB152 (NA 3)	1A64	JAS11	1A203	MAL-4	1A587
GB153 (ICR 7)	1A62	JAS12	1A204	MAN-A1 (CS25)	1A585
GB64/219	1A60	JAS4	1A12	MAN-B1 (CS26)	1A586
GB7018	1A453	JAS5	1A13	MB170	1A736
GB7037	1A454	JAS8	1A114	MB23	1A500
GB7044	1A452	JB01-200	1A455	MB251	1A78
GB7068	1A456	JH158	1A79	MB307	1A737
GB7075	1A455	JH402	1A33	MB500	1A68
GB78	1A284	JH404	1A16	MB61	1A734
GLN-2	1A584	JH406	1A32	MCB	1A505
GLU-1	1A579	JH417	1A152	MH18	1A759
GLU-40	1A582	JH422	1A70	MH20	1A760
GLU-47	1A581	JH642	1A96	MH21	1A761
GSY1025	1A73	JH642 PolHis	1A774	MH22	1A762
GSY1028	1A335	JH646	1S9	MH3402	1A767
GSY1059	1A168	JH647	1S17	MI112	1A423
GSY1127	1A574	JH648	1S16	MI120	1A422
GSY1307	1A102	JH649	1S19	MO101P	1S2
GSY1615	1A496	JH651	1S24	MO1099	1A717
GSY1619	1A495	JH696	1S26	MO1099	1A771
GSY2258	1A334	JH715	1A61	MO1813	1A772
GSY226	1A234	JH818	1A177	MO649	1A773
GSY227	1A235	JH82	1S12	MO99	1S4
GSY260	1A233	JH825	1A249	MP82	1A735
GSY264	1A72	JKB3141	1A330	MS320	1A464
GSY276	1A232	JT175	1A742	Mu5u11	1A389
GSY277	1A231	JT2000	1A743	Mu5u12	1A388
GSY292	1A71	KA10	1A429	Mu5u26	1A387
GSY293	1A360	KA3	1A428	MU8U5U1 (BD54)	1A75
GSY483	1A230	KA31805	1A672	Mu8u5u16	1A145
GSY505	1A361	KA32817	1A673	Mu8u5u6	1A12
GSY908	1A302	KA97103	1A674	Mu8u5u6u41	1A13
H-37	1A391	KE2	1A408	MW10	1A751
HA101	1A476	KI224	1S96	MW10	1A752
HA101-2-10	1A493	KR10	1A656	MY2011	1A466
HA101-2-9	1A492	KS10	1S118	MY2013	1A467
HA101B	1A477	KS13	1S119	N1G17	1A365
HA106	1A494	KS178	1S122	N1G43	1A373
HCR-9	1A369	KS179	1S123	N1G45	1A366
HJS30	1A653	KS181	1S124	N2-2	1S29
HJS31	1A715	KS188	1S125	NA20	1A414
HLL3g	1A445	KS19	1S120	NA20-22	1A413
HPR10	1A178	KS194	1S126	NA64	1A412
HPR12	1A179	KS195	1S127	ng 79	1A758
HPR16	1A180	KS216	1S128	NG1.13	1S42
HPR18	1A181	KS25	1S121	NG1.67	1S63
HS1A21	1A364	KS261	1S129	NG1.82	1S79
IAM1247	1A451	KS265	1S130	NG12.12	1S61
IG-20	1A436	KS276	1S131	NG12.5	1S37
IS115	1A190	KS287	1S132	NG15.4	1S34
IS116	1A191	KS289	1S133	NG17.15	1S35
IS121	1A218	KS297	1S134	NG17.22	1S33

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ORIGINAL CODE	BGSC	ORIGINAL CODE	BGSC	ORIGINAL CODE	BGSC
NG18.6	1S32	PB3315	1A426	QB858	1A84
NG4.14	1S60	PB3394	1A387	QB861	1A156
NG6.13	1S80	PB3395	1A388	QB870	1A122
NH3	1A160	PB3397	1A389	QB879	1A125
NH5	1A74	PB3A	1S5	QB889	1A92
NHO3	1A695	PB70	1A676	QB890	1A126
Ni15	1A504	PB73	1A675	QB917 KIT-8	1A10
Nil (oxr-1)	1A502	PG522	1A236	QB922 KIT-5	1A7
Nil (oxr-2)	1A503	PG524	1A237	QB928 KIT-2	1A4
NP22.1	1A256	PG599	1A377	QB934 KIT-3	1A5
NP4.1	1A257	PG602	1A376	QB935 KIT-6	1A8
NP40	1A309	PG650	1A441	QB936 KIT-7	1A9
NP58	1A341	PG662	1A442	QB943 KIT-4	1A6
OBS14	1A576	PG668	1A443	QB944 KIT-1	1A3
OBS2	1A573	PHOP,PHEA	1A254	QB952	1A171
OBS20	1A577	PHOP12	1A255	QB1097	1A202
OBS30	1A655	PIG18TB	1A183	QB1130	1A288
OIIB	1S74	PIGY1	1A184	QB1133	1A289
OKB105	1A698	PRA2	1A446	QB1180	1A264
OKB120	1A699	PS273	1S109	QB1506	1A93
P18	1S81	PS339	1S110	QUA184	1A282
P20	1S46	PS356	1S111	QUA188	1A283
P7	1S57	PS481	1S112	QUA2	1A280
P9	1S43	PS482	1S113	QUA4	1A281
PB106	1A677	PS499	1S114	R11	1A650
PB1429	1A337	PS832	1A757	R15-13	1S68
PB1439	1A383	PS9	1A141	R21	1A651
PB1440	1A382	PS9W7	1A448	RB1034	1A421
PB1625	1A497	PSL1	1A510	RB1479	1A419
PB1629	1A498	PY179	1S115	RB1949	1A463
PB1630	1A499	PY180	1S116	RB1952	1A420
PB1633	1A380	PY79	1A747	RB308	1A440
PB1640	1A103	QB2,PUR(+)	1A49	RB397	1A679
PB1641	1A378	QB13	1A165	RB403	1A439
PB1653	1A404	QB19	1A88	RB413	1A678
PB1663	1A301	QB39	1A166	RB541	1A512
PB1673	1A390	QB42	1A50	RC220	1A259
PB1693	1A379	QB58	1A51	RC221	1A260
PB1728	1A298	QB99	1A89	recA260	1A746
PB1775	1A381	QB123 KIT-9	1A11	_{RI} B-2	1A583
PB1782	1A299	QB127	1A199	_{RI} F-18	1A308
PB2321	1A595	QB136	1A95	RL48	1S105
PB2328	1A482	QB157	1A200	RL50	1S101
PB2328	1G14	QB200	1A170	RL51	1S102
PB2330	1A598	QB254	1A201	RL52	1S103
PB2333	1A649	QB552	1A160	RL53	1S104
PB2336	1A599	QB553	1A161	RL653	1S106
PB2338	1A596	QB562	1A169	RL654	1S107
PB2353	1A647	QB642	1A164	RL673	1S99
PB2354	1A648	QB666	1A90	RL774	1S100
PB2355	1A597	QB687	1A52	RM125	1A253
PB2398	1G4	QB689	1A167	RM125,MIT	1A363
PB2417	1A384	QB694	1A159	RM22	1A409
PB2427	1G2	QB698	1A53	ROD104	1A485
PB2430	1G5	QB712	1A91	ROD113	1A486
PB2439	1G3	QB752	1A263	RUB2112	1A38
PB2442	1G1	QB752	1A263	RUB331	1S75
PB2443	1G6	QB804	1A150	RUB814	1A35
PB3046 (BD96)	1A85	QB807	1A205	RUB834	1A36
PB3197	1A385	QB813	1A154	RUB836	1A37
PB3233	1A386	QB819	1A54	S19TI	1A374
PB3242	1A433	QB820	1A55	S80TI	1A375
PB3242	1A481	QB821	1A56	SB1	1A59
PB3292	1A300	QB832	1A151	SB1,ARGC-4	1A28

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ORIGINAL CODE	BGSC	ORIGINAL CODE	BGSC	ORIGINAL CODE	BGSC
SB1058	1A224	SL631	1S78	trpD9 (ICR 19)	1A529
SB1059	1A225	SL731	1S49	trpE1 (ICR 1)	1A516
SB1060	1A226	SL767	1S43	trpE194 (SB194)	1A521
SB1115	1A228	SL824	1S52	trpE2 (ICR 6)	1A517
SB112	1A227	SL931	1S45	trpE3 (ICR 14)	1A518
SB1141	1A230	SMY	1A775	trpE4 (ICR 16)	1A519
SB1142	1A231	SPIIB4	1S71	trpE5 (UV 17)	1A520
SB1143	1A232	SPIIB4	1S72	trpF1 (NA 2)	1A531
SB1144	1A233	SPOA3	1S5	trpF10 (ICR 12)	1A539
SB1145	1A234	SR22	1S10	trpF11 (SB 11)	1A540
SB1146	1A235	SSP	1A488	trpF12 (NA 5)	1A541
SB1158	1A456	ST-3	1A198	trpF13 (HA 1)	1A542
SB120	1A69	SU+III	1A14	trpF2 (NA 4)	1A532
SB121	1A132	SU+III	1A459	trpF3 (NA 6)	1A533
SB130	1A133	Sz 15 (I/1)	1A589	trpF4 (NA 7)	1A534
SB133	1A275	Sz 16 (II/33)	1A590	trpF5 (NA 10)	1A535
SB135	1A229	Sz 26 (V/64)	1A592	trpF6 (NA 11)	1A536
SB136	1A131	Sz 27 (VI/180)	1A593	trpF8 (HA2)	1A537
SB137	1A83	Sz 28 (III/321)	1A594	trpF9 (PH 1)	1A538
SB164	1A104	Sz 3 (R15)	1A588	TS-134	1A290
SB168	1A246	Sz 34	1A591	TS-151	1A268
SB193	1A207	TAG-1	1A209	TS-355	1A269
SB19E, ts2pyrG1	1A461	TIBS 57	1A474	TSDNA-A13	1A18
SB19SEM	1A101	TKJ3422	1A514	TSDNA-B19	1A19
SB22	1A319	TKJ6901	1A487	TSDNA-C30	1A20
SB25	1A58	tmsB1	1A312	TSDNA-D23	1A21
SB26	1A80	trpA1 (NG 63)	1A553	TSDNA-E20	1A22
SB270A	1A321	trpA2 (NA 9)	1A554	TSDNA-F133	1A23
SB29	1A206	trpA3 (T 50)	1A555	TSDNA-G34	1A24
SB3 (BD92)	1A31	trpA4 (T 51)	1A556	TSDNA-H151	1A25
SB305	1A322	trpA6 (ICR 17)	1A557	TSDNA-I102	1A26
SB319	1A323	trpA7 (ICR 21)	1A558	TTK24	1A491
SB32	1A208	trpB1 (NG 4)	1A559	UOTO277	1A509
SB419	1A285	trpB10 (ICR 8)	1A566	UTB600	1A490
SB443	1A286	trpB11 (ICR 9)	1A567	UVS1	1A344
SB491	1A2	trpB12 (ICR 13)	1A568	UVS109	1A346
SB491U5	1A403	trpB13 (ICR 15)	1A569	UVS114	1A347
SB491U6	1A397	trpB14 (ICR 18)	1A570	UVS42	1A345
SB5	1A115	trpB15 (ICR 20)	1A571	UVS80	1A343
SB58A	1A320	trpB16 (NG 7)	1A572	UVSSP-42-1	1A489
SB68	1A87	trpB2 (NG 6)	1A560	VA321	1A314
SB69	1A108	trpB5 (NG 14)	1A561	VA322, THR(+)	1A318
SB70	1A173	trpB6 (NG 57)	1A562	VA55	1A316
SCR354	1S69	trpB7 (NG 58)	1A563	VA61	1A317
SCR372	1S70	trpB8 (NG 59)	1A564	VA71, THR(+)	1A315
SCR500	1A66	trpB9 (NG 60)	1A565	VB104	1A348
SCR506	1A67	trpC1 (NG 1)	1A543	VB106	1A349
SCR584	1S11	trpC10 (EMS 2)	1A551	VB107A	1A350
SCR690	1S54	trpC11 (NG 2)	1A552	VB122A	1A351
SG64	1A680	trpC3 (NG 3)	1A544	VB126	1A352
SH	1A270	trpC4 (NG 5)	1A545	VB127	1A353
SH-2	1A273	trpC5 (NG 24)	1A546	VB157	1A354
SH-3	1A272	trpC6 (UV 15)	1A547	VB158	1A355
SH-5	1A271	trpC7 (UV 16)	1A548	VB293	1A356
SL16	1S51	trpC8 (UV 18)	1A549	VB336F	1A358
SL17	1S50	trpC9 (EMS 1)	1A550	VB355B	1A357
SL311	1S56	trpD1 (NA 1)	1A522	VUB192	1A149
SL330	1A306	trpD10 (ICR 22)	1A530	VUB212	1A261
SL344	1A307	trpD2 (NA 3)	1A523	VUB221	1A163
SL346	1S55	trpD4 (NG 61)	1A524	VUB234	1A262
SL401	1S86	trpD5 (NG 62)	1A525	VUB333	1A162
SL55-7	1S87	trpD6 (NG 120)	1A526	VUB79	1A158
SL61	1S44	trpD7 (ICR 10)	1A527	W10	1S45
SL613	1S77	trpD8 (ICR 11)	1A528	W168	1A308

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ORIGINAL CODE	BGSC	ORIGINAL CODE	BGSC	ORIGINAL CODE	BGSC
W168BRY	1A267	XVM _{rS} (l)	1A416	YN118	1A340
WB2281B	1A130	YB886	1A304	YN21	1A339
WB428	1A135	YB886TNR	1A372	YN9	1A182
WB577	1A333	YB965	1A720	YY88	1A311
WB888	1A134	YF127	1A739	Z3	1S49
WH152	1A719	YF171	1A740	Z31	1S28
X8	1S58	YF176	1A741	Z7	1S47

B. SUBTILIS 168 STRAINS INDEXED BY ALLELE

ALLELE	CODE	DESCRIPTION	ALLELE	CODE	DESCRIPTION
(SPβc2)	1A600	(SPβc2) cym-84::Tn917 trpC2	::Tn917/lac	1A749	::Tn917/lac MLS ^R
	1A601	(SPβc2) purM::Tn917 trpC2	abrB6	1S69	abrB6 spo0A12 trpC2
	1A602	(SPβc2) ath-83::Tn917 trpC2	abrB23	1S68	abrB23 pheA1 spo0A12 trpC2
	1A603	(SPβc2) thiA84::Tn917 trpC2	abrB24	1S70	abrB24 spo0A12 trpC2
	1A604	(SPβc2) metD83::Tn917 trpC2	blt-2	1A189	blt-2 trpC2
	1A605	(SPβc2) argF83::Tn917 trpC2	addA5	1A334	addA5 hisH2 metB5
	1A606	(SPβc2) argF82::Tn917 trpC2	addB71	1A702	addB71 amyE SPβ- metB5 sigB xin-1
	1A607	(SPβc2) metC85::Tn917 trpC2	addB72	1A701	addB72 amyE SPβ- metB5 sigB trpC2 xin-1
	1A608	(SPβc2) arg342::Tn917 trpC2	ade	1A437	ade his hsd _R R-M- met nic rib trp tyr ura
	1A609	(SPβc2) pyr-82::Tn917 trpC2		1S31	ade met spolla26 trpC2
	1A610	(SPβc2) pyr-83::Tn917 trpC2		1S73	ade met Sm spo0A16 trpC2
	1A611	(SPβc2) trpC2 urc-83::Tn917	aec	1A356	aec hom-1 trpC2
	1A612	(SPβc2) gltAB81::Tn917 trpC2	aec-56	1A431	aec-56
	1A613	(SPβc2) aroBC84::Tn917 trpC2	aec-59	1A432	aec-59
	1A614	(SPβc2) serA84::Tn917 trpC2	aecB	1A357	aecB lys-1 sul trpC2
	1A615	(SPβc2) lys-82::Tn917 trpC2	ahrC2	1A512	ahrC2
	1A616	(SPβc2) nic-82::Tn917 trpC2	ala-1	1A434	ala-1 leuB8 metB pur thr-5 trpC
	1A617	(SPβc2) pheA82::Tn917 trpC2	alaA84::Tn917	1A623	(SPβc2) alaA84::Tn917 trpC2
	1A618	(SPβc2) leuB84::Tn917 trpC2	ald-1	1A9	ald-1 aroA932 leuB8 trpC2
	1A619	(SPβc2) liv1-82::Tn917 trpC2		1A53	ald-1 degQ36 trpC2
	1A620	(SPβc2) liv3-83::Tn917 trpC2		1A679	ald-1 leuB8 menE312 trpC2
	1A621	(SPβc2) serC82::Tn917 trpC2	ald::	1S134	ald::Tn917 HU297
	1A622	(SPβc2) arg(GH)85::Tn917 trpC2	Tn917 HU297		
	1A623	(SPβc2) alaA84::Tn917 trpC2	alsR1	1A147	alsR1 ccpA1 ilvB 1 trpC2
	1A624	(SPβc2) mth-83::Tn917 trpC2		1A250	alsR1 ilvB 1 trpC2
	1A625	(SPβc2) mth-84::Tn917 trpC2	amm-35	1A336	amm-35 leuB8 metB5 purA16
	1A626	(SPβc2) hisA82::Tn917 trpC2	amt	1A337	amt
	1A627	(SPβc2) trpC2 zaa-84::Tn917	amy-3	1A501	amy-3 aro-10 lmrA2
	1A628	(SPβc2) trpC2 zbj-82::Tn917;	amyE	1A288	amyE dal-1 metB5 sacA321
	1A629	(SPβc2) trpC2 zca-82::Tn917		1A289	amyE aroI906 metB5 sacA321
	1A630	(SPβc2) trpC2 zce-82::Tn917		1A297	amyE aspT1 trpC2
	1A631	(SPβc2) motA::Tn917 trpC2		1A701	addB72 amyE SPβ- metB5 sigB trpC2 xin-1
	1A632	(SPβc2) kinC::Tn917 trpC2		1A702	addB71 amyE SPβ- metB5 sigB xin-1
	1A633	(SPβc2) trpC2 zdi-82::Tn917		1A703	amyE SPβ- metB5 recP149 sigB trpC2 xin-1
	1A634	(SPβc2) trpC2 zci-82::Tn917	amyE ^{+M}	1A182	amyE ^{+M} amyR1 deg-9 metB5 pro(L) purF6 str trpB3
	1A635	(SPβc2) trpC2 proJ::Tn917		1A311	amyE ^{+M} amyR2 deg-9 metB5 pro(L) purF6 str
	1A636	(SPβc2) cgeE::Tn917 trpC2		1A338	amyE ^{+M} amyR1(+M) metB5 pro(L) purF6 trpB3
	1A637	(SPβc2) trpC2 yokH::Tn917		1A339	amyE ^{+M} amyR21(+M)(H) metB5 pro(L) purF6 str trpB3
	1A638	(SPβc2) trpC2 zfg-83::Tn917		1A340	amyE ^{+M} amyR1 aroI116 deg-118 metB5 pro(L) str trpB3
	1A639	(SPβc2) spoVID::Tn917 trpC2		1A341	amyE ^{+M} amyR1 ^{+M} metB5 pro(H) purF6 str trpB3
	1A640	(SPβc2) trpC2 zhb-83::Tn917		1A412	amyE ^{+M} amyR2 metB5 purF6
	1A641	(SPβc2) trpC2 zhc-85::Tn917		1A413	amyE ^{+M} amyR1 metB5
	1A642	(SPβc2) trpC2 yufR::Tn917		1A414	amyE ^{+N} amyR2 metB5 purF6
	1A643	(SPβc2) trpC2 yvaC::Tn917		1A772	amyE::cat Cm pheA1 trpC2
	1A644	(SPβc2) trpC2 zii-83::Tn917		1A717	amyE::erm MLS
	1A645	(SPβc2) trpC2 zjf-85::Tn917		1A771	amyE::erm MLS pheA1 trpC2
	1A646	(SPβc2) trpC2 zfd-81::Tn917		1A474	amyE3 aroI10
	1A687	(SPβc2) trpC2 zba89::Tn917		1A182	amyE ^{+M} amyR1 deg-9 metB5 pro(L) purF6 str trpB3
	1A688	(SPβc2) trpC2 ydaO::Tn917		1A340	amyE ^{+M} amyR1 aroI116 deg-118 metB5 pro(L) str trpB3
	1A689	(SPβc2) trpC2 zdf88::Tn917		1A413	amyE ^{+N} amyR1 metB5
	1A690	(SPβc2) trpC2 zec88::Tn917		1A338	amyE ^{+M} amyR1 ^{+M} metB5 pro ^l purF6 trpB3
	1A691	(SPβc2) trpC2 zfe86::Tn917		1A341	amyE ^{+M} amyR1 ^{+M} metB5 pro ^h purF6 str trpB3
	1A692	(SPβc2) trpC2 zhf86::Tn917		1A311	amyE ^{+M} amyR2 deg-9 metB5 pro ^l purF6 str
	1A693	(SPβc2) trpC2 zhg86::Tn917		1A412	amyE ^{+M} amyR2 metB5 purF6
	1A721	(SPβc2) aroI86::Tn917 trpC2	amyE ^{+N}		
	1A722	(SPβc2) bfmB84::Tn917 trpC2	amyE::cat		
	1A724	(SPβc2) trpC2 zba-88::Tn917	amyE::erm		
	1A727	(SPβc2) trpC2 zeh-82::Tn917			
	1A728	(SPβc2) trpC2 z fj-83::Tn917			
	1A730	(SPβc2) trpC2 zhf-83::Tn917	amyE3		
	1A731	(SPβc2) trpC2 zib-82::Tn917	amyR1		
	1A732	(SPβc2) trpC2 zjd-89::Tn917			
	1A733	(SPβc2) trpC2 zjj-84::Tn917			
		zjj-85::Tn917			
(φ105)	1A421	(φ105) ilvA1 metB5 purA16 xhi-1479 xki-1479	amyR1 ^{+M}		
::Tn917	1A759	::Tn917 MLS ^R			
::Tn917::pTV20	1A760	::Tn917::pTV20 Cm MLS ^R	amyR2		
::Tn917::pTV20	1A762	::Tn917::pTV20 bac-1 Cm MLS ^R			
::Tn917::pTV21 2	1A761	::Tn917::pTV21 2 Cm			

B. subtilis 168 Strains Indexed by Allele

ALLELE	CODE	DESCRIPTION	ALLELE	CODE	DESCRIPTION
amyR2 (cont)	1A414	amyE(+N) amyR2 metB5 purF6	aroB2 (cont)	1A380	aroB2 hisH2 recF33 trpC2
amyR21 ^{M(H)}	1A339	amyE ^M amyR21(+M)(H) metB5 pro(L) purF6 str trpB3		1A404	aroB2 hisA53 hisH2 rna-53 trpC2 tyrA1
aprE	1A751	apr bglS EV bglC 102 his npr	aroB4	1A131	aroB4 hisH2
	1A752	apr bglS EV bglC 102 glgB::lacZ M15 his npr	aroBC84::Tn917	1A613	(SPβc2) aroBC84::Tn917 trpC2
apt-6	1A681	apt-6 ilvA1 pbuG3 pupA3 sacA78 upp	aroC7	1A132	aroC7 trpC2
arg	1A506	arg trp	aroD120	1A408	aroD120 recA4 trpC2
	1A595	arg thyA thyB tscA1		1A654	aroD120 bglS33 trpC2
	1A596	arg thyA thyB tscA23		1A69	aroD120 trpC2
	1A597	arg nadE49 thyA thyB		1A8	aroD120 lys-1 trpC2
	1A598	arg thyA thyB tscC11	aroE1	1A133	aroE1 hisH2
	1A599	arg thyA thyB tscD14		1A207	aroE1 hisA1
	1A647	arg nadE47 thyA thyB		1A229	aroE1
	1A648	arg nadE48 thyA thyB	aroF5	1A134	aroF5
	1A649	arg thyA thyB tscD14	aroA932	1A330	aroA932 bioB141
arg(BCDJ)	1A148	arg(ABCDE)		1A56	aroA932 trpC2
arg(BCDJ)1	1A118	arg(ABCDE)1 metA8 trpC2		1A9	ald-1 aroA932 leuB8 trpC2
arg(GH)2	1A92	arg(GH)2 aroA932 bioB141 sacA321		1A92	arg(GH)2 aroA932 bioB141 sacA321
	1A111	arg(GH)2 azlB101 trpC2	aroH1	1A117	aroH1 cotA73
	1A119	arg(GH)2 leuA164 pheA2 trpC2	arol10	1A474	amyE3 arol10
	1A121	arg(GH)2 pheA2 sdhC109 trpC2	arol86::Tn917	1A721	(SPβc2) arol86::Tn917 trpC2
	1A440	arg(GH)2 hemA1	arol116	1A340	amyE(+M) amyR1 arol116 deg-118 metB5 pro(L) str trpB3
arg(GH)3	1A211	arg(GH)3 pheA12 rplV1	arol906	1A289	amyE arol906 metB5 sacA321
	1A212	arg(GH)3 lys-21 metB5 pheA12 purA16 rplV1		1A4	arol906 dal-1 purE1 trpC2
	1A277	arg(GH)3 lys-21 metB5 pheA12		1A429	arol906 glpT6 trpC2
arg(GH)15	1A253	arg(GH)15 hsd _R R-M- leuB8 SP10 ^S		1A55	arol906 dal-1 metB5 sacA321
	1A363	arg(GH)15 hsd _R R-M- leuB8 rplV	asaA4	1A281	asaA4 leu-2 trpC2
	1A365	arg(GH)15 trpB3		1A283	asaA4 asaB4 leu-2 trpC2
	1A366	arg(GH)15 recA45 trpB3	asaA 2	1A280	asaA 2 leu-2 trpC2
	1A373	arg(GH)15 recD43 trpB3		1A282	asaA 2 asaB1 leu-2 trpC2
	1A409	arg(GH)15 hsd _R R-M- leuB8 recA4	asaB1	1A282	asaA 2 asaB1 leu-2 trpC2
	1A423	arg(GH)15 hsd _R R-M- leuB8 recA4 thr-5	asaB4	1A283	asaA4 asaB4 leu-2 trpC2
	1A510	arg(GH)15 hsd _R R-M- leuB8 recA4 stp thr	aspB66	1A295	aspB66 trpC2
arg(GH)85::Tn917	1A622	(SPβc2) arg(GH)85::Tn917 trpC2	aspH1	1A296	aspH1 trpC2
arg ^S	1A391	arg ^S pyrA	aspT1	1A297	amyE aspT1 trpC2
arg342::Tn917	1A608	(SPβc2) arg342::Tn917 trpC2	ath-83::Tn917	1A602	(SPβc2) ath-83::Tn917 trpC2
argF4	1A28	argF4 hisA1 trpC2	azc-1	1A430	azc-1
	1A39	argF4 trpC2	azlA102	1A112	azlA102 trpC2
	1A125	argF4 metA29 thiB4	azlB101	1A111	arg(GH)2 azlB101 trpC2
	1A136	argF4 hag-2 tagE	azpB80	1A298	aroB2 azpB80 hisH2 trpC2
	1A138	argF4 hag-1 smo-1 trpC2	bac-1	1A758	bac-1
	1A151	argF4 hpr hisA1 pha-1		1A762	::Tn917::pTV20 bac-1 Cm MLS ^R
	1A302	argF4 hisA1 recA4	bfmB	1A471	pdhA1 bfmB metC7 trpC2
	1A312	argF4 flaC51 hag-1 hisA1 ura	bfmB::cat	1A756	bfmB::cat Cm thr-5 trpC2
	1A319	argF4 hisA1 purH4 trpC2	bfmB1	1A472	bfmB1 iur trpC2
	1S44	argF4 hisA1 metB5 pheA12 purA16 pyrA26 spoVB91 trpC2		1A473	bfmB1 strC2 trpC2
	1S84	argF4 cotA leu-2 pyrA26 scoA1	bfmB84::Tn917	1A722	(SPβc2) bfmB84::Tn917 trpC2
	1S85	argF4 kinA2 leu-2 pyrA26	bglS33	1A654	aroD120 bglS33 trpC2
argF82::Tn917	1A606	(SPβc2) argF82::Tn917 trpC2	bglS EV	1A751	apr bglS EV bglC 102 his npr
argF83::Tn917	1A605	(SPβc2) argF83::Tn917 trpC2		1A752	apr bglS EV bglC 102 his npr glgB::lacZ M15 his npr
aro-10	1A501	amy-3 aro-10 lmrA2	bioB141	1A330	aroA932 bioB141
aroA6	1A130	aroA6	bioB141	1A92	arg(GH)2 aroA932 bioB141 sacA321
aroB2	1A36	aroB2 hisH2 metB10 trpC2 tyrA1	bmr ^R	1A753	bmr ^R thr-5 trpC2
	1A83	aroB2 hisH2	bmr::cat	1A754	bmr::cat Cm thr-5 trpC2
	1A103	aroB2 hisH2 recG40 trpC2 tyrA1	bmrR::cat	1A755	bmrR::cat Cm thr-5 trpC2
	1A104	aroB2	bofA::cat	1S100	bofA::cat Cm SPβ
	1A298	aroB2 azpB80 hisH2 trpC2 tyrA1	bofA::Tn917lac	1S96	bofA::Tn917lac pheA1 trpC2
	1A299	aroB2 hisH2 gyrA trpC2 tyrA1	bry	1A267	bry
	1A378	aroB2 hisH2 recD41 trpC2 tyrA1	cafA1	1A381	cafA1 metB10 trpC2
	1A379	aroB2 hisH2 recG39 trpC2 tyrA1	cam-2	1A578	cam-2 trpC2
			car-41	1A13	car-41 leuB8 metB5 purF6
				1A449	car-41 leuB8 metB5 purF6 rpoC105
			ccpA1	1A147	alsR1 ccpA1 ilvB 1 trpC2
				1A480	cdd-1 ddd-3
			cdd-1	1A479	cdd-1 crk-1 dck-3

B. subtilis 168 Strains Indexed by Allele

ALLELE	CODE	DESCRIPTION	ALLELE	CODE	DESCRIPTION
cdr-1	1A655	arol906 cdr-1 trpC2	ctrA1	1A11	ctrA1 sacA321 trpC2
cer-2	1A573	cer-2 trpC2		1A461	ctrA1 ts-2
cer-14	1A576	cer-14 trpC2	cym-1	1A500	cym-1 rpoB1
cer-20	1A577	cer-20 trpC2	cym-84::Tn917	1A600	(SPβc2) cym-84::Tn917 trpC2
cgeE::Tn917	1A636	(SPβc2) cgeE::Tn917 trpC2	cysB3	1A31	cysB3 hisA1 trpC2
citB1	1A326	citB1 gltA2 ilvA8 thyB1	cysC1	1A79	cysC1 trpC2
	1A331	citB1 trpC2	cysC7	1S67	cysC7 furA2 spoIIg279
citB17	1A143	citB17 ilvA1 sacA78 thyB204	cysE14	1A3	cysE14 purA26 trpC2
	1A152	citB17 trpC2		1A97	cysE14 trpC2
citB75	1A120	citB75 trpC2		1A190	cysE14 spo- tufAA-7
citC	1A492	citC met pheA trpC2		1A192	cysE14 efg-1 spo-
	1A493	citC met polA10 trpC2		1A194	cysE14 nea-1 spo-
citC6	1A32	citC6 trpC2		1A195	cysE14 ole-2 spo-
citD 1	1A278	citD 1 trpC2		1A222	cysE14 rplV1 spo-
	1A332	citD 1 ilvA8 thyA1 thyB1		1A241	cysE14 rpsE2
citD 29	1S76	citD 29 dal-1 spo0A 677 str-76 thyA thyB uvr-1		1A662	cysE14 purA16 rpmA1 trpC2
				1A663	cysE14 purA16 rpsK2 trpC2
citG4	1A16	citG4 trpC2	dacA::cat ⁺	1A742	dacA::cat ⁺ trpC2
citH	1A364	citH	dacA ⁺ ::cat ⁺	1A743	dacA ⁺ ::cat ⁺ trpC2
Cm	1A716	Cm sigD::pLM5 trpC2	dacB::cat ⁺	1A745	dacB::cat ⁺ trpC2
	1A754	bmr::cat Cm thr-5 trpC2	dacB ⁺ ::cat ⁺	1A744	dacB ⁺ ::cat ⁺ trpC2
	1A755	bmrR::cat Cm thr-5 trpC2		1A4	arol906 dal-1 purE1 trpC2
	1A756	bfmB::cat Cm thr-5 trpC2		1A55	arol906 dal-1 metB5 sacA321
	1A760	::Tn917::pTV20 Cm MLS ^R		1S76	citD 29 dal-1 spo0A 677 str-76 thyA thyB uvr-1
	1A761	::Tn917::pTV21 2 Cm			
	1A762	::Tn917::pTV20 bac-1 Cm MLS ^R		1A288	amyE dal-1 metB5 sacA321
	1A763	Cm fla/che::pLM19 trpC2	dapE320	1A464	dapE320 thyA1 thyB1 trpC2
	1A767	Cm MLS pheA1 phoA::pCE413 phoB::Tn917 trpC2	dck-3	1A479	dck-1 crk-1 dck-3
	1A772	amyE::cat Cm pheA1 trpC2	ddd-3	1A480	dck-1 ddd-3
	1A773	Cm pheA1 thrC::cat trpC2	ddIA1475	1A463	ddIA1475 ilvA1 metB5 purA16
	1S100	bofA::cat Cm SPβ-		1A202	deg leuB8 trpC2
	1S101	Cm cotA::cat trpC2	deg(H)25	1A159	deg(H)25 narA1
	1S108	Cm cotT::pDE194 pheA1 trpC2	deg(H)32	1A165	deg(H)32 trpC2
	1S112	Cm sspA sspE	deg(H)32	1A95	deg(H)32 leuB8 trpC2
	1S113	Cm sspA sspB sspE	deg(H)100	1A200	deg(H)100 leuB8 trpC2
com-9	1A706	com-9 hisA1 leu-8 lys-21 metB5 thr-5 trpC2	deg(H)200	1A199	deg(H)200 leuB8 trpC2
			deg-9	1A182	amyE(+M) amyR1 deg-9 metB5 pro(L) purF6 str trpB3
com-14::Tn917	1A711	com-14::Tn917 hisA1 leu-8 lys- 21 metB5 purF6 thr-5 trpC2	deg-9	1A311	amyE(+M) amyR2 deg-9 metB5 pro(L) purF6 str
			deg-42	1A201	deg-42 hisA1 sacA321 trpC2
com-18::Tn917	1A712	com-18::Tn917 hisA1 leu-8 lys- 21 metB5 purF6 thr-5 trpC2	deg-118	1A340	amyE(+M) amyR1 aroI116 deg- 118 metB5 pro(L) str trpB3
			dfrA24	1A491	dfrA24 pabA7
com-30	1A708	com-30 hisA1 leu-8 lys-21 metB5 thr-5 trpC2	divI32	1A318	divI32 trpC2
			divIB12	1A146	divIB12 leuB8 metB5 purA16
com-31	1A710	com-31 hisA1 leu-8 lys-21 metB5 thr-5 trpC2	divII55	1A316	divII55 thr-5 trpC2
			divII61	1A317	divII61 thr-5 trpC2
com-44::Tn917	1A713	com-44::Tn917 hisA1 leu-8 lys- 21 metB5 purF6 thr-5 trpC2	divIVA1	1A196	divIVA1 ilvD thyA1 thyB1
			divV32	1A314	divV32 thr-5 trpC2
com-71	1A707	com-71 hisA1 leu-8 metB5 purF6 thr-5 trpC2	divV71	1A315	divV71 trpC2
			dnaA13	1A175	dnaA13 glnA100 pheA1 trpC2
com-104	1A709	com-104 hisA1 leu-8 lys-21 metB5 thr-5 trpC2	dnaA13	1A18	dnaA13 ilvA1 metB5
			dnaA151	1A25	dnaA151 ilvA1 metB5
cotA	1S84	argF4 cotA leu-2 pyrA26 scoA1	dnaB1	1A41	dnaB1 thyA1 thyB1 trpC2
cotA::cat	1S101	Cm cotA::cat trpC2	dnaB134	1A17	dnaB134 ilvA1 thyA1 thyB1
cotA1	1A184	cotA1 trpC2		1A290	dnaB134 thyA1 thyB1 trpC2
cotA73	1A117	aroH1 cotA73	dnaB19	1A19	dnaB19 ilvA1 metB5
cotA8	1A183	cotA8 trpC2	dnaC30	1A20	dnaC30 ilvA1 metB5
cotA::	1S136	cotA::Tn917 HU306	dnaD23	1A21	dnaD23 ilvA1 metB5
Tn917 HU306			dnaE20	1A22	dnaE20 ilvA1 metB5
cotB::cat	1S102	cotB::cat trpC2	dnaI102	1A26	dnaI102 ilvA1 metB5
cotC::cat	1S103	cotC::cat trpC2	dnaN34	1A24	dnaN34 ilvA1 metB5
cotD::cat	1S104	cotD::cat trpC2	dnaX8132	1A74	dnaX8132 hisA1 thr-5
cotE::cat	1S105	cotE::cat trpC2		1A93	dnaX8132 hisA1 sacA321 thr-5
cotF::cat	1S106	cotF::cat trpC2	dppE132::neo	1A737	dppE132::neo pheA1 trpC2
cotF::cat	1S107	cotF::cat trpC2	ebr-2	1A342	ebr-2 hisH2 thyA1 thyB1
cotT::pDE194	1S108	Cm cotT::pDE194 pheA1 trpC2	efg-1	1A192	cysE14 efg-1 spo-
crk-1	1A479	cdd-1 crk-1 dck-3	efg-3	1A238	efg-3 str
			bgIC 102	1A751	apr bgIS EV bgIC 102 his npr
crsB40	1A582	crsB40		1A752	apr bgIS EV bgIC 102
crsC1	1A583	crsC1	fbp-1	1A465	glgB::lacZ M15 his npr fbp-1 hisA1 leuB8 metB5 trpC2
crsC2	1A584	crsC2			
crsD1	1A585	crsD1			
crsE1	1A586	crsE1			
crsF4	1A587	crsF4			

B. subtilis 168 Strains Indexed by Allele

ALLELE	CODE	DESCRIPTION	ALLELE	CODE	DESCRIPTION
metB5 (cont)	1A29	leuB8 metB5 nic-38 purA16	metB5 (cont)	1A702	addB71 amyE SPβ- metB5 sigB
	1A30	ilvA64 leuB8 metB5 purA16			xin-1
	1A55	arol906 dal-1 metB5 sacA321	1A703	amyE SPβ- metB5 recP149 sigB	trpC2 xin-1
	1A68	leuB8 metB5 tsi-23	1A706	com-9 hisA1 leu-8 lys-21	metB5 thr-5 trpC2
	1A75	ilvA1 leuB8 metB5	1A707	com-71 hisA1 leu-8 metB5	purF6 thr-5 trpC2
	1A76	ilvA1 metB5 spcB1	1A708	com-30 hisA1 leu-8 lys-21	metB5 thr-5 trpC2
	1A77	ilvA1 metB5 strB3	1A709	com-104 hisA1 leu-8 lys-21	metB5 thr-5 trpC2
	1A81	ilvA1 leuB8 metB5 polC12	1A710	com-31 hisA1 leu-8 lys-21	metB5 thr-5 trpC2
	1A82	ilvA1 leuB8 metB5 polC12			com-14::Tn917 hisA1 leu-8 lys-
	1A86	ilvA1 leu leuB8 metB5	1A711	com-18::Tn917 hisA1 leu-8 lys-	21 metB5 purF6 thr-5 trpC2
		polA1443	1A712	com-44::Tn917 hisA1 leu-8 lys-	21 metB5 purF6 thr-5 trpC2
	1A98	ilv 1 kauA1 metB5	1A713	com-44::Tn917 hisA1 leu-8 lys-	21 metB5 purF6 thr-5 trpC2
	1A141	hisA1 hsd _R R-M- leuB8 lys-21	1A720	hisB leuA8 metB5 polA5 SPβ-	xin-1
		metB5 nonA1 SP10 ^S thr-5	1A746	Em metB5 recA260 SPβ- trpC2	xin-1
		trpC2 φNR2 ^S	1S2	metB5 spo0A3 thr-5	
	1A145	leuB8 metB5 purA16	1S3	-(metB5)+ spo0A3 sup-44 thr-5	
	1A146	divB12 leuB8 metB5 purA16	1S4	-(metB5)+ -(thr-5)+ spo0A3	trnS-Lys3
	1A168	hisA1 metB5 uvrB1	1S44	argF4 hisA1 metB5 pheA12	purA16 pyrA26 spoVB91 trpC2
	1A182	amyE(+M) amyR1 deg-9 metB5	1S77	metB5 spollA50 thr-5	
		pro(L) purF6 str trpB3	1S97	hisA1 leuA8 metB5 sinR::phl	
	1A197	metB5 minD1 tag-1 thyA thyB1	1S98	hisA1 leuA8 metB5 sinL::kan-50	lys-3 metB10 tagE trpC2
		spo	1A35	aroB2 hisH2 metB10 trpC2	tyrA1
	1A212	arg(GH)3 lys-21 metB5 pheA12	1A36	hisA metB10 trpC2	
		purA16 rplV1	1A38	metB10 purF6 trpC2	
	1A258	ile leu metB5 thyA1 thyB1	1A40	lys-3 metB10 trpC2	
	1A276	ilvA1 metB5 polA1443 polC1	1A381	cafA1 metB10 trpC2	
	1A277	arg(GH)3 lys-21 metB5 pheA12	1A478	lys-3 metB10 spc spcD trpC2	
	1A288	amyE dal-1 metB5 sacA321	1A490	gltB1 leuB8 metB10	
	1A289	amyE arol906 metB5 sacA321	1A719	metB10 trpC2 xylAB 1	
	1A291	gcaD26 leuB8 metB5 purA16	1A263	metC pfk pts1	
	1A292	metB5 minD1 thyA1 thyB1	1A5	glyB133 metC3 treA12 trpC2	
	1A304	metB5 SPβ- trpC2 xin-1	1A60	metC3 pyrA xin-1	
	1A311	amyE(+M) amyR2 deg-9 metB5	1A78	metC3 pyrA xtl-1	
		pro(L) purF6 str	1A279	-(hisA1)+ -(metC3)+ sup-22	trpC2
	1A334	addA5 hisH2 metB5	1A284	metC3 pyrA xhd-1	
	1A336	amm-35 leuB8 metB5 purA16	1A306	metC3 phoR2 tal-1	
	1A338	amyE(+M) amyR1(+M) metB5	1A376	fruC1 metC3 trpC2	
		pro(L) purF6 trpB3	1A377	fruB22 fruC1 metC3 trpC2	
	1A339	amyE(+M) amyR21(+M)(H)	1A483	lyt-1 metC3	
		metB5 pro(L) purF6 str trpB3	1A484	lyt-2 metC3	
	1A340	amyE(+M) amyR1 aroI116 deg-	1S27	metC3 spollIJ87 tal-1	
		118 metB5 pro(L) str trpB3	1S42	metC3 spollIA(A-H)35 tal-1	
	1A341	amyE(+M) amyR1(+M) metB5	1S65	metC3 spollVF88 tal-1	
		pro(H) purF6 str trpB3	1S66	metC3 rpoB2 spoVC285	
	1A387	metB5 purE26	1S78	metC3 rpoB2 sigF63 tal-1	
	1A388	metB5 purE4	1S87	metC3 spoIVG-25 tal-1	
	1A389	metB5 purE5	metC7	1A80	metC7 trpC2
	1A412	amyE(+M) amyR2 metB5 purF6	1A293	guaB3 metC7 purH1 trpC2	
	1A413	amyE(+N) amyR1 metB5	1A294	guaA2 metC7 purH1 trpC2	
	1A414	amyE(+N) amyR2 metB5 purF6	1A468	glms2 metC7 trpC2	
	1A420	ilvA1 metB5 purA16 xhi-1479	1A471	pdhA1 bfmB metC7 trpC2	
		xki-1479	1A738	iolG6 metC7 trpC2	
	1A421	(φ105) ilvA1 metB5 purA16	1A739	gntK4 metC7 trpC2	
		xhi-1479 xki-1479	1A740	gntP9 metC7 trpC2	
	1A445	hisA1 leuB8 lys-21 metB5	1A741	gntR1 metC7 trpC2	
		nonA1 purF6 SP10 ^R thr-5 trpC2	1A607	(SPβc2) metC85::Tn917 trpC2	
	1A446	hisA1 leuB8 lys-21 metB5	metD1	1A84	glyB133 metD1
		nonA1 SP10 ^R trpC2	metD4	1A482	hisH2 metD4 outA7 trpC2
	1A447	hsd _R R- M- leuB8 metB5 SP10 ^R		1G14	hisH2 metD4 outA7 trpC2
	1A449	car-41 leuB8 metB5 purF6			
		rpoC105			
	1A459	leuB8 metB5 SPβ- thr-5 trnS-			
		Lys3			
	1A460	ilvA8 metB5 thyA1 thyB1			
	1A462	leuB8 metB5 tem-1			
	1A463	ddlA1475 ilvA1 metB5 purA16			
	1A465	fbp-1 hisA1 leuB8 metB5 trpC2			
	1A476	hisA1 metB5			
	1A477	-(hisA1)+ -(metB5)+ sup-1			
	1A509	hisA1 hsd _R R-M- metB5 recA4			
	1A701	addB72 amyE SPβ- metB5 sigB			
		trpC2 xin-1			

B. subtilis 168 Strains Indexed by Allele

ALLELE	CODE	DESCRIPTION	ALLELE	CODE	DESCRIPTION
metD4 (cont)	1G4	hisH2 metD4 outD1 trpC2	pdhD22	1A70	pdhD22 trpC2
	1G6	gsp-10 hisH2 metD4 trpC2	pfk	1A263	metC pfk pts1
metD83::Tn917	1A604	(SPβc2) metD83::Tn917 trpC2	pgk	1G13	gerG47 met pgk trpC2
minD1	1A197	metB5 minD1 thyA thyB1 spo ⁻	pha-1	1A150	hpr hisA1 pha-1
	1A292	metB5 minD1 thyA1 thyB1		1A151	argF4 hpr hisA1 pha-1
MLS ^R	1A717	amyE::erm MLS	pheA	1A254	pheA phoP
	1A746	metB5 MLS recA260 SPβ- trpC2		1A492	citC met pheA trpC2
	1A749	::Tn917lac MLS ^R	pheA1	1A57	ilvC1 pheA1 trpC2
	1A759	::Tn917 MLS ^R		1A96	pheA1 trpC2
	1A760	::Tn917::pTV20 Cm MLS ^R		1A174	glnA100 ilvC1 pheA1 trpC2
	1A762	::Tn917::pTV20 bac-1 Cm MLS ^R		1A175	dnaA13 glnA100 pheA1 trpC2
	1A767	Cm MLS pheA1 phoA::pCE413		1A176	glnA103 pheA1 trpC2
	1A771	amyE::erm MLS pheA1 trpC2		1A224	hisH2 pheA1 trpC2
	1S99	MLS ^R spoVK::Tn917HU8 SPβ-		1A225	pheA1 polA5 trpC2
motA::Tn917	1A631	(SPβc2) motA::Tn917 trpC2		1A226	hisH2 pheA1 polA5 trpC2
mreD1	1A485	leuB8 mreD1		1A227	pheA1 trpC2
mth-83::Tn917	1A624	(SPβc2) mth-83::Tn917 trpC2		1A240	glpK21 pheA1 trpC2
mth-84::Tn917	1A625	(SPβc2) mth-84::Tn917 trpC2		1A249	ilvC1 pheA1 strC23
mtlD1	1A54	mtlD1 nasC1 sacA321		1A275	pheA1
mtr-264	1A72	mtr-264		1A698	pheA1 sfp
nadE47	1A647	arg nadE47 thyA thyB		1A699	pheA1 sfp srfA::Tn917
nadE48	1A648	arg nadE48 thyA thyB		1A737	dppE132::neo pheA1 trpC2
nadE49	1A597	arg nadE49 thyA thyB		1A764	flgM 80 pheA1 trpC2
nadE81	1G2	hisH2 nadE81 trpC2		1A767	Cm MLS pheA1 phoA::pCE413
gyrA	1A299	aroB2 hisH2 gyrA trpC2 tyrA1		1A771	amyE::erm MLS pheA1 trpC2
narA1	1A159	deg(H)25 narA1		1A772	amyE::cat Cm pheA1 trpC2
	1A205	narA1 trpC2 ura-1		1A773	Cm pheA1 thrC::cat trpC2
	1A94	narA1 trpC2		1A774	pheA1 rpoC:ⓂHis6-tag) Sp trpC2
nasC1	1A54	mtlD1 nasC1 sacA321		1S108	Cm cotT::pDE194 pheA1 trpC2
nea-1	1A194	cysE14 nea-1 spo-		1S16	pheA1 spo0B136 trpC2
nic	1A410	nic		1S17	pheA1 spo0E11 trpC2
	1A437	ade his hsd _R R-M- met nic rib trp tyr ura		1S19	pheA1 spo0F221 trpC2
	1A438	hsd _R R-M+ met nic rib trp tyr ura		1S24	pheA1 sigH81 trpC2
nic-38	1A29	leuB8 metB5 nic-38 purA16		1S26	pheA1 spoIIJ87 trpC2
nic-82::Tn917	1A616	(SPβc2) nic-82::Tn917 trpC2		1S68	abrB23 pheA1 spo0A12 trpC2
nonA1	1A141	hisA1 hsd _R R-M- leuB8 lys-21 metB5 nonA1 SP10 ^S thr-5 trpC2 φNR2 ^S		1S83	pheA1 spoVF1 trpC2
	1A445	hisA1 leuB8 lys-21 metB5 nonA1 purF6 SP10 ^R thr-5 trpC2		1S9	pheA1 spo0A12 trpC2
	1A446	hisA1 leuB8 lys-21 metB5 nonA1 SP10 ^R trpC2		1S96	bofA::Tn917lac pheA1 trpC2
	1A448	hisA1 hsd _R R-M- leuB8 nonA1 rpoB SP10 ^S thr-5	pheA12	1A66	pheA12 tolA6 trpC2
novB	1A162	ilvA1 novB thyA1		1A67	pheA12 tolA6 trpC2 φ29 ^R
novB75	1A127	novB75 trpC2		1A211	arg(GH)3 pheA12 rpIV1
nprB	1A274	npr		1A212	arg(GH)3 lys-21 metB5 pheA12 purA16 rpIV1
	1A751	apr bgIS EV bgIC 102 his npr		1A277	arg(GH)3 lys-21 metB5 pheA12
	1A752	apr bgIS EV bgIC 102 glgB::lacZ M15 his npr		1S44	argF4 hisA1 metB5 pheA12 purA16 pyrA26 spoVB91 trpC2
odhA5	1A672	odhA5 odhA5 trpC2		1S46	pheA12 spoIVA178
	1A672	odhA5 odhA5 trpC2	pheA2	1A15	pheA2 trpC2
odhB1	1A99	odhB1 ilvA3 trpC2		1A119	arg(GH)2 leuA164 pheA2 trpC2
odhB17	1A673	odhB17 trpC2		1A121	arg(GH)2 pheA2 sdhC109 trpC2
ole-2	1A195	cysE14 ole-2 spo-	pheA82::Tn917	1A617	(SPβc2) pheA82::Tn917 trpC2
opp141	1S28	opp141 trpC2	phoA::pCE413	1A767	Cm MLS pheA1 phoA::pCE413 phoB::Tn917 trpC2
outA7	1A482	hisH2 metD4 outA7 trpC2	phoB::Tn917	1A767	Cm MLS pheA1 phoA::pCE413 phoB::Tn917 trpC2
	1G14	hisH2 metD4 outA7 trpC2	phoP	1A254	pheA phoP
outC25	1G5	hisH2 outC25 trpC2	phoP12	1A255	phoP12
outD1	1G4	hisH2 metD4 outD1 trpC2	phoP22	1A256	phoP22
outE42	1G3	hisH2 outE42 trpC2	phoP4	1A257	phoP4
outF4	1G1	hisH2 outF4 trpC2	phoR2	1A306	metC3 phoR2 tal-1
oxr-1	1A502	oxr-1 thyA thyB	phoR2	1A307	leuB8 pho55 tal-1
oxr-2	1A503	oxr-2 thyA thyB trpC2	phoS5	1A215	polA5 thr-5 trpC2
pabB	1A355	hisH2 pabB trpC2	polA5	1A225	pheA1 polA5 trpC2
pubG1	1A682	ilvA1 pubG1 sacA78 upp xpt		1A226	hisH2 pheA1 polA5 trpC2
pbuG3	1A681	apt-6 ilvA1 pbuG3 pupA3 sacA78 upp		1A720	hisB leuA8 metB5 polA5 SPβ-xin-1
pdhA1	1A471	pdhA1 bfmB metC7 trpC2	polA10	1A493	citC met polA10 trpC2
			polA59	1A214	polA59 thr-5 trpC2
			polA1443	1A86	ilvA1 leu leuB8 metB5 polA1443
				1A276	ilvA1 metB5 polA1443 polC1

B. subtilis 168 Strains Indexed by Allele

ALLELE	CODE	DESCRIPTION	ALLELE	CODE	DESCRIPTION
polC1	1A276	ilvA1 metB5 polA1443 polC1	purF6 (cont)	1A445	hisA1 leuB8 lys-21 metB5
polC12	1A81	ilvA1 leuB8 metB5 polC12 spcB1		1A707	nonA1 purF6 SP10 ^R thr-5 trpC2 com-71 hisA1 leu-8 metB5 purF6 thr-5 trpC2
	1A82	ilvA1 leuB8 metB5 polC12		1A711	com-14::Tn917 hisA1 leu-8 lys- 21 metB5 purF6 thr-5 trpC2
polC133	1A216	polC12 pyrA26 spcB3 strB3		1A712	com-18::Tn917 hisA1 leu-8 lys- 21 metB5 purF6 thr-5 trpC2
	1A23	ilvA1 metB5 polC133		1A713	com-44::Tn917 hisA1 leu-8 lys- 21 metB5 purF6 thr-5 trpC2
pro(AB)	1A217	polC133 thr-5 trpC2		1A449	car-41 leuB8 metB5 purF6 rpoC105
pro(H)	1A652	pro(AB)	purH1	1A293	guaB3 metC7 purH1 trpC2
pro(L)	1A341	amyE(+M) amyR1(+M) metB5 pro(H) purF6 str trpB3		1A294	guaA2 metC7 purH1 trpC2
	1A182	amyE(+M) amyR1 deg-9 metB5 pro(L) purF6 str trpB3		1A319	argF4 hisA1 purH4 trpC2
	1A311	amyE(+M) amyR2 deg-9 metB5 pro(L) purF6 str	purH5	1A386	hisH2 purH5 thr trpC2
	1A338	amyE(+M) amyR1(+M) metB5 pro(L) purF6 trpB3	purM::Tn917	1A601	(SPβc2) purM::Tn917 trpC2
	1A339	amyE(+M) amyR21(+M)(H) metB5 pro(L) purF6 str trpB3	purM1	1A251	purM1 trpC2
	1A340	amyE(+M) amyR1 aroI116 deg- 118 metB5 pro(L) str trpB3	pycA19	1A149	argA19 recA1 trpC2
pro-1	1A435	pro-1	pyr-82::Tn917	1A609	(SPβc2) pyr-82::Tn917 trpC2
ptm-42	1A433	ptm-42	pyr-83::Tn917	1A610	(SPβc2) pyr-83::Tn917 trpC2
	1A481	ptm-42	pyrA	1A60	metC3 pyrA xin-1
ptsI1	1A263	metC pfk ptsI1		1A78	metC3 pyrA xtl-1
pupA3	1A681	apt-6 ilvA1 pbuG3 pupA3 sacA78 upp		1A284	metC3 pyrA xhd-1
pur	1A434	ala-1 leuB8 metB pur thr-5 trpC		1A391	arg ^S pyrA
pur-60	1A382	hisH2 pur-60 trpC2	pyrA1	1S82	pyrA1 spoL1 trpC2
pur-67	1A384	pur-67 thyA1 thyB1	pyrA5	1A115	hisA1 pyrA5 trpC2
purA16	1A29	leuB8 metB5 nic-38 purA16	pyrA26	1A27	pyrA26
	1A30	ilvA64 leuB8 metB5 purA16		1A216	polC12 pyrA26 spcB3 strB3
	1A51	purA16 sac(XY)46		1S44	argF4 hisA1 metB5 pheA12 purA16 pyrA26 spoVB91 trpC2
	1A145	leuB8 metB5 purA16		1S84	argF4 cotA leu-2 pyrA26 scoA1
	1A146	divIB12 leuB8 metB5 purA16		1S85	argF4 kinA2 leu-2 pyrA26
	1A212	arg(GH)3 lys-21 metB5 pheA12 purA16 rplV1	pyrABC	1A402	pyrABC thyA1 thyB1 trpC2
	1A291	gcaD26 leuB8 metB5 purA16	pyrACD	1A403	pyrACD
	1A336	amm-35 leuB8 metB5 purA16	pyrB	1A392	pyrB trpC2
	1A420	ilvA1 metB5 purA16 xhi-1479 xki-1479	pyrC	1A393	pyrB trpC3
	1A421	(φ105) ilvA1 metB5 purA16 xhi-1479 xki-1479	pyrCD	1A394	pyrC trpC2
	1A463	ddlA1475 ilvA1 metB5 purA16	pyrD	1A395	pyrC trpC2
	1A662	cysE14 purA16 rpmA1 trpC2		1A398	pyrCD
	1A663	cysE14 purA16 rpsK2 trpC2		1A333	pyrD
	1S44	argF4 hisA1 metB5 pheA12 purA16 pyrA26 spoVB91 trpC2	pyrD1	1A396	pyrD trpC2
purA26	1A3	cysE14 purA26 trpC2		1A397	pyrD
purD1	1A704	purD1		1A6	ilvA1 pyrD1 thyA1 thyB1 trpC2
purE1	1A156	glpK21 purE1 sacA321	pyrD319	1A466	lys-1 pyrD1 rpoB sas-1
purE1	1A4	arol906 dal-1 purE1 trpC2	pyrDF	1A467	lys-1 pyrD1 rpoB sas-2
purE4	1A388	metB5 purE4	pyrE270	1A323	met pyrD319
purE5	1A389	metB5 purE5	pyrE305	1A399	pyrDF trpC2
purE6	1A320	purE6 trpC2	pyrF	1A321	pyrE270
purE7	1A383	hisH2 purE7 trpC2		1A322	met pyrE305
purE8	1A385	hisH2 purE8 trpC2		1A400	pyrF trpC2
purE26	1A387	metB5 purE26		1A401	pyrF trpC2
purF6	1A12	leuB8 metB5 purF6	pyrR1	1A325	furB1 pyrR1 trpC2
	1A13	car-41 leuB8 metB5 purF6	rec-25	1A497	hisH2 rec-25 trpC2
	1A38	metB10 purF6 trpC2	rec-29	1A498	hisH2 rec-29 trpC2
	1A154	furB gutR met purF6 trpC2	rec-30	1A499	hisH2 rec-30 trpC2
	1A182	amyE(+M) amyR1 deg-9 metB5 pro(L) purF6 str trpB3	rec-80	1A343	hisH2 rec-80 thyA1 thyB1
	1A311	amyE(+M) amyR2 deg-9 metB5 pro(L) purF6 str		1A375	rec-80 thyA1 thyB1 trpC2
	1A338	amyE(+M) amyR1(+M) metB5 pro(L) purF6 trpB3	recA1	1A43	recA1 trpC2
	1A339	amyE(+M) amyR21(+M)(H) metB5 pro(L) purF6 str trpB3		1A73	metB4 recA1 trpC2
	1A341	amyE(+M) amyR1(+M) metB5 pro(H) purF6 str trpB3	recA4	1A149	pycA19 recA1 trpC2
	1A412	amyE(+M) amyR2 metB5 purF6		1A46	recA4 thr-5 trpC2
	1A414	amyE(+N) amyR2 metB5 purF6		1A302	argF4 hisA1 recA4
				1A408	aroD120 recA4 trpC2
				1A409	arg(GH)15 hsd _R R-M- leuB8 recA4
				1A422	hsd _R R-M- leuB6 recA4
				1A423	arg(GH)15 hsd _R R-M- leuB8 recA4 thr-5
				1A509	hisA1 hsd _R R-M- metB5 recA4
				1A510	arg(GH)15 hsd _R R-M- leuB8 recA4 stp thr
				1A514	hisH101 lys-21 recA4 spIB1 thyA thyB uvrB10

B. subtilis 168 Strains Indexed by Allele

ALLELE	CODE	DESCRIPTION	ALLELE	CODE	DESCRIPTION
recA4	1A575	ilvA2 recA4 spcB1 trpC2	rpoB2	1S22	rpoB2 sigh17 trpC2
	1A694	attSP(recA4 trpC2 zef87::Tn917		1S32	rpoB2 spoIIA69 trpC2
recA8	1A213	recA8 thr-5 trpC2		1S33	rpoB2 spoIID66 trpC2
recA45	1A366	arg(GH)15 recA45 trpB3		1S35	rpoB2 spoII E64 trpC2
recA260	1A746	Em metB5 recA260 SPβ- trpC2 xin-1		1S37	rpoB2 spoIIIA(A-H)53 trpC2
				1S45	rpoB2 spoVD156 trpC2
recB2	1A335	metB4 recB2 trpC2		1S55	rpoB2 sapA6 spoIIA69
	1A44	recB2 thr-5 trpC2		1S56	rpoB2 sapB2 spoIIA69
recB3	1A45	recB3 thr-5 trpC2		1S61	rpoB2 sigE55 trpC2
recB19	1A495	metB4 recB19 trpC2		1S64	leuB8 rpoB2 spoIIIC92 tal-1
recD27	1A261	gyrB1 metB4 recD27 trpC2		1S66	metC3 rpoB2 spoVC285
recD41	1A378	aroB2 hisH2 recD41 trpC2 tyrA1	rpoB18	1A308	rpoB18
			rpoB500	1A248	rpoB500 trpC2
recD43	1A373	arg(GH)15 recD43 trpB3	rpoC:::(His6-tag)	1A774	pheA1 rpoC:::(His6-tag) Sp trpC2
recF7	1A494	hisH2 leu met recF7			
recF15	1A163	gyrB1 recF15 thr-5 trpC2	rpoC10	1A405	rpoC10
	1A262	gyrB2 recF15 thr-5 trpC2	rpoC105	1A449	car-41 leuB8 metB5 purF6 rpoC105
	1A372	gyrB1 recF15 SPβ- trpC2 xin			
	1A496	metB4 recF15 trpC2	rpoC121	1A450	rpoC121
recF33	1A380	aroB2 hisH2 recF33 trpC2 tyrA1	rpsE2	1A219	rpsE2
				1A241	cysE14 rpsE2
recG39	1A379	aroB2 hisH2 recG39 trpC2 tyrA1	rpsE302	1A668	rpsE302
			rpsF1	1A664	rpsF1
recG40	1A103	aroB2 hisH2 recG40 trpC2 tyrA1	rpsG3	1A661	rpsG3
			rpsH2	1A658	rplK2 rpsH2
rech342	1A301	hisH2 rech342 trpC2	rpsH3	1A671	rpsH3
recL16	1A47	recL16 thr-5 trpC2	rpsI2	1A656	rpsI2
recM13	1A48	recM13 thr-5 trpC2	rpsK2	1A663	cysE14 purA16 rpsK2 trpC2
recP149	1A703	amyE SPβ- metB5 recP149 sigB trpC2 xin-1	rpsL	1A287	rpsL tmsA1 trpC2
			rpsL1	1A191	rpsL1 thr-5 trpC2 tufAA-2
relA	1A766	lys relA trpC2		1A223	rpsL1 tmsB853
rib	1A437	ade his hsd _{RI} R-M- met nic rib trp tyr ura	sacA78	1A142	ilvA1 sacA78 thyA112
				1A143	citB17 ilvA1 sacA78 thyB204
	1A438	hsd _{RI} R-M+ met nic rib trp tyr ura		1A144	ilvA1 sacA78 thyA112 thyB204
				1A681	apt-6 ilvA1 pbuG3 pupA3 sacA78 upp
	1A685	hsd _{RI} R-M+ rib trpC2 tyr-1 ura			
	1A718	his hsd _{RI} R-M+ Km lacZ- M15 met rib trpC2 tyr ura	sacA321	1A682	ilvA1 pubG1 sacA78 upp xpt
rib-2	1A210	rib-2		1A11	ctrA1 sacA321 trpC2
rna-53	1A390	hisA53 rna-53		1A49	sacA321
	1A404	aroB2 hisA53 hisH2 rna-53 trpC2 tyrA1		1A52	sacA321 treA12 trpC2
rplA1	1A665	rplA1 rplJ1 rplL1		1A54	mtID1 nasC1 sacA321
rplC1	1A101	rplC1 rplV1 str-2		1A55	arol906 dal-1 metB5 sacA321
	1A220	rplC1		1A90	hisA1 sacA321 trpC2
rplE1	1A657	rplE1		1A91	fruB138 sacA321 trpC2
rplE3	1A666	rplE3		1A92	arg(GH)2 aroA932 bioB141 sacA321
rplJ1	1A665	rplA1 rplJ1 rplL1			
rplK2	1A658	rplK2 rpsH2		1A93	dnaX8132 hisA1 sacA321 thr-5
rplK6	1A475	rplK6 thr-5 trpC2		1A126	hisH2 leuB8 sacA321 thiC5
rplL1	1A665	rplA1 rplJ1 rplL1		1A156	glpK21 purE1 sacA321
	1A667	rplL1		1A160	gyrB1 sacA321
rplU1	1A670	rplU1		1A201	deg-42 hisA1 sacA321 trpC2
rplV	1A363	arg(GH)15 hsd _{RI} R-M- leuB8 rplV		1A288	amyE dal-1 metB5 sacA321
rplV1	1A88	rplV1 sac(XY)32 trpC2	sacB182	1A289	amyE aroI906 metB5 sacA321
	1A101	rplC1 rplV1 str-2	sacP1	1A169	hisA1 sacB182 trpC2
	1A177	guaB1 rplV1		1A170	sacP1 trpC2
	1A211	arg(GH)3 pheA12 rplV1	degQ36	1A171	hisH leuB8 sacP1 sac(XY)189
	1A212	arg(GH)3 lys-21 metB5 pheA12 purA16 rplV1		1A53	ald-1 degQ36 trpC2
			sacR47	1A164	sacR47
	1A218	rplV1	sac(XY)189	1A171	hisH leuB8 sacP1 sac(XY)189
	1A222	cysE14 rplV1 spo-	sac(XY)32	1A88	rplV1 sac(XY)32 trpC2
	1A660	rplV1	sac(XY)43	1A161	sac(XY)43
rplX2	1A669	rplX2	sac(XY)46	1A50	sac(XY)46 trpC2
rpmA1	1A662	cysE14 purA16 rpmA1 trpC2	sacT3	1A51	purA16 sac(XY)46
rpmD2	1A659	rpmD2	sapA6	1A166	sacT3 trpC2
rpoA:::cat	1A676	rpoA:::cat trpC2	sapB2	1S55	rpoB2 sapA6 spoIIA69
	1A677	gerD97::Tn917 rpoA:::cat	sas-1	1S56	rpoB2 sapB2 spoIIA69
rpoB	1A448	hisA1 hsd _{RI} R-M- leuB8 nonA1 rpoB SP10 ^S thr-5	sas-2	1A466	lys-1 pyrD1 rpoB sas-1
			scoA1	1A467	lys-1 pyrD1 rpoB sas-2
	1A466	lys-1 pyrD1 rpoB sas-1	sdhA2	1S84	argF4 cotA leu-2 pyrA26 scoA1
	1A467	lys-1 pyrD1 rpoB sas-2	sdhA2	1A33	sdhA2 trpC2
rpoB1	1A500	cym-1 rpoB1	sdhB103	1A674	leu-2 sdhB103 trpC2
			sdhC109	1A121	arg(GH)2 pheA2 sdhC109 trpC2

B. subtilis 168 Strains Indexed by Allele

ALLELE	CODE	DESCRIPTION	ALLELE	CODE	DESCRIPTION
ser	1S29	ser spoIIA2	spo0A12	1S10	spo0A12 trpC2
ser-22	1A129	ser-22 trpC2		1S11	spo0A12 tolB24 trpC2
serA84::Tn917	1A614	(SPβc2) serA84::Tn917 trpC2		1S12	spo0A12 trpF7
serC82::Tn917	1A621	(SPβc2) serC82::Tn917 trpC2		1S68	abrB23 pheA1 spo0A12 trpC2
serR1	1A128	serR1 trpC2		1S69	absA6 spo0A12 trpC2
sfp	1A698	pheA1 sfp		1S70	absB24 spo0A12 trpC2
	1A699	pheA1 sfp srfA::Tn917	spo0A13	1S13	spo0A13 trpC2
sigA1	1A579	sigA1	spo0A16	1S73	ade met Sm spo0A16 trpC2
sigA4	1A580	sigA4	spo0A170	1S14	spo0A170 tyr
sigA47	1A581	sigA47	spo0A::	1S133	spo0A::Tn917 HU289
sigB	1A701	addB72 amyE SPβ- metB5 sigB trpC2 xin-1	Tn917 HU289		
	1A702	addB71 amyE SPβ- metB5 sigB xin-1	spo0A332	1S15	spo0A332 trpC2
	1A703	amyE SPβ- metB5 recP149 sigB trpC2 xin-1	spo0A 677	1S53	spo0A 677
sigB::cat	1A675	furB1 sigB::cat trpC2		1S76	citD 29 dal-1 spo0A 677 str-76 thyA thyB uvr-1
sigD::pLM5	1A716	Cm sigD::pLM5 trpC2	spo0B(TS)	1S90	lys-1 spo0B(TS)
sigE55	1S61	rpoB2 sigE55 trpC2		1S91	lys-1 spo0B(TS)
sigF1	1S86	sigF1 trpC2	spo0B12	1S54	spo0B12
sigF63	1S78	metC3 rpoB2 sigF63 tal-1	spo0B136	1S16	pheA1 spo0B136 trpC2
sigH4	1S20	sigH4 str trpC2	spo0E11	1S17	pheA1 spo0E11 trpC2
sigH14	1S21	sigH14 trpC2	spo0F221	1S19	pheA1 spo0F221 trpC2
sigH17	1S22	rpoB2 sigH17 trpC2	spo0J93	1S94	spo0J93 trpC2
sigH37	1S23	sigH37 trpC2	spo0J::	1S129	spo0J::Tn917 HU261
sigH81	1S24	pheA1 sigH81 trpC2	Tn917 HU261		
sigH116	1S25	sigH116 trpC2	spo-331	1S75	spo-331 thyA1 thyB1 trpC2
sinI::kan-50	1S98	hisA1 leuA8 metB5 sinI::kan-50	spoIIA2	1S29	ser spoIIA2
sinR::phl	1S97	hisA1 leuA8 metB5 sinR::phl	spoIIA4	1S71	spoIIA4 trpC2
Sm	1S73	ade met Sm spo0A16 trpC2		1S72	spoIIA4 trpC2
smo-1	1A138	argF4 hag-1 smo-1 trpC2	spoIIA5	1S74	spoIIA5
Sp	1A774	pheA1 rpoC::His6-tag Sp trpC2	spoIIA12	1S30	spoIIA12
SP10 ^R	1A445	hisA1 leuB8 lys-21 metB5 nonA1 purF6 SP10 ^R thr-5 trpC2	spoIIA26	1S31	ade met spoIIA26 trpC2
	1A446	hisA1 leuB8 lys-21 metB5 nonA1 SP10 ^R trpC2	spoIIA37	1S79	spoIIA37 trpC2
	1A447	hsd _R R- M- leuB8 metB5 SP10 ^R	spoIIA42	1S80	spoIIA42 trpC2
SP10 ^S	1A141	hisA1 hsd _R R- M- leuB8 lys-21 metB5 nonA1 SP10 ^S thr-5 trpC2 φNR2 ^S	spoIIA50	1S77	metB5 spoIIA50 thr-5
	1A253	arg(GH)15 hsd _R R- M- leuB8 SP10 ^S	spoIIA69	1S32	rpoB2 spoIIA69 trpC2
	1A448	hisA1 hsd _R R- M- leuB8 nonA1 rpoB SP10 ^S thr-5		1S55	rpoB2 sapA6 spoIIA69
spc	1A478	lys-3 metB10 spc spcD trpC2	spoIIA176	1S81	spoIIA176 trpC2
spcB1	1A76	ilvA1 metB5 spcB1	spoIIA176	1S49	spoIIA176 trpC2
	1A81	ilvA1 leuB8 metB5 polC12 spcB1	spoIID66	1S33	rpoB2 spoIID66 trpC2
	1A575	ilvA2 recA4 spcB1 trpC2	spoIID298	1S43	spoIID298 trpC2
spcB3	1A216	polC12 pyrA26 spcB3 strB3	spoIID::	1S115	spoIID::Tn917 HU8
spcD	1A478	lys-3 metB10 spc spcD trpC2	Tn917 HU8		
Spo ⁻	1A190	cysE14 Spo ⁻ tufAA-7	spoIID::	1S135	spoIID::Tn917 HU298
	1A192	cysE14 efg-1 Spo ⁻	Tn917 HU298		
	1A193	kan-2 Spo ⁻	spoIIE61	1S34	spoIIE61 trpC2
	1A194	cysE14 nea-1 Spo ⁻	spoIIE64	1S35	rpoB2 spoIIE64 trpC2
	1A195	cysE14 ole-2 Spo ⁻	spoIIE::	1S116	spoIIE::Tn917 HU7
	1A197	metB5 minD1 tag-1 thyA thyB1	Tn917 HU7		
	1A222	cysE14 rplV1 Spo ⁻	spoIIE::	1S124	spoIIE::Tn917 HU181
	1A269	spo- thyA1 thyB1 trpC2 ts-355	Tn917 HU181		
Spo ^{Con}	1A61	furF5 Spo ^{Con}	spoIIG41	1S60	leuB8 spoIIG41 tal-1
Spo ^{Ts}	1A508	fus Spo ^{Con}	spoIIG279	1S67	cysC7 furA2 spoIIG279
spo0A3	1S1	spo0A3	spoIIG::	1S138	spoIIG::Tn917 HU325
	1S2	metB5 spo0A3 thr-5	Tn917 HU325		
	1S3	-(metB5)+ spo0A3 sup-44 thr-5	spoIIM::	1S125	spoIIM::Tn917 HU188
	1S4	-(metB5)+ -(thr-5)+ spo0A3 trnS-Lys3	Tn917 HU188		
	1S5	spo0A3 trpC2	spoIIM::	1S132	spoIIM::Tn917 HU287
spo0A5	1S6	spo0A5	Tn917 HU287		
spo0A6	1S7	metB4 spo0A6 trpC2	spoIIIA(A-H)7	1S36	ilvC1 spoIIIA(A-H)7 trpC2
spo0A9	1S8	spo0A9 trpC2	spoIIIA(A-H)35	1S42	metC3 spoIIIA(A-H)35 tal-1
spo0A12	1S9	pheA1 spo0A12 trpC2	spoIIIA(A-H)53	1S37	rpoB2 spoIIIA(A-H)53 trpC2
			spoIIIA(A-H)::	1S119	spoIIIA(A-H)::Tn917 HU13
			Tn917 HU13		
			spoIIIB2	1S48	spoIIIB2 trpC2
			spoIIIB::	1S121	spoIIIB::Tn917 HU25
			Tn917 HU25		
			spoIIIC11	1S40	spoIIIC11
			spoIIIC92	1S64	leuB8 rpoB2 spoIIIC92 tal-1
			spoIIIC94	1S38	spoIIIC94 trpC2
			spoIIID83	1S39	spoIIID83 trpC2
			spoIIIE36	1S63	spoIIIE36 trpC2

B. subtilis 168 Strains Indexed by Allele

ALLELE	CODE	DESCRIPTION	ALLELE	CODE	DESCRIPTION
spolIJ87	1S26	pheA1 spolIJ87 trpC2	spIB1 (cont)	1A514	hisH101 lys-21 recA4 spIB1 thyA thyB uvrB10
	1S27	metC3 spolIJ87 tal-1	sspA	1S109	sspA
spolVA178	1S46	pheA12 spolVA178		1S111	sspA sspB
spolVA::	1S126	spolVA::Tn917 HU194		1S112	Cm sspA sspE
Tn917 HU194				1S113	Cm sspA sspB sspE
spolVB165	1S57	spolVB165 trp	sspB	1S110	sspB
spolVC133	1S47	spolVC133 trpC2		1S111	sspA sspB
spolVC::	1S128	spolVC::Tn917 HU215		1S113	Cm sspA sspB sspE
Tn917 HU215			sspE	1S112	Cm sspA sspE
spolVD::	1S118	spolVD::Tn917 HU10		1S113	Cm sspA sspB sspE
Tn917 HU10				1S114	sspE
spolVF ^{TS}	1S89	spolVF ^{TS} trpC2	stp	1A510	arg(GH)15 hsd _R R-M- leuB8 recA4 stp thr
	1S92	lys-1 spolVF ^{TS}	str	1A182	amyE(+M) amyR1 deg-9 metB5 pro(L) purF6 str trpB3
spolVF88	1S65	metC3 spolVF88 tal-1		1A238	efg-3 str
spolVF152	1S58	spolVF152 trpC2		1A270	str sul
spolVFA::	1S123	spolVFA::Tn917 HU179		1A271	hutP1 str sul
Tn917 HU179				1A272	hutH1 str sul
spoL1	1S82	pyrA1 spoL1 trpC2		1A273	hutCR1 str sul
spoVA89	1S50	spoVA89 trpC2		1A311	amyE(+M) amyR2 deg-9 metB5 pro(L) purF6 str
spoVA::	1S127	spoVA::Tn917 HU195		1A339	amyE(+M) amyR21(+M)(H) metB5 pro(L) purF6 str trpB3
Tn917 HU195				1A340	amyE(+M) amyR1 aroI116 deg-118 metB5 pro(L) str trpB3
spoVA::	1S131	spoVA::Tn917 HU276		1A341	amyE(+M) amyR1(+M) metB5 pro(H) purF6 str trpB3
Tn917 HU276				1S20	sigH4 str trpC2
spoVM::	1S137	spoVM::Tn917 HU324	str-2	1A101	rplC1 rpIV1 str-2
Tn917 HU324			str-76	1S76	citD 29 dal-1 spo0A 677 str-76 thyA thyB uvr-1
spoVB	1S93	lys-1 spoVB	strB3	1A77	ilvA1 metB5 strB3
spoVB91	1S44	argF4 hisA1 metB5 pheA12 purA16 pyrA26 spoVB91 trpC2		1A198	strB3
spoVC285	1S66	metC3 rpoB2 spoVC285		1A216	polC12 pyrA26 spcB3 strB3
spoVD156	1S45	rpoB2 spoVD156 trpC2	strC2	1A473	bfmB1 strC2 trpC2
spoVE85	1S51	spoVE85 trpC2	strC23	1A249	ilvC1 pheA1 strC23
spoVF	1S41	spoVF trpC2	suf-1	1A367	leuA169 suf-1 trpC2
spoVF1	1S83	pheA1 spoVF1 trpC2	suh-428	1A135	suh-428
spoVF224	1S52	spoVF224 trpC2	sul	1A270	str sul
spoVG::	1S130	spoVG::Tn917 HU265		1A271	hutP1 str sul
Tn917 HU265				1A272	hutH1 str sul
spoVIA513	1S88	spoVIA513 trpC2		1A273	hutCR1 str sul
spoVID::Tn917	1A639	(SPβc2) spoVID::Tn917 trpC2		1A344	met-14 sul thyA1 thyB1 trpC2 uvrB10
spoVK517	1S95	spoVK517 trpC2		1A345	met-14 sul thyA1 thyB1 trpC2 uvrB42
spoVK::	1S99	MLS ^R spoVK::Tn917HU8 SPβ-		1A354	sul trpC2
Tn917HU8				1A357	aecB lys-1 sul trpC2
spoVK::	1S117	spoVK::Tn917HU8		1A358	lysC lys-1 sul trpC2
Tn917HU8				1A488	met-14 spIB1 sul thyA1 thyB1 trpC2
spoVK::	1S122	spoVK::Tn917HU178		1A489	met-14 spIB1 sul thyA1 thyB1 trpC2 uvrB42
Tn917HU178				1A695	hisH2 sul ten trpC2
SPβ ⁻	1A100	SPβ ⁻ trpC2	sup-1	1A477	-(hisA1)+ -(metB5)+ sup-1
	1A304	metB5 SPβ ⁻ trpC2 xin-1	sup-22	1A279	-(hisA1)+ -(metC3)+ sup-22 trpC2
	1A372	gyrB1 recF15 SPβ ⁻ trpC2 xin	sup-44	1A260	-(met)+ ile leu sup-44 thyA1 thyB1
	1A457	ilvA2 ilvD15 SPβ ⁻ thyA5 thyB5 trpC2		1A264	-(hisA1)+ sup-44 thr -5
	1A458	ilvA2 SPβ ⁻ thyA5 thyB5 trpC2		1S3	-(metB5)+ spo0A3 sup-44 thr -5
	1A459	leuB8 metB5 SPβ ⁻ thr-5 trnS-Lys3	sup-67	1A368	leuD117 sup-67 trpC2
	1A686	SPβ ⁻ trpC2 zae86::Tn917	tag-1	1A197	metB5 minD1 tag-1 thyA thyB1 metB5 minD1 spo- thyA1 thyB1
	1A694	SPβ ⁻ recA4 trpC2 zef87::Tn917		1A209	tag-1 thyA1 thyB1 trpC2
	1A701	addB72 amyE SPβ ⁻ metB5 sigB trpC2 xin-1	tagE	1A136	argF4 hag-2 tagE
	1A702	addB71 amyE SPβ ⁻ metB5 sigB xin-1		1A35	lys-3 metB10 tagE trpC2
	1A703	amyE SPβ ⁻ metB5 recP149 sigB trpC2 xin-1		1A486	leuB8 tagF1
	1A720	hisB leuA8 metB5 polA5 SPβ ⁻ xin-1		1A306	metC3 phoR2 tal-1
	1A746	Em metB5 recA260 SPβ ⁻ trpC2 xin-1		1A307	leuB8 pho5 tal-1
	1A747	SPβ ⁻		1S27	metC3 spolIJ87 tal-1
	1S99	MLS ^R spoVK::Tn917HU8 SPβ-			
	1S100	bofA::cat Cm SPβ-			
srfA::Tn917	1A699	pheA1 srfA::Tn917			
spIB1	1A488	met-14 spIB1 sul thyA1 thyB1 trpC2			
	1A489	met-14 spIB1 sul thyA1 thyB1 trpC2 uvrB42			

B. subtilis 168 Strains Indexed by Allele

ALLELE	CODE	DESCRIPTION	ALLELE	CODE	DESCRIPTION	
tal-1 (cont)	1S42	metC3 spoIIIA(A-H)35 tal-1	thr-5 (cont)	1S2	metB5 spo0A3 thr-5	
	1S60	leuB8 spoIIIG41 tal-1		1S3	-(metB5)+ spo0A3 sup-44 thr-5	
	1S64	leuB8 rpoB2 spoIIIC92 tal-1		1S4	-(metB5)+ -(thr-5)+ spo0A3	
	1S65	metC3 spoIVF88 tal-1			trnS-Lys3	
	1S78	metC3 rpoB2 sigF63 tal-1		1S77	metB5 spoIIIA50 thr-5	
	1S87	metC3 spoIVG-25 tal-1		thrC::cat	1A773	Cm pheA1 thrC::cat trpC2
				thyA	1A197	metB5 minD1 tag-1 thyA thyB1
tem-1	1A462	leuB8 metB5 tem-1		metB5 minD1 spo- thyA1		
ten	1A695	hisH2 sul ten trpC2		thyB1		
thiA78	1A122	glpK21 glyB133 thiA78 treA12	1A419	thyA thyB trpC2 xhi-1479 xki-1479		
thiA84::Tn917	1A603	(SPβc2) thiA84::Tn917 trpC2	1A502	oxr-1 thyA thyB		
thiB4	1A125	argF4 metA29 thiB4	1A503	oxr-2 thyA thyB trpC2		
thiC5	1A126	hisH2 leuB8 sacA321 thiC5	1A504	lyt-15 thyA thyB trpC2 xin-15		
thr	1A386	hisH2 purH5 thr trpC2	1A511	lys-3 thyA thyB trpC2		
	1A510	arg(GH)15 hsd _R R-M- leuB8	1A514	hisH101 lys-21 recA4 splB1		
thr-5	1A10	hisA1 thr-5 trpC2		thyA thyB uvrB10		
	1A14	-(metB5)+ -(thr-5)+ leuB8 trnS-Lys3	1A595	arg thyA thyB tscA1		
	1A42	thr-5 trpC2	1A596	arg thyA thyB tscA23		
	1A44	recB2 thr-5 trpC2	1A597	arg nadE49 thyA thyB		
	1A45	recB3 thr-5 trpC2	1A598	arg thyA thyB tscC11		
	1A46	recA4 thr-5 trpC2	1A599	arg thyA thyB tscD14		
	1A47	recL16 thr-5 trpC2	1A647	arg nadE47 thyA thyB		
	1A48	recM13 thr-5 trpC2	1A648	arg nadE48 thyA thyB		
	1A74	dnaX8132 hisA1 thr-5	1A649	arg thyA thyB tscD14		
	1A93	dnaX8132 hisA1 sacA321 thr-5	1S76	citD 29 dal-1 spo0A 677 str-76		
	1A141	hisA1 hsd _R R-M- leuB8 lys-21 metB5 nonA1 SP10 ^S thr-5 trpC2 φNR2 ^S	thyA1	1A6	ilvA1 pyrD1 thyA1 thyB1 trpC2	
		1A163	gyrB1 recF15 thr-5 trpC2	1A17	dnaB134 ilvA1 thyA1 thyB1	
		1A191	rpsL1 thr-5 trpC2 tufAA-2	1A41	dnaB1 thyA1 thyB1 trpC2	
		1A213	recA8 thr-5 trpC2	1A162	ilvA1 novB thyA1	
		1A214	polA59 thr-5 trpC2	1A185	thyA1 thyB1 trpC2	
		1A215	polA5 thr-5 trpC2	1A187	ksgA618 thyA1 thyB1 trpC2	
		1A217	polC133 thr-5 trpC2	1A188	ksgA619 thyA1 thyB1 trpC2	
		1A242	hisA1 thr-5 trpC2	1A196	divIVA1 ilvD thyA1 thyB1	
		1A262	gyrB2 recF15 thr-5 trpC2	1A197	metB5 minD1 tag-1 thyA thyB1	
		1A264	-(hisA1)+ sup-44 thr-5		metB5 minD1 spo- thyA1	
		1A313	thr-5 trpC2		thyB1	
		1A314	divV32 thr-5 trpC2	1A209	tag-1 thyA1 thyB1 trpC2	
		1A316	divII55 thr-5 trpC2	1A230	ilvD6 thyA1 trpC2	
		1A317	divII61 thr-5 trpC2	1A243	thyA1 thyB1 trpC2	
		1A423	arg(GH)15 hsd _R R-M- leuB8	1A258	ile leu metB5 thyA1 thyB1	
			recA4 thr-5	1A259	-(met)+ ile leu thyA1 thyB1	
		1A434	ala-1 leuB8 metB pur thr-5 trpC		trnS-Lys3	
		1A445	hisA1 leuB8 lys-21 metB5 nonA1 purF6 SP10 ^R thr-5 trpC2	1A260	-(met)+ ile leu sup-44 thyA1	
		1A448	hisA1 hsd _R R-M- leuB8 nonA1 rpoB SP10 ^S thr-5		thyB1	
		1A459	leuB8 metB5 SPβ- thr-5 trnS-Lys3	1A268	thyA1 thyB1 tmsA151 trpC2	
		1A475	rplK6 thr-5 trpC2	1A269	spo- thyA1 thyB1 trpC2 ts-355	
	thr-5	1A706	com-9 hisA1 leu-8 lys-21 metB5 thr-5 trpC2	1A290	dnaB134 thyA1 thyB1 trpC2	
		1A707	com-71 hisA1 leu-8 metB5 purF6 thr-5 trpC2	1A292	metB5 minD1 thyA1 thyB1	
		1A708	com-30 hisA1 leu-8 lys-21 metB5 thr-5 trpC2	1A300	glyA thyA1 thyB1 trpC2	
		1A709	com-104 hisA1 leu-8 lys-21 metB5 thr-5 trpC2	1A327	gltA2 ilvA8 thyA1 thyB1	
		1A710	com-31 hisA1 leu-8 lys-21 metB5 thr-5 trpC2	1A332	citD 1 ilvA8 thyA1 thyB1	
		1A711	com-14::Tn917 hisA1 leu-8 lys-21 metB5 purF6 thr-5 trpC2	1A342	ebr-2 hisH2 thyA1 thyB1	
		1A712	com-18::Tn917 hisA1 leu-8 lys-21 metB5 purF6 thr-5 trpC2	1A343	hisH2 rec-80 thyA1 thyB1	
		1A713	com-44::Tn917 hisA1 leu-8 lys-21 metB5 purF6 thr-5 trpC2	1A344	met-14 sul thyA1 thyB1 trpC2	
			1A753	bmr ^R thr-5 trpC2		uvrB10
			1A754	bmr::cat Cm thr-5 trpC2	1A345	met-14 sul thyA1 thyB1 trpC2
			1A755	bmrR::cat Cm thr-5 trpC2		uvrB42
			1A756	bfmB::cat Cm thr-5 trpC2	1A346	hisH2 thyA1 thyB1 uvrC109
			1G7	gerA(ABC)11 thr-5 trpC2	1A347	hisH2 thyA1 thyB1 uvrC114
					1A374	thyA1 thyB1 trpC2 uvrB19
					1A375	rec-80 thyA1 thyB1 trpC2
					1A384	pur-67 thyA1 thyB1
				1A402	pyrABC thyA1 thyB1 trpC2	
			1A460	ilvA8 metB5 thyA1 thyB1		
			1A464	dapE320 thyA1 thyB1 trpC2		
			1A487	thyA1 thyB1 urg-1		
			1A488	met-14 splB1 sul thyA1 thyB1		
				trpC2		
			1A489	met-14 splB1 sul thyA1 thyB1		
				trpC2 uvrB42		
			1S75	spo-331 thyA1 thyB1 trpC2		

B. subtilis 168 Strains Indexed by Allele

ALLELE	CODE	DESCRIPTION	ALLELE	CODE	DESCRIPTION
thyA5	1A457	ilvA2 ilvD15 SPβ- thyA5 thyB5 trpC2	thyB5	1A457	ilvA2 ilvD15 SPβ- thyA5 thyB5 trpC2
	1A458	ilvA2 SPβ- thyA5 thyB5 trpC2		1A458	ilvA2 SPβ- thyA5 thyB5 trpC2
thyA112	1A142	ilvA1 sacA78 thyA112	thyB204	1A143	citB17 ilvA1 sacA78 thyB204
	1A144	ilvA1 sacA78 thyA112 thyB204		1A144	ilvA1 sacA78 thyA112 thyB204
thyA	1A456	ilvD6 thyA thyB1	tmsA1	1A287	rpsL tmsA1 trpC2
thyB	1A419	thyA thyB trpC2 xhi-1479 xki-1479	tmsA151	1A268	thyA1 thyB1 tmsA151 trpC2
	1A502	oxr-1 thyA thyB	tmsB853	1A223	rpsL1 tmsB853
	1A503	oxr-2 thyA thyB trpC2	tolA6	1A66	pheA12 tolA6 trpC2
	1A504	lyt-15 thyA thyB trpC2 xin-15		1A67	pheA12 tolA6 trpC2 φ29 ^R
	1A511	lys-3 thyA thyB trpC2	tolB24	1S11	spo0A12 tolB24 trpC2
	1A514	hisH101 lys-21 recA4 spIB1 thyA thyB uvrB10	treA12	1A5	glyB133 metC3 treA12 trpC2
	1A595	arg thyA thyB tscA1		1A52	sacA321 treA12 trpC2
	1A596	arg thyA thyB tscA23		1A122	glpK21 glyB133 thiA78 treA12
	1A597	arg nadE49 thyA thyB		1A167	treA12 trpC2
	1A598	arg thyA thyB tscC11	trnS-Lys3	1A14	-(metB5)+ -(thr-5)+ leuB8 trnS-Lys3
	1A599	arg thyA thyB tscD14		1A259	-(met)+ ile leu thyA1 thyB1 trnS-Lys3
	1A647	arg nadE47 thyA thyB		1A459	leuB8 metB5 SPβ- thr-5 trnS-Lys3
	1A648	arg nadE48 thyA thyB		1S4	-(metB5)+ -(thr-5)+ spo0A3 trnS-Lys3
	1A649	arg thyA thyB tscD14	trp	1A437	ade his hsd _R R-M- met nic rib trp tyr ura
	1S76	citD 29 dal-1 spo0A 677 str-76 thyA thyB uvr-1		1A438	hsd _R R-M+ met nic rib trp tyr ura
thyB1	1A6	ilvA1 pyrD1 thyA1 thyB1 trpC2		1A506	arg trp
	1A17	dnaB134 ilvA1 thyA1 thyB1		1S57	spoIVB165 trp
	1A41	dnaB1 thyA1 thyB1 trpC2	trpA1	1A553	trpA1
	1A185	thyA1 thyB1 trpC2	trpA2	1A554	trpA2
	1A187	ksgA618 thyA1 thyB1 trpC2	trpA3	1A555	trpA3
	1A188	ksgA619 thyA1 thyB1 trpC2	trpA4	1A556	trpA4
	1A196	divIVA1 ilvD thyA1 thyB1	trpA5	1A62	trpA5
	1A197	metB5 minD1 tag-1 thyA thyB1	trpA6	1A557	trpA6
		metB5 minD1 spo- thyA1 thyB1	trpA7	1A558	trpA7
	1A197	metB5 minD1 tag-1 thyA thyB1	trpB1	1A559	trpB1
		metB5 minD1 spo- thyA1 thyB1	trpB2	1A560	trpB2
	1A209	tag-1 thyA1 thyB1 trpC2	trpB3	1A182	amyE(+M) amyR1 deg-9 metB5 pro(L) purF6 str trpB3
	1A243	thyA1 thyB1 trpC2	trpB3	1A338	amyE(+M) amyR1(+M) metB5 pro(L) purF6 trpB3
	1A258	ile leu metB5 thyA1 thyB1	trpB3	1A339	amyE(+M) amyR21(+M)(H) metB5 pro(L) purF6 str trpB3
	1A259	-(met)+ ile leu thyA1 thyB1 trnS-Lys3	trpB3	1A340	amyE(+M) amyR1 aroI116 deg-118 metB5 pro(L) str trpB3
	1A260	-(met)+ ile leu sup-44 thyA1 thyB1	trpB3	1A341	amyE(+M) amyR1(+M) metB5 pro(H) purF6 str trpB3
	1A268	thyA1 thyB1 tmsA151 trpC2	trpB3	1A365	arg(GH)15 trpB3
	1A269	spo- thyA1 thyB1 trpC2 ts-355	trpB3	1A366	arg(GH)15 recA45 trpB3
	1A290	dnaB134 thyA1 thyB1 trpC2	trpB3	1A373	arg(GH)15 recD43 trpB3
	1A292	metB5 minD1 thyA1 thyB1	trpB4	1A63	trpB4
	1A300	glyA thyA1 thyB1 trpC2	trpB5	1A561	trpB5
	1A326	citB1 gltA2 ilvA8 thyB1	trpB6	1A562	trpB6
	1A327	gltA2 ilvA8 thyA1 thyB1	trpB7	1A563	trpB7
	1A332	citD 1 ilvA8 thyA1 thyB1	trpB8	1A564	trpB8
	1A342	ebr-2 hisH2 thyA1 thyB1	trpB9	1A565	trpB9
	1A343	hisH2 rec-80 thyA1 thyB1	trpB10	1A566	trpB10
	1A344	met-14 sul thyA1 thyB1 trpC2 uvrB10	trpB11	1A567	trpB11
	1A345	met-14 sul thyA1 thyB1 trpC2 uvrB42	trpB12	1A568	trpB12
	1A346	hisH2 thyA1 thyB1 uvrC109	trpB13	1A569	trpB13
	1A347	hisH2 thyA1 thyB1 uvrC114	trpB14	1A570	trpB14
	1A374	thyA1 thyB1 trpC2 uvrB19	trpB15	1A571	trpB15
	1A375	rec-80 thyA1 thyB1 trpC2	trpB16	1A572	trpB16
	1A384	pur-67 thyA1 thyB1	trpC	1A434	ala-1 leuB8 metB pur thr-5 trpC
	1A402	pyrABC thyA1 thyB1 trpC2	trpC1	1A543	trpC1
	1A456	ilvD6 thyA thyB1	trpC2	1A1	trpC2
	1A460	ilvA8 metB5 thyA1 thyB1		1A3	cysE14 purA26 trpC2
	1A464	dapE320 thyA1 thyB1 trpC2		1A4	arol906 dal-1 purE1 trpC2
	1A487	thyA1 thyB1 urg-1		1A5	glyB133 metC3 treA12 trpC2
	1A488	met-14 spIB1 sul thyA1 thyB1 trpC2		1A6	ilvA1 pyrD1 thyA1 thyB1 trpC2
	1A489	met-14 spIB1 sul thyA1 thyB1 trpC2 uvrB42		1A7	gltA292 trpC2
	1S75	spo-331 thyA1 thyB1 trpC2		1A8	arod120 lys-1 trpC2

B. subtilis 168 Strains Indexed by Allele

ALLELE	CODE	DESCRIPTION
trpC2 (cont)	1A9	ald-1 aroA932 leuB8 trpC2
	1A10	hisA1 thr -5 trpC2
	1A11	ctrA1 sacA321 trpC2
	1A15	pheA2 trpC2
	1A28	argF4 hisA1 trpC2
	1A31	cysB3 hisA1 trpC2
	1A32	citC6 trpC2
	1A33	sdhA2 trpC2
	1A34	furC1 trpC2
	1A35	lys-3 metB10 tagE trpC2
	1A36	aroB2 hisH2 metB10 trpC2 tyrA1
	1A37	hisA metB10 trpC2
	1A38	metB10 purF6 trpC2
	1A39	argF4 trpC2
	1A40	lys-3 metB10 trpC2
	1A41	dnaB1 thyA1 thyB1 trpC2
	1A42	thr -5 trpC2
	1A43	recA1 trpC2
	1A44	recB2 thr -5 trpC2
	1A45	recB3 thr -5 trpC2
	1A46	recA4 thr -5 trpC2
	1A47	recL16 thr -5 trpC2
	1A48	recM13 thr -5 trpC2
	1A50	sac(XY)46 trpC2
	1A52	sacA321 treA12 trpC2
	1A53	ald-1 degQ36 trpC2
	1A56	aroA932 trpC2
	1A57	ilvC1 pheA1 trpC2
	1A58	hisH2 trpC2
	1A59	hisA1 trpC2
	1A66	pheA12 tolA6 trpC2
	1A67	pheA12 tolA6 trpC2 ϕ 29 ^R
	1A69	aroD120 trpC2
	1A70	pdhD22 trpC2
	1A71	gltA1 trpC2
	1A73	metB4 recA1 trpC2
	1A79	cysC1 trpC2
	1A80	metC7 trpC2
	1A87	hisH2 trpC2 tyrA1
	1A88	rplV1 sac(XY)32 trpC2
	1A90	hisA1 sacA321 trpC2
	1A91	fruB138 sacA321 trpC2
	1A94	narA1 trpC2
	1A95	deg(H)32 leuB8 trpC2
	1A96	pheA1 trpC2
	1A97	cysE14 trpC2
	1A99	odhB1 ilvA3 trpC2
	1A100	SP β - trpC2
	1A102	trpC2 trpS1
	1A103	aroB2 hisH2 recG40 trpC2 tyrA1
	1A105	gtaB290 trpC2
	1A106	gtaC33 trpC2
	1A107	gtaC10 trpC2
	1A109	ilvB2 trpC2
	1A110	ilvD15 trpC2
	1A111	arg(GH)2 aziB101 trpC2
	1A112	aziA102 trpC2
	1A113	furB1 trpC2
	1A114	leuB6 trpC2
	1A115	hisA1 pyrA5 trpC2
	1A116	leuB7 trpC2
	1A118	arg(ABCDE)1 metA8 trpC2
	1A119	arg(GH)2 leuA164 pheA2 trpC2
	1A120	citB75 trpC2
	1A121	arg(GH)2 pheA2 sdhC109 trpC2
	1A123	furE1 trpC2
	1A127	novB75 trpC2
	1A128	serR1 trpC2
	1A129	ser-22 trpC2
	1A132	aroC7 trpC2

ALLELE	CODE	DESCRIPTION
trpC2 (cont)	1A138	argF4 hag-1 smo-1 trpC2
	1A139	flaA4 hag-1 lys trpC2
	1A141	hisA1 hsd _R R'M' leuB8 lys-21 metB5 nonA1 SP10 ^S thr -5 trpC2 ϕ NR2 ^S
	1A147	alsR1 ccpA1 ilvB 1 trpC2
	1A149	pycA19 recA1 trpC2
	1A152	citB17 trpC2
	1A153	sigD2 lys trpC2
	1A154	furB gutR met purF6 trpC2
	1A155	glpD6 trpC2
	1A157	glpP18 ilvC1 trpC2
	1A16	citG4 trpC2
	1A163	gyrB1 recF15 thr -5 trpC2
	1A165	deg(H)32 trpC2
	1A166	sacT3 trpC2
	1A167	treA12 trpC2
	1A169	hisA1 sacB182 trpC2
	1A170	sacP1 trpC2
	1A172	ilvB 1 trpC2
	1A174	glnA100 ilvC1 pheA1 trpC2
	1A175	dnaA13 glnA100 pheA1 trpC2
	1A176	glnA103 pheA1 trpC2
	1A178	hpr-10 trpC2
	1A179	hpr-12 trpC2
	1A183	cotA8 trpC2
	1A184	cotA1 trpC2
	1A185	thyA1 thyB1 trpC2
	1A187	ksgA618 thyA1 thyB1 trpC2
	1A188	ksgA619 thyA1 thyB1 trpC2
	1A189	blt-2 trpC2
	1A191	rpsL1 thr -5 trpC2 tufAA-2
	1A199	deg(H)200 leuB8 trpC2
	1A200	deg(H)100 leuB8 trpC2
	1A201	deg-42 hisA1 sacA321 trpC2
	1A202	deg leuB8 trpC2
	1A203	ilvB3 trpC2
	1A204	ilvA3 trpC2
	1A205	narA1 trpC2 ura-1
	1A206	trpC2 tyrA1
	1A209	tag-1 thyA1 thyB1 trpC2
	1A213	recA8 thr -5 trpC2
	1A214	polA59 thr -5 trpC2
	1A215	polA5 thr -5 trpC2
	1A217	polC133 thr -5 trpC2
	1A224	hisH2 pheA1 trpC2
	1A225	pheA1 polA5 trpC2
	1A226	hisH2 pheA1 polA5 trpC2
	1A227	pheA1 trpC2
	1A228	ilvB 5 trpC2
	1A230	ilvD6 thyA1 trpC2
	1A231	ilvA2 trpC2
	1A232	ilvD4 trpC2
	1A233	ilvD2 trpC2
	1A234	metB2 trpC2
	1A235	metB3 trpC2
	1A239	glpD8 ilvC1 trpC2
	1A240	glpK21 pheA1 trpC2
	1A242	hisA1 thr -5 trpC2
	1A243	thyA1 thyB1 trpC2
	1A246	trpC2
	1A248	rpoB500 trpC2
	1A250	alsR1 ilvB 1 trpC2
	1A251	purM1 trpC2
	1A261	gyrB1 metB4 recD27 trpC2
	1A262	gyrB2 recF15 thr -5 trpC2
	1A268	thyA1 thyB1 tmsA151 trpC2
	1A269	spo- thyA1 thyB1 trpC2 ts-355
	1A278	citD 1 trpC2
	1A279	-(hisA1)+ -(metC3)+ sup-22 trpC2
	1A280	asaA 2 leu-2 trpC2
	1A281	asaA4 leu-2 trpC2

B. subtilis 168 Strains Indexed by Allele

ALLELE	CODE	DESCRIPTION
trpC2 (cont)	1A282	asaA 2 asaB1 leu-2 trpC2
	1A283	asaA4 asaB4 leu-2 trpC2
	1A287	rpsL tmsA1 trpC2
	1A290	dnaB134 thyA1 thyB1 trpC2
	1A293	guaB3 metC7 purH1 trpC2
	1A294	guaA2 metC7 purH1 trpC2
	1A295	aspB66 trpC2
	1A296	aspH1 trpC2
	1A297	amyE aspT1 trpC2
	1A298	aroB2 azpB80 hisH2 trpC2 tyrA1
	1A299	aroB2 hisH2 gyrA trpC2 tyrA1
	1A300	glyA thyA1 thyB1 trpC2
	1A301	hisH2 recH342 trpC2
	1A303	trpC2
	1A304	metB5 SPβ- trpC2 xin-1
	1A305	trpC2 urs-77
	1A313	thr-5 trpC2
	1A314	divV32 thr-5 trpC2
	1A315	divV71 trpC2
	1A316	divI155 thr-5 trpC2
	1A317	divI161 thr-5 trpC2
	1A318	divI32 trpC2
	1A319	argF4 hisA1 purH4 trpC2
	1A320	purE6 trpC2
	1A325	furB1 pyrR1 trpC2
	1A329	trpC2
	1A331	citB1 trpC2
	1A335	metB4 recB2 trpC2
	1A344	met-14 sul thyA1 thyB1 trpC2 uvrB10
	1A345	met-14 sul thyA1 thyB1 trpC2 uvrB42
	1A350	lysS1 trpC2
	1A352	trpC2 trpS1
	1A354	sul trpC2
	1A355	hisH2 pabB trpC2
	1A356	aec hom-1 trpC2
	1A357	aecB lys-1 sul trpC2
	1A358	lysC lys-1 sul trpC2
	1A360	hom-1 trpC2
	1A367	leuA169 suf-1 trpC2
	1A368	leuD117 sup-67 trpC2
	1A369	trpC2 uvrB9
	1A372	gyrB1 recF15 SPβ- trpC2 xin
	1A374	thyA1 thyB1 trpC2 uvrB19
	1A375	rec-80 thyA1 thyB1 trpC2
	1A376	fruC1 metC3 trpC2
	1A377	fruB22 fruC1 metC3 trpC2
	1A378	aroB2 hisH2 recD41 trpC2 tyrA1
	1A379	aroB2 hisH2 recG39 trpC2 tyrA1
	1A380	aroB2 hisH2 recF33 trpC2 tyrA1
	1A381	cafA1 metB10 trpC2
	1A382	hisH2 pur-60 trpC2
	1A383	hisH2 purE7 trpC2
	1A385	hisH2 purE8 trpC2
	1A386	hisH2 purH5 thr trpC2
	1A392	pyrB trpC2
	1A394	pyrC trpC2
	1A395	pyrC trpC2
	1A396	pyrD trpC2
	1A399	pyrDF trpC2
	1A400	pyrF trpC2
	1A401	pyrF trpC2
	1A402	pyrABC thyA1 thyB1 trpC2
	1A404	aroB2 hisA53 hisH2 rna-53 trpC2 tyrA1
	1A408	aroD120 recA4 trpC2
	1A411	his trpC2

ALLELE	CODE	DESCRIPTION
trpC2 (cont)	1A419	thyA thyB trpC2 xhi-14/9 xki-1479
	1A428	met trpC2 ts-39-2
	1A429	arol906 glpT6 trpC2
	1A436	hsd _R R-M- trpC2
	1A439	leuB8 menC315 trpC2
	1A442	gutA2 leuB8 trpC2
	1A443	gutB2 leuB8 trpC2
	1A445	hisA1 leuB8 lys-21 metB5 nonA1 purF6 SP10 ^R thr-5 trpC2
	1A446	hisA1 leuB8 lys-21 metB5 nonA1 SP10 ^R trpC2
	1A453	ilvB2 trpC2
	1A454	leuA169 trpC2
	1A455	trpC2 uvrB9
	1A457	ilvA2 ilvD15 SPβ ⁻ thyA5 thyB5 trpC2
	1A458	ilvA2 SPβ ⁻ thyA5 thyB5 trpC2
	1A464	dapE320 thyA1 thyB1 trpC2
	1A465	fbp-1 hisA1 leuB8 metB5 trpC2
	1A468	glms2 metC7 trpC2
	1A471	pdhA1 bfmB metC7 trpC2
	1A472	bfmB1 iur trpC2
	1A473	bfmB1 strC2 trpC2
	1A475	rplK6 thr-5 trpC2
	1A478	lys-3 metB10 spc spcD trpC2
	1A482	hisH2 metD4 outA7 trpC2
	1A488	met-14 splB1 sul thyA1 thyB1 trpC2
	1A489	met-14 splB1 sul thyA1 thyB1 trpC2 uvrB42
	1A492	citC met pheA trpC2
	1A493	citC met polA10 trpC2
	1A495	metB4 recB19 trpC2
	1A496	metB4 recF15 trpC2
	1A497	hisH2 rec-25 trpC2
	1A498	hisH2 rec-29 trpC2
	1A499	hisH2 rec-30 trpC2
	1A503	oxr-2 thyA thyB trpC2
	1A504	lyt-15 thyA thyB trpC2 xin-15
	1A505	mc ^S trpC2 uv ^S
	1A511	lys-3 thyA thyB trpC2
	1A573	cer-2 trpC2
	1A575	ilvA2 recA4 spcB1 trpC2
	1A576	cer-14 trpC2
	1A577	cer-20 trpC2
	1A578	cam-2 trpC2
	1A588	hemA1 trpC2
	1A589	hemB1 trpC2
	1A590	hemC33 trpC2
	1A591	hemD11 trpC2
	1A592	hemE64 trpC2
	1A593	hemH180 trpC2
	1A594	hemY321 trpC2
	1A600	(SPβc2) cym-84::Tn917 trpC2
	1A601	(SPβc2) purM::Tn917 trpC2
	1A602	(SPβc2) ath-83::Tn917 trpC2
	1A603	(SPβc2) thiA84::Tn917 trpC2
	1A604	(SPβc2) metD83::Tn917 trpC2
	1A605	(SPβc2) argF83::Tn917 trpC2
	1A606	(SPβc2) argF82::Tn917 trpC2
	1A607	(SPβc2) metC85::Tn917 trpC2
	1A608	(SPβc2) arg342::Tn917 trpC2
	1A609	(SPβc2) pyr-82::Tn917 trpC2
	1A610	(SPβc2) pyr-83::Tn917 trpC2
	1A611	(SPβc2) trpC2 urc-83::Tn917
	1A612	(SPβc2) gltAB81::Tn917 trpC2
	1A613	(SPβc2) aroBC84::Tn917 trpC2
	1A614	(SPβc2) serA84::Tn917 trpC2
	1A615	(SPβc2) lys-82::Tn917 trpC2
	1A616	(SPβc2) nic-82::Tn917 trpC2
	1A617	(SPβc2) pheA82::Tn917 trpC2
	1A618	(SPβc2) leuB84::Tn917 trpC2

B. subtilis 168 Strains Indexed by Allele

ALLELE	CODE	DESCRIPTION	ALLELE	CODE	DESCRIPTION
trpC2 (cont)	1A619	(SPβc2) liv1-82::Tn917 trpC2	trpC2 (cont)	1A718	his hsd _{RI} R-M ⁺ Km lacZ- M15
	1A620	(SPβc2) liv3-83::Tn917 trpC2			met rib trpC2 tyr ura
	1A621	(SPβc2) serC82::Tn917 trpC2	1A719		metB10 trpC2 xylAB 1
	1A622	(SPβc2) arg(GH)85::Tn917 trpC2	1A721	(SPβc2) aroI86::Tn917 trpC2	
	1A623	(SPβc2) alaA84::Tn917 trpC2	1A722	(SPβc2) bfmB84::Tn917 trpC2	
	1A624	(SPβc2) mth-83::Tn917 trpC2	1A724	(SPβc2) trpC2 zba-88::Tn917	
	1A625	(SPβc2) mth-84::Tn917 trpC2	1A727	(SPβc2) trpC2 zeh-82::Tn917	
	1A626	(SPβc2) hisA82::Tn917 trpC2	1A728	(SPβc2) trpC2 zjf-83::Tn917	
	1A627	(SPβc2) trpC2 zaa-84::Tn917	1A730	(SPβc2) trpC2 zhf-83::Tn917	
	1A628	(SPβc2) trpC2 zbj-82::Tn917;	1A731	(SPβc2) trpC2 zib-82::Tn917	
	1A629	(SPβc2) trpC2 zca-82::Tn917	1A732	(SPβc2) trpC2 zjd-89::Tn917	
	1A630	(SPβc2) trpC2 zce-82::Tn917	1A733	(SPβc2) trpC2 zjj-85::Tn917	
	1A631	(SPβc2) motA::Tn917 trpC2	1A737	dppE132::neo pheA1 trpC2	
	1A632	(SPβc2) kinC::Tn917 trpC2	1A738	iolG6 metC7 trpC2	
	1A633	(SPβc2) trpC2 zdi-82::Tn917	1A739	gntK4 metC7 trpC2	
	1A634	(SPβc2) trpC2 zci-82::Tn917	1A740	gntP9 metC7 trpC2	
	1A635	(SPβc2) trpC2 proJ::Tn917	1A741	gntR1 metC7 trpC2	
	1A636	(SPβc2) cgeE::Tn917 trpC2	1A742	dacA::cat ⁺ trpC2	
	1A637	(SPβc2) trpC2 yokH::Tn917	1A743	dacA ⁺ ::cat ⁺ trpC2	
	1A638	(SPβc2) trpC2 zfg-83::Tn917	1A744	dacB ⁺ ::cat ⁺ trpC2	
	1A639	(SPβc2) spoVID::Tn917 trpC2	1A745	dacB::cat ⁺ trpC2	
	1A640	(SPβc2) trpC2 zhb-83::Tn917	1A746	metB5 MLS recA260 SPβ ⁻ trpC2	
	1A641	(SPβc2) trpC2 zhc-85::Tn917			xin-1
	1A642	(SPβc2) trpC2 yufR::Tn917	1A753	bmr ^R thr-5 trpC2	
	1A643	(SPβc2) trpC2 yvaC::Tn917	1A754	bmr::cat Cm thr-5 trpC2	
	1A644	(SPβc2) trpC2 zii-83::Tn917	1A755	bmrR::cat Cm thr-5 trpC2	
	1A645	(SPβc2) trpC2 zjf-85::Tn917	1A756	bfmB::cat Cm thr-5 trpC2	
	1A646	(SPβc2) trpC2 zfd-81::Tn917	1A763	Cm fla/che::pLM19 trpC2	
	1A654	aroD120 bglS33 trpC2	1A764	flgM 80 pheA1 trpC2	
	1A655	aroI906 cdr-1 trpC2	1A765	lys trpC2	
	1A662	cysE14 purA16 rpmA1 trpC2	1A766	lys relA trpC2	
	1A663	cysE14 purA16 rpsK2 trpC2	1A767	Cm MLS pheA1 phoA::pCE413	
	1A672	odhA5 odhA5 trpC2			phoB::Tn917 trpC2
	1A673	odhB17 trpC2	1A771	amyE::erm MLS pheA1 trpC2	
	1A674	leu-2 sdhB103 trpC2	1A772	amyE::cat Cm pheA1 trpC2	
	1A675	furB1 sigB::cat trpC2	1A773	Cm pheA1 thrC::cat trpC2	
	1A676	rpoA::cat trpC2	1A774	pheA1 rpoC:ⓂHis6-tag) Sp	
	1A678	leuB8 menB325 trpC2			trpC2
	1A679	ald-1 leuB8 menE312 trpC2	1G1	hisH2 outF4 trpC2	
	1A685	hsd _{RI} R-M ⁺ rib trpC2 tyr-1 ura	1G2	hisH2 nadE81 trpC2	
	1A686	SPβ ⁻ trpC2 zae86::Tn917	1G3	hisH2 outE42 trpC2	
	1A687	(SPβc2) trpC2 zba89::Tn917	1G4	hisH2 metD4 outD1 trpC2	
	1A688	(SPβc2) trpC2 ydaO::Tn917	1G5	hisH2 outC25 trpC2	
	1A689	(SPβc2) trpC2 zdf88::Tn917	1G6	gsp-10 hisH2 metD4 trpC2	
	1A690	(SPβc2) trpC2 zec88::Tn917	1G7	gerA(ABC)11 thr-5 trpC2	
	1A691	SPβc2 trpC2 zfe86::Tn917	1G8	gerB(ABC)18 trpC2	
	1A692	(SPβc2) trpC2 zhf86::Tn917	1G9	gerD19 trpC2	
	1A693	(SPβc2) trpC2 zhg86::Tn917	1G10	gerF45 trpC2	
	1A694	attSP(recA4 trpC2	1G11	gerCC58 trpC2 tzm wrd	
		zef87::Tn917	1G13	gerG47 met pgk trpC2	
	1A695	hisH2 sul ten trpC2	1G14	hisH2 metD4 outA7 trpC2	
	1A700	trpC2	1S5	spo0A3 trpC2	
	1A701	addB72 amyE SPβ ⁻ metB5 sigB	1S7	metB4 spo0A6 trpC2	
		trpC2 xin-1	1S8	spo0A9 trpC2	
	1A703	amyE SPβ ⁻ metB5 recP149 sigB	1S9	pheA1 spo0A12 trpC2	
		trpC2 xin-1	1S10	spo0A12 trpC2	
	1A706	com-9 hisA1 leu-8 lys-21	1S11	spo0A12 toIB24 trpC2	
		metB5 thr-5 trpC2	1S13	spo0A13 trpC2	
	1A707	com-71 hisA1 leu-8 metB5	1S15	spo0A332 trpC2	
		purF6 thr-5 trpC2	1S16	pheA1 spo0B136 trpC2	
	1A708	com-30 hisA1 leu-8 lys-21	1S17	pheA1 spo0E11 trpC2	
		metB5 thr-5 trpC2	1S19	pheA1 spo0F221 trpC2	
	1A709	com-104 hisA1 leu-8 lys-21	1S20	sigH4 str trpC2	
		metB5 thr-5 trpC2	1S21	sigH14 trpC2	
	1A710	com-31 hisA1 leu-8 lys-21	1S22	rpoB2 sigH17 trpC2	
		metB5 thr-5 trpC2	1S23	sigH37 trpC2	
	1A711	com-14::Tn917 hisA1 leu-8 lys-	1S24	pheA1 sigH81 trpC2	
		21 metB5 purF6 thr-5 trpC2	1S25	sigH116 trpC2	
	1A712	com-18::Tn917 hisA1 leu-8 lys-	1S26	pheA1 spoIIJ87 trpC2	
		21 metB5 purF6 thr-5 trpC2	1S28	opp141 trpC2	
	1A713	com-44::Tn917 hisA1 leu-8 lys-	1S31	ade met spoIIA26 trpC2	
		21 metB5 purF6 thr-5 trpC2	1S32	rpoB2 spoIIA69 trpC2	
	1A716	Cm sigD::pLM5 trpC2	1S33	rpoB2 spoIID66 trpC2	

B. subtilis 168 Strains Indexed by Allele

ALLELE	CODE	DESCRIPTION	ALLELE	CODE	DESCRIPTION
trpC2 (cont)	1S34	spoilE61 trpC2	trpE26	1A65	trpE26
	1S35	rpoB2 spoilE64 trpC2	trpE194	1A521	trpE194
	1S36	ilvC1 spoilIA(A-H)7 trpC2	trpF1	1A531	trpF1
	1S37	rpoB2 spoilIA(A-H)53 trpC2	trpF2	1A532	trpF2
	1S38	spoilIC94 trpC2	trpF3	1A533	trpF3
	1S39	spoilID83 trpC2	trpF4	1A534	trpF4
	1S41	spoVF trpC2	trpF5	1A535	trpF5
	1S43	spoilD298 trpC2	trpF6	1A536	trpF6
	1S44	argF4 hisA1 metB5 pheA12 purA16 pyrA26 spoVB91 trpC2	trpF7	1S12	spoOA12 trpF7
	1S45	rpoB2 spoVD156 trpC2	trpF8	1A537	trpF8
	1S47	spoilVC133 trpC2	trpF9	1A538	trpF9
	1S48	spoilIB2 trpC2	trpF10	1A539	trpF10
	1S49	spoilB131 trpC2	trpF11	1A540	trpF11
	1S50	spoVA89 trpC2	trpF12	1A541	trpF12
	1S51	spoVE85 trpC2	trpF13	1A542	trpF13
	1S52	spoVF224 trpC2	trpS1	1A102	trpC2 trpS1
	1S58	spoilVF152 trpC2		1A352	trpC2 trpS1
	1S59	kinA96 trpC2		1A353	trpS1
	1S61	rpoB2 sigE55 trpC2	ts-2	1A461	ctrA1 ts-2
	1S63	spoilIE36 trpC2	ts-355	1A269	spo- thyA1 thyB1 trpC2 ts-355
	1S68	abrB23 pheA1 spoOA12 trpC2	ts-39-2	1A428	met trpC2 ts-39-2
	1S69	absA6 spoOA12 trpC2	tscA1	1A595	arg thyA thyB tscA1
	1S70	absB24 spoOA12 trpC2	tscA23	1A596	arg thyA thyB tscA23
	1S71	spoilA4 trpC2	tscC11	1A598	arg thyA thyB tscC11
	1S72	spoilA4 trpC2	tscD14	1A599	arg thyA thyB tscD14
	1S73	ade met Sm spoOA16 trpC2		1A649	arg thyA thyB tscD14
	1S75	spo-331 thyA1 thyB1 trpC2	tsi-23	1A68	leuB8 metB5 tsi-23
	1S79	spoilA37 trpC2	tufAA-2	1A191	rpsL1 thr-5 trpC2 tufAA-2
	1S80	spoilA42 trpC2	tufAA-7	1A190	cysE14 spo- tufAA-7
	1S81	spoilA176 trpC2	tyr	1A437	ade his hsd _R R ^M - met nic rib trp tyr ura
	1S82	pyrA1 spoL1 trpC2		1A438	hsd _R R ^M + met nic rib trp tyr ura
	1S83	pheA1 spoVF1 trpC2		1A718	his hsd _R R ^M + Km lacZ- M15 met rib trpC2 tyr ura
	1S86	sigF1 trpC2		1S14	spoOA170 tyr
	1S88	spoVIA513 trpC2	tyr-1	1A685	hsd _R R ^M + rib trpC2 tyr-1 ura
	1S89	spoilVF(TS) trpC2	tyrA1	1A36	aroB2 hisH2 metB10 trpC2 tyrA1
	1S94	spoOJ93 trpC2		1A87	hisH2 trpC2 tyrA1
	1S95	spoVK517 trpC2		1A103	aroB2 hisH2 recG40 trpC2 tyrA1
	1S96	bofA::Tn917lac pheA1 trpC2		1A108	hisA1 tyrA1
	1S101	Cm cotA::cat trpC2		1A173	hisH2 tyrA1
	1S102	cotB::cat trpC2		1A206	trpC2 tyrA1
	1S103	cotC::cat trpC2		1A298	aroB2 azpB80 hisH2 trpC2 tyrA1
	1S104	cotD::cat trpC2		1A299	aroB2 hisH2 gyrA trpC2 tyrA1
	1S105	cotE::cat trpC2		1A378	aroB2 hisH2 recD41 trpC2 tyrA1
	1S106	cotF::cat trpC2		1A379	aroB2 hisH2 recG39 trpC2 tyrA1
	1S107	cotF::cat trpC2		1A380	aroB2 hisH2 recF33 trpC2 tyrA1
	1S108	Cm cotT::pDE194 pheA1 trpC2		1A404	aroB2 hisA53 hisH2 rna-53 trpC2 tyrA1
trpC3	1A393	pyrB trpC3	tzm	1G11	gerCC58 trpC2 tzm wrd
	1A544	trpC3	upp	1A681	apt-6 ilvA1 pbuG3 pupA3 sacA78 upp
trpC4	1A545	trpC4	upp	1A682	ilvA1 pubG1 sacA78 upp xpt
trpC5	1A546	trpC5	ura	1A137	hag-3 hisA1 ura
trpC6	1A547	trpC6		1A140	hag-2 hisA1 ifm-1 ura uvrB1
trpC7	1A548	trpC7		1A312	argF4 flaC51 hag-1 hisA1 ura
trpC8	1A549	trpC8		1A437	ade his hsd _R R ^M - met nic rib trp tyr ura
trpC9	1A550	trpC9		1A438	hsd _R R ^M -M+ met nic rib trp tyr ura
trpC10	1A551	trpC10		1A685	hsd _R R ^M -M+ rib trpC2 tyr-1 ura
trpC11	1A552	trpC11		1A718	his hsd _R R ^M -M+ Km lacZ- M15 met rib trpC2 tyr ura
trpD1	1A522	trpD1	ura-1	1A205	narA1 trpC2 ura-1
trpD2	1A64	trpD2	ura-3	1A236	fruA20 ura-3
trpD3	1A523	trpD3		1A237	fruB22 ura-3
trpD4	1A524	trpD4		1A441	gutR1 ura-3
trpD5	1A525	trpD5			
trpD6	1A526	trpD6			
trpD7	1A527	trpD7			
trpD8	1A528	trpD8			
trpD9	1A529	trpD9			
trpD10	1A530	trpD10			
trpE1	1A516	trpE1			
trpE2	1A517	trpE2			
trpE3	1A518	trpE3			
trpE4	1A519	trpE4			
trpE5	1A520	trpE5			

B. subtilis 168 Strains Indexed by Allele

ALLELE	CODE	DESCRIPTION
urc-83::Tn917	1A611	(SPβc2) trpC2 urc-83::Tn917
urg-1	1A487	thyA1 thyB1 urg-1
urs-77	1A305	trpC2 urs-77
uv ^S	1A505	mc ^S trpC2 uv ^S
uvr-1	1S76	citD 29 dal-1 spo0A 677 str-76 thyA thyB uvr-1
uvrB1	1A140	hag-2 hisA1 ifm-1 ura uvrB1
	1A168	hisA1 metB5 uvrB1
uvrB9	1A369	trpC2 uvrB9
	1A455	trpC2 uvrB9
uvrB10	1A344	met-14 sul thyA1 thyB1 trpC2 uvrB10
	1A514	hisH101 lys-21 recA4 splB1 thyA thyB uvrB10
uvrB19	1A374	thyA1 thyB1 trpC2 uvrB19
uvrB42	1A345	met-14 sul thyA1 thyB1 trpC2 uvrB42
	1A489	met-14 splB1 sul thyA1 thyB1 trpC2 uvrB42
uvrC109	1A346	hisH2 thyA1 thyB1 uvrC109
uvrC114	1A347	hisH2 thyA1 thyB1 uvrC114
virM	1A416	virM
	1A418	virM virS
virS	1A417	virS
	1A418	virM virS
wrd	1G11	gerCC58 trpC2 tzm wrd
lacA1	1A680	lacA1 lacR1
lacR1	1A680	lacA1 lacR1
xhd-1	1A284	metC3 pyrA xhd-1
xhi-1479	1A419	thyA thyB trpC2 xhi-1479 xki- 1479
	1A420	ilvA1 metB5 purA16 xhi-1479 xki-1479
	1A421	(φ105) ilvA1 metB5 purA16 xhi-1479 xki-1479
xin	1A372	gyrB1 recF15 SPβ- trpC2 xin
xin-1	1A60	metC3 pyrA xin-1
	1A304	metB5 SPβ ⁻ trpC2 xin-1
	1A701	addB72 amyE SPβ ⁻ metB5 sigB trpC2 xin-1
	1A702	addB71 amyE SPβ ⁻ metB5 sigB xin-1
	1A703	amyE SPβ ⁻ metB5 recP149 sigB trpC2 xin-1
	1A720	hisB leuA8 metB5 polA5 SPβ- xin-1
	1A746	Em metB5 recA260 SPβ- trpC2 xin-1
xin-15	1A504	lyt-15 thyA thyB trpC2 xin-15
xki-1479	1A419	thyA thyB trpC2 xhi-1479 xki- 1479
	1A420	ilvA1 metB5 purA16 xhi-1479 xki-1479
	1A421	(φ105) ilvA1 metB5 purA16 xhi-1479 xki-1479
xpt	1A682	ilvA1 pubG1 sacA78 upp xpt
xtl-1	1A78	metC3 pyrA xtl-1
xylAB 1	1A719	metB10 trpC2 xylAB 1
xynA8	1A651	lys-3 xynA8
xynB7	1A650	lys-3 xynB7
ydaO::Tn917	1A688	(SPβc2) trpC2 ydaO::Tn917
proJ::Tn917	1A635	(SPβc2) trpC2 proJ::Tn917
yokH::Tn917	1A637	(SPβc2) trpC2 yokH::Tn917
yufR::Tn917	1A642	(SPβc2) trpC2 yufR::Tn917
yvaC::Tn917	1A643	(SPβc2) trpC2 yvaC::Tn917
zaa-84::Tn917	1A627	(SPβc2) trpC2 zaa-84::Tn917
zae86::Tn917	1A686	SPβ ⁻ trpC2 zae86::Tn917
zba-88::Tn917	1A724	(SPβc2) trpC2 zba-88::Tn917
zba89::Tn917	1A687	(SPβc2) trpC2 zba89::Tn917
zjb-82::Tn917;	1A628	(SPβc2) trpC2 zjb-82::Tn917;
zca-82::Tn917	1A629	(SPβc2) trpC2 zca-82::Tn917
zce-82::Tn917	1A630	(SPβc2) trpC2 zce-82::Tn917
zci-82::Tn917	1A634	(SPβc2) trpC2 zci-82::Tn917
zdf88::Tn917	1A689	(SPβc2) trpC2 zdf88::Tn917

ALLELE	CODE	DESCRIPTION
zdi-82::Tn917	1A633	(SPβc2) trpC2 zdi-82::Tn917
zec88:Tn917	1A690	(SPβc2) trpC2 zec88:Tn917
zef87::Tn917	1A694	SPβ ⁻ recA4 trpC2 zef87::Tn917
zeh-82::Tn917	1A727	(SPβc2) trpC2 zeh-82::Tn917
zfd-81::Tn917	1A646	(SPβc2) trpC2 zfd-81::Tn917
zfe86::Tn917	1A691	(SPβc2) trpC2 zfe86::Tn917
zfg-83::Tn917	1A638	(SPβc2) trpC2 zfg-83::Tn917
zfg-83::Tn917	1A728	(SPβc2) trpC2 zfg-83::Tn917
zhh-83::Tn917	1A640	(SPβc2) trpC2 zhh-83::Tn917
zhc-85::Tn917	1A641	(SPβc2) trpC2 zhc-85::Tn917
zhf-83::Tn917	1A730	(SPβc2) trpC2 zhf-83::Tn917
zhf86::Tn917	1A692	(SPβc2) trpC2 zhf86::Tn917
zhg86::Tn917	1A693	(SPβc2) trpC2 zhg86::Tn917
zib-82::Tn917	1A731	(SPβc2) trpC2 zib-82::Tn917
zii-83::Tn917	1A644	(SPβc2) trpC2 zii-83::Tn917
zjd-89::Tn917	1A732	(SPβc2) trpC2 zjd-89::Tn917
zjf-85::Tn917	1A645	(SPβc2) trpC2 zjf-85::Tn917
zjj-85:Tn917	1A733	(SPβc2) trpC2 zjj-85:Tn917
φ29 ^R	1A67	pheA12 tolA6 trpC2 φ29 ^R
φNR2 ^S	1A141	hisA1 hsdR ^R M ⁻ leuB8 lys-21 metB5 nonA1 SP10 ^S thr-5 trpC2 φNR2 ^S

Alleles and Phenotypes of BGSC *Bacillus subtilis* Strains

Gene	Genome Location	Function	Gene Product	Synonyms	Mutant Phenotypes
<i>abrB</i>	(44846 ← 45136)	regulation of transition state genes (negative for <i>abrB</i> , <i>aprE</i> , <i>ftsAZ</i> , <i>kinC</i> , <i>motAB</i> , <i>nprE</i> , <i>pbpE</i> , <i>rbs</i> , <i>spoOH</i> , <i>spoVG</i> , <i>spoOE</i> , <i>tycA</i> ; positive for <i>comK</i> , <i>hpr</i>)	transcriptional regulator	<i>cpsX</i>	Partial suppression of <i>spo0</i> mutant phenotypes, including antibiotic sensitivity, exoenzyme secretion
<i>addA</i>	1139280 → 1142978	DNA repair	ATP-dependent deoxyribonuclease (subunit A)	<i>addA</i> or <i>addB</i>	sensitivity to DNA damaging agents
<i>addB</i>	1135793 → 1139293	DNA repair	ATP-dependent deoxyribonuclease (subunit B)		sensitivity to DNA damaging agents
<i>aec</i> <i>aecB</i> <i>ahrC</i>	(2521599 ← 2522048)	negative regulation of arginine biosynthesis; positive regulation of arginine catabolism (<i>roc</i> operons)	transcriptional regulator	May be <i>lysC</i> May be <i>lysC</i>	aminoethyl cysteine resistance (700 µg/ml) aminoethyl cysteine resistance (700 µg/ml) arginine hydroxamate resistance (100 µg/ml) in the presence of ornithine
<i>ald</i>	3277380 → 3278516	utilization of L-alanine	(EC 1.4.1.1) L-alanine dehydrogenase	<i>spoVN</i> , probably <i>alaA</i>	<i>ald-1</i> : unable to grow on L-alanine as sole carbon or nitrogen source; Tn917 insertion additionally blocks sporulation at stage V; <i>alaA</i> : auxotrophy for L-alanine
<i>alsR</i>	3710555 → 3711463	regulation of the α -acetolactate operon (<i>alsSD</i>)	transcriptional regulator (LysR family)		constitutive acetolactate synthase
<i>amm</i> <i>amt</i> <i>amyE</i>	327171 → 329153	starch degradation	(EC 3.2.1.1) amyA α -amylase	<i>amyR</i>	glutamate requirement 3-amino tyrosine resistance (700 µg/ml) <i>amyE^N</i> : electrophoretic variant; <i>amyE^T</i> : hyperactivity; <i>amyR</i> : regulation of amylase synthesis
<i>aprE</i>	(1103895 ← 1105040)	secreted protease	(EC 3.4.21.62) serine alkaline protease (subtilisin E)	<i>sprE</i>	reduction in extracellular protease activity
<i>apt</i> <i>arg(BCDJ)</i>	(2822166 ← 2822678) 1194506 → 1198731	purine metabolism arginine biosynthesis	adenine phosphoribosyltransferase operon encodes four enzymes in arginine biosynthesis pathway	originally <i>argO</i> ; later <i>argABCDE</i>	resistance to 2-fluoroadenine requires arginine
<i>argF</i>	1202927 → 1203886	arginine biosynthesis	(EC 2.1.3.3) ornithine carbamoyltransferase		requires arginine or citrulline
<i>arg(GH)</i>	(3010823 ← 3012208)	arginine biosynthesis	operon encodes argininosuccinate synthase and argininosuccinate lyase	originally <i>argA</i>	requires arginine, ornithine, or citrulline
<i>arg-342</i> <i>arg^S</i> <i>aroA</i>	(3044519 ← 3045595)	shikimate pathway	(EC 4.1.2.15) 3-deoxy-D-arabino-heptulosonate 7-phosphate synthase chorismate mutase-isozyme 3	probably <i>proAB</i> may be <i>pyrA</i> <i>aroG</i>	requires proline, arginine, ornithine, or citrulline sensitivity to arginine requires phenylalanine, tyrosine, and tryptophan
<i>aroB</i>	(2377253 ← 2378341)	shikimate pathway	(EC 4.6.1.3) 3-dehydroquinate synthase		requires shikimic acid (or phenylalanine, tyrosine, and tryptophan)
<i>aroC</i>	(2411940 ← 2412707)	shikimate pathway	(EC 4.2.1.10) 3-dehydroquinate dehydratase		requires shikimic acid (or phenylalanine, tyrosine, and tryptophan)
<i>aroD</i>	(2643896 ← 2644738)	shikimate pathway	(EC 1.1.1.25) shikimate 5-dehydrogenase		requires shikimic acid

Alleles and Phenotypes of BGSC *B. subtilis* Strains (continued)

Gene	Genome Location	Function	Gene Product	Synonyms	Mutant Phenotypes
<i>aroE</i>	(2367195 ← 2368481)	shikimate pathway	(EC 2.5.1.19) 5-enolpyruvoylshikimate-3-phosphate synthase		requires phenylalanine, tyrosine, and tryptophan
<i>aroF</i>	(2378403 ← 2379509)	shikimate pathway	(EC 4.6.1.4) chorismate synthase		requires phenylalanine, tyrosine, and tryptophan
<i>aroH</i>	(2376873 ← 2377256)	aromatic amino acids biosynthesis	(EC 5.4.99.5) chorismate mutase (isozymes 1 and 2)		requires phenylalanine, tyrosine, and tryptophan
<i>aroI</i>	339597 → 340157	shikimate pathway	(EC 2.7.1.71) shikimate kinase		requires phenylalanine, tyrosine, and tryptophan
<i>asaA</i>			arsenate reductase?	probably <i>yqcM</i>	sensitive to sodium arsenate (1 mM); <i>asa2</i> is large deletion
<i>asaB</i>					arsenate resistance (1 mM sodium arsenate; introduced from W23)
<i>aspH</i>				may be <i>ansR</i>	constitutive aspartase
<i>aspT</i>					deficient in high affinity aspartate transport
<i>ath</i>					requirement for adenine + thiamine
<i>azc</i>					resistance to L-azetidin-2-carboxylic acid (500 µg/ml)
<i>azlA</i>				probably in <i>ilvBC</i>	4-azaleucine resistance (40 µg/ml)
<i>azlB</i>	(2729022 ← 2729495)	negative regulation of the <i>azlBCD</i> operon	transcriptional regulator (Lrp/AsnC family)	<i>yrdG</i>	4-azaleucine resistance (40 µg/ml)
<i>azp</i>					resistance to azopyrimidines (50 µg/ml HPUra)
<i>bac</i>					reduction in bacilysin synthesis
<i>bfmB</i>				<i>bfmBAA</i> , <i>bfmBAB</i> , or <i>bfmBB</i>	requires branched fatty acid or valine or isoleucine
<i>bglC</i>	1939853 → 1941379	cellulose degradation	(EC 3.2.1.4) endo-1,4-β-glucanase	<i>eglS</i>	deficient in cellulose degradation
<i>bglS</i>	(4010631 ← 4011359)	lichenan degradation	(EC 3.2.1.73) endo-β-1,3-1,4 glucanase	<i>bgl</i> , <i>licS</i>	deficient in lichenan degradation
<i>bioB</i>	(3089563 ← 3090570)	biotin biosynthesis	biotin synthetase		biotin auxotrophy
<i>blt</i>	2716242 → 2717444		multidrug-efflux transporter	<i>acfA</i> , <i>bmr2</i> , <i>bmt</i>	chromosomal amplification leads to multidrug resistance via efflux
<i>bmr</i>	2493888 → 2495057		multidrug-efflux transporter	<i>bmr1</i>	chromosomal amplification leads to multidrug resistance via efflux
<i>bmrR</i>	2495130 → 2495969	positive regulation of the <i>bmrUR</i> operon	transcriptional regulator		
<i>bofA</i>	29770 → 30033	inhibitor of the pro-σ ^K processing machinery	integral membrane protein		null allele has moderately reduce sporulation
<i>bry</i>					bryamycin resistance
<i>cafA</i>					caffeine resistance (4-8 mg/ml)
<i>cam-2</i>					chloramphenicol resistance (20 µg/ml)
<i>car</i>					fails to grow on trehalose, maltose, or sucrose
<i>ccpA</i>	(3043240 ← 3044244)	carbon catabolite control; glucose regulation of several genes; mediates catabolite repression	transcriptional regulator (LacI family)	<i>graR</i> , <i>alsA</i>	loss of glucose repression for amylase and acetoin production
<i>cdd</i>	(2610203 ← 2610613)		(EC 3.5.4.5) cytidine/deoxycytidine deaminase		unable to grow on cytidine or deoxycytidine as sole pyrimidine source
<i>cdr</i>					resistance to Cd ²⁺
<i>cer</i>					resistance to cerulenin
<i>cgeE</i>	(2145256 ← 2146035)	maturation of the outermost layer of the spore		<i>cgeBC</i>	spores may have altered hydrophobicity or other surface properties

Alleles and Phenotypes of BGSC *B. subtilis* Strains (continued)

Gene	Genome Location	Function	Gene Product	Synonyms	Mutant Phenotypes
<i>citB</i>	1925935 → 1928664	citric acid cycle	(EC 4.2.1.3) aconitate hydratase		unable to grow on lactate-glutamate; autolytic, poor sporulation
<i>citC</i>	(2978789 ← 2980060)	citric acid cycle	(EC 1.1.1.42) isocitrate dehydrogenase		unable to grow on lactate-glutamate; autolytic, poor sporulation
<i>citD</i>					unable to grow on lactate-glutamate; autolytic, poor sporulation; deletion of <i>citK</i> and <i>kauA</i>
<i>citG</i>	(3388083 ← 3389471)	citric acid cycle	(EC 4.2.1.2) fumarate hydratase		unable to grow on lactate-glutamate; autolytic, poor sporulation
<i>citH</i>	(2977807 ← 2978745)	citric acid cycle	(EC 1.1.1.37) malate dehydrogenase	<i>mdh</i>	unable to grow on lactate-glutamate; autolytic, poor sporulation
<i>com-9</i>		competence for transformation			poorly transformable
<i>com-14</i>		competence for transformation			poorly transformable
:: <i>Tn917</i>					
<i>com-18</i>		competence for transformation			poorly transformable
:: <i>Tn917</i>					
<i>com-30</i>		competence for transformation			poorly transformable
<i>com-31</i>		competence for transformation			poorly transformable
<i>com-44</i>		competence for transformation			poorly transformable
:: <i>Tn917</i>					
<i>com-71</i>		competence for transformation			poorly transformable
<i>com-104</i>		competence for transformation			poorly transformable
<i>cotA</i>	(683179 ← 684720)	protein composition of the spore coat	spore coat protein (outer)	<i>pig</i>	colonies fail to form sporulation pigment
<i>cotB</i>	(3713796 ← 3714938)	protein composition of the spore coat	spore coat protein (outer)		no known effect on spore morphology, resistance, or germination properties
<i>cotC</i>	(1904250 ← 1904606)	protein composition of the spore coat	spore coat protein (outer)		no known effect on spore morphology, resistance, or germination properties
<i>cotD</i>	(2332026 ← 2332253)	protein composition of the spore coat	spore coat protein (inner)		no known effect on spore morphology, resistance, or germination properties
<i>cotE</i>	1774435 → 1774980	outer coat assembly	morphogenic protein		spores lack outer coats; lysozyme sensitive, defective germination
<i>cotF</i>	4166318 → 4166800	protein composition of the spore coat	spore coat protein		no known effect on spore morphology, resistance, or germination properties
<i>cotT</i>	(1280096 ← 1280419)	protein composition of the spore coat	spore coat protein (inner)		slow germination on glucose, fructose, and L-asparagine
<i>crk</i>					resistance to fluorocytidine
<i>crsB</i>					sporulates in the presence of excess carbon sources
<i>crsC</i>					sporulates in the presence of excess carbon sources
<i>crsD</i>					sporulates in the presence of excess carbon sources
<i>crsE</i>				probably <i>rpoC</i>	sporulates in the presence of excess carbon sources
<i>crsF</i>					sporulates in the presence of excess carbon sources
<i>ctrA</i>	(3809746 ← 3811353)	pyrimidine biosynthesis	(EC 6.3.4.2) CTP synthetase		requires cytidine in the absence of NH ₄ ⁺
<i>cym</i>					requirement for cysteine or methionine
<i>cysB</i>					cysteine requirement
<i>cysC</i>					cysteine, methionine, sulfite, sulfide requirement
<i>cysE</i>	112797 → 113450	cysteine biosynthesis	(EC 2.3.1.30) serine acetyltransferase	<i>cysA</i>	cysteine requirement

Alleles and Phenotypes of BGSC *B. subtilis* Strains (continued)

Gene	Genome Location	Function	Gene Product	Synonyms	Mutant Phenotypes
<i>dacA</i>	17532 → 18863	peptidoglycan biosynthesis	(EC 3.4.16.4) D-alanyl-D-alanine carboxypeptidase (penicillin-binding protein 5)		null mutant: grows normally; forespores develop abnormally, are 10-fold less heat resistant than wild type
<i>dacB</i>	(2422617 ← 2423765)	spore cortex synthesis (peptidoglycan biosynthesis)	(EC 3.4.16.4) D-alanyl-D-alanine carboxypeptidase (penicillin-binding protein 5*)		null mutant: refractile spores that are resistance to chemicals but extremely sensitive to heat
<i>dal</i> <i>dapE</i> <i>dck</i> <i>ddd</i> <i>ddIA</i>	516929 → 518098	peptidoglycan biosynthesis	(EC 5.1.1.1) D-alanine racemase	<i>alr</i> possibly <i>yaaFG</i> probably <i>cdd</i>	D-alanine requirement temperature sensitive peptidoglycan synthesis Deoxycytidine kinase negative
	507805 → 508869	peptidoglycan biosynthesis	(EC 6.3.2.4) D-alanyl-D-alanine ligase A		temperature sensitive peptidoglycan synthesis
<i>degSU</i>	(3643667 ← 3645596)	regulation of extracellular degradative enzymes production and other stationary phase events		formerly <i>sacU</i>	H alleles increase exoenzyme production, decrease motility and competence, and alter sporulation regulation
<i>degQ</i>	(3256168 ← 3256308)	regulation of extracellular degradative enzymes production and other stationary phase events		<i>sacQ</i>	Hy alleles: increased exoenzyme production, decreased motility and competence, and altered sporulation regulation
<i>dfrA</i>	(2295844 ← 2296350)	glycine/purine/DNA precursor synthesis, conversion of dUMP to dTMP	(EC 1.5.1.3) dihydrofolate reductase	<i>tmp</i>	trimethoprim resistance (0.5 µg/ml)
<i>divI</i>				probably <i>divIB</i> ; formerly <i>divD</i>	temperature-sensitive cell division
<i>divIB</i>	1593100 → 1593891	probably stabilizing or promoting the assembly of the division complex (septum formation)	cell-division initiation protein	<i>dds</i> , <i>tms-12</i>	temperature-sensitive cell division
<i>divII</i> <i>divIVA</i>	1611922 → 1612416	initiation of cell division and correct placement of the septum	cell-division initiation protein	formerly <i>divC</i> <i>ylmJ</i> ; formerly <i>divA</i> formerly <i>divB</i>	temperature-sensitive cell division temperature-sensitive cell division; minicell production temperature-sensitive cell division
<i>divV</i> <i>dnaA</i>	410 → 1750	initiation of chromosome replication (DNA synthesis)		formerly <i>divB</i> <i>dnaH</i> , <i>dnaJ</i> , <i>dnaK</i>	temperature sensitive replication; no growth
<i>dnaB</i>	(2963222 ← 2964640)	initiation of chromosome replication (DNA synthesis)	membrane attachment protein		temperature sensitive replication; no growth
<i>dnaC</i> <i>dnaD</i>	(4156679 ← 4158043) (2344675 ← 2345373)	DNA synthesis replicative initiation of chromosome replication (DNA synthesis)	(EC 3.6.1.-) DNA helicase		temperature sensitive replication; no growth temperature sensitive replication; no growth
<i>dnaE</i> <i>dnaI</i> <i>dnaN</i>	(2990342 ← 2993689) (2962259 ← 2963194) 1939 → 3075	DNA synthesis DNA synthesis DNA synthesis	DNA polymerase III (α subunit) helicase loader (EC 2.7.7.7) DNA polymerase III (β subunit)	<i>ytxA</i> , <i>dnaY</i> <i>dnaG</i> , <i>dnaK</i>	temperature sensitive replication; no growth temperature sensitive replication; no growth temperature sensitive replication; no growth
<i>dnaX</i>	26812 → 28503	DNA synthesis	(EC 2.7.7.7) DNA polymerase III (γ and τ subunits)	<i>dnaH</i> , <i>dna-8132</i>	temperature sensitive replication; no growth
<i>dppE</i>	1363617 → 1365266	dipeptide transport	dipeptide ABC transporter (dipeptide-binding protein)	<i>dciAE</i>	renders proline auxotrophs unable to grow on Pro-Gly dipeptides
<i>ebrAB</i> <i>fbp</i>	(1863933 ← 1864617) 4127237 → 4129252	transport/binding protein gluconeogenesis	multidrug resistance protein (EC 3.1.3.11) fructose-1,6-bisphosphatase	<i>yydE</i> ; formerly <i>fdpA</i>	ethidium bromide resistance (10 µg/ml) Fails to grow on gluconeogenic carbon sources in the presence of <i>bfd</i> mutation
<i>flaA</i>					flagellaless

Alleles and Phenotypes of BGSC *B. subtilis* Strains (continued)

Gene	Genome Location	Function	Gene Product	Synonyms	Mutant Phenotypes
<i>flaC</i>					flagellaless
<i>flgM</i>	(3639345 ← 3639611)	coupling late flagellar gene expression to assembly of hook-basal body complex	anti-sigma factor repressor of σ^D -dependent transcription		
<i>fnd</i>					fluoroindole resistance (50 µg/ml)
<i>fruA</i>	1508661 → 1510568	phosphotransferase system (PTS)	fructose-specific enzyme IIBC component		unable to grow on fructose as carbon source
<i>fruB</i>	1507735 → 1508646	fructose utilization	(EC 2.7.1.56) fructose-1-phosphate kinase		unable to grow on fructose as carbon source
<i>fruC</i>					unable to grow on fructose as carbon source
<i>ftt</i>					fluorotryptophan resistance (50 µg/ml)
<i>furA</i>					5-fluorouracil resistance (1 µg/ml)
<i>furB</i>					5-fluorouracil resistance (40 µg/ml) in the presence of uracil (40 µg/ml)
<i>furC</i>					5-fluorouracil resistance (40 µg/ml) in the presence of uracil (40 µg/ml)
<i>furE</i>					5-fluorouracil resistance (40 µg/ml) in the presence of uracil (40 µg/ml)
<i>furF</i>					5-fluorouracil resistance (40 µg/ml) in the presence of uracil (40 µg/ml)
<i>fus</i>	130683 → 132761		elongation factor G	<i>efg</i>	fusidic acid resistance (3 µg/ml)
<i>gcaD</i>	56350 → 57720	peptidoglycan and lipopolysaccharide biosynthesis	(EC 2.7.7.23) UDP-N-acetyl-glucosamine pyrophosphorylase	<i>tms, tms26</i>	temperature-sensitive growth
<i>gerA(ABC)</i>	3389841 → 3391289	germination response to L-alanine and related amino acids (earliest stage)			germination defective
<i>gerB(ABC)</i>	3687872 → 3691553	germination response to combination of glucose, fructose, L-asparagine, and KCl			germination defective
<i>gerCC</i>	(2381157 ← 2382203)	menaquinone biosynthesis (germination)	(EC 2.5.1.30) heptaprenyl diphosphate synthase component II	<i>gerC58</i>	germination defective
<i>gerD</i>	(158514 ← 159071)	germination response to L-alanine and combination of glucose, fructose, L-asparagine, and KCl (early stage)			germination defective
<i>gerE</i>	(2903828 ← 2904052)	required for the expression of late spore coat genes (germination)	transcriptional regulator		germination defective
<i>gerF</i>					germination defective
<i>gerG</i>					germination defective
<i>gerJ</i>				<i>tzm</i>	germination defective; white on tetrazolium agar
<i>glgB</i>	(3168841 ← 3170724)	starch and glycogen biosynthesis	(EC 2.4.1.18) 1,4- α -glucan branching enzyme		defective glycogen synthesis
<i>glmS</i>	200263 → 202065		(EC 2.6.1.16) L-glutamine-D-fructose-6-phosphate amidotransferase	<i>gcaA, ybxD</i>	requires glucosamine on minimal media; spores produced with limiting glucosamine have defective cortex
<i>glnA</i>	1877669 → 1879003		(EC 6.3.1.2) glutamine synthetase		requires glutamine (500 µg/ml) in minimal media
<i>glnR</i>	1877201 → 1877608	negative regulation of the glutamine synthetase gene (<i>glnA</i>)	transcriptional regulator		
<i>glpD</i>	1004480 → 1006147	glycerol utilization	(EC 1.1.99.5) glycerol-3-phosphate dehydrogenase		inability to use glycerol as carbon source
<i>glpK</i>	1002849 → 1004339	glycerol utilization	(EC 2.7.1.30) glycerol kinase		inability to use glycerol as carbon source
<i>glpP</i>	1001249 → 1001827	control of <i>glpD</i> transcription	antiterminator		inability to use glycerol as carbon source

Alleles and Phenotypes of BGSC *B. subtilis* Strains (continued)

Gene	Genome Location	Function	Gene Product	Synonyms	Mutant Phenotypes
<i>glpT</i>	(233983 ← 235317)	uptake of glycerol-3-phosphate	glycerol-3-phosphate permease	<i>ybeE</i>	fosfomycin resistant (200 µg/ml)
<i>gltA</i>	(2009326 ← 2013888)	glutamate biosynthesis	(EC 1.4.1.13) glutamate synthase (large subunit)		requires glutamate or aspartate
<i>gltB</i>	(2007828 ← 2009309)	glutamate biosynthesis	(EC 1.4.1.13) glutamate synthase (small subunit)		requires glutamate or aspartate
<i>glyA</i>	(3788245 ← 3789492)	glycine/serine/threonine metabolism	(EC 2.1.2.1) serine hydroxymethyltransferase	<i>glyC</i>	requires glycine
<i>glyB</i>					requires for glycine
<i>gntK</i>	4113349 → 4114890	gluconate utilization	(EC 2.7.1.12) gluconate kinase		inability to utilize gluconate
<i>gntP</i>	4114919 → 4116265	gluconate utilization	gluconate permease		inability to utilize gluconate
<i>gntR</i>	4112625 → 4113356	negative regulation of gluconate operon	transcriptional regulator		constitutive expression of gnt operon
<i>gsiB</i>	494057 → 494428	general stress response	general stress protein		null mutant has no known phenotype
<i>gsp-10</i>				probably <i>gerA</i>	germination and outgrowth defective
<i>gtaB</i>	3664689 → 3665567	glucosylation of teichoic acid	(EC 2.7.7.9) UTP-glucose-1-phosphate uridylyltransferase		smooth colonies; resistant to ö25, ö29, SP10
<i>gtaC</i>					smooth colonies; resistant to ö25, ö29, SP10
<i>guaB</i>	15913 → 17379	GMP biosynthesis	(EC 1.1.1.205) inositol-monophosphate dehydrogenase	<i>guaA</i>	requires guanine
<i>gutA</i>				<i>may be ydjk</i>	inability to use sorbitol as carbon source
<i>gutB</i>	667183 → 668244		(EC 1.1.1.14) sorbitol dehydrogenase		inability to use sorbitol as carbon source
<i>gutR</i>	(664492 ← 666981)	positive regulation of the sorbitol dehydrogenase gene (<i>gutB</i>)	transcriptional regulator		constitutive mutation allows growth on xylitol
<i>gyrA</i>	6993 → 9458	initiation of replication cycle and DNA elongation	(EC 5.99.1.3) DNA gyrase (subunit A)	<i>nalA</i>	resistance to naladixic acid (50 µg/ml)
<i>gyrB</i>	4866 → 6782	initiation of replication cycle and DNA elongation	(EC 5.99.1.3) DNA gyrase (subunit B)	<i>novA</i>	resistance to novobiocin (2 µg/ml)
<i>hag</i>	(3634047 ← 3634961)	flagellar synthesis	flagellin protein		<i>hag-1</i> : strain 168 antigen; <i>hag-2</i> : strain W23 antigen; <i>hag-3</i> : straight filament
<i>hemA</i>	(2876866 ← 2878233)	porphyrin biosynthesis	(EC 1.2.1.-) glutamyl-tRNA reductase		requires heme
<i>hemB</i>	(2873302 ← 2874276)	porphyrin biosynthesis	(EC 4.2.1.24) δ-aminolevulinic acid dehydratase (porphobilinogen synthase)		requires heme
<i>hemC</i>	(2875051 ← 2875995)	hydroxymethylbilane synthesis from porphobilinogen (porphyrin biosynthesis)	(EC 4.3.1.8) porphobilinogen deaminase (hydroxymethylbilane synthase)		requires heme
<i>hemD</i>	(2874273 ← 2875061)	cyclisation of hydroxymethylbilane (porphyrin biosynthesis)	(EC 4.2.1.75) uroporphyrinogen III cosynthase		requires heme
<i>hemE</i>	1085590 → 1086651	porphyrin biosynthesis	(EC 4.1.1.37) uroporphyrinogen III decarboxylase		requires heme
<i>hemH</i>	1086723 → 1087655	incorporation of iron into protoporphyrin IX (porphyrin biosynthesis)	(EC 4.99.1.1) ferrochelatase	<i>hemF</i>	requires heme
<i>hemY</i>	1087670 → 1089082	late steps of protoheme IX synthesis (porphyrin biosynthesis)	(EC 1.3.3.4) protoporphyrinogen IX and coproporphyrinogen III oxidase	<i>hemG</i>	requires heme

Alleles and Phenotypes of BGSC *B. subtilis* Strains (continued)

Gene	Genome Location	Function	Gene Product	Synonyms	Mutant Phenotypes
<i>hisA</i>	(3583377 ← 3584114)	histidine biosynthesis	(EC 5.3.1.16) phosphoribosylformimino-5-aminoimidazole carboxamide ribotide isomerase		requires histidine
<i>hisB</i>	(3584750 ← 3585334)	histidine biosynthesis	(EC 4.2.1.19) imidazoleglycerol-phosphate dehydratase		requires histidine
<i>hisH</i>	(3584111 ← 3584749)	histidine biosynthesis	(EC 2.4.2.-) amidotransferase		requires histidine
<i>hom</i>	(3313886 ← 3315187)	threonine/methionine biosynthesis	(EC 1.1.1.3) homoserine dehydrogenase		requires threonine and methionine
<i>hpr</i>	(1072581 ← 1073192)	negative regulation of sporulation and extracellular proteases (<i>aprE</i> , <i>nprE</i> , <i>sin</i>)	transcriptional regulator	<i>catA</i> , <i>scoC</i>	hyperproduces extracellular proteases
<i>hsd_{BI}</i>		restriction-modification			possesses Bsu 1247I restriction-modification system
<i>hsd_{CI}</i>		restriction-modification			possesses Bsu 1247II restriction-modification system
<i>hsd_{RI}</i>		restriction-modification			M ⁻ : deficient in restriction methylase; R ⁻ : deficient in restriction endonuclease
<i>hutCR</i>		histidine utilization			renders <i>hut</i> operon constitutive and insensitive to catabolite repression
<i>hutH</i>	4040840 → 4042366	histidine utilization	(EC 4.3.1.3) histidase		inability to utilize histidine
<i>hutP</i>	4040272 → 4040727	positive regulation of the histidine utilization operon (<i>hutPHUIGM</i>)	transcriptional regulator	<i>hutP1</i>	inability to utilize histidine
<i>ifm</i>					increased flagella and motility
<i>ilvA</i>	(2292010 ← 2293278)	isoleucine biosynthesis	(EC 4.2.1.16) threonine dehydratase		requires isoleucine
<i>ilvB</i>	(2894347 ← 2896071)	valine/isoleucine biosynthesis	(EC 4.1.3.18) acetolactate synthase (acetohydroxy-acid synthase) (large subunit)		requires isoleucine and valine
<i>ilvC</i>	(2892781 ← 2893809)	valine/isoleucine biosynthesis	(EC 1.1.1.86) keto-acid reductoisomerase (acetohydroxy-acid isomero-reductase)		requires isoleucine and valine
<i>ilvD</i>	(2300003 ← 2301679)	valine/isoleucine biosynthesis	(EC 4.2.1.9) dihydroxy-acid dehydratase		requires isoleucine and valine
<i>inh</i>				probably <i>tyrA</i>	inhibition by histidine (50 µg/ml)
<i>iolG</i>	(4074575 ← 4075609)	myo-inositol catabolism	(EC 1.1.1.18) myo-inositol 2-dehydrogenase	<i>iol</i> , <i>idh</i>	inability to utilize inositol
<i>iur</i>					inhibition by uracil
<i>kan</i>					kanamycin resistance (50 µg/ml)
<i>kauA</i>					defective in branched-chain α-keto acid transport
<i>kinA</i>	1469428 → 1471248	initiation of sporulation	(EC 2.7.3.-) two-component sensor histidine kinase	<i>spoIIF</i> , <i>spoIIJ</i> , <i>gsiC</i> , <i>scoB</i> , <i>scoD</i>	null mutants cause oligosporogeny (stage 0-II) in liquid media, delayed sporulation on agar
<i>ksgA</i>	50638 → 51516	high level kasugamycin resistance	(EC 2.1.1.-) dimethyladenosine transferase		resistance to kasugamycin (40 µg/ml)
<i>lacA</i>	(3502083 ← 3504146)		(EC 3.2.1.23) β-galactosidase	<i>yvfN</i>	null mutations eliminate endogenous α-galactosidase
<i>lacR</i>	(3507722 ← 3508714)	negative regulation of β-galactosidase gene (<i>lacA</i>)	transcriptional regulator (LacI family)	<i>yvfJ</i>	up mutations cause overproduction of α-galactosidase
<i>leuA</i>	(2891238 ← 2892794)	leucine biosynthesis	(EC 4.1.3.12) 2-isopropylmalate synthase		leucine auxotrophy
<i>leuB</i>	(2890120 ← 2891217)	leucine biosynthesis	(EC 1.1.1.85) 3-isopropylmalate dehydrogenase		leucine auxotrophy

Alleles and Phenotypes of BGSC *B. subtilis* Strains (continued)

Gene	Genome Location	Function	Gene Product	Synonyms	Mutant Phenotypes
<i>leuD</i>	(2888040 ← 2888639)	leucine biosynthesis	(EC 4.2.1.33) 3-isopropylmalate dehydratase (small subunit)		leucine auxotrophy
<i>liv</i>				deletion within <i>ilvBNC-leuACBD</i> <i>lin-2, yccB</i>	requires leucine, isoleucine, and valine
<i>lmrA</i>	(289686 ← 290252)	negative regulation of lincomycin operon	transcriptional regulator		lincomycin resistance (80-100 µg/ml)
<i>lys</i>	(2436179 ← 2437498)	lysine biosynthesis	(EC 4.1.1.20) diaminopimelate decarboxylase		lysine auxotrophy
<i>lysC</i>	(2908623 ← 2909849)	diaminopimelate/lysine biosynthesis	(EC 2.7.2.4) aspartokinase II α (aa 1-408) and β subunits (aa 246-408)	<i>ask, aecA</i>	aminoethyl cysteine resistance (700 µg/ml)
<i>lysS</i>	88724 → 90223	aminoacyl-tRNA synthetase	(EC 6.1.1.6) lysyl-tRNA synthetase		temperature-sensitive growth
<i>lyt</i>					reduction in autolytic enzymes; cells grow as long chains
<i>menB</i>	(3147981 ← 3148796)	dihydroxynaphthoic acid synthetase	menaquinone biosynthesis		resistance to aminoglycosides (2 µg/ml kanamycin); menaquinone deficient; supplement with menadione
<i>menC</i>				probably <i>menD</i>	resistance to aminoglycosides (2 µg/ml kanamycin); menaquinone deficient; supplement with menadione
<i>menE</i>	(3146430 ← 3147890)	menaquinone biosynthesis	(EC 6.2.1.26) O-succinylbenzoic acid-CoA ligase		resistance to aminoglycosides (2 µg/ml kanamycin); menaquinone deficient; supplement with menadione
<i>metA</i>				possibly <i>yjcl</i>	requires methionine, cystathionine, or homocysteine
<i>metB</i>	2304619 → 2305293	methionine biosynthesis	(EC 2.3.1.46) homoserine O-succinyltransferase		requires methionine or homocysteine
<i>metC</i>	(1382784 ← 1385072)	methionine biosynthesis	(EC 2.1.1.14) cobalamin-independent methionine synthase		requires methionine
<i>metD</i>				possibly <i>yjcJ</i>	requires methionine
<i>minD</i>	(2857038 ← 2857844)	cell-division inhibition (septum placement)	ATPase activator of MinC	<i>divIVB1</i>	minicell production
<i>motA</i>	(1433899 ← 1434711)	flagellar motor rotation	motility protein A	<i>mot</i>	paralyzed flagella
<i>mreD</i>	(2858579 ← 2859097)		cell-shape determining protein	<i>rodB</i>	cell wall defective; salt dependent growth
<i>mth</i>				probably <i>thr-hom</i>	Requires threonine plus either methionine or homocysteine; probably deletion in thr-hom region
<i>mtlD</i>	451189 → 452289		(EC 1.1.1.17) mannitol-1-phosphate dehydrogenase	<i>mtlB</i>	inability to utilize mannitol as carbon source
<i>mtr</i>				<i>mtrA</i> or <i>mtrB</i>	5-methyl-tryptophan resistance (1 mg/ml); derepression of trp operon
<i>nadE</i>	337860 → 338678	NAD biosynthesis	(EC 6.3.5.1) NH ₃ -dependent NAD ⁺ synthetase	<i>outB, tscBGH, gsp-81, narAB</i>	temperature-sensitive growth
<i>narA</i>	(3771380 ← 3772405)	nitrate assimilation, anaerobic respiration	(EC 1.7.99.4) assimilatory nitrate reductase (catalytic subunit)	<i>narB, nasBB</i>	inability to use nitrate as nitrogen source
<i>nasC</i>	(357875 ← 360007)				inability to use nitrate as nitrogen source
<i>nea</i>					neamine resistance (10 µg/ml)
<i>nic</i>				probably in <i>nadABC</i> or <i>nifS</i>	nicotinic acid requirement
<i>nonA</i>					permissive for infection by phages SP10 and δNR2
<i>novB</i>					resistance to novobiocin (2 µg/ml)
<i>odhA</i>	(2108043 ← 2110856)		(EC 1.2.4.2) 2-oxoglutarate dehydrogenase (E1 subunit)	<i>citK</i>	inability to grow on lactate-glutamate as carbon source

Alleles and Phenotypes of BGSC *B. subtilis* Strains (continued)

Gene	Genome Location	Function	Gene Product	Synonyms	Mutant Phenotypes
<i>odhB</i>	(2106760 ← 2108013)		(EC 2.3.1.61) 2-oxoglutarate dehydrogenase complex (dihydrolipoamide transsuccinylase, E2 subunit)	<i>citM</i>	inability to grow on lactate-glutamate as carbon source
<i>ole</i> <i>opp(ABCDEF)</i>	1219321 → 1224922	required for initiation of sporulation, competence development, and oligopeptide transport	oligopeptide ABC transporter (ATP-binding protein)	<i>spo0K</i>	oleandomycin resistance (200 µg/ml) null mutants display delayed sporulation and resistance to bialaphos
<i>outA</i> <i>outC</i> <i>outD</i> <i>outE</i> <i>outF</i> <i>oxr</i> <i>pabA</i>	84287 → 84871	folate and tryptophan biosynthesis	(EC 4.1.3.- (EC 4.1.3.27) para-aminobenzoate synthase glutamine amidotransferase (subunit B) anthranilate synthase (subunit II) (EC 4.1.3.-) para-aminobenzoate synthase (subunit A)	<i>trpG, trpX, gat</i>	temperature-sensitive outgrowth of spores temperature-sensitive outgrowth of spores temperature-sensitive outgrowth of spores temperature-sensitive outgrowth of spores oxolinic acid resistance Requires para-aminobenzoic acid and tryptophan
<i>pabB</i>	82861 → 84273	folate biosynthesis	(EC 4.1.3.-) para-aminobenzoate synthase (subunit A)	<i>pab</i>	para-aminobenzoic acid requirement
<i>pbuG</i> <i>pdhA</i>	1527731 → 1528846		(EC 1.2.4.1) pyruvate dehydrogenase (E1 α subunit)	<i>aceA</i>	resistance to 8-azaguanine requires acetate
<i>pdhD</i>	1531275 → 1532687		(EC 1.8.1.4) dihydrolipoamide dehydrogenase E3 subunit of both pyruvate dehydrogenase and 2-oxoglutarate dehydrogenase complexes	<i>citL</i>	unable to grow on lactate-glutamate as carbon source
<i>pfk</i>	(2985661 ← 2986620)	glycolysis	(EC 2.7.1.11) 6-phosphofructokinase		growth on fructose; slow growth on glycerol or malate; no growth on glucose or mannose
<i>pgk</i>	(3479260 ← 3480444)	glycolysis	(EC 2.7.2.3) phosphoglycerate kinase		grows on glucose plus acetate or glycerol plus malate, but not on any of these carbon sources alone
<i>pha</i> <i>pheA</i>	(2850544 ← 2851401)	phenylalanine biosynthesis	(EC 4.2.1.51) prephenate dehydratase		resistance to phage SPO1 requires phenylalanine
<i>phoA</i>	(1016535 ← 1017920)	phosphorus metabolism	(EC 3.1.3.1) alkaline phosphatase A	<i>phoAIV</i>	reduction in phosphate-starvation induced APase (60-75%)
<i>phoB</i>	(619813 ← 621201)	phosphorus metabolism	(EC 3.1.3.1) alkaline phosphatase III	<i>phoAIII</i>	reduction in phosphate-starvation induced APase (25-40%); reduction in sporulation APase
<i>phoP</i>	(2976873 ← 2977595)	phosphate regulation (<i>phoA</i> , <i>phoB</i> , <i>phoD</i> , <i>resABCDE</i>)	two-component response regulator		required for starvation-induced accumulation of APase
<i>phoR</i>	(2975141 ← 2976880)	involved in phosphate regulation	two-component sensor histidine kinase		required for starvation-induced accumulation of APase
<i>phoS</i> <i>polA</i>	(2972255 ← 2974897)	replication and DNA repair	(EC 2.7.7.7) DNA polymerase I		constitutive alkaline phosphatase production sensitive to MMS (methyl methanesulphonate, 350 µg/ml)

Alleles and Phenotypes of BGSC *B. subtilis* Strains (continued)

Gene	Genome Location	Function	Gene Product	Synonyms	Mutant Phenotypes
<i>polC</i>	1726524 → 1730837	initiation of replication cycle and DNA elongation	(EC 2.7.7.7) DNA polymerase III (α subunit)	<i>mut-1</i> , <i>dnaF</i> , <i>dnaP</i>	polC133: temperature sensitive growth; polC12: HPUra resistance (8 ig/ml); allele1: temperature sensitive, mutator proline auxotrophy high production of exoproteases low production of exoproteases
<i>pro(AB)</i> <i>pro(H)</i> <i>pro(L)</i> <i>proJ</i> <i>ptm</i> <i>ptsI</i>	1379069 → 1380316 (2014989 ← 2016104) 1459117 → 1460769	proline biosynthesis proline biosynthesis general energy coupling protein of PTS; transfers phosphate from PEP to HPr	 glutamate 5-kinase (EC 2.7.3.9) phosphotransferase system (PTS) enzyme I	 <i>yohA</i>	 pyrithmine resistance no growth on phosphotransferase system sugars
<i>pupA</i> <i>purA</i>	(4154641 ← 4155933)	purine biosynthesis	(EC 6.3.4.4) AMP biosynthesis adenylosuccinate synthetase	<i>probably deoD</i>	adenosine phosphorylase negative adenine requirement
<i>purB</i>	699738 → 701033	purine biosynthesis	(EC 4.3.2.2) purine biosynthesis adenylosuccinate lyase		adenine requirement
<i>purD</i>	709653 → 710921	purine biosynthesis	(EC 6.3.4.13) phosphoribosylglycinamide synthetase		adenine or hypoxanthine requirement
<i>purE</i>	698121 → 698609	purine biosynthesis	(EC 4.1.1.21) phosphoribosyl-aminoimidazole carboxylase I	<i>purB33</i>	adenine, guanine, or hypoxanthine requirement
<i>purF</i>	704946 → 706376	purine biosynthesis	(EC 2.4.2.14) phosphoribosyl-pyrophosphate amidotransferase	<i>purB6</i>	adenine, guanine, or hypoxanthine requirement
<i>purH</i>	708099 → 709637	purine biosynthesis	(EC 2.1.2.3) phosphoribosylaminoimidazole carboxy formyl formyltransferase	<i>purJ</i>	adenine requirement
<i>purM</i>	706478 → 707518	purine biosynthesis	inosine-monophosphate cyclohydrolase (EC 6.3.3.1) phosphoribosylaminoimidazole synthetase		adenine and thiamine requirement
<i>pycA</i>	1553590 → 1557036		(EC 6.4.1.1) pyruvate carboxylase		requires citric acid cycle compounds in minimal media
<i>pyrA</i>	1622056 → 1623150	pyrimidine biosynthesis	(EC 6.3.5.5) carbamoyl-phosphate synthetase		arginine-sensitive growth
<i>pyrB</i>	1619875 → 1620789	pyrimidine biosynthesis	(EC 2.1.3.2) aspartate carbamoyltransferase		requires pyrimidine source
<i>pyrC</i> <i>pyrD</i>	1620773 → 1622059 1627117 → 1628052	pyrimidine biosynthesis pyrimidine biosynthesis	(EC 3.5.2.3) dihydroorotase (EC 1.3.3.1) dihydroorotase dehydrogenase	<i>pyrX</i>	requires pyrimidine source requires pyrimidine source
<i>pyrE</i>	1628719 → 1629369	pyrimidine biosynthesis	(EC 2.4.2.10) orotate phosphoribosyltransferase		requires pyrimidine source
<i>pyrF</i>	1628021 → 1628740	pyrimidine biosynthesis	(EC 4.1.1.23) orotidine 5'-phosphate decarboxylase		requires pyrimidine source
<i>pyrR</i>	1617708 → 1618253	attenuation (antitermination) of the pyrimidine operon (<i>pyrPBCADFE</i>) in the presence of UMP (pyrimidine biosynthesis)	transcriptional attenuator and uracil phosphoribosyltransferase activity (minor)		

Alleles and Phenotypes of BGSC *B. subtilis* Strains (continued)

Gene	Genome Location	Function	Gene Product	Synonyms	Mutant Phenotypes
<i>rapA</i>	1315338 → 1316474	prevents sporulation by dephosphorylating Spo0F-P (and thus the phosphorelay)	response regulator aspartate phosphatase	<i>gsiAA, spo0L</i>	null mutant sporulates in the presence of excess carbon sources
<i>recA</i>	1764015 → 1765058 3437 → 4549	DNA repair and genetic recombination	multifunctional SOS repair regulator	<i>recE</i>	impaired in recombination and repair
<i>recB</i>		DNA repair and genetic recombination			
<i>recD</i>		DNA repair and genetic recombination			
<i>recF</i>		DNA repair and genetic recombination			
<i>recG</i>		DNA repair and genetic recombination			
<i>recH</i>		DNA repair and genetic recombination			
<i>recL</i>		DNA repair and genetic recombination			
<i>recP</i>		DNA repair and genetic recombination			
<i>recR</i>		DNA repair and genetic recombination			
<i>relA</i>		28865 → 29461 (2819794 ← 2821998)			
<i>rib</i>					requirement for riboflavin
<i>rna-53</i>					temperature-sensitive RNA synthesis
<i>rplA</i>	119107 → 119805	ribosome, large subunit	ribosomal protein L1 (BL1)		altered electrophoretic mobility; chloramphenicol resistance (5 µg/ml)
<i>rplC</i>	135710 → 136339	ribosome, large subunit	ribosomal protein L3 (BL3)		altered electrophoretic mobility; possible micrococcal resistance (50 µg/ml)
<i>rplE</i>	141193 → 141732	ribosome, large subunit	ribosomal protein L5 (BL6)		altered electrophoretic mobility
<i>rplJ</i>	120057 → 120557	ribosome, large subunit	ribosomal protein L10 (BL5)	<i>relC, tsp</i>	altered electrophoretic mobility
<i>rplK</i>	118588 → 119013	ribosome, large subunit	ribosomal protein L11 (BL11)		altered electrophoretic mobility; thiostrepton resistance (1 µg/ml)
<i>rplL</i>	120604 → 120975	ribosome, large subunit	ribosomal protein L12 (BL9)		altered electrophoretic mobility
<i>rplU</i>	(2854779 ← 2855087)	ribosome, large subunit	ribosomal protein L21 (BL20)		altered electrophoretic mobility
<i>rplV</i>	138495 → 138836	ribosome, large subunit	ribosomal protein L22 (BL17)		altered electrophoretic mobility; erythromycin resistance (2 µg/ml)
<i>rplX</i>	140855 → 141166	ribosome, large subunit	ribosomal protein L24 (BL23) (histone-like protein HPB12)		altered electrophoretic mobility
<i>rpmA</i>	(2854141 ← 2854425)	ribosome, large subunit	ribosomal protein L27 (BL24)		altered electrophoretic mobility
<i>rpmD</i>	143873 → 144052	ribosome, large subunit	ribosomal protein L30 (BL27)		altered electrophoretic mobility
<i>rpoA</i>	148929 → 149873	transcription	(EC 2.7.7.6) RNA polymerase (α subunit)		
<i>rpoB</i>	121916 → 125497	transcription	(EC 2.7.7.6) RNA polymerase (β subunit)		rifampin resistance (50 µg/ml); allele 2: low rifampin resistance (2 µg/ml)
<i>rpoC</i>	125559 → 129158	transcription	(EC 2.7.7.6) RNA polymerase (β' subunit)		lipiarmycin (10 µg/ml) and streptolydigin (40 µg/ml) resistance
<i>rpsE</i>	143359 → 143859	ribosome, small subunit	ribosomal protein S5		altered electrophoretic mobility; spectinomycin resistance (125 µg/ml)
<i>rpsF</i>	(4198653 ← 4198940)	ribosome, small subunit	ribosomal protein S6 (BS9)		altered electrophoretic mobility
<i>rpsG</i>	130159 → 130629	ribosome, small subunit	ribosomal protein S7 (BS7)		altered electrophoretic mobility
<i>rpsH</i>	141972 → 142370	ribosome, small subunit	ribosomal protein S8 (BS8)		altered electrophoretic mobility
<i>rpsI</i>	154299 → 154691	ribosome, small subunit	ribosomal protein S9		altered electrophoretic mobility
<i>rpsK</i>	148357 → 148752	ribosome, small subunit	ribosomal protein S11 (BS11)		altered electrophoretic mobility
<i>rpsL</i>	129701 → 130117	ribosome, small subunit	ribosomal protein S12 (BS12)	<i>strA, fun</i>	altered electrophoretic mobility; streptomycin resistance, slower growth, reduced sporulation

Alleles and Phenotypes of BGSC *B. subtilis* Strains (continued)

Gene	Genome Location	Function	Gene Product	Synonyms	Mutant Phenotypes
<i>sacA</i>	(3901006 ← 3902448)	sucrose metabolism	(EC 3.2.1.26) sucrose-6-phosphate hydrolase	<i>ipa-50d</i>	inability to utilize sucrose (except in a deg mutant strain)
<i>sacB</i>	3535072 → 3536493	sucrose metabolism	(EC 2.4.1.10) levansucrase		levanase negative
<i>sacP</i>	(3902445 ← 3903827)	sucrose transport	(EC 2.7.1.69) phosphotransferase system (PTS) sucrose-specific enzyme IIBC component	<i>ipa-49d</i>	inability to utilize sucrose
<i>sacR</i>					constitutive levansucrase and sucrose synthesis
<i>sacT</i>	(3904938 ← 3905768)	positive regulation of <i>sacA</i> and <i>sacP</i>	transcriptional antiterminator	<i>ipa-47d</i>	constitutive sucrose synthesis
<i>sac(XY)</i>	3941028 → 3943303	positive regulation of levansucrase and sucrose synthesis (sucrose regulation)		<i>sacS</i>	constitutive levansucrase and sucrose synthesis
<i>sapA</i>					allows synthesis of sporulation alkaline phosphatase in Spo ⁻ strains
<i>sapB</i>					allows synthesis of sporulation alkaline phosphatase in Spo ⁻ strains
<i>sas</i>				<i>spoIIA</i>	intragenic suppressor of <i>spoIIA69</i>
<i>scoA</i>					"sporulation control;" delayed sporulation, elevated protease levels
<i>sdhA</i>	(2905438 ← 2907198)	citric acid cycle	(EC 1.3.99.1) succinate dehydrogenase (flavoprotein subunit)	<i>citF</i>	no growth on lactate-glutamate as carbon sources; autolytic
<i>sdhB</i>	(2904674 ← 2905435)	citric acid cycle	(EC 1.3.99.1) succinate dehydrogenase (iron-sulfur protein)		no growth on lactate-glutamate as carbon sources; autolytic
<i>sdhC</i>	(2907232 ← 2907840)	citric acid cycle	succinate dehydrogenase (cytochrome b558 subunit)		no growth on lactate-glutamate as carbon sources; autolytic
<i>serA</i>	2410320 → 2411897	serine biosynthesis	(EC 1.1.1.95) phosphoglycerate dehydrogenase		requirement for serine or glycine
<i>serC</i>	(1074762 ← 1075841)	serine biosynthesis	(EC 2.6.1.52) phosphoserine aminotransferase	<i>yhaF</i>	requirement for serine
<i>serR</i>					resistant to serine (50 µg/ml)
<i>sfp</i>	(407222 ← 407719)	surfactin production			null mutant: no surfactin synthesis
<i>sigA</i>	(2599490 ← 2600605)	general vegetative sigma factor	RNA polymerase major sigma factor σ^A	<i>rpoD</i> , <i>crsA</i>	<i>crsA</i> alleles: sporulate in the presence of repressing levels of glucose and other carbon sources
<i>sigB</i>	522413 → 523207	general stress sigma factor (class II genes)	RNA polymerase σ^B	<i>rpoF</i>	null mutant: no obvious growth or sporulation phenotype, but blocks expression of many general stress response genes
<i>sigD</i>	1715885 → 1716649	flagellar synthesis, motility, chemotaxis, autolysis	RNA polymerase σ^D	<i>flaB</i>	null mutant: filamentous growth; blocks flagellar synthesis, motility, chemotaxis, autolysin formation
<i>sigE</i>	1604166 → 1604885	early mother cell-specific gene expression	RNA polymerase sporulation-specific σ^E	<i>spoIIGB</i>	null mutations: block sporulation at stage II; two septa formed
<i>sigF</i>	(2442658 ← 2443425)	early forespore-specific gene expression	RNA polymerase sporulation-specific sigma factor σ^F	<i>spoIIAC</i>	null mutations: block sporulation at stage II; two septa formed
<i>sigH</i>	116597 → 117253	expression of vegetative and early stationary-phase genes	RNA polymerase σ^H	<i>spoOH</i>	null mutations: block sporulation before septum formation
<i>sinI</i>	2551722 → 2551895	prevents SinR from binding to its target sequence on <i>aprE</i>	antagonist of SinR		null mutations: reduced frequency of spore formation

Alleles and Phenotypes of BGSC *B. subtilis* Strains (continued)

Gene	Genome Location	Function	Gene Product	Synonyms	Mutant Phenotypes
<i>sinR</i>	2551929 → 2552264	regulation of post-exponential-phase responses genes (positive regulation of <i>comK</i> ; negative regulation of <i>aprE</i> , <i>kinB</i> , <i>sigD</i> , <i>spo0A</i> , <i>spoIIA</i> , <i>spoIIE</i> , <i>spoIIG</i>)	transcriptional regulator	<i>sin</i> , <i>flaD</i>	null mutations: blocks flagellar synthesis, motility, chemotaxis, autolysin formation; overexpression on plasmid: blocks sporulation
<i>smo</i> <i>SP10^R</i> <i>SP10^S</i> <i>spcB</i> <i>spcD</i> <i>spl(AB)</i>					smooth colony morphology resistant to phage SP10 sensitive to phage SP10
<i>spl(AB)</i>	1461177 → 1462205	repair of UV radiation-induced DNA damage during spore germination	spore photoproduct lyase	<i>spl</i> , <i>ssp-1</i>	spores are UV-sensitive
<i>spo0A</i>	(2517301 ← 2518104)	central role in the initiation of sporulation (negative regulation of <i>abrB</i> , <i>kinA</i> , <i>kinC</i> , <i>spo0A</i> ; positive regulation of <i>spoIIA</i> , <i>spoIIE</i> , <i>spoIIG</i>) (stage 0 sporulation)	two-component response regulator	<i>spo0C</i> , <i>spo0G</i> , <i>spoIIL</i> , <i>sof-1</i>	null mutation: blocks sporulation at stage 0; <i>sof</i> , <i>rvtA</i> : suppress null mutations in <i>spo0B</i> and <i>spo0F</i>
<i>spo0B</i>	(2853242 ← 2853820)	stage 0 sporulation	sporulation initiation phosphoprotein	<i>spo0D</i>	blocks sporulation at stage 0
<i>spo0E</i>	1430150 → 1430407	specific dephosphorylation of Spo0A-P (stage 0 sporulation)	negative sporulation regulatory phosphatase		null mutation: no block; nonsense mutations in distal portion of gene: block sporulation at stage 0
<i>spo0F</i>	(3808603 ← 3808977)	initiation of sporulation (stage 0 sporulation)	two-component response regulator		blocks sporulation at stage 0
<i>spo0J</i>	(4204764 ← 4205612)	positioning chromosome near the pole of cell before asymmetric septation, specifying its orientation, and imposing directionality on its transport through septum (stage 0 sporulation)	antagonist of Soj	<i>spoCM</i>	blocks sporulation at stage 0
<i>spoIIAA</i>	(2443437 ← 2444227)	stage II sporulation; regulation of σ^F activity			null mutations: block sporulation at stage II; normal septum formation
<i>spoIIB</i>	(2862555 ← 2863553)	endospore development (stage II sporulation)			null mutations: oligosporogenous; block sporulation at stage II
<i>spoIID</i>	(3775777 ← 3776808)	dissolution of the asymmetric septum (stage II sporulation)		<i>spoIIC</i>	null mutations: block sporulation at stage II; peptidoglycan layer in asymmetric septum fails to dissolve
<i>spoIIE</i>	70536 → 73019	dephosphorylates SpoIIAA-P and overcomes SpoIIAB-mediated inhibition of σ^F (stage II sporulation)	serine phosphatase	<i>spoIIH</i> , <i>spoIIK</i>	null mutations: block sporulation at stage II; asymmetric septum remains straight and thick
<i>spoIIG</i>	1603174 → 1604103	processing of pro- σ^E (SpoIIGB) to active sigma-E (stage II sporulation)	protease		null mutations: block sporulation at stage II; normal septum formation
<i>spoIIM</i>	(2449631 ← 2450275)	dissolution of the septal cell wall (stage II sporulation)			null mutations: block sporulation at stage II; peptidoglycan layer in asymmetric septum fails to dissolve
<i>spoIIIA(A-H)</i>	(2531628 ← 2536889)	stage III sporulation			null mutations: block sporulation at stage III after complete engulfment
<i>spoIIIB</i> <i>spoIIIC</i>	2700607 → 2701023	late mother cell-specific gene expression (stage IV sporulation)	Probably <i>spoIIIA</i> RNA polymerase sporulation-specific sigma factor (sigma-K) (C-terminal half)	<i>sigK</i> , <i>spoIVD</i> , <i>spoIVE</i>	null mutations: block sporulation at stage III blocks sporulation at stage IV; phase-gray, coatless forespores with incomplete cortex

Alleles and Phenotypes of BGSC *B. subtilis* Strains (continued)

Gene	Genome Location	Function	Gene Product	Synonyms	Mutant Phenotypes
<i>spoIID</i>	(3747475 ← 3747756)	regulation of genes controlled by mother cell-specific sigma factors E and K (stage III sporulation)	transcriptional regulator		null mutations: block sporulation at stage III
<i>spoIIE</i>	1751668 → 1754031	chromosome partitioning through the septum into the forespore compartment (stage III sporulation)	DNA translocase		allele 36: defective segregation of forespore chromosome; forespores complete engulfment, then lyse
<i>spoIIJ</i>	(4213031 ← 4213816)	σ^G activity at stage III (stage III sporulation)		<i>spo0J87</i>	null mutations: block sporulation at stage III
<i>spoIVA</i>	(2385432 ← 2386910)	spore cortex formation and coat assembly (stage IV sporulation)		<i>spoVP</i>	null mutations: block sporulation at stage IV; cortex forms improperly; coat proteins accumulate as swirls in mother cell cytoplasm
<i>spoIVB</i>	(2518380 ← 2519657)	intercompartmental signaling of pro- σ^K processing in the mother-cell (stage IV sporulation)			null mutations: block sporulation at stage IV; block cortex and coat formation
<i>spoIVC(AB)</i>		stage IV sporulation			blocks sporulation at stage IV; phase-gray, coatless forespores with incomplete cortex
<i>spoIVD</i>			large deletion overlapping <i>spoIIIC</i>		blocks sporulation at stage IV; phase-gray, coatless forespores with incomplete cortex
<i>spoIVF(AB)</i>	(2855234 ← 2856887)	stage IV sporulation			blocks sporulation at stage IV; phase-gray, coatless forespores with incomplete cortex; <i>spoIVFA</i> mutants have temperature-sensitive sporulation
<i>spoL</i>					"decadent" sporulation; block of sporulation stops at heterogeneous stages in sporulation
<i>spoVA</i>	(2437604 ← 2442536)	stage V sporulation			blocks sporulation at stage V; phase-white spores, partially resistant to toluene and lysozyme but sensitive to CHCl_3 and heat; normal cortex, some coat
<i>spoVB</i>	2828825 → 2830381	spore cortex synthesis (stage V sporulation)		<i>spoIII F</i>	blocks sporulation at stage V; heat-sensitive spores with defective cortex
<i>spoVC</i>	59502 → 60068	thermosensitive mutant blocks spore coat formation (stage V sporulation)			blocks sporulation at stage V; allele -285: at restrictive temperature, arrests coat formation
<i>spoVD</i>	1583616 → 1585553	spore morphogenesis (spore cortex) (stage V sporulation)	penicillin-binding protein		blocks sporulation at stage V; forms striated cortex, immature coat
<i>spoVE</i>	1589717 → 1590817	spore cortex synthesis (stage V sporulation)			blocks sporulation at stage V; well developed coat; no cortex
<i>spoVF(AB)</i>	1743758 → 1744651	stage V sporulation	dipicolinate synthase subunits		blocks sporulation at stage V; heat sensitive spores
<i>spoVG</i>	55864 → 56157	spore cortex synthesis (stage V sporulation)			null mutation: minicell formation during growth, oligosporogenic block of sporulation at stage V;
<i>spoVK</i>	1873444 → 1874412	disruption leads to the production of immature spores (stage V sporulation)		<i>spoVJ</i>	blocks sporulation at stage V; immature spores sensitive to lysozyme, organic solvents, heat
<i>spoVM</i>	1654845 → 1654925	spore cortex and coat synthesis (stage V sporulation)			blocks sporulation at stage V; phase gray spores with deficient cortex, thin coat
<i>spoVIA</i>		stage VI sporulation			blocks sporulation at stage VI; incomplete coat, lysozyme sensitive spores, slow germination
<i>spoVID</i>	(2870122 ← 2871849)	assembly of the spore coat (stage VI sporulation)			blocks sporulation at stage VI; defective coat, lysozyme sensitive spores, slow germination
<i>srfA</i>	376537 → 402697	surfactin production and competence	surfactin synthetase	<i>comL</i>	null mutation: blocks competence development and surfactin synthesis, reduces sporulation frequency

Alleles and Phenotypes of BGSC *B. subtilis* Strains (continued)

Gene	Genome Location	Function	Gene Product	Synonyms	Mutant Phenotypes
<i>sspA</i>	(3024517 ← 3024726)	spore resistance properties	small acid-soluble spore protein (α -type SASP)		spores are slightly more sensitive to heat, significantly more sensitive to UV radiation
<i>sspB</i>	(1049511 ← 1049714)	spore resistance properties	small acid-soluble spore protein (β -type SASP)		enhances effect of <i>sspA</i> mutations; no detectable phenotype alone
<i>sspE</i>	937406 → 937660	spore resistance properties	small acid-soluble spore protein (γ -type SASP)		null mutation: slow outgrowth upon germination in the absence of externally supplied amino acids
<i>stp</i>					reported to increase plasmid stability
<i>strB</i>					streptomycin resistance (200 μ g/ml)
<i>strC</i>					streptomycin resistance (1 μ g/ml), glucose requirement
<i>suf</i>					suppresses <i>leuA169</i> frameshift
<i>suh</i>					may be leaky <i>hisH</i>
<i>sul</i>	85734 → 86591	dihydrofolate biosynthesis	(EC 2.5.1.15) dihydropteroate synthase		sulfanilamide resistance (500 μ g/ml)
<i>sup-1</i>					nonsense suppressor
<i>sup-22</i>					nonsense suppressor
<i>sup-44</i>					nonsense suppressor
<i>sup-67</i>					nonsense suppressor
<i>tagE</i>	(3677459 ← 3679480)	teichoic acid biosynthesis	(EC 2.4.1.52) UDP-glucose:polyglycerol phosphate glucosyltransferase	<i>rodD</i> , <i>gtaA</i> , <i>gtaD</i>	cell wall defective
<i>tagF</i>	(3675219 ← 3677459)	teichoic acid biosynthesis	CDP-glycerol:polyglycerol phosphate glycerophosphotransferase	<i>rodC</i>	cell wall defective
<i>tal</i>					$\hat{\alpha}$ -thienylalanine resistant (100 μ g/ml)
<i>tem</i>					temperature-sensitive RNA and protein synthesis
<i>ten</i>					transfection enhancement for phage SP82 DNA
<i>thiA</i>	955403 → 957175	biosynthesis of the pyrimidine moiety of thiamin (thiamin biosynthesis)			thiamine requirement
<i>thiB</i>					thiamine requirement
<i>thiC</i>	(3929503 ← 3930171)	thiamine biosynthesis	(EC 2.5.1.3) thiamine-phosphate pyrophosphorylase	<i>ipa-26d</i> , <i>ywbK</i>	thiamine requirement
<i>thrB</i>	(3311902 ← 3312831)	threonine biosynthesis	(EC 2.7.1.39) homoserine kinase	<i>thrA</i>	threonine requirement
<i>thrC</i>	(3312828 ← 3313886)	threonine biosynthesis	(EC 4.2.99.2) threonine synthase	<i>thrB</i>	threonine requirement
<i>thyA</i>	1901474 → 1902313	deoxyribonucleotide biosynthesis	(EC 2.1.1.45) thymidylate synthase A		thymine requirement in conjunction with <i>thyB</i> mutation
<i>thyB</i>	(2296347 ← 2297141)	deoxyribonucleotide biosynthesis	(EC 2.1.1.45) thymidylate synthase B		thymine requirement in conjunction with <i>thyA</i> mutation
<i>tmsA</i>					temperature-sensitive growth
<i>tmsB</i>					temperature-sensitive growth
<i>tolA</i>					tolerance of bacteriophage ϕ 29
<i>tolB</i>					tolerance of bacteriophage ϕ 29
<i>treA</i>	851357 → 853042		(EC 3.2.1.93) trehalose-6-phosphate hydrolase	<i>treC</i>	inability to grow on trehalose
<i>trnS-Lys3</i>	528818 → 528893	transfer RNA	tRNA-Lys		<i>sup-3</i> nonsense suppressor
<i>trpA</i>	(2370749 ← 2371552)	tryptophan biosynthesis	(EC 4.2.1.10) tryptophan synthase (α subunit)		tryptophan requirement

Alleles and Phenotypes of BGSC *B. subtilis* Strains (continued)

Gene	Genome Location	Function	Gene Product	Synonyms	Mutant Phenotypes
<i>trpB</i>	(2371545 ← 2372747)	tryptophan biosynthesis	(EC 4.2.1.20) tryptophan synthase (β subunit)		tryptophan requirement
<i>trpC</i>	(2373380 ← 2374132)	tryptophan biosynthesis	(EC 4.1.1.48) indol-3-glycerol phosphate synthase		tryptophan or indole requirement
<i>trpD</i>	(2374125 ← 2375138)	tryptophan biosynthesis	(EC 2.4.2.18) anthranilate phosphoribosyltransferase		tryptophan or indole requirement
<i>trpE</i>	(2375110 ← 2376657)	tryptophan biosynthesis	(EC 4.1.3.27) anthranilate synthase		tryptophan, indole, or anthranilate requirement
<i>trpF</i>	(2372728 ← 2373375)	tryptophan biosynthesis	(EC 5.3.1.24) phosphoribosyl anthranilate isomerase		tryptophan or indole requirement
<i>trpS</i>	(1217585 ← 1218577)	aminoacyl-tRNA synthetase	(EC 6.1.1.2) tryptophanyl-tRNA synthetase		5-fluorotryptophan resistance (50 µg/ml)
<i>ts-2</i>					temperature-sensitive growth
<i>ts-355</i>					temperature-sensitive growth
<i>ts-39-2</i>					temperature-sensitive growth
<i>tscA1</i>					temperature-sensitive growth
<i>tscC11</i>					temperature-sensitive growth
<i>tscD14</i>					temperature-sensitive growth
<i>tsi-23</i>					temperature-sensitive growth
<i>tufA</i>	132881 → 134071		elongation factor Tu		kanamycin resistance (200 µg/ml)
<i>tyrA</i>	(2368492 ← 2369607)	tyrosine biosynthesis	(EC 1.3.1.12) prephenate dehydrogenase		tyrosine requirement
<i>upp</i>	(3787481 ← 3788110)	pyrimidine salvage	(EC 2.4.2.9) uracil phosphoribosyltransferase	<i>ipc-35d</i>	in the absence of deoxyadenosine, 5-fluorouracil resistance (10 µg/ml) uracil requirement
<i>ura</i>				<i>cysC-pyr region</i>	requirement for uracil and cysteine and methionine
<i>urc</i>					uracil glycosidase
<i>urg</i>				<i>carA or carB</i>	uracil-sensitive growth
<i>urs</i>					UV sensitivity
<i>uvr</i>					UV sensitivity
<i>uvrB</i>	(3612005 ← 3613990)	excision of ultraviolet light-induced pyrimidine dimers in DNA	excinuclease ABC (subunit B)	<i>dinA, uvrA</i>	UV sensitivity
<i>uvrC</i>	(2910194 ← 2911990)	excision of ultraviolet light-induced pyrimidine dimers in DNA	(EC 4.1.99.3) excinuclease ABC (subunit C)	<i>uvrB</i>	UV sensitivity
<i>uv^S</i>					sensitive to ultraviolet radiation
<i>virM</i>					virginamycin M resistance (50 µg/ml)
<i>virS</i>					virginamycin S resistance (13 µg/ml)
<i>wrd</i>					slow growth on PGYE medium, normal on MA medium
<i>xhd</i>					induced PBSX phage lacks heads
<i>xhi</i>				<i>probably xre</i>	heat-inducible PBSX
<i>xin</i>				<i>probably xre</i>	induction defective PBSX
<i>xki</i>					PBSX particles fail to kill strain W23
<i>xpt</i>	(2318682 ← 2319266)	purine biosynthesis	(EC 2.4.2.7) xanthine phosphoribosyltransferase		resistance to 8-azaxanthine
<i>xtI</i>					induced PBSX phage lack tails
<i>xyl(AB)</i>	1891162 → 1894149	xylose metabolism			unable to utilize xylose
<i>xynA</i>	(2053853 ← 2054494)	xylan degradation	(EC 3.2.1.8) endo-1,4-β-xylanase		unable to degrade xylan
<i>xynB</i>	1888028 → 1889629	xylan degradation	xylan β-1,4-xylosidase	<i>ynaK</i>	unable to degrade xylan
<i>ydaO</i>	485985 → 487808	unknown			no known phenotype

Alleles and Phenotypes of BGSC *B. subtilis* Strains (continued)

<i>yokH</i>	(2276762 ← 2277319)	unknown	no known phenotype
<i>yufR</i>	3243849 → 3245195	unknown	no known phenotype
<i>yvaC</i>	(3445299 ← 3447194)	unknown	no known phenotype
<i>zaa-zjj</i>			silent transposon insertions; letters after "z" in mnemonic give approximate map position in percent, where a = 0, b = 1, c = 2, etc. (zaa = 0%, zab = 1%, zjj = 99%)
<i>29^R</i>			resistant to phage ø29
<i>NR2^S</i>			sensitive to phage øNR2
