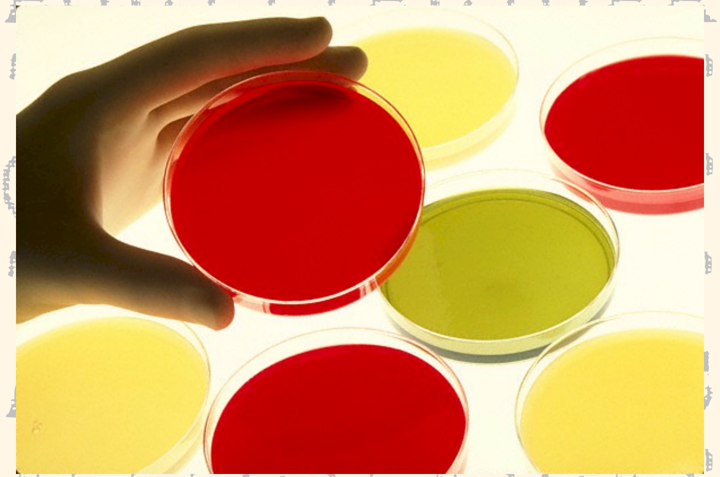
BACILLUS SUBTILIS 168



BACILLUS GENETIC STOCK CENTER
CATALOG OF STRAINS
SEVENTH EDITION
VOLUME 1

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

The *Bacillus* Genetic Stock Center
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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 *Bacilllus 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.

Please note: The BGSC catalog has been updated since this catalog was created. The online catalog on the BGSC website (https://bgsc.org/index.php) more accurately reflects the strains available from our collection. If you would like a full list of the B. subtilis strains in our collection, please email asc-microbioservice@osu.edu with your request.

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***Bacillus subtilis 168* Strain Indexes**

(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 and cloning vectors 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 then provided facilities and administrative support. The Director of the BGSC, Dr. Daniel R. Zeigler, oversaw the BGSC for many years before retiring in 2021. The *Bacillus* Genetic Stock Center is no longer funded by the NSF and is now supported by the Infectious Disease Institute at the Ohio State University.

What kinds of cultures are available from the BGSC?

This catalog lists only the *Bacillus subtilis* 168 cultures available from the BGSC. The BGSC maintains and distributes a wide range of other strains, however. Included in our collection as of December 1999 (and described in other existing and planned catalogs) are:

- **146 characterized environmental isolates and mutant strains derived from *Bacillus thuringiensis*;**
- **19 bacteriophages of *B. thuringiensis* and *B. cereus;***
- **54 *B. subtilis* plasmid-bearing strains;**
- **17 *B. subtilis* isolates from non-168 backgrounds;**
- **39 genetically characterized wild-type and mutant strains of *Bacillus licheniformis;***
- **38 genetically characterized wild-type and mutant strains of *Bacillus megaterium;***
- **16 genetically characterized wild-type and mutant strains of *Bacillus stearothermophilus;***
- **45 isolates from other related species, including *B. cereus, B. amyloliquefaciens, B. globigii, B. niger, B. pumilus, B. sphaericus, B. badius, B. polymyxa, B. subtilis natto, Brevibacillus brevis, Brevibacillus laterosporus, Paenibacillus vorticalis,* and *Paenibacillus dendritiformus;***
- **114 *Escherichia coli* strains bearing shuttle plasmids or cloned *Bacillus* DNA;**
- **The strain collections of Stanley A. Zahler and the late Ernst W. Freese.**
- **Note that we do not have or ever intend to obtain any pathogenic strains of *Bacillus anthracis!* We simply do not have the experience, facilities, permission, or desire to deal with any serious human pathogen.**

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

What you can do to help the BGSC

- *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:** asc-microbioservice@osu.edu
- **Internet:** https://bgsc.org/index.php
- **Phone:** 614-292-2275
- **Mail:** The Ohio State University
  484 West Twelfth Avenue
  Biological Sciences Building 556
  Columbus, OH 43210
  USA

Non-profit and for-profit users should supply a full shipping address, billing address, email address, phone number, and BGSC IDs of the requested strains. We make every effort to respond to all inquiries within one working day of receipt, together with an estimated delivery date if an order has been placed.

Pricing information

- *Academic, Government, and Non-Profit Users*--Users may purchase cultures as needed for a 55.00 USD per culture charge. If purchasing many cultures, users may pay a fee of 285.00 USD to receive up to 20 strains over the course of a year.

- *For-profit Corporate Users*--Users may purchase cultures as needed for a 179.00 USD per culture charge. If purchasing many cultures, users may pay a fee of 2850.00 USD to receive up to 50 strains over the course of a year.
- *Shipping:* Shipping and handling charges will be included in the quoted price. The shipping rate for domestic destinations is 15.00 USD and 60.00 USD for international destinations.

Important Notice

Please read this notice before ordering materials from this catalog!

THE MATERIALS OFFERED IN THIS CATALOG MAY BE OWNED BY PERSONS OR FIRMS OTHER THAN THE OHIO STATE UNIVERSITY OR THE *BACILLUS* GENETIC STOCK CENTER. USE OF THE MATERIALS FOR ANY PUPOSE OTHER THAN RESEARCH MAY CONSTITUTE A VIOLATION OF THE RIGHTS OF THESE PARTIES AND MAY SUBJCT THE RECIPIENT TO LEGAL LIABILITY. IT IS THE RESPONSIBILITY OF THE USER (NOT EMPLOYEES OF THE *BACILLUS* GENETIC STOCK CENTER) TO DETERMINE THE PROPRIETARY STATUS OF ANY OF THESE MATERIALS.

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- **(iii) the freedom from claims by others of intellectual or other property rights in Materials or in any such methods. The provision of the Material to Recipient shall not alter any pre-existing right to the Materials.**

BACILLUS SUBTILIS 168 STRAINS INDEXED BY BGSC ACCESSION NUMBER

BGSC	**ORIGINAL CODE**	**DESCRIPTION**	**SOURCE**	**DONOR**	**REF**
1A1	168	*trpC2*	Giles N	Shapiro JA	30
1A2	SB491	prototrophic	Lederberg J	Lederberg J	155
1A3	QB944 KIT-1	*cysE14 purA26 trpC2*	Dedonder RA	Dedonder RA	60
1A4	QB928 KIT-2	*aroI906 dal-1 purE1 trpC2*	Dedonder RA	Dedonder RA	60
1A5	QB934 KIT-3	*glyB133 metC3 treA12 trpC2*	Dedonder RA	Dedonder RA	60
1A6	QB943 KIT-4	*ilvA1 pyrD1 thyA1 thyB1 trpC2*	Dedonder RA	Dedonder RA	60
1A7	QB922 KIT-5	*gltA292 trpC2*	Dedonder RA	Dedonder RA	60
1A8	QB935 KIT-6	*aroD120 lys-1 trpC2*	Dedonder RA	Dedonder RA	60
1A9	QB936 KIT-7	*ald-1 aroA932 leuB8 trpC2*	Dedonder RA	Dedonder RA	60
1A10	QB917 KIT-8	*hisA1 thr-5 trpC2*	Dedonder RA	Dedonder RA	60
1A11	QB123 KIT-9	*ctrA1 sacA321 trpC2*	Dedonder RA	Dedonder RA	60
1A12	Mu8u5u6	*leuB8 metB5 purF6*	Seuoka N	Shapiro JA	292
1A13	Mu8u5u6u41	*car-41 leuB8 metB5 purF6*	Sueoka N	Shapiro JA	150
1A14	SU+III 168SU$^{+}\gamma$	*-(metB5)+ -(thr-5)+ leuB8 trnS-Lys3*	Georgopoulos C	Sonenshein AL	96
1A15	BR63	*pheA2 trpC2*	Reilly BE	Sonenshein AL	216
1A16	JH404	*citG4 trpC2*	Hoch JA	Hoch JA	225
1A17	CU403,TS-134	*dnaB134 ilvA1 thyA1 thyB1*	Mendelson NH	Mendelson NH	176
1A18	TSDNA-A13	*dnaA13 ilvA1 metB5*	Karamata D	Brown NC	146
1A19	TSDNA-B19	*dnaB19 ilvA1 metB5*	Karamata D	Brown NC	146
1A20	TSDNA-C30	*dnaC30 ilvA1 metB5*	Karamata D	Brown NC	146
1A21	TSDNA-D23	*dnaD23 ilvA1 metB5*	Karamata D	Brown NC	146
1A22	TSDNA-E20	*dnaE20 ilvA1 metB5*	Karamata D	Brown NC	146
1A23	TSDNA-F133	*ilvA1 metB5 polC133*	Karamata D	Brown NC	146
1A24	TSDNA-G34	*dnaN34 ilvA1 metB5*	Karamata D	Brown NC	146
1A25	TSDNA-H151	*dnaA151 ilvA1 metB5*	Karamata D	Brown NC	146
1A26	TSDNA-I102	*dnaI102 ilvA1 metB5*	Karamata D	Brown NC	146
1A27	BD97	*pyrA26*	Dubnau D	Karamata D	65
1A28	C-4 SB1 BC38	*argF4 hisA1 trpC2*	Marmur J	Copeland JC	166
1A29	BC50	*leuB8 metB5 nic-38 purA16*	Copeland JC	Copeland JC	45
1A30	BC53	*ilvA64 leuB8 metB5 purA16*	Copeland JC	Copeland JC	44
1A31	SB3 (BD92)	*cysB3 hisA1 trpC2*	Nester EW	Copeland JC	159
1A32	JH406	*citC6 trpC2*	Hoch JA	Hoch JA	225
1A33	JH402	*sdhA2 trpC2*	Hoch JA	Hoch JA	225
1A34	CU635	*furC1 trpC2*	Zahler SA	Zahler SA	300
1A35	RUB814	*tagE lys-3 metB10 trpC2*	Young FE	Yasbin RE	293
1A36	RUB834	*aroB2 hisH2 metB10 trpC2 tyrA1*	Young FE	Yasbin RE	293
1A37	RUB836	*hisA metB10 trpC2*	Young FE	Yasbin RE	293
1A38	RUB2112	*metB10 purF6 trpC2*	Young FE	Young FE	293
1A39	BR85	*argF4 trpC2*	Reilly BE	Young FE	294
1A40	BR151	*lys-3 metB10 trpC2*	Reilly BE	Young FE	294
1A41	DNA-1	*dnaB1 thyA1 thyB1 trpC2*	Sueoka N	Sueoka N	261
1A42	BD170	*thr-5 trpC2*	Dubnau DA	Dubnau DA	64
1A43	BD194	*recA1 trpC2*	Dubnau DA	Garro AJ	64
1A44	BD191	*recB2 thr-5 trpC2*	Dubnau DA	Garro AJ	64
1A45	BD193	*recB3 thr-5 trpC2*	Dubnau DA	Garro AJ	64
1A46	BD224	*recA4 thr-5 trpC2*	Dubnau DA	Garro AJ	64
1A47	BD241	*recL16 thr-5 trpC2*	Dubnau DA	Garro AJ	64
1A48	BD246	*reCm13 thr-5 trpC2*	Dubnau DA	Garro AJ	64
1A49	QB2,PUR(+)	*sacA321*	Dedonder RA	Dedonder RA	59, 158
1A50	QB42	*sac(XY)46 trpC2*	Dedonder RA	Dedonder RA	158
1A51	QB58	*purA16 sac(XY)46*	Dedonder RA	Dedonder RA	59
1A52	QB687	*sacA321 treA12 trpC2*	Dedonder RA	Dedonder RA	159
1A53	QB698	*ald-1 degQ36 trpC2*	Dedonder RA	Dedonder RA	159
1A54	QB819	*mtlD1 nasC1 sacA321*	Dedonder RA	Dedonder RA	159
1A55	QB820	*aroI906 dal-1 metB5 sacA321*	Dedonder RA	Dedonder RA	159
1A56	QB821	*aroA932 trpC2*	Dedonder RA	Dedonder RA	59
1A57	BR95	*ilvC1 pheA1 trpC2*	Reilly BE	Garro AJ	216
1A58	SB25	*hisH2 trpC2*	Lederberg J	Mahler I	191
1A59	SB1	*hisA1 trpC2*	Lederberg J	Mahler I	190
1A60	GB64/219	*metC3 pyrA xin-1*	Garro AJ	Garro AJ	92
1A61	JH715	*furF5* spo^{-}	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)	*trpA5*	Carlton BC	Garro AJ	285
1A63	GB151 (NG 14)	*trpB4*	Carlton BC	Garro AJ	285
1A64	GB152 (NA 3)	*trpD2*	Carlton BC	Garro AJ	285
1A65	BS166	*trpE26*	Yanofsky C	Spizizen J	30
1A66	SCR500	*pheA12 tolA6 trpC2*	Ito J	Ito J	135
1A67	SCR506	*pheA12 tolA6 trpC2* $\phi29^R$	Ito J	Ito J	136
1A68	MB500	*leuB8 metB5 tsi-23*	Hoch JA	Mahler I	246
1A69	SB120	*aroD120 trpC2*	Nester EW	Lepesant J-A	127
1A70	JH422	*citL22 trpC2*	Hoch JA	Hoch JA	125
1A71	GSY292	*gltA1 trpC2*	Anagnostopoulos C	Lepesant J-A	9, 61
1A72	GSY264	*mtr-264*	Anagnostopoulos C	Hoch JA	128
1A73	GSY1025	*metB4 recA1 trpC2*	Anagnostopoulos C	Lepesant JA	124
1A74	NH5	*dnaX8132 hisA1 thr-5*	Harford N	Lepesant J-A	109
1A75	MU8U5U1 (BD54)	*ilvA1 leuB8 metB5*	Dubnau DA	Brown NC	292
1A76	BD54,spcB	*ilvA1 metB5 spcB1*	Brown NC	Brown NC	164
1A77	BD54,strB	*ilvA1 metB5 strB3*	Brown NC	Brown NC	164
1A78	MB251	*metC3 pyrA xtl-1*	Garro AJ	Garro AJ	93
1A79	JH158	*cysC1 trpC2*	Hoch JA	Brown NC	123, 126
1A80	SB26	*metC7 trpC2*	Lederberg J	Brown NC	155
1A81	BD54,spcB,azp	*ilvA1 leuB8 metB5 polC12 spcB1*	Brown NC	Brown NC	164
1A82	BD54,azp	*ilvA1 leuB8 metB5 polC12*	Brown NC	Brown NC	164
1A83	SB137	*aroB2 hisH2*	Lederberg J	Lederberg J	191
1A84	QB858	*glyB133 metD1*	Lepesant J-A	Lepesant J-A	156
1A85	PB3046 (BD96)	*furA1*	Dubnau DA	Brown NC	209
1A86	1443	*ilvA1 leu leuB8 metB5 polA1443*	Gross J	Brown NC	21,117
1A87	SB68	*hisH2 trpC2 tyrA1*	Lederberg J	Lederberg J	155
1A88	QB19	*rplV1 sac(XY)32 trpC2*	Lepesant JA	Lepesant JA	158
1A89	QB99	*hisH2 leuB8*	Lepesant JA	Lepesant JA	60
1A90	QB666	*hisA1 sacA321 trpC2*	Lepesant JA	Lepesant JA	60
1A91	QB712	*fruB138 sacA321 trpC2*	Lepesant JA	Lepesant JA	156
1A92	QB889	*arg(GH)2 aroA932 bioB141 sacA321*	Lepesant JA	Lepesant JA	156
1A93	QB1506	*dnaX8132 hisA1 sacA321 thr-5*	Lepesant JA	Lepesant JA	156
1A94	CU495	*narA1 trpC2*	Zahler SA	Zahler SA	302
1A95	QB136	*leuB8 deg(H)32 trpC2*	Lepesant J-A	Lepesant J-A	152
1A96	JH642	*pheA1 trpC2*	Hoch JA	Hoch JA	58
1A97	CU135	*cysE14 trpC2*	Zahler SA	Zahler SA	300
1A98	CU968	*ilvΔ1 kauA1 metB5*	Zahler SA	Zahler SA	302
1A99	CU173	*citM1 ilvA3 trpC2*	Zahler SA	Zahler SA	80, 300
1A100	CU1065	SPβ^- *trpC2*	Zahler SA	Zahler SA	303
1A101	SB19SEM BC110	*rplC1 rplV1 str-2*	Nester EW	Copeland JC	66
1A102	GSY1307	*trpC2 trpS1*	Anagnostopoulos C	Copeland JC	258
1A103	PB1640	*aroB2 hisH2 recG40 trpC2 tyrA1*	Mazza PG	Mazza PG	172
1A104	SB164	*aroB2*	Lederberg J	Lederberg J	155
1A105	BR290	*gtaB290 trpC2*	Young FE	Streips UN	294
1A106	C33	*gtaC33 trpC2*	Young FE	Streips UN	293
1A107	C10	*gtaC10 trpC2*	Young FE	Streips UN	293
1A108	SB69	*hisA1 tyrA1*	Lederberg J	Lederberg J	155
1A109	CU229	*ilvB2 trpC2*	Zahler SA	Zahler SA	281
1A110	CU219	*ilvD15 trpC2*	Zahler SA	Zahler SA	300
1A111	CU456	*arg(GH)2 azlB101 trpC2*	Zahler SA	Zahler SA	300
1A112	CU457	*azlA102 trpC2*	Zahler SA	Zahler SA	282
1A113	CU626	*furB1 trpC2*	Zahler SA	Zahler SA	300
1A114	CU134 (JAS8)	*leuB6 trpC2*	Zahler SA	Shapiro JA	300
1A115	SB5	*hisA1 pyrA5 trpC2*	Potvin B	Zahler SA	127
1A116	BR54 (JAS9)	*leuB7 trpC2*	Reilly BE	Shapiro JA	216
1A117	CU776	*aroH1 cotA73*	Zahler SA	Zahler SA	300
1A118	CU785	*arg(ABCDE)1 metA8 trpC2*	Zahler SA	Zahler SA	300
1A119	CU810	*arg(GH)2 leuA164 pheA2 trpC2*	Zahler SA	Zahler SA	300
1A120	CU872	*citB75 trpC2*	Zahler SA	Zahler SA	300
1A121	CU893	*arg(GH)2 pheA2 sdhC109 trpC2*	Freese E	Zahler SA	300
1A122	QB870	*glpK21 glyB133 thiA78 treA12*	Lepesant J-A	Zahler SA	156
1A123	CU973	*furE1 trpC2*	Zahler SA	Zahler SA	300
1A125	QB879	*argF4 metA29 thiB4*	Lepesant J-A	Zahler SA	156
1A126	QB890	*hisH2 leuB8 sacA321 thiC5*	Lepesant J-A	Zahler SA	156

B. subtilis 168 Strains Indexed by BGSC Accession Number

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

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BGSC	ORIGINAL CODE	DESCRIPTION	SOURCE	DONOR	REF
1A188	KSG619	*ksgA619 thyA1 thyB1 trpC2*	Kobayashi Y	Kobayashi Y	272
1A189	168BLT	*blt-2 trpC2*	Rogolsky M	Rogolsky M	219
1A190	IS115	*cysE14* Spo$^-$ *tuf-7*	Smith I	Smith I	250
1A191	IS116	*rpsL1 thr-5 trpC2 tuf-2*	Smith I	Smith I	250
1A192	IS126	*cysE14 fus-1* Spo$^-$	Smith I	Smith I	98
1A193	IS153 CYS$^+$	*kan-2* Spo$^-$	Smith I	Smith I	97
1A194	IS154	*cysE14 nea-1* Spo$^-$	Smith I	Smith I	97
1A195	IS155	*cysE14 ole-2* Spo$^-$	Smith I	Smith I	97
1A196	CU403,DIVIVA	*divIVA1 ilvD thyA1 thyB1*	Reeve JN	Reeve JN	215
1A197	CU403,DIVIVB,SPO$^-$	*minD1 metB5* Spo$^-$ *thyA1 thyB1*	Reeve JN	Reeve JN	215
1A198	ST-3	*strB3*	Hoch JA	Hoch JA	123
1A199	QB127	*leuB8 deg(H)200 trpC2*	Dedonder RA	Dedonder RA	152
1A200	QB157	*leuB8 deg(H)100 trpC2*	Dedonder RA	Dedonder RA	59
1A201	QB254	*hisA1 sacA321 deg-42 trpC2*	Dedonder RA	Dedonder RA	158
1A202	WB1097	*leuB8 deg trpC2*	Dedonder RA	Dedonder RA	259
1A203	JAS11	*ilvB3 trpC2*	Shapiro JA	Shapiro JA	243
1A204	JAS12	*ilvA3 trpC2*	Shapiro JA	Shapiro JA	243
1A205	QB8087	*narA1 trpC2 ura-1*	Dedonder RA	Dedonder RA	59
1A206	SB29	*trpC2 tyrA1*	Lederberg J	Lederberg J	191
1A207	SB193	*aroE1 hisA1*	Lederberg J	Lederberg J	155
1A208	SB32	*hisH2*	Lederberg J	Lederberg J	190
1A209	TAG-1	*tag-1 thyA1 thyB1 trpC2*	Mendelson NH	Mendelson NH	176
1A210	BD35	*rib-2*	Greer S	Dubnau DA	65
1A211	BD40	*arg(GH)3 pheA12 rplV1*	Dubnau DA	Dubnau DA	65
1A212	BD108	*arg(GH)3 lys-21 metB5 pheA12 purA16 rplV1*	Dubnau DA	Dubnau DA	63
1A213	BD237	*recA8 thr-5 trpC2*	Dubnau DA	Dubnau DA	64
1A214	BD274	*polA59 thr-5 trpC2*	Dubnau DA	Dubnau DA	63
1A215	BD291	*polA5 thr-5 trpC2*	Dubnau DA	Dubnau DA	63
1A216	BD332	*polC12 pyrA26 spcB3 strB3*	Dubnau DA	Dubnau DA	63
1A217	BD336	*polC133 thr-5 trpC2*	Dubnau DA	Dubnau DA	**63**
1A218	IS121	*rplV1*	Smith I	Smith I	250
1A219	IS158	*rpsE2*	Smith I	Smith I	97
1A220	IS164	*rplC1*	Smith I	Smith I	97
1A221	IS165	*lmrA2*	Smith I	Smith I	97
1A222	IS166	*cysE14 rplV1* Spo$^-$	Smith I	Smith I	97
1A223	170-1	*rpsL1 tmsB853*	Smith I	Smith I	252
1A224	SB1058	*hisH2 pheA1 trpC2*	Lederberg J	Lederberg J	155
1A225	SB1059	*pheA1 polA5 trpC2*	Lederberg J	Lederberg J	155
1A226	SB1060	*hisH2 pheA1 polA5 trpC2*	Lederberg J	Lederberg J	155
1A227	SB112	*pheA1 trpC2*	Lederberg J	Lederberg J	191
1A228	CU373 SB1115	*ilvB 5 trpC2*	Zahler SA	Lederberg J	300
1A229	SB135	*aroE1*	Lederberg J	Lederberg J	155
1A230	GSY483 SB1141	*ilvD6 thyA1 trpC2*	Anagnostopoulos C	Lederberg J	155
1A231	GSY277 SB1142	*ilvA2 trpC2*	Lederberg J	Lederberg J	19
1A232	GSY276 SB1143	*ilvD4 trpC2*	Lederberg J	Lederberg J	19
1A233	GSY260 SB1144	*ilvD2 trpC2*	Lederberg J	Lederberg J	19
1A234	GSY226 SB1145	*metB2 trpC2*	Lederberg J	Lederberg J	19
1A235	GSY227 SB1146	*metB3 trpC2*	Lederberg J	Lederberg J	19
1A236	PG522	*fruA20 ura-3*	Gay P	Gay P	95
1A237	PG524	*fruB22 ura-3*	Gay P	Gay P	95
1A238	TS3	*fus-3 str*	Ron EZ	Ron EZ	3
1A239	BR95,GLPD8	*glpD8 ilvC1 trpC2*	Rutberg B	Rutberg B	161
1A240	BR95,GLPK	*glpK21 pheA1 trpC2*	Rutberg B	Rutberg B	161
1A241	JAS1	*cysE14 rpsE2*	Shapiro JA	Shapiro JA	243
1A242	BD99	*hisA1 thr-5 trpC2*	Dubnau DA	Mahler I	63
1A243	168TT	*thyA1 thyB1 trpC2*	Rothman F	Marmur J	77
1A246	SB168 168	*trpC2*	Lederberg J	Lederberg J	30
1A248	LS11	*rpoB500 trpC2*	Sonenshein AL	Sonenshein AL	255
1A249	JH825	*ilvC1 pheA1 strC23*	Hoch JA	Hoch JA	123
1A250	CU466	*alsR1 ilvBΔ1 trpC2*	Zahler SA	Zahler SA	302
1A251	CU869	*purM1 trpC2*	Zahler SA	Zahler SA	301
1A253	RM125	*arg(GH)15 leuB8* $hsd_{RI}R^-M^-$ SP10^S	Uozumi T	Uozumi T	277
1A254	PHOP,PHEA	*pheA phoP*	Cozzarelli NR	Mahler I	46

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1A255	PHOP12	*phoP12*	Hoch JA	Mahler I	123
1A256	NP22.1	*phoP22*	Grant W	Mahler I	100
1A257	NP4.1	*phoP4*	Grant W	Mahler I	100
1A258	103	*ile leu metB5 thyA1 thyB1*	Farmer JL	Arnaud M	76
1A259	RC220 103SU+3	*-(met)+ ile leu trnS-Lys3 thyA1 thyB1*	Halvorson HO	Arnaud M	107
1A260	RC221 103SU+44	*-(met)+ ile leu sup-44 thyA1 thyB1*	Halvorson HO	Arnaud M	107
1A261	VUB212	*metB4 gyrB1 recD27 trpC2*	Harford N	Dedonder RA	109
1A262	VUB234	*gyrB2 recF15 thr-5 trpC2*	Harford N	Dedonder RA	109
1A263	QB752	*metC pfk ptsI1*	Dedonder RA	Dedonder RA	59
1A264	QB1180	*-(hisA1)+ sup-44 thr-5*	Dedonder RA	Dedonder RA	59
1A267	168BRY	*bry*	Sonenshein AL	Sonenshein AL	253
1A268	TS-151	*thyA1 thyB1 tmsA151 trpC2*	Mendelson NH	Mendelson NH	176
1A269	TS-355	*spo*$^{-}$ *thyA1 thyB1 trpC2 ts-355*	Mendelson NH	Mendelson NH	176
1A270	SH	prototroph *str sul*	Magasanik B	Magasanik B	37
1A271	SH-5	*hutP1 str sul*	Magasanik B	Magasanik B	37
1A272	SH-3	*hutH1 str sul*	Magasanik B	Magasanik B	37
1A273	SH-2	*hutCR1 str sul*	Magasanik B	Magasanik B	37
1A274	512	*npr*	Millet J	Streips UN	179
1A275	SB133	*pheA1*	Lederberg J	Lederberg J	191
1A276	2355	*ilvA1 metB5 polA1443 polC1*	Gross J	Brown NC	102
1A277	BC37,PUR^{+}	*arg(GH)3 lys-21 metB5 pheA12*	Copeland JC	Copeland JC	43
1A278	CU296	*citDΔ1 trpC2*	Zahler SA	Zahler SA	302
1A279	CU79	*-(hisA1)+ -(metC3)+ sup-22 trpC2*	Zahler SA	Zahler SA	300
1A280	QUA2	*asaAΔ2 leu-2 trpC2*	Adams, A.	Adams, A.	2
1A281	QUA4	*asaA4 leu-2 trpC2*	Adams, A.	Adams, A.	2
1A282	QUA184	*asaAΔ2 asaB1 leu-2 trpC2*	Adams, A.	Adams, A.	1
1A283	QUA188	*asaA4 asaB4 leu-2 trpC2*	Adams, A.	Adams, A.	1
1A284	GB78	*metC3 pyrA xhd-1*	Garro, AJ	Garro, AJ	92
1A285	SB419	*inh-1*	Lederberg, J	Lederberg, J	192
1A286	SB443	*inh-491*	Lederberg, J	Lederberg, J	191
1A287	168S^{R}	*rpsL tmsA1 trpC2*	McDonald WC	McDonald WC	173
1A288	QB1130	*amyE dal-1 metB5 sacA321*	Dedonder RA	Dedonder RA	259
1A289	QB1133	*amyE aroI906 metB5 sacA321*	Dedonder RA	Dedonder RA	259
1A290	TS-134	*dnaB134 thyA1 thyB1 trpC2*	Mendelson NH	Mendelson NH	176
1A291	BC102	*leuB8 metB5 purA16 gcaD26*	Copeland JC	Copeland JC	45
1A292	CU403,DIVIVB	*minD1 metB5 thyA1 thyB1*	Mendelson NH	Mendelson NH	215
1A293	61676	*guaB3 metC7 purH1 trpC2*	Heinz J	Freese E	113
1A294	61677	*guaA2 metC7 purH1 trpC2*	Heinz J	Freese E	113
1A295	C66	*aspB66 trpC2*	Hoch JA	Freese E	123
1A296	61501	*aspH1 trpC2*	Diesterhaft M	Freese E	131
1A297	60348	*amyE aspT1 trpC2*	Freese E	Freese E	284
1A298	PB1728	*aroB2 azpB80 hisH2 trpC2 tyrA1*	Mazza PG	Mazza PG	34
1A299	PB1782	*aroB2 hisH2 gyrA trpC2 tyrA1*	Mazza PG	Mazza PG	34
1A300	PB3292	*glyA thyA1 thyB1 trpC2*	Mazza PG	Mazza PG	34
1A301	PB1663	*hisH2 recH342 trpC2*	Prozorov AA	Mazza PG	213
1A302	GSY908	*argF4 hisA1 recA4*	Anagnostopoulos C	Anagnostopoulos C	9
1A303	1604	*trpC2*	Smith DA	Moir A	181
1A304	YB886	*metB5* SPβ^{-} *trpC2 xin-1*	Yasbin R	Yasbin R	288
1A305	CU1459	*trpC2 urs-77*	Zahler SA	Zahler SA	300
1A306	SL330	*metC3 phoR2 tal-1*	Piggot PJ	Piggot PJ	204
1A307	305.7	*leuB8 phoS5 tal-1*	Piggot PJ	Piggot PJ	207
1A308	W168,RIF-18 DB31	*rpoB18*	Sueoka N	Doi RH	261
1A309	NP40	prototrophic	Jensen RA	Jensen RA	141
1A311	YY88	*amyE*$^{(+M)}$ *amyR2 metB5 pro(L) purF6 deg-9 str*	Yondea YS	Zalkin H	290
1A312	tmsB1	*argF4 flaC51 hag-1 hisA1 ura*	Simon MI	Ordal GW	247
1A313	BR77	*thr-5 trpC2*	Reilly BE	Ordal GW	294
1A314	VA321	*divV32 thr-5 trpC2*	Simon MI	Ordal GW	278
1A315	VA71,THR(+)	*divV71 trpC2*	Simon MI	Ordal GW	278
1A316	VA55	*divII55 thr-5 trpC2*	Simon MI	Ordal GW	278
1A317	VA61	*divII61 thr-5 trpC2*	Simon MI	Ordal GW	278
1A318	VA322,THR(+)	*divI32 trpC2*	Simon MI	Ordal GW	278
1A319	SB22	*argF4 hisA1 purH4 trpC2*	Lederberg J	Lederberg J	155
1A320	SB58A	*purE6 trpC2*	Lederberg J	Lederberg J	155

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1A321	SB270A	*pyrE270*	Lederberg J	Lederberg J	155
1A322	SB305	*met pyrE305*	Lederberg J	Lederberg J	155
1A323	SB319	*met pyrD319*	Lederberg J	Lederberg J	155
1A325	CU641	*furB1 pyrR1 trpC2*	Zahler SA	Zahler SA	300
1A326	CU806	*citB1 gltA2 ilvA8 thyB1*	Zahler SA	Zahler SA	302
1A327	CU809	*gltA2 ilvA8 thyA1 thyB1*	Zahler SA	Zahler SA	302
1A329	168M	*trpC2*	Zahler SA	Zahler SA	302
1A330	JKB3141	*aroA932 bioB141*	Pai CH	Zahler SA	201
1A331	CU281	*citB1 trpC2*	Zahler SA	Zahler SA	300
1A332	CU927	*citDΔ1 ilvA8 thyA1 thyB1*	Zahler SA	Zahler SA	300
1A333	WB577	*pyrD*	Nester EW	Nester EW	189
1A334	GSY2258	*addA5 hisH2 metB5*	Anagnostopoulos C	Anagnostopoulos C	9
1A335	GSY1028	*metB4 recB2 trpC2*	Anagnostopoulos C	Saito H	124
1A336	BD77	*amm-35 leuB8 metB5 purA16*	Dubnau D	Dubnau D	63
1A337	PB1429	*amt*	Polsinelli M	Polsinelli M	209
1A338	6160	*amyE*$^{(+M)}$ *amyR1*$^{(+M)}$ *metB5 pro*^{L} *purF6 trpB3*	Ikeda Y	Yoneda YS	132
1A339	YN21	*amyE*$^{(+M)}$ *amyR21*$^{(+M)(H)}$ *metB5 pro*^{L} *purF6 str trpB3*	Yoneda YS	Yoneda YS	289
1A340	YN118	*amyE*$^{(+M)}$ *amyR1 aroI116 metB5 pro*^{L} *deg-118 str trpB3*	Yoneda YS	Yamane K	290
1A341	NP58	*amyE*$^{(+M)}$ *amyR1*$^{(+M)}$ *metB5 pro*^{H} *purF6 str trpB3*	Uehara H	Yoneda YS	276
1A342	168EBR	*ebr-2 hisH2 thyA1 thyB1*	Munakata N	Munakata N	185
1A343	UVS80	*hisH2 rec-80 thyA1 thyB1*	Munakata N	Munakata N	185
1A344	UVS1	*met-14 sul thyA1 thyB1 trpC2 uvrB10*	Munakata N	Munakata N	185
1A345	UVS42	*met-14 sul thyA1 thyB1 trpC2 uvrB42*	Munakata N	Munakata N	185
1A346	UVS109	*hisH2 thyA1 thyB1 uvrC109*	Munakata N	Munakata N	185
1A347	UVS114	*hisH2 thyA1 thyB1 uvrC114*	Munakata N	Munakata N	185
1A348	VB104	*lys-1 lysS2*	Steinberg W	Zuber PA	214
1A349	VB106	*lysS2 metB3*	Steinberg W	Zuber PA	214
1A350	VB107A	*lysS1 trpC2*	Steinberg W	Zuber PA	257
1A351	VB122A	*lys-1 lysS1*	Steinberg W	Zuber PA	257
1A352	VB126	*trpC2 trpS1*	Steinberg W	Zuber PA	257
1A353	VB127	*trpS1*	Steinberg W	Zuber PA	257
1A354	VB157	*sul trpC2*	Steinberg W	Zuber PA	257
1A355	VB158	*hisH2 pabB trpC2*	Steinberg W	Zuber PA	257
1A356	VB293	*aec hom-1 trpC2*	Steinberg W	Zuber PA	257
1A357	VB355B	*aecB lys-1 sul trpC2*	Steinberg W	Zuber PA	257
1A358	VB336F	*aecA lys-1 sul trpC2*	Steinberg W	Zuber PA	257
1A360	GSY293	*hom-1 trpC2*	Anagnostopoulos C	Anagnostopoulos C	9
1A361	GSY505	*ilvA6*	Anagnostopoulos C	Anagnostopoulos C	9
1A363	RM125,MIT	*arg(GH)15 leuB8 hsd*$_{RI}$*R*$^{-}$*M*$^{-}$ *rplV*	Mahler I	Mahler I	165
1A364	HS1A21	*citH*	Hanson RS	Hanson RS	108
1A365	N1G17	*arg(GH)15 trpB3*	Kada T	Kada T	143
1A366	N1G45	*arg(GH)15 recA45 trpB3*	Kada T	Kada T	143
1A367	CU812	*leuA169 suf-1 trpC2*	Zahler SA	Zahler SA	300
1A368	CU850	*leuD117 sup-67 trpC2*	Zahler SA	Zahler SA	300
1A369	HCR-9	*trpC2 uvrB9*	Okubo S	Matsumoto K	198
1A372	YB886TNR	*gyrB1 recF15 SPb*^{S} *trpC2 xin*	Dean DH	Perkins JB	54
1A373	N1G43	*arg(GH)15 recD43 trpB3*	Kada T	Kada T	143
1A374	S19TI	*thyA1 thyB1 trpC2 uvrB19*	Matsumoto K	Matsumoto K	170
1A375	S80TI	*rec-80 thyA1 thyB1 trpC2*	Matsumoto K	Matsumoto K	170
1A376	PG602	*fruC1 metC3 trpC2*	Gay P	Gay P	95
1A377	PG599	*fruB22 fruC1 metC3 trpC2*	Gay P	Gay P	95
1A378	PB1641	*aroB2 hisH2 recD41 trpC2 tyrA1*	Mazza GP	Mazza GP	172
1A379	PB1693	*aroB2 hisH2 recG39 trpC2 tyrA1*	Mazza GP	Mazza GP	14
1A380	PB1633	*aroB2 hisH2 recF33 trpC2 tyrA1*	Mazza GP	Mazza GP	172
1A381	PB1775	*cafA1 metB10 trpC2*	Mazza PG	Mazza PG	33
1A382	PB1440	*hisH2 pur-60 trpC2*	Mazza PG	Mazza PG	163
1A383	PB1439	*hisH2 purE7 trpC2*	Mazza PG	Mazza PG	163
1A384	PB2417	*pur-67 thyA1 thyB1*	Mazza PG	Mazza PG	163
1A385	PB3197	*hisH2 purE8 trpC2*	Mazza PG	Mazza PG	163
1A386	PB3233	*hisH2 purH5 thr trpC2*	Mazza PG	Mazza PG	163

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1A387	Mu5u26	*metB5 purB26*	Chilton MD	Mazza PG	38
1A388	Mu5u12	*metB5 purE4*	Chilton MD	Mazza PG	38
1A389	Mu5u11	*metB5 purE5*	Chilton MD	Mazza PG	38
1A390	PB1673	*hisA53 rna-53*	Riva S	Mazza PG	218
1A391	H-37	*arg(S) pyrA*	Jensen R	Potvin BW	140,210
1A392	168MIU8	*pyrB trpC2*	Potvin BW	Potvin BW	211
1A393	168MIU16	*pyrB trpC3*	Potvin BW	Potvin BW	211
1A394	168MIU7	*pyrC trpC2*	Potvin BW	Potvin BW	211
1A395	168MIU17	*pyrC trpC2*	Potvin BW	Potvin BW	211
1A396	168MIU18	*pyrD trpC2*	Potvin BW	Potvin BW	211
1A397	SB491U6	*pyrD*	Potvin BW	Potvin BW	211
1A398	17A-42	*pyrCD*	Greer SB	Potvin BW	101
1A399	168MIU1	*pyrDF trpC2*	Potvin BW	Potvin BW	211
1A400	168MIU9	*pyrF trpC2*	Potvin BW	Potvin BW	211
1A401	168SU7	*pyrF trpC2*	Potvin BW	Potvin BW	211
1A402	168TUT	*pyrABC thyA1 thyB1 trpC2*	Romig W	Potvin BW	221
1A403	SB491U5	*pyrACD*	Potvin BW	Potvin BW	211
1A404	PB1653	*aroB2 hisA53 hisH2 rna-53 trpC2 tyrA1*	Riva S	Sonenshein AL	218
1A405	DR10	*rpoC10*	Rothstein D	Sonenshein AL	224
1A408	KE2	*aroD120 recA4 trpC2*	Epstein K	Sonenshein AL	69
1A409	RM22	*arg(GH)15 leuB8* $hsd_{RI}R^{-}M^{-}$ *recA4*	Sonenshein AL	Sonenshein AL	253
1A410	BS122	*nic*	Yanofsky C	Spizizen J	30
1A411	BS168NT	*his trpC2*	Young F	Spizizen J	293
1A412	NA64	$amyE^{(+M)}$ *amyR2 metB5 purF6*	Yoneda Y	Yamane K	290
1A413	NA20-22	$amyE^{(+N)}$ *amyR1 metB5*	Yoneda Y	Yamane K	291
1A414	NA20	$amyE^{(+N)}$ *amyR2 metB5 purF6*	Yoneda Y	Yamane K	291
1A415	2M(I)S(I)	prototrophic	Cocito C	Cocito C	40
1A416	XVM(R)S(I)	*virM*	Cocito C	Cocito C	40
1A417	9M(I)S(R)	*virS*	Cocito C	Cocito C	39
1A418	91'M(R)S(R)	*virM virS*	Cocito C	Cocito C	39
1A419	RB1479	*thyA thyB trpC2 xhi-1479 xki-1479*	Buxton RS	Buxton RS	31
1A420	RB1952	*ilvA1 metB5 purA16 xhi-1479 xki-1479*	Buxton RS	Buxton RS	31
1A421	RB1034	(ϕ105) *ilvA1 metB5 purA16 xhi-1479 xki-1479*	Buxton RS	Buxton RS	31
1A422	MI120	*leuB6* $hsd_{RI}R^{-}M^{-}$ *recA4*	Tanaka T	Tanaka T	269
1A423	MI112	*arg(GH)15 leuB8 recA4 thr-5* $hsd_{RI}R^{-}M^{-}$	Tanaka T	Tanaka T	269
1A424	FB7	*fnd-7*	Bazzicalupo M	Bazzicalupo M	22
1A425	FB8	*fnd-8*	Bazzicalupo M	Bazzicalupo M	22
1A426	PB3315	*fnd-15*	Bazzicalupo M	Bazzicalupo M	22
1A427	FB21	*ftr-21*	Bazzicalupo M	Bazzicalupo M	22
1A428	KA3	*met trpC2 ts-39-2*	Lindgren V	Lindgren V	160
1A429	KA10	*aroI906 glpT6 trpC2*	Lindgren V	Lindgren V	160
1A430	FB6	*azc-1*	Polsinelli M	Polsinelli M	91
1A431	FB56	*aec-56*	Polsinelli M	Polsinelli M	171
1A432	FB59	*aec-59*	Polsinelli M	Polsinelli M	171
1A433	PB3242	*ptm-42*	Polsinelli M	Polsinelli M	208
1A434	FB74	*ala-1 leuB8 metB pur thr-5 trpC*	Polsinelli M	Polsinelli M	208
1A435	FB12	*pro-1*	Polsinelli M	Polsinelli M	208
1A436	IG-20	$hsd_{RI}R^{-}M^{-}$ *trpC2*	Bron S	Bron S	27
1A437	8G-5	*ade his* $hsd_{RI}R^{-}M^{-}$ *met nic rib trp tyr ura*	Bron S	Bron S	27
1A438	6G-R	$hsd_{RI}R^{-}M^{+}$ *met nic rib trp tyr ura*	Bron S	Bron S	27
1A439	RB403	*leuB8 menC315 trpC2*	Taber HW	Taber HW	265
1A440	RB308	*arg(GH)2 hemA1*	Ivanovics G	Taber HW	137
1A441	PG650	*gutR1 ura-3*	Gay P	Gay P	94
1A442	PG662	*gutA2 leuB8 trpC2*	Gay P	Gay P	36
1A443	PG668	*gutB2 leuB8 trpC2*	Gay P	Gay P	36
1A445	HLL3g	*hisA1 leuB8 lys-21 metB5 nonA1 purF6* SP10(R) *thr-5 trpC2*	Saito H	Witmer HJ	229
1A446	PRA2	*hisA1 leuB8 lys-21 metB5 nonA1* SP10(R) *trpC2*	Saito H	Witmer HJ	228
1A447	1019	*hsrM1 leuB8 metB5* SP10(R)	Saito H	Witmer HJ	229
1A448	PS9W7	*hisA1 hsrM1 leuB8 nonA1 rpoB* SP10(S) *thr-5*	Saito H	Witmer HJ	229
1A449	LS105	*car-41 leuB8 metB5 purF6 rpoC105*	Sonenshein AL	Sonenshein AL	254

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BGSC	ORIGINAL CODE	DESCRIPTION	SOURCE	DONOR	REF
1A450	LS121	*rpoC121*	Sonenshein AL	Sonenshein AL	253
1A451	IAM1247	$hsd_{BI}R^{+}M^{+}$ $hsd_{CI}R^{+}M^{+}$	Saito H	Witmer HJ	229
1A452	GB7044	*ilvB2 leuA169*	Garro AJ	Garro AJ	92
1A453	GB7018,CU229	*ilvB2 trpC2*	Zahler SA	Garro AJ	281
1A454	GB7037,CU614	*leuA169 trpC2*	Zahler SA	Garro AJ	281
1A455	GB7075	*trpC2 uvrB9*	Garro AJ	Garro AJ	92
1A456	GB7068	*ilvD6 thyA*Δ *thyB1*	Garro AJ	Garro AJ	92
1A457	CU1428	*ilvA2 ilvD15* SPβ^{S} *thyA5 thyB5 trpC2*	Zahler SA	Zahler SA	79
1A458	CU1430	*ilvA2* SPβ^{S} *thyA5 thyB5 trpC2*	Zahler SA	Zahler SA	79
1A459	SU+III	*leuB8 metB5* SPβ^{S} *trnS-Lys3 thr-5*	Hemphill HE	Zahler SA	283
1A460	CU403	*ilvA8 metB5 thyA1 thyB1*	Zahler SA	Zahler SA	300
1A461	SB19E,ts2pyrG1	*ctrA1 ts-2*	Takahashi I	Takahashi I	266
1A462	6TR1	*leuB8 metB5 tem-1*	Siegel E	Siegel E	245
1A463	RB1949	*ddlA1475 ilvA1 metB5 purA16*	Buxton RS	Buxton RS	32
1A464	MS320	*dapE320 thyA1 thyB1 trpC2*	Buxton RS	Buxton RS	32
1A465	61656	*fbp-1 hisA1 leuB8 metB5 trpC2*	Iijima T	Freese E	85
1A466	MY2011	*lys-1 pyrD1 rpoB sas-1*	Yudkin MD	Yudkin MD	299
1A467	MY2013	*lys-1 pyrD1 rpoB sas-2*	Yudkin MD	Yudkin MD	299
1A468	60984	*glmS2 metC7 trpC2*	Freese EB	Freese E	84
1A471	61494	*aceA1 bfmB metC7 trpC2*	Willecke K	Freese E	25
1A472	61539	*bfmB1 iur trpC2*	Iijima T	Freese E	25
1A473	61571	*bfmB1 strC2 trpC2*	Iijima T	Freese E	25
1A474	TIBS 57	*amyE3 aroI10*	Trenk HL	Turner HR	274
1A475	IS169	*rplK6 thr-5 trpC2*	Smith I	Smith I	251
1A476	HA101	*hisA1 metB5*	Okuba S	Steward C	199
1A477	HA101B	*-(hisA1)+ -(metB5)+ sup-1*	Okuba S	Steward C	199
1A478	M5	*lys-3 metB10 spc spcD trpC2*	Chambliss G	Chambliss G	118
1A479	22-4	*cdd-1 crk-1 dck-3*	Takahashi I	Takahashi I	266
1A480	ddd-3	*cdd-1 ddd-3*	Takahashi I	Takahashi I	266
1A481	PB3242	*ptm-42*	Galizzi A	Galizzi A	89
1A482	PB2328	*hisH2 metD4 outA7 trpC2*	Galizzi A	Galizzi A	89
1A483	FJ3	*lyt-1 metC3*	Rogers HJ	Buxton RS	78
1A484	FJ6	*lyt-2 metC3*	Rogers HJ	Buxton RS	78
1A485	ROD104	*leuB8 mreD1*	Rogers HJ	Buxton RS	147
1A486	ROD113	*leuB8 tagF1*	Rogers HJ	Buxton RS	147
1A487	TKJ6901	*thyA1 thyB1 urg-1*	Munakata N	Munakata N	167
1A488	SSP	*met-14 splB1 sul thyA1 thyB1 trpC2*	Munakata N	Munakata N	187
1A489	UVSSP-42-1	*met-14 splB1 sul thyA1 thyB1 trpC2 uvrB42*	Munakata N	Munakata N	186
1A490	UTB600	*gltB1 leuB8 metB10*	Kane J	Kane J	144
1A491	TTK24	*dfrA24 pabA7*	Kane J	Kane J	144
1A492	HA101-2-9	*citC met pheA trpC2*	Peebles C	Hadden C	203
1A493	HA101-2-10	*citC met polA10 trpC2*	Peebles C	Hadden C	203
1A494	HA106	*hisH2 leu met recF7*	Strauss B	Hadden C	110, 260
1A495	GSY1619	*metB4 recB19 trpC2*	Harford N	Hadden C	110
1A496	GSY1615	*metB4 recF15 trpC2*	Harford N	Hadden C	110
1A497	PB1625	*hisH2 rec-25 trpC2*	Mazza G	Hadden C	172
1A498	PB1629	*hisH2 rec-29 trpC2*	Mazza G	Hadden C	172
1A499	PB1630	*hisH2 rec-30 trpC2*	Mazza G	Hadden C	172
1A500	MB23	*cym-1 rpoB1*	Piggot PJ	Piggot PJ	205
1A501	EE1	*amy-3 aro-10 lmrA2*	Eng E	Dean DH	54
1A502	Nil (oxr-1)	*oxr-1 thyA thyB*	Mandelstam J	Mandelstam J	280
1A503	Nil (oxr-2)	*oxr-2 thyA thyB trpC2*	Mandelstam J	Mandelstam J	280
1A504	Ni15	*lyt-15 thyA thyB trpC2 xin-15*	Karamata D	Karamata D	145
1A505	MCB	MC^{S} *trpC2* UC^{S}	Trautner TA	Trautner TA	273
1A506	222	*arg trp*	Hiroka H	Hiroka H	122, 236
1A507	FUS426	*fus* Spo(Ts)	Kobayashi T	Kobayashi T	121
1A508	FUS429	*fus* Spo(Con)	Kobayashi T	Kobayashi T	121
1A509	UOTO277	*hisA1* $hsd_{RI}R^{-}M^{-}$ *metB5 recA4*	Shimotsu H	Shimotsu H	244
1A510	PSL1	*arg(GH)15 leuB8* $hsd_{RI}R^{-}M^{-}$ *recA4 stp thr*	Pene J	Pene J	200
1A511	BD393	*lys-3 thyA thyB trpC2*	Dubnau D	Dubnau D	63

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1A512	RB541	*ahrC2*	Baumberg S	Baumberg S	20
1A513	CU403,DIVIVB1	*minD1 metB5 tag-1 thyA thyB1*	Mendelson NH	Mendelson NH	176
1A514	TKJ3422	*hisH101 lys-21 recA4 splB1 thyA thyB uvrB10*	Munakata N	Munakata N	184
1A516	trpE1 (ICR 1)	*trpE1*	Carlton BC	Carlton BC	285
1A517	trpE2 (ICR 6)	*trpE2*	Carlton BC	Carlton BC	285
1A518	trpE3 (ICR 14)	*trpE3*	Carlton BC	Carlton BC	285
1A519	trpE4 (ICR 16)	*trpE4*	Carlton BC	Carlton BC	285
1A520	trpE5 (UV 17)	*trpE5*	Carlton BC	Carlton BC	285
1A521	trpE194 (SB194)	*trpE194*	Carlton BC	Carlton BC	285
1A522	trpD1 (NA 1)	*trpD1*	Carlton BC	Carlton BC	285
1A523	trpD2 (NA 3)	*trpD3*	Carlton BC	Carlton BC	285
1A524	trpD4 (NG 61)	*trpD4*	Carlton BC	Carlton BC	285
1A525	trpD5 (NG 62)	*trpD5*	Carlton BC	Carlton BC	285
1A526	trpD6 (NG 120)	*trpD6*	Carlton BC	Carlton BC	285
1A527	trpD7 (ICR 10)	*trpD7*	Carlton BC	Carlton BC	285
1A528	trpD8 (ICR 11)	*trpD8*	Carlton BC	Carlton BC	285
1A529	trpD9 (ICR 19)	*trpD9*	Carlton BC	Carlton BC	285
1A530	trpD10 (ICR 22)	*trpD10*	Carlton BC	Carlton BC	285
1A531	trpF1 (NA 2)	*trpF1*	Carlton BC	Carlton BC	285
1A532	trpF2 (NA 4)	*trpF2*	Carlton BC	Carlton BC	285
1A533	trpF3 (NA 6)	*trpF3*	Carlton BC	Carlton BC	285
1A534	trpF4 (NA 7)	*trpF4*	Carlton BC	Carlton BC	285
1A535	trpF5 (NA 10)	*trpF5*	Carlton BC	Carlton BC	285
1A536	trpF6 (NA 11)	*trpF6*	Carlton BC	Carlton BC	285
1A537	trpF8 (HA2)	*trpF8*	Carlton BC	Carlton BC	285
1A538	trpF9 (PH 1)	*trpF9*	Carlton BC	Carlton BC	285
1A539	trpF10 (ICR 12)	*trpF10*	Carlton BC	Carlton BC	285
1A540	trpF11 (SB 11)	*trpF11*	Carlton BC	Carlton BC	285
1A541	trpF12 (NA 5)	*trpF12*	Carlton BC	Carlton BC	285
1A542	trpF13 (HA 1)	*trpF13*	Carlton BC	Carlton BC	285
1A543	trpC1 (NG 1)	*trpC1*	Carlton BC	Carlton BC	285
1A544	trpC3 (NG 3)	*trpC3*	Carlton BC	Carlton BC	285
1A545	trpC4 (NG 5)	*trpC4*	Carlton BC	Carlton BC	285
1A546	trpC5 (NG 24)	*trpC5*	Carlton BC	Carlton BC	285
1A547	trpC6 (UV 15)	*trpC6*	Carlton BC	Carlton BC	285
1A548	trpC7 (UV 16)	*trpC7*	Carlton BC	Carlton BC	285
1A549	trpC8 (UV 18)	*trpC8*	Carlton BC	Carlton BC	285
1A550	trpC9 (EMS 1)	*trpC9*	Carlton BC	Carlton BC	285
1A551	trpC10 (EMS 2)	*trpC10*	Carlton BC	Carlton BC	285
1A552	trpC11 (NG 2)	*trpC11*	Carlton BC	Carlton BC	285
1A553	trpA1 (NG 63)	*trpA1*	Carlton BC	Carlton BC	285
1A554	trpA2 (NA 9)	*trpA2*	Carlton BC	Carlton BC	285
1A555	trpA3 (T 50)	*trpA3*	Carlton BC	Carlton BC	285
1A556	trpA4 (T 51)	*trpA4*	Carlton BC	Carlton BC	285
1A557	trpA6 (ICR 17)	*trpA6*	Carlton BC	Carlton BC	285
1A558	trpA7 (ICR 21)	*trpA7*	Carlton BC	Carlton BC	285
1A559	trpB1 (NG 4)	*trpB1*	Carlton BC	Carlton BC	285
1A560	trpB2 (NG 6)	*trpB2*	Carlton BC	Carlton BC	285
1A561	trpB5 (NG 14)	*trpB5*	Carlton BC	Carlton BC	285
1A562	trpB6 (NG 57)	*trpB6*	Carlton BC	Carlton BC	285
1A563	trpB7 (NG 58)	*trpB7*	Carlton BC	Carlton BC	285
1A564	trpB8 (NG 59)	*trpB8*	Carlton BC	Carlton BC	285
1A565	trpB9 (NG 60)	*trpB9*	Carlton BC	Carlton BC	285
1A566	trpB10 (ICR 8)	*trpB10*	Carlton BC	Carlton BC	285
1A567	trpB11 (ICR 9)	*trpB11*	Carlton BC	Carlton BC	285
1A568	trpB12 (ICR 13)	*trpB12*	Carlton BC	Carlton BC	285
1A569	trpB13 (ICR 15)	*trpB13*	Carlton BC	Carlton BC	285
1A570	trpB14 (ICR 18)	*trpB14*	Carlton BC	Carlton BC	285

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1A571	trpB15 (ICR 20)	*trpB15*	Carlton BC	Carlton BC	285
1A572	trpB16 (NG 7)	*trpB16*	Carlton BC	Carlton BC	285
1A573	OBS2	*cer-2 trpC2*	Zeigler DR	Zeigler DR	304
1A574	GSY1127	*hisH2 ilvC1/ilvC(+)*	Anagnostopoulos C	Anagnostopoulos C	237
1A575	CU3497	*ilvA2 recA4 spcB1 trpC2*	Zahler SA	Zahler SA	300
1A576	OBS14	*cer-14 trpC2*	Zeigler D	Zeigler D	304
1A577	OBS20	*cer-20 trpC2*	Zeigler D	Zeigler D	304
1A578	168 cam2	*cam-2 trpC2*	Bott KF	Bott KF	10
1A579	GLU-1	*sigA1*	Takahashi I	Takahashi I	267
1A580	FRU-4	*sigA4*	Takahashi I	Takahashi I	267
1A581	GLU-47	*sigA47*	Takahashi I	Takahashi I	267
1A582	GLU-40	*crsB40*	Takahashi I	Takahashi I	267
1A583	RIB-2	*crsC1*	Takahashi I	Takahashi I	267
1A584	GLN-2	*crsC2*	Takahashi I	Takahashi I	267
1A585	MAN-A1 (CS25)	*crsD1*	Takahashi I	Takahashi I	263
1A586	MAN-B1 (CS26)	*crsE1*	Takahashi I	Takahashi I	263
1A587	MAL-4	*crsF4*	Takahashi I	Takahashi I	267
1A588	Sz 3 (R15)	*hemA1 trpC2*	Miczák A	Miczák A	11
1A589	Sz 15 (I/1)	*hemB1 trpC2*	Miczák A	Miczák A	23
1A590	Sz 16 (II/33)	*hemC33 trpC2*	Miczák A	Miczák A	23
1A591	Sz 34	*hemD11 trpC2*	Miczák A	Miczák A	178
1A592	Sz 26 (V/64)	*hemE64 trpC2*	Miczák A	Miczák A	23
1A593	Sz 27 (VI/180)	*hemH180 trpC2*	Miczák A	Miczák A	23
1A594	Sz 28 (III/321)	*hemY321 trpC2*	Miczák A	Miczák A	23
1A595	PB2321	*arg thyA thyB tscA1*	Galizzi A	Galizzi A	90
1A596	PB2338	*arg thyA thyB tscA23*	Galizzi A	Galizzi A	90
1A597	PB2355	*arg thyA thyB nadE49*	Galizzi A	Galizzi A	90
1A598	PB2330	*arg thyA thyB tscC11*	Galizzi A	Galizzi A	90
1A599	PB2336	*arg thyA thyB tscD14*	Galizzi A	Galizzi A	90
1A600	CU4120	(SPβc2) *cym-84*::Tn*917 trpC2*	Zahler SA	Zahler SA	279
1A601	CU4121	(SPβc2) *purM*::Tn*917 trpC2*	Zahler SA	Zahler SA	279
1A602	CU4122	(SPβc2) *ath-83*::Tn*917 trpC2*	Zahler SA	Zahler SA	279
1A603	CU4123	(SPβc2) *thiA84*::Tn*917 trpC2*	Zahler SA	Zahler SA	279
1A604	CU4124	(SPβc2) *metD83*::Tn*917 trpC2*	Zahler SA	Zahler SA	279
1A605	CU4125	(SPβc2) *argF83*::Tn*917 trpC2*	Zahler SA	Zahler SA	279
1A606	CU4126	(SPβc2) *argF82*::Tn*917 trpC2*	Zahler SA	Zahler SA	279
1A607	CU4127	(SPβc2) *metC85*::Tn*917 trpC2*	Zahler SA	Zahler SA	279
1A608	CU4128	(SPβc2) *arg342*::Tn*917 trpC2*	Zahler SA	Zahler SA	279
1A609	CU4129	(SPβc2) *pyr-82*::Tn*917 trpC2*	Zahler SA	Zahler SA	279
1A610	CU4130	(SPβc2) *pyr-83*::Tn*917 trpC2*	Zahler SA	Zahler SA	279
1A611	CU4131	(SPβc2) *trpC2 urc-83*::Tn*917*	Zahler SA	Zahler SA	279
1A612	CU4132	(SPβc2) *gltAB81*::Tn*917 trpC2*	Zahler SA	Zahler SA	279
1A613	CU4133	(SPβc2) *aroBC84*::Tn*917 trpC2*	Zahler SA	Zahler SA	279
1A614	CU4134	(SPβc2) *serA84*::Tn*917 trpC2*	Zahler SA	Zahler SA	279
1A615	CU4135	(SPβc2) *lys-82*::Tn*917 trpC2*	Zahler SA	Zahler SA	279
1A616	CU4136	(SPβc2) *nic-82*::Tn*917 trpC2*	Zahler SA	Zahler SA	279
1A617	CU4137	(SPβc2) *pheA82*::Tn*917 trpC2*	Zahler SA	Zahler SA	279
1A618	CU4138	(SPβc2) *leuB84*::Tn*917 trpC2*	Zahler SA	Zahler SA	279
1A619	CU4139	(SPβc2) *liv1-82*::Tn*917 trpC2*	Zahler SA	Zahler SA	279
1A620	CU4140	(SPβc2) *liv3-83*::Tn*917 trpC2*	Zahler SA	Zahler SA	279
1A621	CU4141	(SPβc2) *serC82*::Tn*917 trpC2*	Zahler SA	Zahler SA	279
1A622	CU4142	(SPβc2) *arg(GH)85*::Tn*917 trpC2*	Zahler SA	Zahler SA	279
1A623	CU4143	(SPβc2) *alaA84*::Tn*917 trpC2*	Zahler SA	Zahler SA	279
1A624	CU4144	(SPβc2) *mth-83*::Tn*917 trpC2*	Zahler SA	Zahler SA	279
1A625	CU4145	(SPβc2) *mth-84*::Tn*917 trpC2*	Zahler SA	Zahler SA	279
1A626	CU4146	(SPβc2) *hisA82*::Tn*917 trpC2*	Zahler SA	Zahler SA	279
1A627	CU4147	(SPβc2) *trpC2 zaa-84*::Tn*917*	Zahler SA	Zahler SA	279
1A628	CU4148	(SPβc2) *trpC2 zbj-82*::Tn*917;*	Zahler SA	Zahler SA	82, 279
1A629	CU4149	(SPβc2) *trpC2 zca-82*::Tn*917*	Zahler SA	Zahler SA	279
1A630	CU4150	(SPβc2) *trpC2 zce-82*::Tn*917*	Zahler SA	Zahler SA	82, 279
1A631	CU4151	(SPβc2) *trpC2 motA*::Tn*917*	Zahler SA	Zahler SA	82, 279
1A632	CU4152	(SPβc2) *trpC2 kinC*::Tn*917*	Zahler SA	Zahler SA	82, 279

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1A633	CU4153	(SPβc2) *trpC2* *zdi-82*::Tn917	Zahler SA	Zahler SA	82, 279
1A634	CU4154	(SPβc2) *trpC2* *zci-82*::Tn917	Zahler SA	Zahler SA	82, 279
1A635	CU4155	(SPβc2) *trpC2* *proJ*::Tn917	Zahler SA	Zahler SA	82, 279
1A636	CU4156	(SPβc2) *trpC2* *cgeE*::Tn917	Zahler SA	Zahler SA	82, 279
1A637	CU4157	(SPβc2) *trpC2* *yokH*::Tn917	Zahler SA	Zahler SA	82, 279
1A638	CU4158	(SPβc2) *trpC2* *zfg-83*::Tn917	Zahler SA	Zahler SA	82, 279
1A639	CU4159	(SPβc2) *trpC2* *spoVID*::Tn917	Zahler SA	Zahler SA	82, 279
1A640	CU4160	(SPβc2) *trpC2* *zhb-83*::Tn917	Zahler SA	Zahler SA	279
1A641	CU4161	(SPβc2) *trpC2* *zhc-85*::Tn917	Zahler SA	Zahler SA	82, 279
1A642	CU4162	(SPβc2) *trpC2* *yufR*::Tn917	Zahler SA	Zahler SA	82, 279
1A643	CU4163	(SPβc2) *trpC2* *yvaC*::Tn917	Zahler SA	Zahler SA	82, 279
1A644	CU4164	(SPβc2) *trpC2* *zii-83*::Tn917	Zahler SA	Zahler SA	279
1A645	CU4165	(SPβc2) *trpC2* *zjf-85*::Tn917	Zahler SA	Zahler SA	279
1A646	CU2111	(SPβc2 *zfd-81*::Tn917) *trpC2*	Zahler SA	Zahler SA	279
1A647	PB2353	*arg thyA thyB nadE47*	Galizzi A	Galizzi A	90
1A648	PB2354	*arg thyA thyB nadE48*	Galizzi A	Galizzi A	90
1A649	PB2333	*arg thyA thyB tscD14*	Galizzi A	Galizzi A	90
1A650	R11	*lys-3 xynB7*	Roncero MIG	Roncero MIG	222
1A651	R21	*lys-3 xynA8*	Roncero MIG	Roncero MIG	222
1A652	146	*pro(AB)*	Harwood CR	Harwood CR	111
1A653	HJS30	*glnA200*	Schreier HJ	Schreier HJ	239
1A654	BG314	*aroD120 bglS33 trpC2*	Borriss R	Borriss R	24
1A655	OBS30	*aroI906 cdr-1 trpC2*	Zeigler D	Zeigler D	304
1A656	KR10	*rpsI2*	Dabbs ER	Dabbs ER	51
1A657	DA9	*rplE1*	Dabbs ER	Dabbs ER	49
1A658	DA65	*rplK2 rpsH2*	Dabbs ER	Dabbs ER	49
1A659	DA63	*rpmD2*	Dabbs ER	Dabbs ER	48
1A660	DA14	*rplV1*	Dabbs ER	Dabbs ER	48
1A661	DA49	*rpsG3*	Dabbs ER	Dabbs ER	48
1A662	DB65	*cysE14 purA16 rpmA1 trpC2*	Dabbs ER	Dabbs ER	51
1A663	DB14	*cysE14 purA16 rpsK2 trpC2*	Dabbs ER	Dabbs ER	48
1A664	DA36	*rpsF1*	Dabbs ER	Dabbs ER	50
1A665	DA463	*rplA1 rplJ1 rplL1*	Dabbs ER	Dabbs ER	52
1A666	DA73	*rplE3*	Dabbs ER	Dabbs ER	48
1A667	DA46	*rplL1*	Dabbs ER	Dabbs ER	49
1A668	CA302	*rpsE302*	Dabbs ER	Dabbs ER	53
1A669	DA47	*rplX2*	Dabbs ER	Dabbs ER	48
1A670	DA32	*rplU1*	Dabbs ER	Dabbs ER	53
1A671	DA34	*rpsH3*	Dabbs ER	Dabbs ER	48
1A672	KA31805	*citK5 trpC2*	Rutberg L	Rutberg L	225
1A673	KA32817	*citM17 trpC2*	Hederstedt L	Hederstedt L	35
1A674	KA97103	*leu-2 sdhB103 trpC2*	Hederstedt L	Hederstedt L	112
1A675	PB73	*furB1 sigB::cat trpC2*	Price CW	Price CW	67
1A676	PB70	*rpoA::cat trpC2*	Price CW	Price CW	262
1A677	PB106	*gerD97*::Tn917 *rpoA::cat*	Price CW	Price CW	212
1A678	RB413	*leuB8 menB325 trpC2*	Taber HW	Taber HW	265
1A679	RB397	*ald-1 leuB8 menE312 trpC2*	Taber HW	Taber HW	265
1A680	SG64	*lacA1 lacR1*	Errington J	Errington J	73
1A681	ED179	*apt-6 ilvA1 pbuG3 pupA3 sacA78 upp*	Saxild HH	Saxild HH	234
1A682	ED193	*ilvA1 pbuG1 sacA78 upp xpt*	Saxild HH	Saxild HH	234
1A683	ED249	*his*	Saxild HH	Saxild HH	234
1A684	BM1	*met*	Alonso JC	Alonso JC	7
1A685	6GM	*hsd*$_{RI}$*R*$^-$*M*$^+$ *rib trpC2 tyr-1 ura*	Bron S	Bron S	105
1A686	CU4617	SPβ$^-$ *trpC2 zae86*::Tn917	Zahler SA	Zahler SA	300
1A687	CU4619	(SPβc2) *trpC2* *zba89*::Tn917	Zahler SA	Zahler SA	300
1A688	CU4620	(SPβc2) *trpC2* *ydaO*::Tn917	Zahler SA	Zahler SA	82, 300
1A689	CU4621	(SPβc2) *trpC2* *zdf88*::Tn917	Zahler SA	Zahler SA	300
1A690	CU4624	(SPβc2) *trpC2* *zec88*:Tn917	Zahler SA	Zahler SA	300
1A691	CU4626	(SPβc2) *trpC2* *zfe86*::Tn917	Zahler SA	Zahler SA	300
1A692	CU4627	(SPβc2) *trpC2* *zhf86*::Tn917	Zahler SA	Zahler SA	300

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1A693	CU4628	(SPβc2) *trpC2 zhg86::*Tn*917*	Zahler SA	Zahler SA	300
1A694	CU4553	SPβ$^-$ *recA4 trpC2 zef87::*Tn*917*	Zahler SA	Zahler SA	300
1A695	NHO3	*hisH2 sul ten trpC2*	Zahler SA	Zahler SA	300
1A698	OKB105	*pheA1 sfp*	Zuber P	Zuber P	188
1A699	OKB120	*pheA1 sfp srfA::*Tn*917*	Zuber P	Zuber P	188
1A700	168	*trpC2*	Anagnostopoulos	Anagnostopoulos	30
1A701	BG126	*addB72 amyE* attSPβ *metB5 sigB trpC2 xin-1*	Alonso JC	Alonso JC	8
1A702	BG124	*addB71 amyE* attSPβ *metB5 sigB xin-1*	Alonso JC	Alonso JC	6
1A703	BG101	*amyE attSPb metB5 recP149 sigB trpC2 xin-1*	Alonso JC	Alonso JC	8
1A704	60173	*purD1*	Saxild HH	Saxild HH	234
1A706	FB91	*com-9 hisA1 leu-8 lys-21 metB5 thr-5 trpC2*	Mastromei G	Mastromei G	75
1A707	FB92	*com-71 hisA1 leu-8 metB5 purB6 thr-5 trpC2*	Mastromei G	Mastromei G	75
1A708	FB93	*com-30 hisA1 leu-8 lys-21 metB5 thr-5 trpC2*	Mastromei G	Mastromei G	75
1A709	FB94	*com-104 hisA1 leu-8 lys-21 metB5 thr-5 trpC2*	Mastromei G	Mastromei G	75
1A710	FB108	*com-31 hisA1 leu-8 lys-21 metB5 thr-5 trpC2*	Mastromei G	Mastromei G	75
1A711	FBT14	*com-14::*Tn*917 hisA1 leu-8 lys-21 metB5 purB6 thr-5 trpC2*	Mastromei G	Mastromei G	75
1A712	FBT18	*com-18::*Tn*917 hisA1 leu-8 lys-21 metB5 purB6 thr-5 trpC2*	Mastromei G	Mastromei G	75
1A713	FBT44	*com-44::*Tn*917 hisA1 leu-8 lys-21 metB5 purB6 thr-5 trpC2*	Mastromei G	Mastromei G	75
1A715	HJS31	*glnR57*	Schreier HJ	Schreier HJ	238
1A716	CB100	Cm *sigD::pLM5 trpC2*	Marquez-Magaña LM	Marquez-Magaña LM	114
1A717	MO1099	*amyE::erm* Em	Stragier P	Stragier P	104
1A718	6GM15	*his* Km *lacZ-ΔM15 met* $hsd_{RI}R^-M^+$ *rib trpC2 tyr ura*	Bron S	Bron S	106
1A719	WH152	*metB10 trpC2 xylABΔ1*	Hillen W	Hillen W	227
1A720	YB965	*hisB leuA8 metB5 polA5* SPβ$^-$ *xin-1*	Yasbin R	Bol D	287
1A721	CU4834	(SPβc2) *aroI86::*Tn*917 trpC2*	Zahler SA	Zahler SA	300
1A722	CU4199	(SPβc2) *bfmB84::*Tn*917 trpC2*	Zahler SA	Zahler SA	300
1A724	CU4836	(SPβc2) *trpC2 zba-88::*Tn*917*	Zahler SA	Zahler SA	300
1A727	CU3574	(SPβc2) *trpC2 zeh-82::*Tn*917*	Zahler SA	Zahler SA	300
1A728	CU3737	(SPβc2) *trpC2 zfj-83::*Tn*917*	Zahler SA	Zahler SA	300
1A730	CU3757	(SPβc2) *trpC2 zhf-83::*Tn*917*	Zahler SA	Zahler SA	300
1A731	CU3522	(SPβc2) *trpC2 zib-82::*Tn*917*	Zahler SA	Zahler SA	300
1A732	CU4665	(SPβc2) *trpC2 zjd-89::*Tn*917*	Zahler SA	Zahler SA	300
1A733	CU4845	(SPβc2) *trpC2 zjj-85:*Tn*917*	Zahler SA	Zahler SA	300
1A734	MB61	*rapA::cat*	Mueller JP	Mueller JP	182
1A735	MP82	*gsiB::neo*	Mueller JP	Mueller JP	182
1A736	MB170	*kinA82*	Mueller JP	Mueller JP	183
1A737	MB307	*dppE132::neo pheA1 trpC2*	Mueller JP	Mueller JP	169
1A738	61668	*iolG6 metC7 trpC2*	Fujita Y	Fujita Y	87
1A739	YF127	*gntK4 metC7 trpC2*	Fujita Y	Fujita Y	86
1A740	YF171	*gntP9 metC7 trpC2*	Fujita Y	Fujita Y	86
1A741	YF176	*gntR1 metC7 trpC2*	Fujita Y	Fujita Y	88
1A742	JT175	*dacA::cat+ trpC2*	Buchanan CE	Buchanan CE	271
1A743	JT2000	*dacA+::cat+ trpC2*	Buchanan CE	Buchanan CE	271
1A744	CB11	$dacB^+::cat^+$ *trpC2*	Buchanan CE	Buchanan CE	28
1A745	CB36	$dacB::cat^+$ *trpC2*	Buchanan CE	Buchanan CE	28
1A746	recA260	Em *metB5 recA260* SPβ$^-$ *trpC2 xin-1*	Yasbin R	Yasbin R	287
1A747	PY79	prototroph SPβ-	Youngman P	Youngman P	298
1A748	1012M15	*glgB::lacZΔM15 Km leu met* $hsd_{RI}R^-M^+$	Bron S	Bron S	26
1A749	5:7	*::*Tn*917lac* MLS^R	Mendelson NH	Salhi B	231
1A751	MW10	*bglCΔ102 bglSΔEV npr apr his*	Borris R	Borris R	286
1A752	MW10	*bglCΔ102 bglSΔEV npr apr his glgB::lacZΔM15*	Borris R	Borris R	286
1A753	1R4	*thr-5 trpC2* bmr^R	Neyfakh AA	Neyfakh AA	195
1A754	BD170/bmr::cat	*thr-5 trpC2 bmr::cat* Cm	Neyfakh AA	Neyfakh AA	194
1A755	BD170/bmrR::cat	*thr-5 trpC2 bmrR::cat* Cm	Neyfakh AA	Neyfakh AA	194
1A756	BD170/bfmB::cat	*thr-5 trpC2 bfmB::cat* Cm	Neyfakh AA	Neyfakh AA	194
1A757	PS832	prototrophic	Setlow P	Setlow P	242
1A758	ng 79	*bac-1*	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::pTV21Δ2* Cm	Demain A	Demain A	120
1A762	MH22	*::Tn917::pTV20 bac-1* Cm MLS^R	Demain A	Demain A	120
1A763	CB138	*trpC2 fla/che::pLM19* Cm	Chamberlin MJ	Ordal G	168
1A764	CB149	*trpC2 pheA1 flgMΔ80*	Chamberlin MJ	Ordal GW	180
1A765	BR16	*trpC2 lys*	Strauch M	Strauch M	264
1A766	BR17	*trpC2 lys relA*	Strauch M	Strauch M	264
1A767	MH3402	*trpC2 pheA1 phoA::pCE413 phoB::*Tn*917* Cm MLS	Hulett FM	Hulett FM	130
1A771	MO1099	*trpC2 pheA1 amyE::ery* MLS	Stragier P	Stragier P	104
1A772	MO1813	*trpC2 pheA1 amyE::cat* Cm	Stragier P	Stragier P	104
1A773	MO649	*trpC2 pheA1 thrC::cat* Cm	Stragier P	Stragier P	104
1A774	JH642PolHis	*trpC2 pheA1 rpoC::*(His_6*-tag) Sp*	Moran CP	Moran CP	253
1A775	SMY	prototrophic	Sonenshein LS	Henkin T	103
1G1	PB2442	*hisH2 outF4 trpC2*	Galizzi A	Galizzi A	4
1G2	PB2427	*hisH2 nadE81 trpC2*	Galizzi A	Gallizi A	5
1G3	PB2439	*hisH2 outE42 trpC2*	Galizzi A	Gallizi A	4
1G4	PB2398	*hisH2 metD4 outD1 trpC2*	Galizzi A	Gallizi A	5
1G5	PB2430	*hisH2 outC25 trpC2*	Gallizi A	Gallizi A	4
1G6	PB2443	*gsp-10 hisH2 metD4 trpC2*	Gallizi A	Gallizi A	4
1G7	4744	*gerA(ABC)11 thr-5 trpC2*	Smith DA	Moir A	248
1G8	4592	*gerB(ABC)18 trpC2*	Smith DA	Moir A	181
1G9	4593	*gerD19 trpC2*	Smith DA	Moir A	181
1G10	4728	*gerF45 trpC2*	Smith DA	Moir A	181
1G11	1558	*gerCC58 trpC2 tzm wrd*	Smith DA	Moir A	181
1G12	4751	*gerE36 leu-2*	Smith DA	Moir A	248
1G13	61111	*gerG47 met pgk trpC2*	Freese E	Smith D	83
1G14	PB2328	*hisH2 metD4 outA7 trpC2*	Galizzi A	Galizzi A	89
1L1	CU1065(ϕ3T)	(ϕ3T) $\text{SP}\beta^-$ *trpC2*	Zahler SA	Hemphill HE	300
1L2	CU1065(Z)	(Zeta) $\text{SP}\beta^-$	Zahler SA	Hemphill HE	300
1L4	SU+III(SPβ)	(SPβ) *leuB8 metB5 thr-5*	Hemphill HE	Hemphill HE	283
1L5	CU1147	(SPβc2) *trpC2*	Zahler SA	Zahler SA	223
1L6	168(SPO2)	(SPO2) *trpC2*	Okubo S	Sonenshein AL	197
1L7	GB1061	(SPO2 *ind-1) hisA1 thr-5 trpC2*	Garro AJ	Garro AJ	92
1L8	168(SP16)	(SP16) *trpC2*	Thorne CB	Thorne CB	174, 270
1L9	168(ρ6)	(ρ6) *trpC2*	Dean DH	Dean DH	55
1L10	168(ρ10)	(ρ10) *trpC2*	Dean DH	Dean DH	55
1L11	168(ϕ105)	(ϕ105) *trpC2*	Rutberg L	Rutberg L	226
1L12	GB1064 BD99	(ϕ105 *ind-1) hisA1 thr-5 trpC2*	Garro AJ	Garro AJ	92
1L13	JAS50	(ϕ105 *d50) ilv leuB7 trpC2*	Shapiro JA	Shapiro JA	243
1L15	168(ρ14)	(ρ14) *trpC2*	Dean DH	Dean DH	55
1L16	168(ϕdo7)	(ϕDO7) *trpC2*	Kroyer JM	Dean DH	151
1L17	GB113	(ϕ105K *sus7) -(met)+ -(thr-5)+ leuB8 sup-3*	Garro AJ	Garro AJ	12
1L18	GB114	(ϕ105L *sus9) -(met)+ -(thr-5)+ leuB8 trnS-Lys3*	Garro AJ	Garro AJ	12
1L19	GB1115	(ϕ105J *sus11) -(met)+ -(thr-5)+ leuB8 sup-3*	Garro AJ	Garro AJ	12
1L20	GB1116	(ϕ105F *sus12) -(met)+ -(thr-5)+ leuB8 sup-3*	Garro AJ	Garro AJ	12
1L21	GB1117	(ϕ105B *sus14) -(met)+ -(thr-5)+ leuB8 sup-3*	Garro AJ	Garro AJ	12
1L22	GB1118	(ϕ105B *sus14) -(met)+ -(thr-5)+ leuB8 sup-3*	Garro AJ	Garro AJ	12
1L23	GB1119	(ϕ105C *sus19) -(met)+ -(thr-5)+ leuB8 sup-3*	Garro AJ	Garro AJ	12
1L24	GB1120	(ϕ105E *tsN9) -(met)+ -(thr-5)+ leuB8 sup-3*	Garro AJ	Garro AJ	12
1L25	GB1121	(ϕ105H *tsN34) -(met)+ -(thr-5)+ leuB8 sup-3*	Garro AJ	Garro AJ	12
1L26	3610(ϕ3T)	(ϕ3T)	Tucker R	Thorne CB	54, 56
1L27	DBS-15(ρ11)	(ρ11) *pheA2 trpC2*	Perkins JB	Dean DH	54, 56
1L28	ϕ105 DI:29t	(ϕ105DI:29t) *trpC2*	Flock JI	Flock JI	81
1L29	ϕ105 DI:1t	(ϕ105DI:1t) *trpC2*	Flock JI	Flock JI	81
1L30	CU2058	*(*SPβc2 *int-5::sup3-1)* (SPβc2) *-(metB5)+ dal-1*	Zahler SA	Zahler SA	162
1L31	CU2059	*(*SPβc2 *int-5::sup44-1)* (SPβc2) *-(metB5)+ dal-1*	Zahler SA	Zahler SA	162
1L32	1A304(ϕ105)	(ϕ105) *metB10* SPβ- *trpC2 xin-1*	Ellis DM	Ellis DM	68
1L33	CU1160(Z)	(Zeta) *thyA thyB trpC2*	Hemphill HE	Hemphill HE	115

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1L34	ϕ105 DI:1t	(ϕ105DI:1t) *metB10* SPβ- *trpC2 xin-1*	Lampel J	Lampel J	116
1L35	168(ϕ105J9)	(ϕ105J9) *trpC2*	Errington J	Errington J	71
1L36	UOT-0994	(ϕCM) Cm *hisA1 metB51*	Kawamura H	Kawamura H	240
1L37	UOT-0756	(ϕCL) Cm *hisA1 leuB8 metB51 nonB1 trpC2*	Kawamura H	Kawamura H	240
1L38	UOT-0531	(ϕPA14) *leuB8 metB51 nonB1 trpC2*	Kawamura H	Kawamura H	241
1L39	CU267(ϕ105J23)	(ϕ105J23) *ilvB2 leuB16 trpC2*	Errington J	Errington J	142
1L40	CU267(ϕ105J27)	(ϕ105J27) *ilvB2 leuB16 trpC2*	Errington J	Errington J	142
1L41	UOT-0533	(ϕ105spo0F+) *leuB8 metB51 nonB1 spo0F77 trpC2*	Kawamura F	Kawamura F	148
1L42	CU267(ϕ105J106)	(ϕ105J106) *ilvB2 leuB16 trpC2*	Errington J	Errington J	70
1L43	566(ϕ105DS1)	(ϕ105DS1) *-(spoIIAA562)*+ *-(sigF561)*+	Mandelstam J	Mandelstam J	233
1L44	MB75(ϕ105J13)	(ϕ105J13) *-(lys-1)*+ *metC3 tal-1*	Errington J	Errington J	71
1L45	522(ϕ105J45)	(ϕ105J45) *-(gerE36)*+ *trpC2*	Mandelstam J	Mandelstam J	138
1L46	CU448(ϕ105J38)	(ϕ105J38) *-(arg(GH)2)*+ *ilvA1 pheA2 trpC2*	Errington J	Errington J	72
1L47	488.1(ϕ105J39)	(ϕ105J39) *-(spo0B136)*+ *lys-1*	Errington J	Errington J	72
1L48	221.1 (ϕ105J40)	(ϕ105J40) *-(spo0F221)*+ *trpC2*	Errington J	Errington J	72
1L49	SG5(ϕ105J65)	(ϕ105J65) *-(thr-5)*+ *pheA12*	Errington J	Errington J	70
1L50	23.1(ϕ105J78)	(ϕ105J78) *-(spoIVC)*+ *trpC2*	Errington J	Errington J	72
1L51	17.2(ϕ105J80)	(ϕ105J80) *-(sigH)*+ *metC3 tal-1*	Errington J	Errington J	72
1L52	517(ϕ105J81)	(ϕ105J81) *-(spoVK517)*+ *trpC2*	Errington J	Errington J	72
1L53	298.2(ϕ105J85)	(ϕ105J85) *-(spoIID298)*+ *pheA12*	Errington J	Errington J	72
1L54	43.6(ϕ105J94)	(ϕ105J94) *-(spo0A43)*+ *trpC2*	Errington J	Errington J	72
1L55	55.2(ϕ105J114)	(ϕ105J114) *-(spoIIG55)*+ *rpoB2 trpC2*	Errington J	Errington J	70
1L56	87.2	(ϕ105J93) *leuA8 spoIIIJ87 tal-1*	Errington J	Errington J	72
1S1	3NA	*spo0A3*	Schaeffer P	Schaeffer P	177
1S2	184	*metB5 spo0A3 thr-5*	Salas M	Arnaud M	230
1S3	FR24	*-(metB5)*+ *spo0A3 sup-44 thr-5*	Salas M	Arnaud M	175
1S4	FR32	*-(metB5)*+ *-(thr-5)*+ *spo0A3 trnS-Lys3*	Salas M	Arnaud M	175
1S5	PB3A	*spo0A3 trpC2*	Spizizen J	Rogolsky M	256
1S6	5NA	*spo0A5*	Schaeffer P	Schaeffer P	133
1S7	6U	*metB4 spo0A6 trpC2*	Schaeffer P	Schaeffer P	133
1S8	9V	*spo0A9 trpC2*	Schaeffer P	Schaeffer P	133
1S9	JH646	*pheA1 spo0A12 trpC2*	Hoch JA	Hoch JA	275
1S10	SR22	*spo0A12 trpC2*	Ito J	Ito J	135
1S11	SCR584	*spo0A12 tolB24 trpC2*	Ito J	Ito J	135
1S12	JH82	*spo0A12 trpF7*	Hoch JA	Hoch JA	123
1S13	13V	*spo0A13 trpC2*	Schaeffer P	Schaeffer P	133
1S14	170-2	*spo0A170 tyr*	Takahashi I	Takahashi I	268
1S15	B332H	*spo0A332 trpC2*	Rogolsky M	Rogolsky M	220
1S16	JH648	*pheA1 spo0B136 trpC2*	Hoch JA	Hoch JA	123
1S17	JH647	*pheA1 spo0E11 trpC2*	Hoch JA	Hoch JA	123
1S19	JH649	*pheA1 spo0F221 trpC2*	Hoch JA	Hoch JA	123
1S20	B4NA	*sigH4 str trpC2*	Rogolsky M	Rogolsky M	220
1S21	B14NG	*sigH14 trpC2*	Rogolsky M	Rogolsky M	220
1S22	E22	*rpoB2 sigH17 trpC2*	Piggot PJ	Young M	206
1S23	B37NA	*sigH37 trpC2*	Rogolsky M	Rogolsky M	220
1S24	JH651	*pheA1 sigH81 trpC2*	Hoch JA	Hoch JA	123
1S25	B116NG	*sigH116 trpC2*	Rogolsky M	Rogolsky M	220
1S26	JH696	*pheA1 spoIIIJ87 trpC2*	Hoch JA	Hoch JA	123
1S27	87	*metC3 spoIIIJ87 tal-1*	Hranueli D	Young M	129
1S28	Z31	*opp(ABCDEF)(ABCDEF)141 trpC2*	Coote JG	Mandelstam J	42
1S29	N2-2	*ser spoIIA2*	Takahashi I	Takahashi I	268
1S30	12U	*spoIIA12*	Schaeffer P	Schaeffer P	133
1S31	26U	*ade met spoIIA26 trpC2*	Schaeffer P	Schaeffer P	133
1S32	NG18.6	*rpoB2 spoIIA69 trpC2*	Piggot PJ	Young M	206
1S33	NG17.22	*rpoB2 spoIID66 trpC2*	Piggot PJ	Young M	206
1S34	NG15.4	*spoIIE61 trpC2*	Piggot PJ	Young M	206
1S35	NG17.15	*rpoB2 spoIIE64 trpC2*	Piggot PJ	Young M	206
1S36	7Z	*ilvC1 spoIIIA(A-H)7 trpC2*	Schaeffer P	Schaeffer P	133
1S37	NG12.5	*rpoB2 spoIIIA(A-H)53 trpC2*	Piggot PJ	Young M	206
1S38	94U	*spoIIIC94 trpC2*	Schaeffer P	Schaeffer P	133

B. subtilis 168 Strains Indexed by BGSC Accession Number

BGSC	ORIGINAL CODE	DESCRIPTION	SOURCE	DONOR	REF
1S39	83U	*spoIIID83 trpC2*	Schaeffer P	Schaeffer P	133
1S40	11T	*spoIIIC11*	Schaeffer P	Schaeffer P	133
1S41	168DPA(-)	*spoVF trpC2*	Halvorson HO	Arnaud M	306
1S42	NG1.13	*metC3 spoIIIA(A-H)35 tal-1*	Piggot PJ	Young M	206
1S43	P9	*spoIID298 trpC2*	Coote JG	Mandelstam J	42
1S44	91	*argF4 hisA1 metB5 pheA12 purA16 pyrA26 spoVB91 trpC2*	Hranueli D	Young M	129
1S45	SL931	*rpoB2 spoVD156 trpC2*	Piggot PJ	Piggot PJ	204
1S46	P20	*pheA12 spoIVA178*	Coote JG	Mandelstam J	42
1S47	Z7	*spoIVC133 trpC2*	Coote JG	Coote JG	41
1S48	A3	*spoIIIB2 trpC2*	Piggot PJ	Young M	206
1S49	Z3	*spoIIB131 trpC2*	Coote JG	Mandelstam J	42
1S50	89	*spoVA89 trpC2*	Hranueli D	Young M	129
1S51	85	*spoVE85 trpC2*	Hranueli D	Young M	129
1S52	SL824	*spoVF224 trpC2*	Piggot PJ	Piggot PJ	204
1S53	667	*spo0AΔ677*	Ito J	Ito J	135
1S54	SCR690	*spo0B12*	Ito J	Ito J	135
1S55	306.1	*rpoB2 sapA6 spoIIA69*	Piggot PJ	Piggot PJ	207
1S56	300.1	*rpoB2 sapB2 spoIIA69*	Piggot PJ	Piggot PJ	207
1S57	P7	*spoIVB165 trp*$^-$	Coote JG	Mandelstam J	42
1S58	X8	*spoIVF152 trpC2*	Coote JG	Mandelstam J	42
1S59	96	*kinA96 trpC2*	Hranueli D	Young M	129
1S60	41.1	*leuB8 spoIIG41 tal-1*	Young M	Young M	297
1S61	NG12.12	*rpoB2 sigE55 trpC2*	Piggot PJ	Young M	206
1S63	NG1.67	*spoIIIE36 trpC2*	Piggot PJ	Young M	206
1S64	92	*leuB8 rpoB2 spoIIIC92 tal-1*	Hranueli D	Young M	129
1S65	88	*metC3 spoIVF88 tal-1*	Hranueli D	Young M	129
1S66	285	*metC3 rpoB2 spoVC285*	Young, M	Young, M	296
1S67	279.6	*cysC7 furA2 spoIIG279*	Young, M	Young, M	297
1S68	R15-13	*abrB23 pheA1 spo0A12 trpC2*	Hoch JA	Mahler I	123
1S69	SCR354	*abrB6 spo0A12 trpC2*	Ito J	Ito J	136
1S70	SCR372	*abrB24 spo0A12 trpC2*	Ito J	Ito J	136
1S71	4Z	*spoIIA4 trpC2*	Schaeffer P	Schaeffer P	133
1S72	4Z	*spoIIA4 trpC2*	Schaeffer P	Schaeffer P	133
1S73	16U ATM16 SPIIB	*ade met Sm spo0A16 trpC2*	Schaeffer P	Schaeffer P	235
1S74	4SA2 OIIB	*spoIIA5*	Schaeffer P	Schaeffer P	235
1S75	RUB331	*spo-331 thyA1 thyB1 trpC2*	Wilson GA	Wilson GA	295
1S76	ASB298	*citDΔ29 dal-1 spo0AΔ677 str-76 thyA thyB uvr-1*	Burke WF	Burke WF	29
1S77	SL613 50.2	*metB5 spoIIA50 thr-5*	Piggot PJ	Piggot PJ	204
1S78	SL631 63.2	*metC3 rpoB2 sigF63 tal-1*	Piggot PJ	Piggot PJ	204
1S79	NG1.82	*spoIIA37 trpC2*	Piggot PJ	Mandelstam J	206
1S80	NG6.13	*spoIIA42 trpC2*	Piggot PJ	Mandelstam J	206
1S81	P18	*spoIIA176 trpC2*	Coote JG	Mandelstam J	42
1S82	DB16	*pyrA1 spoL1 trpC2*	Balassa G	Pasteur Institute	17
1S83	AB12	*pheA1 spoVF1 trpC2*	Balassa G	Pasteur Institute	18
1S84	EV15	*argF4 cotA leu-2 pyrA26 scoA1*	Balassa G	Pasteur Institute	16
1S85	EC21	*argF4 leu-2 pyrA26 kinA2*	Balassa G	Pasteur Institute	16
1S86	SL401	*sigF1 trpC2*	Piggot PJ	Piggot PJ	204
1S87	SL55-7	*metC3 spoIVG-25 tal-1*	Piggot PJ	Jenkinson HF	204
1S88	513	*spoVIA513 trpC2*	Jenkinson HF	Jenkinson HF	139
1S89	181	*spoIVF(TS) trpC2*	Mandelstam J	Mandelstam J	154
1S90	580	*lys-1 spo0B(TS)*	Mandelstam J	Mandelstam J	154
1S91	581	*lys-1 spo0B(TS)*	Mandelstam J	Mandelstam J	154
1S92	587	*lys-1 spoIVF(TS)*	Mandelstam J	Mandelstam J	154
1S93	590	*lys-1 spoVB*	Mandelstam J	Mandelstam J	153
1S94	93.2	*spo0J93 trpC2*	Errington J	Errington J	70
1S95	517	*spoVK517 trpC2*	Errington J	Errington J	70
1S96	KI224	*bofA*::Tn*917lac pheA1 trpC2*	Grossman AD	Grossman AD	134
1S97	IS720	*hisA1 leuA8 metB5 sinR::phl*	Smith I	Smith I	15, 249

BGSC	ORIGINAL CODE	DESCRIPTION	SOURCE	DONOR	REF
1S98	IS875	*hisA1 leuA8 metB5 sinI::kan-50* Spo^{-}	Smith I	Smith I	249
1S99	RL673	MLS^{R} *spoVK::*Tn*917HU8* SPβ^{-}	Losick R	Cutting S	74
1S100	RL774	*bofA::cat* Cm SPβ^{-}	Losick R	Cutting S	217
1S101	RL50	Cm *cotA::cat trpC2*	Losick R	Driks A	62
1S102	RL51	*cotB::cat trpC2*	Losick R	Driks A	62
1S103	RL52	*cotC::cat trpC2*	Losick R	Driks A	62
1S104	RL53	*cotD::cat trpC2*	Losick R	Driks A	62
1S105	RL48	*cotE*Δ*::cat trpC2*	Losick R	Losick R	305
1S106	RL653	*cotF::cat trpC2*	Losick R	Cutting S	47
1S107	RL654	*cotF*Δ*::cat trpC2*	Losick R	Cutting S	47
1S108	DB200	Cm *cotT*::pDE194 *pheA1 trpC2*	Aronson I	Aronson I	13
1S109	PS273	*sspA*$^{\Delta}$	Setlow P	Setlow P	242
1S110	PS339	*sspB*$^{\Delta}$	Setlow P	Setlow P	242
1S111	PS356	*sspA*$^{\Delta}$ *sspB*$^{\Delta}$	Setlow P	Setlow P	242
1S112	PS481	*sspA*$^{\Delta}$ *sspE*$^{\Delta}$ Cm	Setlow P	Setlow P	242
1S113	PS482	*sspA*$^{\Delta}$ *sspB*$^{\Delta}$ *sspE*$^{\Delta}$ Cm	Setlow P	Setlow P	242
1S114	PS499	*sspE*$^{\Delta}$	Setlow P	Setlow P	242
1S115	PY179	*spoIID::*Tn*917ΩHU8*	Youngman P	Youngman P	232
1S116	PY180	*spoIIE::*Tn*917ΩHU7*	Youngman P	Youngman P	232
1S117	KS8	*spoVK::*Tn917Ω*HU8*	Sandman K	Youngman P	232
1S118	KS10	*spoIVD::*Tn*917*Ω*HU10*	Sandman K	Youngman P	232
1S119	KS13	*spoIIIA(A-H)::*Tn*917*Ω*HU13*	Sandman K	Youngman P	232
1S120	KS19	*kinA::*Tn*917*Ω*HU19*	Sandman K	Youngman P	232
1S121	KS25	*spoIIIB::*Tn*917*Ω*HU25*	Sandman K	Youngman P	232
1S122	KS178	*spoVK::*Tn*917*Ω*HU178*	Sandman K	Youngman P	232
1S123	KS179	*spoIVFA::*Tn*917*Ω*HU179*	Sandman K	Youngman P	232
1S124	KS181	*spoIIE::*Tn*917*Ω*HU181*	Sandman K	Youngman P	232
1S125	KS188	*spoIIM::*Tn*917*Ω*HU188*	Sandman K	Youngman P	232
1S126	KS194	*spoIVA::*Tn*917*Ω*HU194*	Sandman K	Youngman P	232
1S127	KS195	*spoVA::*Tn*917*Ω*HU195*	Sandman K	Youngman P	232
1S128	KS215	*spoIVC::*Tn*917*Ω*HU215*	Sandman K	Youngman P	232
1S129	KS261	*spo0J::*Tn*917*Ω*HU261*	Sandman K	Youngman P	232
1S130	KS265	*spoVG::*Tn*917*Ω*HU265*	Sandman K	Youngman P	232
1S131	KS276	*spoVA::*Tn*917*Ω*HU276*	Sandman K	Youngman P	232
1S132	KS287	*spoIIM::*Tn*917*Ω*HU287*	Sandman K	Youngman P	232
1S133	KS289	*spo0A::*Tn*917*Ω*HU289*	Sandman K	Youngman P	232
1S134	KS297	*ald::*Tn*917*Ω*HU297*	Sandman K	Youngman P	232
1S135	KS298	*spoIID::*Tn*917*Ω*HU298*	Sandman K	Youngman P	232
1S136	KS306	*cotA::*Tn*917*Ω*HU306*	Sandman K	Youngman P	232
1S137	KS324	*spoVM::*Tn*917*Ω*HU324*	Sandman K	Youngman P	232
1S138	KS325	*spoIIG::*Tn*917*Ω*HU325*	Sandman K	Youngman P	232

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B. SUBTILIS 168 STRAINS BY ORIGINAL CODE

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168MIU8	**1A392**
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B. subtilis 168 Strains Indexed by Original Code

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MO101P	**1S2**
MO1099	**1A717**
MO1099	**1A771**
MO1813	**1A772**
MO649	**1A773**
MO99	**1S4**
MP82	**1A735**
MS320	**1A464**
Mu5u11	**1A389**
Mu5u12	**1A388**
Mu5u26	**1A387**
MU8U5U1 (BD54)	**1A75**
Mu8u5u16	**1A145**
Mu8u5u6	**1A12**
Mu8u5u6u41	**1A13**
MW10	**1A751**
MW10	**1A752**
MY2011	**1A466**
MY2013	**1A467**
N1G17	**1A365**
N1G43	**1A373**
N1G45	**1A366**
N2-2	**1S29**
NA20	**1A414**
NA20-22	**1A413**
NA64	**1A412**
ng 79	**1A758**
NG1.13	**1S42**
NG1.67	**1S63**
NG1.82	**1S79**
NG12.12	**1S61**
NG12.5	**1S37**
NG15.4	**1S34**
NG17.15	**1S35**
NG17.22	**1S33**

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

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ORIGINAL CODE	BGSC
SB1058	**1A224**
SB1059	**1A225**
SB1060	**1A226**
SB1115	**1A228**
SB112	**1A227**
SB1141	**1A230**
SB1142	**1A231**
SB1143	**1A232**
SB1144	**1A233**
SB1145	**1A234**
SB1146	**1A235**
SB1158	**1A456**
SB120	**1A69**
SB121	**1A132**
SB130	**1A133**
SB133	**1A275**
SB135	**1A229**
SB136	**1A131**
SB137	**1A83**
SB164	**1A104**
SB168	**1A246**
SB193	**1A207**
SB19E,ts2pyrG1	**1A461**
SB19SEM	**1A101**
SB22	**1A319**
SB25	**1A58**
SB26	**1A80**
SB270A	**1A321**
SB29	**1A206**
SB3 (BD92)	**1A31**
SB305	**1A322**
SB319	**1A323**
SB32	**1A208**
SB419	**1A285**
SB443	**1A286**
SB491	**1A2**
SB491U5	**1A403**
SB491U6	**1A397**
SB5	**1A115**
SB58A	**1A320**
SB68	**1A87**
SB69	**1A108**
SB70	**1A173**
SCR354	**1S69**
SCR372	**1S70**
SCR500	**1A66**
SCR506	**1A67**
SCR584	**1S11**
SCR690	**1S54**
SG64	**1A680**
SH	**1A270**
SH-2	**1A273**
SH-3	**1A272**
SH-5	**1A271**
SL16	**1S51**
SL17	**1S50**
SL311	**1S56**
SL330	**1A306**
SL344	**1A307**
SL346	**1S55**
SL401	**1S86**
SL55-7	**1S87**
SL61	**1S44**
SL613	**1S77**

ORIGINAL CODE	BGSC
SL631	**1S78**
SL731	**1S49**
SL767	**1S43**
SL824	**1S52**
SL931	**1S45**
SMY	**1A775**
SPIIB4	**1S71**
SPIIB4	**1S72**
SPOA3	**1S5**
SR22	**1S10**
SSP	**1A488**
ST-3	**1A198**
SU+III	**1A14**
SU+III	**1A459**
Sz 15 (I/1)	**1A589**
Sz 16 (II/33)	**1A590**
Sz 26 (V/64)	**1A592**
Sz 27 (VI/180)	**1A593**
Sz 28 (III/321)	**1A594**
Sz 3 (R15)	**1A588**
Sz 34	**1A591**
TAG-1	**1A209**
TIBS 57	**1A474**
TKJ3422	**1A514**
TKJ6901	**1A487**
tmsB1	**1A312**
trpA1 (NG 63)	**1A553**
trpA2 (NA 9)	**1A554**
trpA3 (T 50)	**1A555**
trpA4 (T 51)	**1A556**
trpA6 (ICR 17)	**1A557**
trpA7 (ICR 21)	**1A558**
trpB1 (NG 4)	**1A559**
trpB10 (ICR 8)	**1A566**
trpB11 (ICR 9)	**1A567**
trpB12 (ICR 13)	**1A568**
trpB13 (ICR 15)	**1A569**
trpB14 (ICR 18)	**1A570**
trpB15 (ICR 20)	**1A571**
trpB16 (NG 7)	**1A572**
trpB2 (NG 6)	**1A560**
trpB5 (NG 14)	**1A561**
trpB6 (NG 57)	**1A562**
trpB7 (NG 58)	**1A563**
trpB8 (NG 59)	**1A564**
trpB9 (NG 60)	**1A565**
trpC1 (NG 1)	**1A543**
trpC10 (EMS 2)	**1A551**
trpC11 (NG 2)	**1A552**
trpC3 (NG 3)	**1A544**
trpC4 (NG 5)	**1A545**
trpC5 (NG 24)	**1A546**
trpC6 (UV 15)	**1A547**
trpC7 (UV 16)	**1A548**
trpC8 (UV 18)	**1A549**
trpC9 (EMS 1)	**1A550**
trpD1 (NA 1)	**1A522**
trpD10 (ICR 22)	**1A530**
trpD2 (NA 3)	**1A523**
trpD4 (NG 61)	**1A524**
trpD5 (NG 62)	**1A525**
trpD6 (NG 120)	**1A526**
trpD7 (ICR 10)	**1A527**
trpD8 (ICR 11)	**1A528**

ORIGINAL CODE	BGSC
trpD9 (ICR 19)	**1A529**
trpE1 (ICR 1)	**1A516**
trpE194 (SB194)	**1A521**
trpE2 (ICR 6)	**1A517**
trpE3 (ICR 14)	**1A518**
trpE4 (ICR 16)	**1A519**
trpE5 (UV 17)	**1A520**
trpF1 (NA 2)	**1A531**
trpF10 (ICR 12)	**1A539**
trpF11 (SB 11)	**1A540**
trpF12 (NA 5)	**1A541**
trpF13 (HA 1)	**1A542**
trpF2 (NA 4)	**1A532**
trpF3 (NA 6)	**1A533**
trpF4 (NA 7)	**1A534**
trpF5 (NA 10)	**1A535**
trpF6 (NA 11)	**1A536**
trpF8 (HA2)	**1A537**
trpF9 (PH 1)	**1A538**
TS-134	**1A290**
TS-151	**1A268**
TS-355	**1A269**
TSDNA-A13	**1A18**
TSDNA-B19	**1A19**
TSDNA-C30	**1A20**
TSDNA-D23	**1A21**
TSDNA-E20	**1A22**
TSDNA-F133	**1A23**
TSDNA-G34	**1A24**
TSDNA-H151	**1A25**
TSDNA-I102	**1A26**
TTK24	**1A491**
UOTO277	**1A509**
UTB600	**1A490**
UVS1	**1A344**
UVS109	**1A346**
UVS114	**1A347**
UVS42	**1A345**
UVS80	**1A343**
UVSSP-42-1	**1A489**
VA321	**1A314**
VA322,THR(+)	**1A318**
VA55	**1A316**
VA61	**1A317**
VA71,THR(+)	**1A315**
VB104	**1A348**
VB106	**1A349**
VB107A	**1A350**
VB122A	**1A351**
VB126	**1A352**
VB127	**1A353**
VB157	**1A354**
VB158	**1A355**
VB293	**1A356**
VB336F	**1A358**
VB355B	**1A357**
VUB192	**1A149**
VUB212	**1A261**
VUB221	**1A163**
VUB234	**1A262**
VUB333	**1A162**
VUB79	**1A158**
W10	**1S45**
W168	**1A308**

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

B. SUBTILIS 168 STRAINS INDEXED BY ALLELE

ALLELE	CODE	DESCRIPTION
(SPβc2)	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
	1A619	(SPβc2) liv1-82::Tn917 trpC2
	1A620	(SPβc2) liv3-83::Tn917 trpC2
	1A621	(SPβc2) serC82::Tn917 trpC2
	1A622	(SPβc2) arg(GH)85::Tn917 trpC2
	1A623	(SPβc2) alaA84::Tn917 trpC2
	1A624	(SPβc2) mth-83::Tn917 trpC2
	1A625	(SPβc2) mth-84::Tn917 trpC2
	1A626	(SPβc2) hisA82::Tn917 trpC2
	1A627	(SPβc2) trpC2 zaa-84::Tn917
	1A628	(SPβc2) trpC2 zbj-82::Tn917;
	1A629	(SPβc2) trpC2 zca-82::Tn917
	1A630	(SPβc2) trpC2 zce-82::Tn917
	1A631	(SPβc2) motA::Tn917 trpC2
	1A632	(SPβc2) kinC::Tn917 trpC2
	1A633	(SPβc2) trpC2 zdi-82::Tn917
	1A634	(SPβc2) trpC2 zci-82::Tn917
	1A635	(SPβc2) trpC2 proJ::Tn917
	1A636	(SPβc2) cgeE::Tn917 trpC2
	1A637	(SPβc2) trpC2 yokH::Tn917
	1A638	(SPβc2) trpC2 zfg-83::Tn917
	1A639	(SPβc2) spoVID::Tn917 trpC2
	1A640	(SPβc2) trpC2 zhb-83::Tn917
	1A641	(SPβc2) trpC2 zhc-85::Tn917
	1A642	(SPβc2) trpC2 yufR::Tn917
	1A643	(SPβc2) trpC2 yvaC::Tn917
	1A644	(SPβc2) trpC2 zii-83::Tn917
	1A645	(SPβc2) trpC2 zjf-85::Tn917
	1A646	(SPβc2) trpC2 zfd-81::Tn917
	1A687	(SPβc2) trpC2 zba89::Tn917
	1A688	(SPβc2) trpC2 ydaO::Tn917
	1A689	(SPβc2) trpC2 zdf88::Tn917
	1A690	(SPβc2) trpC2 zec88:Tn917
	1A691	(SPβc2) trpC2 zfe86::Tn917
	1A692	(SPβc2) trpC2 zhf86::Tn917
	1A693	(SPβc2) trpC2 zhg86::Tn917
	1A721	(SPβc2) aroI86::Tn917 trpC2
	1A722	(SPβc2) bfmB84::Tn917 trpC2
	1A724	(SPβc2) trpC2 zba-88::Tn917
	1A727	(SPβc2) trpC2 zeh-82::Tn917
	1A728	(SPβc2) trpC2 zfj-83::Tn917
	1A730	(SPβc2) trpC2 zhf-83::Tn917
	1A731	(SPβc2) trpC2 zib-82::Tn917
	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
::Tn917	1A759	::Tn917 MLS^R
::Tn917::pTV20	1A760	::Tn917::pTV20 Cm MLS^R
::Tn917::pTV20	1A762	::Tn917::pTV20 bac-1 Cm MLS^R
::Tn917::pTV21Δ2	1A761	::Tn917::pTV21Δ2 Cm
::Tn917lac	1A749	::Tn917lac MLS
abrB6	1S69	abrB6 spo0A12 trpC2
abrB23	1S68	abrB23 pheA1 spo0A12 trpC2
abrB24	1S70	abrB24 spo0A12 trpC2
blt-2	1A189	blt-2 trpC2
addA5	1A334	addA5 hisH2 metB5
addB71	1A702	addB71 amyE SPβ- metB5 sigB xin-1
addB72	1A701	addB72 amyE SPβ- metB5 sigB trpC2 xin-1
ade	1A437	ade his hsd$_{RI}$R-M- met nic rib trp tyr ura
	1S31	ade met spoIIA26 trpC2
	1S73	ade met Sm spo0A16 trpC2
aec	1A356	aec hom-1 trpC2
aec-56	1A431	aec-56
aec-59	1A432	aec-59
aecB	1A357	aecB lys-1 sul trpC2
ahrC2	1A512	ahrC2
ala-1	1A434	ala-1 leuB8 metB pur thr-5 trpC
alaA84::Tn917	1A623	(SPβc2) alaA84::Tn917 trpC2
ald-1	1A9	ald-1 aroA932 leuB8 trpC2
	1A53	ald-1 degQ36 trpC2
	1A679	ald-1 leuB8 menE312 trpC2
ald:: Tn917 HU297	1S134	ald::Tn917 HU297
alsR1	1A147	alsR1 ccpA1 ilvB 1 trpC2
	1A250	alsR1 ilvB 1 trpC2
amm-35	1A336	amm-35 leuB8 metB5 purA16
amt	1A337	amt
amy-3	1A501	amy-3 aro-10 lmrA2
amyE	1A288	amyE dal-1 metB5 sacA321
	1A289	amyE aroI906 metB5 sacA321
	1A297	amyE aspT1 trpC2
	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
amyE^{+M}	1A182	amyE^{+M} amyR1 deg-9 metB5 pro(L) purF6 str trpB3
	1A311	amyE^{+M} amyR2 deg-9 metB5 pro(L) purF6 str
	1A338	amyE^{+M} amyR1(+M) metB5 pro(L) purF6 trpB3
	1A339	amyE^{+M} amyR21(+M)(H) metB5 pro(L) purF6 str trpB3
	1A340	amyE^{+M} amyR1 aroI116 deg-118 metB5 pro(L) str trpB3
	1A341	amyE^{+M} amyR1^{+M} metB5 pro(H) purF6 str trpB3
	1A412	amyE^{+M} amyR2 metB5 purF6
amyE^{+N}	1A413	amyE^{+N} amyR1 metB5
	1A414	amyE^{+N} amyR2 metB5 purF6
amyE::cat	1A772	amyE::cat Cm pheA1 trpC2
amyE::erm	1A717	amyE::erm MLS
	1A771	amyE::erm MLS pheA1 trpC2
amyE3	1A474	amyE3 aroI10
amyR1	1A182	amyE^{+M} amyR1 deg-9 metB5 pro(L) purF6 str trpB3
	1A340	amyE^{+M} amyR1 aroI116 deg-118 metB5 pro(L) str trpB3
	1A413	amyE^{+N} amyR1 metB5
amyR1^{+M}	1A338	amyE^{+M} amyR1^{+M} metB5 pro^L purF6 trpB3
	1A341	amyE^{+M} amyR1^{+M} metB5 pro^H purF6 str trpB3
amyR2	1A311	amyE^{+M} amyR2 deg-9 metB5 pro^L purF6 str
	1A412	amyE^{+M} amyR2 metB5 purF6

ALLELE	CODE	DESCRIPTION
amyR2 (cont)	1A414	amyE(+N) amyR2 metB5 purF6
amyR21$^{+M(H)}$	1A339	amyE^{+M} amyR21(+M)(H) metB5 pro(L) purF6 str trpB3
aprE	1A751	apr bglS EV bglC 102 his npr
	1A752	apr bglS EV bglC 102 glgB::lacZ M15 his npr
apt-6	1A681	apt-6 ilvA1 pbuG3 pupA3 sacA78 upp
arg	1A506	arg trp
	1A595	arg thyA thyB tscA1
	1A596	arg thyA thyB tscA23
	1A597	arg nadE49 thyA thyB
	1A598	arg thyA thyB tscC11
	1A599	arg thyA thyB tscD14
	1A647	arg nadE47 thyA thyB
	1A648	arg nadE48 thyA thyB
	1A649	arg thyA thyB tscD14
arg(BCDJ)	1A148	arg(ABCDE)
arg(BCDJ)1	1A118	arg(ABCDE)1 metA8 trpC2
arg(GH)2	1A92	arg(GH)2 aroA932 bioB141 sacA321
	1A111	arg(GH)2 azlB101 trpC2
	1A119	arg(GH)2 leuA164 pheA2 trpC2
	1A121	arg(GH)2 pheA2 sdhC109 trpC2
	1A440	arg(GH)2 hemA1
arg(GH)3	1A211	arg(GH)3 pheA12 rplV1
	1A212	arg(GH)3 lys-21 metB5 pheA12 purA16 rplV1
	1A277	arg(GH)3 lys-21 metB5 pheA12
arg(GH)15	1A253	arg(GH)15 hsd$_{RI}$R-M- leuB8 SP10^{S}
	1A363	arg(GH)15 hsd$_{RI}$R-M- leuB8 rplV
	1A365	arg(GH)15 trpB3
	1A366	arg(GH)15 recA45 trpB3
	1A373	arg(GH)15 recD43 trpB3
	1A409	arg(GH)15 hsd$_{RI}$R-M- leuB8 recA4
	1A423	arg(GH)15 hsd$_{RI}$R-M- leuB8 recA4 thr-5
	1A510	arg(GH)15 hsd$_{RI}$R-M- leuB8 recA4 stp thr
arg(GH)85::Tn917	1A622	(SPβc2) arg(GH)85::Tn917 trpC2
arg^{S}	1A391	arg^{S} pyrA
arg342::Tn917	1A608	(SPβc2) arg342::Tn917 trpC2
argF4	1A28	argF4 hisA1 trpC2
	1A39	argF4 trpC2
	1A125	argF4 metA29 thiB4
	1A136	argF4 hag-2 tagE
	1A138	argF4 hag-1 smo-1 trpC2
	1A151	argF4 hpr hisA1 pha-1
	1A302	argF4 hisA1 recA4
	1A312	argF4 flaC51 hag-1 hisA1 ura
	1A319	argF4 hisA1 purH4 trpC2
	1S44	argF4 hisA1 metB5 pheA12 purA16 pyrA26 spoVB91 trpC2
	1S84	argF4 cotA leu-2 pyrA26 scoA1
	1S85	argF4 kinA2 leu-2 pyrA26
argF82::Tn917	1A606	(SPβc2) argF82::Tn917 trpC2
argF83::Tn917	1A605	(SPβc2) argF83::Tn917 trpC2
aro-10	1A501	amy-3 aro-10 lmrA2
aroA6	1A130	aroA6
aroB2	1A36	aroB2 hisH2 metB10 trpC2 tyrA1
	1A83	aroB2 hisH2
	1A103	aroB2 hisH2 recG40 trpC2 tyrA1
	1A104	aroB2
	1A298	aroB2 azpB80 hisH2 trpC2 tyrA1
	1A299	aroB2 hisH2 gyrA trpC2 tyrA1
	1A378	aroB2 hisH2 recD41 trpC2 tyrA1
	1A379	aroB2 hisH2 recG39 trpC2 tyrA1
aroB2 (cont)	1A380	aroB2 hisH2 recF33 trpC2 tyrA1
	1A404	aroB2 hisA53 hisH2 rna-53 trpC2 tyrA1
aroB4	1A131	aroB4 hisH2
aroBC84::Tn917	1A613	(SPβc2) aroBC84::Tn917 trpC2
aroC7	1A132	aroC7 trpC2
aroD120	1A408	aroD120 recA4 trpC2
	1A654	aroD120 bglS33 trpC2
	1A69	aroD120 trpC2
	1A8	aroD120 lys-1 trpC2
aroE1	1A133	aroE1 hisH2
	1A207	aroE1 hisA1
	1A229	aroE1
aroF5	1A134	aroF5
aroA932	1A330	aroA932 bioB141
	1A56	aroA932 trpC2
	1A9	ald-1 aroA932 leuB8 trpC2
	1A92	arg(GH)2 aroA932 bioB141 sacA321
aroH1	1A117	aroH1 cotA73
aroI10	1A474	amyE3 aroI10
aroI86::Tn917	1A721	(SPβc2) aroI86::Tn917 trpC2
aroI116	1A340	amyE(+M) amyR1 aroI116 deg-118 metB5 pro(L) str trpB3
aroI906	1A289	amyE aroI906 metB5 sacA321
	1A4	aroI906 dal-1 purE1 trpC2
	1A429	aroI906 glpT6 trpC2
	1A55	aroI906 dal-1 metB5 sacA321
	1A655	aroI906 cdr-1 trpC2
asaA4	1A281	asaA4 leu-2 trpC2
	1A283	asaA4 asaB4 leu-2 trpC2
asaAΔ2	1A280	asaAΔ2 leu-2 trpC2
	1A282	asaAΔ2 asaB1 leu-2 trpC2
asaB1	1A282	asaAΔ2 asaB1 leu-2 trpC2
asaB4	1A283	asaA4 asaB4 leu-2 trpC2
aspB66	1A295	aspB66 trpC2
aspH1	1A296	aspH1 trpC2
aspT1	1A297	amyE aspT1 trpC2
ath-83::Tn917	1A602	(SPβc2) ath-83::Tn917 trpC2
azc-1	1A430	azc-1
azlA102	1A112	azlA102 trpC2
azlB101	1A111	arg(GH)2 azlB101 trpC2
azpB80	1A298	aroB2 azpB80 hisH2 trpC2 tyrA1
bac-1	1A758	bac-1
	1A762	::Tn917::pTV20 bac-1 Cm MLS^{R}
bfmB	1A471	pdhA1 bfmB metC7 trpC2
bfmB::cat	1A756	bfmB::cat Cm thr-5 trpC2
bfmB1	1A472	bfmB1 iur trpC2
	1A473	bfmB1 strC2 trpC2
bfmB84::Tn917	1A722	(SPβc2) bfmB84::Tn917 trpC2
bglS33	1A654	aroD120 bglS33 trpC2
bglS EV	1A751	apr bglSΔEV bglC 102 his npr
	1A752	apr bglSΔEV bglC 102 glgB::lacZ M15 his npr
bioB141	1A330	aroA932 bioB141
bioB141	1A92	arg(GH)2 aroA932 bioB141 sacA321
bmr^{R}	1A753	bmr^{R} thr-5 trpC2
bmr::cat	1A754	bmr::cat Cm thr-5 trpC2
bmrR::cat	1A755	bmrR::cat Cm thr-5 trpC2
bofA::cat	1S100	bofA::cat Cm SPβ-
bofA::Tn917lac	1S96	bofA::Tn917lac pheA1 trpC2
bry	1A267	bry
cafA1	1A381	cafA1 metB10 trpC2
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 ilvBΔ1 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
cdr-1	1A655	aroI906 cdr-1 trpC2
cer-2	1A573	cer-2 trpC2
cer-14	1A576	cer-14 trpC2
cer-20	1A577	cer-20 trpC2
cgeE::Tn917	1A636	(SPβc2) cgeE::Tn917 trpC2
citB1	1A326	citB1 gltA2 ilvA8 thyB1
	1A331	citB1 trpC2
citB17	1A143	citB17 ilvA1 sacA78 thyB204
	1A152	citB17 trpC2
citB75	1A120	citB75 trpC2
citC	1A492	citC met pheA trpC2
	1A493	citC met polA10 trpC2
citC6	1A32	citC6 trpC2
citDΔ1	1A278	citDΔ1 trpC2
	1A332	citDΔ1 ilvA8 thyA1 thyB1
citDΔ29	1S76	citDΔ29 dal-1 spo0AΔ677 str-76 thyA thyB uvr-1
citG4	1A16	citG4 trpC2
citH	1A364	citH
Cm	1A716	Cm sigD::pLM5 trpC2
	1A754	bmr::cat Cm thr-5 trpC2
	1A755	bmrR::cat Cm thr-5 trpC2
	1A756	bfmB::cat Cm thr-5 trpC2
	1A760	::Tn917::pTV20 Cm MLS^R
	1A761	::Tn917::pTV21Δ2 Cm
	1A762	::Tn917::pTV20 bac-1 Cm MLS^R
	1A763	Cm fla/che::pLM19 trpC2
	1A767	Cm MLS pheA1 phoA::pCE413 phoB::Tn917 trpC2
	1A772	amyE::cat Cm pheA1 trpC2
	1A773	Cm pheA1 thrC::cat trpC2
	1S100	bofA::cat Cm SPβ-
	1S101	Cm cotA::cat trpC2
	1S108	Cm cotT::pDE194 pheA1 trpC2
	1S112	Cm sspAΔ sspEΔ
	1S113	Cm sspAΔ sspBΔ sspEΔ
com-9	1A706	com-9 hisA1 leu-8 lys-21 metB5 thr-5 trpC2
com-14::Tn917	1A711	com-14::Tn917 hisA1 leu-8 lys-21 metB5 purF6 thr-5 trpC2
com-18::Tn917	1A712	com-18::Tn917 hisA1 leu-8 lys-21 metB5 purF6 thr-5 trpC2
com-30	1A708	com-30 hisA1 leu-8 lys-21 metB5 thr-5 trpC2
com-31	1A710	com-31 hisA1 leu-8 lys-21 metB5 thr-5 trpC2
com-44::Tn917	1A713	com-44::Tn917 hisA1 leu-8 lys-21 metB5 purF6 thr-5 trpC2
com-71	1A707	com-71 hisA1 leu-8 metB5 purF6 thr-5 trpC2
com-104	1A709	com-104 hisA1 leu-8 lys-21 metB5 thr-5 trpC2
cotA	1S84	argF4 cotA leu-2 pyrA26 scoA1
cotA::cat	1S101	Cm cotA::cat trpC2
cotA1	1A184	cotA1 trpC2
cotA73	1A117	aroH1 cotA73
cotA8	1A183	cotA8 trpC2
cotA::Tn917ΩHU306	1S136	cotA::Tn917ΩHU306
cotB::cat	1S102	cotB::cat trpC2
cotC::cat	1S103	cotC::cat trpC2
cotD::cat	1S104	cotD::cat trpC2
cotEΔ::cat	1S105	cotEΔ::cat trpC2
cotF::cat	1S106	cotF::cat trpC2
cotFΔ::cat	1S107	cotFΔ::cat trpC2
cotT::pDE194	1S108	Cm cotT::pDE194 pheA1 trpC2
crk-1	1A479	cdd-1 crk-1 dck-3
crsB40	1A582	crsB40
crsC1	1A583	crsC1
crsC2	1A584	crsC2
crsD1	1A585	crsD1
crsE1	1A586	crsE1
crsF4	1A587	crsF4

ALLELE	CODE	DESCRIPTION
ctrA1	1A11	ctrA1 sacA321 trpC2
	1A461	ctrA1 ts-2
cym-1	1A500	cym-1 rpoB1
cym-84::Tn917	1A600	(SPβc2) cym-84::Tn917 trpC2
cysB3	1A31	cysB3 hisA1 trpC2
cysC1	1A79	cysC1 trpC2
cysC7	1S67	cysC7 furA2 spoIIG279
cysE14	1A3	cysE14 purA26 trpC2
	1A97	cysE14 trpC2
	1A190	cysE14 spo- tufAA-7
	1A192	cysE14 efg-1 spo-
	1A194	cysE14 nea-1 spo-
	1A195	cysE14 ole-2 spo-
	1A222	cysE14 rplV1 spo-
	1A241	cysE14 rpsE2
	1A662	cysE14 purA16 rpmA1 trpC2
	1A663	cysE14 purA16 rpsK2 trpC2
dacA::cat$^+$	1A742	dacA::cat$^+$ trpC2
dacA$^+$::cat$^+$	1A743	dacA$^+$::cat$^+$ trpC2
dacB::cat$^+$	1A745	dacB::cat$^+$ trpC2
dacB$^+$::cat$^+$	1A744	dacB$^+$::cat$^+$ trpC2
dal-1	1A4	aroI906 dal-1 purE1 trpC2
	1A55	aroI906 dal-1 metB5 sacA321
	1S76	citDΔ29 dal-1 spo0AΔ677 str-76 thyA thyB uvr-1
	1A288	amyE dal-1 metB5 sacA321
dapE320	1A464	dapE320 thyA1 thyB1 trpC2
dck-3	1A479	cdd-1 crk-1 dck-3
ddd-3	1A480	cdd-1 ddd-3
ddlA1475	1A463	ddlA1475 ilvA1 metB5 purA16
deg	1A202	deg leuB8 trpC2
deg(H)25	1A159	deg(H)25 narA1
deg(H)32	1A165	deg(H)32 trpC2
deg(H)32	1A95	deg(H)32 leuB8 trpC2
deg(H)100	1A200	deg(H)100 leuB8 trpC2
deg(H)200	1A199	deg(H)200 leuB8 trpC2
deg-9	1A182	amyE(+M) amyR1 deg-9 metB5 pro(L) purF6 str trpB3
deg-9	1A311	amyE(+M) amyR2 deg-9 metB5 pro(L) purF6 str
deg-42	1A201	deg-42 hisA1 sacA321 trpC2
deg-118	1A340	amyE(+M) amyR1 aroI116 deg-118 metB5 pro(L) str trpB3
dfrA24	1A491	dfrA24 pabA7
divI32	1A318	divI32 trpC2
divIB12	1A146	divIB12 leuB8 metB5 purA16
divII55	1A316	divII55 thr-5 trpC2
divII61	1A317	divII61 thr-5 trpC2
divIVA1	1A196	divIVA1 ilvD thyA1 thyB1
divV32	1A314	divV32 thr-5 trpC2
divV71	1A315	divV71 trpC2
dnaA13	1A175	dnaA13 glnA100 pheA1 trpC2
dnaA13	1A18	dnaA13 ilvA1 metB5
dnaA151	1A25	dnaA151 ilvA1 metB5
dnaB1	1A41	dnaB1 thyA1 thyB1 trpC2
dnaB134	1A17	dnaB134 ilvA1 thyA1 thyB1
	1A290	dnaB134 thyA1 thyB1 trpC2
dnaB19	1A19	dnaB19 ilvA1 metB5
dnaC30	1A20	dnaC30 ilvA1 metB5
dnaD23	1A21	dnaD23 ilvA1 metB5
dnaE20	1A22	dnaE20 ilvA1 metB5
dnaI102	1A26	dnaI102 ilvA1 metB5
dnaN34	1A24	dnaN34 ilvA1 metB5
dnaX8132	1A74	dnaX8132 hisA1 thr-5
	1A93	dnaX8132 hisA1 sacA321 thr-5
dppE132::neo	1A737	dppE132::neo pheA1 trpC2
ebr-2	1A342	ebr-2 hisH2 thyA1 thyB1
efg-1	1A192	cysE14 efg-1 spo-
efg-3	1A238	efg-3 str
bglCΔ102	1A751	apr bglSΔEV bglCΔ102 his npr
	1A752	apr bglSΔEV bglCΔ102 glgB::lacZΔM15 his npr
fbp-1	1A465	fbp-1 hisA1 leuB8 metB5 trpC2

B. subtilis **168 Strains Indexed by Allele**

ALLELE	CODE	DESCRIPTION
fla/che::pLM19	1A763	Cm fla/che::pLM19 trpC2
flaA4	1A139	flaA4 hag-1 lys trpC2
sigD2	1A153	sigD2 lys trpC2
flaC51	1A312	argF4 flaC51 hag-1 hisA1 ura
flgM 80	1A764	flgM 80 pheA1 trpC2
fnd-7	1A424	fnd-7
fnd-8	1A425	fnd-8
fnd-15	1A426	fnd-15
fruA20	1A236	fruA20 ura-3
fruB138	1A91	fruB138 sacA321 trpC2
fruB22	1A237	fruB22 ura-3
	1A377	fruB22 fruC1 metC3 trpC2
fruC1	1A376	fruC1 metC3 trpC2
fruC1	1A377	fruB22 fruC1 metC3 trpC2
ftr-21	1A427	ftr-21
furA1	1A85	furA1
furA2	1S67	cysC7 furA2 spoIIG279
furB	1A154	furB gutR met purF6 trpC2
furB1	1A113	furB1 trpC2
	1A325	furB1 pyrR1 trpC2
	1A675	furB1 sigB::cat trpC2
furC1	1A34	furC1 trpC2
furE1	1A123	furE1 trpC2
furF5	1A61	furF5 spo-
fus	1A192	cysE14 fus-1 Spo$^-$
	1A507	fus Spo(Ts)
	1A508	fus Spo(Con)
pabA7	1A491	dfrA24 pabA7
gcaD26	1A291	gcaD26 leuB8 metB5 purA16
gerA(ABC)11	1G7	gerA(ABC)11 thr-5 trpC2
gerB(ABC)18	1G8	gerB(ABC)18 trpC2
gerCC58	1G11	gerCC58 trpC2 tzm wrd
gerD19	1G9	gerD19 trpC2
gerD97::Tn917	1A677	gerD97::Tn917 rpoA::cat
gerE36	1G12	gerE36 leu-2
gerF45	1G10	gerF45 trpC2
gerG47	1G13	gerG47 met pgk trpC2
glgB::lacZ M15	1A748	glgB::lacZ M15 hsd$_{RI}$R-M+ Km leu met
	1A752	apr bglS EV bglC 102 glgB::lacZ M15 his npr
glmS2	1A468	glmS2 metC7 trpC2
glnA100	1A174	glnA100 ilvC1 pheA1 trpC2
	1A175	dnaA13 glnA100 pheA1 trpC2
glnA103	1A176	glnA103 pheA1 trpC2
glnA200	1A653	glnA200
glnR57	1A715	glnR57
glpD6	1A155	glpD6 trpC2
glpD8	1A239	glpD8 ilvC1 trpC2
glpK21	1A122	glpK21 glyB133 thiA78 tre-12
	1A156	glpK21 purE1 sacA321
	1A240	glpK21 pheA1 trpC2
glpP18	1A157	glpP18 ilvC1 trpC2
glpT6	1A429	aroI906 glpT6 trpC2
gltA1	1A71	gltA1 trpC2
gltA2	1A326	citB1 gltA2 ilvA8 thyB1
	1A327	gltA2 ilvA8 thyA1 thyB1
gltA292	1A7	gltA292 trpC2
gltAB81::Tn917	1A612	(SPβc2) gltAB81::Tn917 trpC2
gltB1	1A490	gltB1 leuB8 metB10
glyA	1A300	glyA thyA1 thyB1 trpC2
glyB133	1A122	glpK21 glyB133 thiA78 tre-12
	1A5	glyB133 metC3 tre-12 trpC2
	1A84	glyB133 metD1
gntK4	1A739	gntK4 metC7 trpC2
gntP9	1A740	gntP9 metC7 trpC2
gntR1	1A741	gntR1 metC7 trpC2
rapA::cat	1A734	rapA::cat
gsiB::neo	1A735	gsiB::neo
gsp-10	1G6	gsp-10 hisH2 metD4 trpC2
gtaB290	1A105	gtaB290 trpC2
gtaC10	1A107	gtaC10 trpC2
gtaC33	1A106	gtaC33 trpC2
guaA2	1A294	guaA2 metC7 purH1 trpC2
guaB1	1A177	guaB1 rplV1
guaB3	1A293	guaB3 metC7 purH1 trpC2
gutA2	1A442	gutA2 leuB8 trpC2
gutB2	1A443	gutB2 leuB8 trpC2
gutR	1A154	furB gutR met purF6 trpC2
gutR1	1A441	gutR1 ura-3
gyrB1	1A160	gyrB1 sacA321
	1A163	gyrB1 recF15 thr-5 trpC2
	1A261	gyrB1 metB4 recD27 trpC2
	1A372	gyrB1 recF15 SPβ- trpC2 xin
gyrB2	1A262	gyrB2 recF15 thr-5 trpC2
hag-1	1A138	argF4 hag-1 smo-1 trpC2
	1A139	flaA4 hag-1 lys trpC2
	1A312	argF4 flaC51 hag-1 hisA1 ura
hag-2	1A136	argF4 hag-2 tagE
	1A140	hag-2 hisA1 ifm-1 ura uvrB1
hag-3	1A137	hag-3 hisA1 ura
hemA1	1A440	arg(GH)2 hemA1
	1A588	hemA1 trpC2
hemB1	1A589	hemB1 trpC2
hemC33	1A590	hemC33 trpC2
hemD11	1A591	hemD11 trpC2
hemE64	1A592	hemE64 trpC2
hemH180	1A593	hemH180 trpC2
hemY321	1A594	hemY321 trpC2
his	1A411	his trpC2
	1A437	ade his hsd$_{RI}$R-M- met nic rib trp tyr ura
	1A683	his
	1A718	his hsd$_{RI}$R-M+ Km lacZ- M15 met rib trpC2 tyr ura
	1A751	apr bglS EV bglC 102 his npr
	1A752	apr bglS EV bglC 102 glgB::lacZ M15 his npr
hisA	1A37	hisA metB10 trpC2
hisA1	1A10	hisA1 thr-5 trpC2
	1A28	argF4 hisA1 trpC2
	1A31	cysB3 hisA1 trpC2
	1A59	hisA1 trpC2
	1A74	dnaX8132 hisA1 thr-5
	1A90	hisA1 sacA321 trpC2
	1A93	dnaX8132 hisA1 sacA321 thr-5
	1A108	hisA1 tyrA1
	1A115	hisA1 pyrA5 trpC2
	1A137	hag-3 hisA1 ura
	1A140	hag-2 hisA1 ifm-1 ura uvrB1
	1A141	hisA1 hsd$_{RI}$R-M- leuB8 lys-21 metB5 nonA1 SP10^S thr-5 trpC2 φNR2^S
	1A150	hpr hisA1 pha-1
	1A151	argF4 hpr hisA1 pha-1
	1A168	hisA1 metB5 uvrB1
	1A169	hisA1 sacB182 trpC2
	1A201	deg-42 hisA1 sacA321 trpC2
	1A207	aroE1 hisA1
	1A242	hisA1 thr-5 trpC2
	1A264	-(hisA1)+ sup-44 thr-5
	1A279	-(hisA1)+ -(metC3)+ sup-22 trpC2
	1A302	argF4 hisA1 recA4
	1A312	argF4 flaC51 hag-1 hisA1 ura
	1A319	argF4 hisA1 purH4 trpC2
	1A445	hisA1 leuB8 lys-21 metB5 nonA1 purF6 SP10^R thr-5 trpC2
	1A446	hisA1 leuB8 lys-21 metB5 nonA1 SP10^R trpC2
	1A448	hisA1 hsd$_{RI}$R-M- leuB8 nonA1 rpoB SP10^S thr-5
	1A465	fbp-1 hisA1 leuB8 metB5 trpC2
	1A476	hisA1 metB5
	1A477	-(hisA1)+ -(metB5)+ sup-1

B. subtilis **168 Strains Indexed by Allele**

ALLELE	CODE	DESCRIPTION
hisA1 (cont)	1A509	hisA1 hsd$_{RI}$R-M- metB5 recA4
	1A706	com-9 hisA1 leu-8 lys-21 metB5 thr-5 trpC2
	1A707	com-71 hisA1 leu-8 metB5 purF6 thr-5 trpC2
	1A708	com-30 hisA1 leu-8 lys-21 metB5 thr-5 trpC2
	1A709	com-104 hisA1 leu-8 lys-21 metB5 thr-5 trpC2
	1A710	com-31 hisA1 leu-8 lys-21 metB5 thr-5 trpC2
	1A711	com-14::Tn917 hisA1 leu-8 lys-21 metB5 purF6 thr-5 trpC2
	1A712	com-18::Tn917 hisA1 leu-8 lys-21 metB5 purF6 thr-5 trpC2
	1A713	com-44::Tn917 hisA1 leu-8 lys-21 metB5 purF6 thr-5 trpC2
	1S44	argF4 hisA1 metB5 pheA12 purA16 pyrA26 spoVB91 trpC2
	1S97	hisA1 leuA8 metB5 sinR::phl
	1S98	hisA1 leuA8 metB5 sinI::kan-50
hisA53	1A390	hisA53 rna-53
	1A404	aroB2 hisA53 hisH2 rna-53 trpC2 tyrA1
hisA82::Tn917	1A626	(SPβc2) hisA82::Tn917 trpC2
hisB	1A720	hisB leuA8 metB5 polA5 SPβ-xin-1
hisH	1A171	hisH leuB8 sacP1 sac(XY)189
hisH2	1A36	aroB2 hisH2 metB10 trpC2 tyrA1
	1A58	hisH2 trpC2
	1A83	aroB2 hisH2
	1A87	hisH2 trpC2 tyrA1
	1A89	hisH2 leuB8
	1A103	aroB2 hisH2 recG40 trpC2 tyrA1
	1A126	hisH2 leuB8 sacA321 thiC5
	1A131	aroB4 hisH2
	1A133	aroE1 hisH2
	1A173	hisH2 tyrA1
	1A208	hisH2
	1A224	hisH2 pheA1 trpC2
	1A226	hisH2 pheA1 polA5 trpC2
	1A298	aroB2 azpB80 hisH2 trpC2 tyrA1
	1A299	aroB2 hisH2 gyrA trpC2 tyrA1
	1A301	hisH2 recH342 trpC2
	1A334	addA5 hisH2 metB5
	1A342	ebr-2 hisH2 thyA1 thyB1
	1A343	hisH2 rec-80 thyA1 thyB1
	1A346	hisH2 thyA1 thyB1 uvrC109
	1A347	hisH2 thyA1 thyB1 uvrC114
	1A355	hisH2 pabB trpC2
	1A378	aroB2 hisH2 recD41 trpC2 tyrA1
	1A379	aroB2 hisH2 recG39 trpC2 tyrA1
	1A380	aroB2 hisH2 recF33 trpC2 tyrA1
	1A382	hisH2 pur-60 trpC2
	1A383	hisH2 purE7 trpC2
	1A385	hisH2 purE8 trpC2
	1A386	hisH2 purH5 thr trpC2
	1A404	aroB2 hisA53 hisH2 rna-53 trpC2 tyrA1
	1A482	hisH2 metD4 outA7 trpC2
	1A494	hisH2 leu met recF7
	1A497	hisH2 rec-25 trpC2
	1A498	hisH2 rec-29 trpC2
	1A499	hisH2 rec-30 trpC2
	1A574	hisH2 ilvC1/ilvC(+)
	1A695	hisH2 sul ten trpC2
	1G1	hisH2 outF4 trpC2
	1G14	hisH2 metD4 outA7 trpC2
hisH2 (cont)	1G3	hisH2 outE42 trpC2
	1G4	hisH2 metD4 outD1 trpC2
	1G5	hisH2 outC25 trpC2
	1G6	gsp-10 hisH2 metD4 trpC2
hisH101	1A514	hisH101 lys-21 recA4 splB1 thyA thyB uvrB10
hom-1	1A356	aec hom-1 trpC2
	1A360	hom-1 trpC2
hpr	1A150	hpr hisA1 pha-1
	1A151	argF4 hpr hisA1 pha-1
hpr-10	1A178	hpr-10 trpC2
hpr-12	1A179	hpr-12 trpC2
hpr-16	1A180	hpr-16
hpr-18	1A181	hpr-18
hsd$_{BI}^+$	1A451	hsd$_{BI}^+$ hsd$_{CI}^+$
hsd$_{CI}^+$	1A451	hsd$_{BI}^+$ hsd$_{CI}^+$
hsd$_{RI}$R$^-$M$^-$	1A447	hsd$_{RI}$R$^-$ M$^-$ leuB8 metB5 SP10^R
	1A141	hisA1 hsd$_{RI}$R$^-$M$^-$ leuB8 lys-21 metB5 nonA1 SP10^S thr-5 trpC2 φNR2^S
	1A253	arg(GH)15 hsd$_{RI}$R$^-$M$^-$ leuB8 SP10^S
	1A363	arg(GH)15 hsd$_{RI}$R$^-$M$^-$ leuB8 rplV
	1A409	arg(GH)15 hsd$_{RI}$R$^-$M$^-$ leuB8 recA4
	1A422	hsd$_{RI}$R$^-$ M$^-$ leuB6 recA4
	1A423	arg(GH)15 hsd$_{RI}$R$^-$M$^-$ leuB8 recA4 thr-5
hsd$_{RI}$R$^-$M$^-$	1A436	hsd$_{RI}$R$^-$ M$^-$ trpC2
	1A437	ade his hsd$_{RI}$R-M- met nic rib trp tyr ura
	1A448	hisA1 hsd$_{RI}$R$^-$M$^-$ leuB8 nonA1 rpoB SP10^S thr-5
	1A509	hisA1 hsd$_{RI}$R$^-$M$^-$ metB5 recA4
	1A510	arg(GH)15 hsd$_{RI}$R$^-$M$^-$ leuB8 recA4 stp thr
	1A438	hsd$_{RI}$R$^-$M$^+$ met nic rib trp tyr ura
	1A685	hsd$_{RI}$R$^-$M$^+$ rib trpC2 tyr-1 ura
	1A718	his hsd$_{RI}$R$^-$M$^+$ Km lacZ- M15 met rib trpC2 tyr ura
	1A748	glgB::lacZ M15 hsd$_{RI}$R$^-$M$^+$ Km leu met
hutCR1	1A273	hutCR1 str sul
hutH1	1A272	hutH1 str sul
hutP1	1A271	hutP1 str sul
ifm-1	1A140	hag-2 hisA1 ifm-1 ura uvrB1
ile	1A258	ile leu metB5 thyA1 thyB1
	1A259	-(met)+ ile leu thyA1 thyB1 trnS-Lys3
	1A260	-(met)+ ile leu sup-44 thyA1 thyB1
ilvA1	1A6	ilvA1 pyrD1 thyA1 thyB1 trpC2
	1A17	dnaB134 ilvA1 thyA1 thyB1
	1A18	dnaA13 ilvA1 metB5
	1A19	dnaB19 ilvA1 metB5
	1A20	dnaC30 ilvA1 metB5
	1A21	dnaD23 ilvA1 metB5
	1A22	dnaE20 ilvA1 metB5
	1A23	ilvA1 metB5 polC133
	1A24	dnaN34 ilvA1 metB5
	1A25	dnaA151 ilvA1 metB5
	1A26	dnaI102 ilvA1 metB5
	1A75	ilvA1 leuB8 metB5
	1A76	ilvA1 metB5 spcB1
	1A77	ilvA1 metB5 strB3
	1A81	ilvA1 leuB8 metB5 polC12 spcB1
	1A82	ilvA1 leuB8 metB5 polC12
	1A86	ilvA1 leu leuB8 metB5 polA1443
	1A142	ilvA1 sacA78 thyA112
	1A143	citB17 ilvA1 sacA78 thyB204
	1A144	ilvA1 sacA78 thyA112 thyB204
	1A162	ilvA1 novB thyA1

B. subtilis **168 Strains Indexed by Allele**

ALLELE	CODE	DESCRIPTION
ilvA1 (cont)	1A276	ilvA1 metB5 polA1443 polC1
	1A420	ilvA1 metB5 purA16 xhi-1479 xki-1479
	1A421	(φ105) ilvA1 metB5 purA16 xhi-1479 xki-1479
	1A463	ddlA1475 ilvA1 metB5 purA16
	1A681	apt-6 ilvA1 pbuG3 pupA3 sacA78 upp
	1A682	ilvA1 pubG1 sacA78 upp xpt
ilvA2	1A231	ilvA2 trpC2
	1A457	ilvA2 ilvD15 SPβ- thyA5 thyB5 trpC2
	1A458	ilvA2 SPβ- thyA5 thyB5 trpC2
	1A575	ilvA2 recA4 spcB1 trpC2
ilvA3	1A99	odhB1 ilvA3 trpC2
	1A204	ilvA3 trpC2
ilvA6	1A361	ilvA6
ilvA8	1A326	citB1 gltA2 ilvA8 thyB1
	1A327	gltA2 ilvA8 thyA1 thyB1
	1A332	citD 1 ilvA8 thyA1 thyB1
	1A460	ilvA8 metB5 thyA1 thyB1
ilvA64	1A30	ilvA64 leuB8 metB5 purA16
ilvB2	1A109	ilvB2 trpC2
	1A452	ilvB2 leuA169
	1A453	ilvB2 trpC2
ilvB3	1A203	ilvB3 trpC2
ilvB 1	1A147	alsR1 ccpA1 ilvB 1 trpC2
	1A172	ilvB 1 trpC2
	1A250	alsR1 ilvB 1 trpC2
ilvB 5	1A228	ilvB 5 trpC2
ilvC1	1A57	ilvC1 pheA1 trpC2
	1A157	glpP18 ilvC1 trpC2
	1A174	glnA100 ilvC1 pheA1 trpC2
	1A239	glpD8 ilvC1 trpC2
	1A249	ilvC1 pheA1 strC23
	1S36	ilvC1 spoIIIA(A-H)7 trpC2
ilvC1/ilvC(+)	1A574	hisH2 ilvC1/ilvC(+)
ilvD	1A196	divIVA1 ilvD thyA1 thyB1
ilvD2	1A233	ilvD2 trpC2
ilvD4	1A232	ilvD4 trpC2
ilvD6	1A230	ilvD6 thyA1 trpC2
	1A456	ilvD6 thyA thyB1
ilvD15	1A110	ilvD15 trpC2
	1A457	ilvA2 ilvD15 SPβ- thyA5 thyB5 trpC2
ilv 1	1A98	ilv 1 kauA1 metB5
inh-1	1A285	inh-1
inh-491	1A286	inh-491
iolG6	1A738	iolG6 metC7 trpC2
iur	1A472	bfmB1 iur trpC2
kan-2	1A193	kan-2 spo-
kauA1	1A98	ilv 1 kauA1 metB5
kinA2	1S85	argF4 kinA2 leu-2 pyrA26
kinA82	1A736	kinA82
kinA96	1S59	kinA96 trpC2
kinA::Tn917 HU19	1S120	kinA::Tn917 HU19
Km	1A718	his hsd$_{RI}$R-M+ Km lacZ- M15 met rib trpC2 tyr ura
	1A748	glgB::lacZ M15 hsd$_{RI}$R-M+ Km leu met
ksgA618	1A187	ksgA618 thyA1 thyB1 trpC2
ksgA619	1A188	ksgA619 thyA1 thyB1 trpC2
lacZ- M15	1A718	his hsd$_{RI}$R-M+ Km lacZ- M15 met rib trpC2 tyr ura
leu	1A86	ilvA1 leu leuB8 metB5 polA1443
	1A258	ile leu metB5 thyA1 thyB1
	1A259	-(met)+ ile leu thyA1 thyB1 trnS-Lys3
	1A260	-(met)+ ile leu sup-44 thyA1 thyB1
	1A494	hisH2 leu met recF7
leu (cont)	1A748	glgB::lacZ M15 hsd$_{RI}$R-M+ Km leu met
leu-2	1A280	asaA 2 leu-2 trpC2
	1A281	asaA4 leu-2 trpC2
	1A282	asaA 2 asaB1 leu-2 trpC2
	1A283	asaA4 asaB4 leu-2 trpC2
	1A674	leu-2 sdhB103 trpC2
	1G12	gerE36 leu-2
	1S84	argF4 cotA leu-2 pyrA26 scoA1
	1S85	argF4 kinA2 leu-2 pyrA26
leu-8	1A706	com-9 hisA1 leu-8 lys-21 metB5 thr-5 trpC2
	1A707	com-71 hisA1 leu-8 metB5 purF6 thr-5 trpC2
	1A708	com-30 hisA1 leu-8 lys-21 metB5 thr-5 trpC2
	1A709	com-104 hisA1 leu-8 lys-21 metB5 thr-5 trpC2
	1A710	com-31 hisA1 leu-8 lys-21 metB5 thr-5 trpC2
	1A711	com-14::Tn917 hisA1 leu-8 lys-21 metB5 purF6 thr-5 trpC2
	1A712	com-18::Tn917 hisA1 leu-8 lys-21 metB5 purF6 thr-5 trpC2
	1A713	com-44::Tn917 hisA1 leu-8 lys-21 metB5 purF6 thr-5 trpC2
leuA8	1A720	hisB leuA8 metB5 polA5 SPβ- xin-1
	1S97	hisA1 leuA8 metB5 sinR::phl
	1S98	hisA1 leuA8 metB5 sinI::kan-50
leuA164	1A119	arg(GH)2 leuA164 pheA2 trpC2
leuA169	1A367	leuA169 suf-1 trpC2
	1A452	ilvB2 leuA169
	1A454	leuA169 trpC2
leuB6	1A114	leuB6 trpC2
	1A422	hsd$_{RI}$R-M- leuB6 recA4
leuB7	1A116	leuB7 trpC2
leuB8	1A9	ald-1 aroA932 leuB8 trpC2
	1A12	leuB8 metB5 purF6
	1A13	car-41 leuB8 metB5 purF6
	1A14	-(metB5)+ -(thr-5)+ leuB8 trnS-Lys3
	1A29	leuB8 metB5 nic-38 purA16
	1A30	ilvA64 leuB8 metB5 purA16
	1A68	leuB8 metB5 tsi-23
	1A75	ilvA1 leuB8 metB5
	1A81	ilvA1 leuB8 metB5 polC12 spcB1
	1A82	ilvA1 leuB8 metB5 polC12
	1A86	ilvA1 leu leuB8 metB5 polA1443
	1A89	hisH2 leuB8
	1A95	deg(H)32 leuB8 trpC2
	1A126	hisH2 leuB8 sacA321 thiC5
	1A141	hisA1 hsd$_{RI}$R-M- leuB8 lys-21 metB5 nonA1 SP10^{S} thr-5 trpC2 φNR2^{S}
	1A145	leuB8 metB5 purA16
	1A146	divIB12 leuB8 metB5 purA16
	1A171	hisH leuB8 sacP1 sac(XY)189
	1A199	deg(H)200 leuB8 trpC2
	1A200	deg(H)100 leuB8 trpC2
	1A202	deg leuB8 trpC2
	1A253	arg(GH)15 hsd$_{RI}$R-M- leuB8 SP10^{S}
	1A291	gcaD26 leuB8 metB5 purA16
	1A307	leuB8 phoS5 tal-1
	1A336	amm-35 leuB8 metB5 purA16
	1A363	arg(GH)15 hsd$_{RI}$R-M- leuB8 rplV
	1A409	arg(GH)15 hsd$_{RI}$R-M- leuB8 recA4
	1A423	arg(GH)15 hsd$_{RI}$R-M- leuB8 recA4 thr-5
	1A434	ala-1 leuB8 metB pur thr-5 trpC

B. subtilis 168 Strains Indexed by Allele

ALLELE	CODE	DESCRIPTION
leuB8 (cont)	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
	1A447	hsd$_{RI}$R- M- leuB8 metB5 SP10^R
	1A448	hisA1 hsd$_{RI}$R-M- leuB8 nonA1 rpoB SP10^S thr-5
	1A449	car-41 leuB8 metB5 purF6 rpoC105
	1A459	leuB8 metB5 SPβ- thr-5 trnS-Lys3
	1A462	leuB8 metB5 tem-1
	1A465	fbp-1 hisA1 leuB8 metB5 trpC2
	1A485	leuB8 mreD1
	1A486	leuB8 tagF1
	1A490	gltB1 leuB8 metB10
	1A510	arg(GH)15 hsd$_{RI}$R-M- leuB8 recA4 stp thr
	1A678	leuB8 menB325 trpC2
	1A679	ald-1 leuB8 menE312 trpC2
	1S60	leuB8 spoIIG41 tal-1
	1S64	leuB8 rpoB2 spoIIIC92 tal-1
leuB84::Tn917	1A618	(SP(sc2) leuB84::Tn917 trpC2
leuD117	1A368	leuD117 sup-67 trpC2
liv1-82::Tn917	1A619	(SPβc2) liv1-82::Tn917 trpC2
liv3-83::Tn917	1A620	(SPβc2) liv3-83::Tn917 trpC2
lmrA2	1A221	lmrA2
	1A501	amy-3 aro-10 lmrA2
lys	1A139	flaA4 hag-1 lys trpC2
	1A153	sigD2 lys trpC2
	1A765	lys trpC2
	1A766	lys relA trpC2
lys-1	1A8	aroD120 lys-1 trpC2
	1A348	lys-1 lysS2
lys-1	1A351	lys-1 lysS1
	1A357	aecB lys-1 sul trpC2
	1A358	lysC lys-1 sul trpC2
	1A466	lys-1 pyrD1 rpoB sas-1
	1A467	lys-1 pyrD1 rpoB sas-2
	1S90	lys-1 spo0B(TS)
	1S91	lys-1 spo0B(TS)
	1S92	lys-1 spoIVF(TS)
	1S93	lys-1 spoVB
lys-21	1A141	hisA1 hsd$_{RI}$R-M- leuB8 lys-21 metB5 nonA1 SP10^S thr-5 trpC2 φNR2^S
	1A212	arg(GH)3 lys-21 metB5 pheA12 purA16 rplV1
	1A277	arg(GH)3 lys-21 metB5 pheA12
	1A445	hisA1 leuB8 lys-21 metB5 nonA1 purF6 SP10^R thr-5 trpC2
	1A446	hisA1 leuB8 lys-21 metB5 nonA1 SP10^R trpC2
	1A514	hisH101 lys-21 recA4 splB1 thyA thyB uvrB10
	1A706	com-9 hisA1 leu-8 lys-21 metB5 thr-5 trpC2
	1A708	com-30 hisA1 leu-8 lys-21 metB5 thr-5 trpC2
	1A709	com-104 hisA1 leu-8 lys-21 metB5 thr-5 trpC2
	1A710	com-31 hisA1 leu-8 lys-21 metB5 thr-5 trpC2
	1A711	com-14::Tn917 hisA1 leu-8 lys-21 metB5 purF6 thr-5 trpC2
	1A712	com-18::Tn917 hisA1 leu-8 lys-21 metB5 purF6 thr-5 trpC2
	1A713	com-44::Tn917 hisA1 leu-8 lys-21 metB5 purF6 thr-5 trpC2
lys-3	1A35	lys-3 metB10 tagE trpC2
	1A40	lys-3 metB10 trpC2
	1A478	lys-3 metB10 spc spcD trpC2

ALLELE	CODE	DESCRIPTION
lys-3 (cont)	1A511	lys-3 thyA thyB trpC2
	1A650	lys-3 xynB7
	1A651	lys-3 xynA8
lys-82::Tn917	1A615	(SPβc2) lys-82::Tn917 trpC2
lysC	1A358	lysC lys-1 sul trpC2
lysS1	1A350	lysS1 trpC2
	1A351	lys-1 lysS1
lysS2	1A348	lys-1 lysS2
	1A349	lysS2 metB3
lyt-1	1A483	lyt-1 metC3
lyt-15	1A504	lyt-15 thyA thyB trpC2 xin-15
lyt-2	1A484	lyt-2 metC3
mc^S	1A505	mc^S trpC2 uv^S
menB325	1A678	leuB8 menB325 trpC2
menC315	1A439	leuB8 menC315 trpC2
menE312	1A679	ald-1 leuB8 menE312 trpC2
met	1A154	furB gutR met purF6 trpC2
	1A259	-(met)+ ile leu thyA1 thyB1 trnS-Lys3
	1A260	-(met)+ ile leu sup-44 thyA1 thyB1
	1A322	met pyrE305
	1A323	met pyrD319
	1A428	met trpC2 ts-39-2
	1A437	ade his hsd$_{RI}$R$^-$M$^-$ met nic rib trp tyr ura
	1A438	hsd$_{RI}$R$^-$M$^+$ met nic rib trp tyr ura
	1A492	citC met pheA trpC2
	1A493	citC met polA10 trpC2
	1A494	hisH2 leu met recF7
	1A684	met
	1A718	his hsd$_{RI}$R$^-$M$^+$ Km lacZ- M15 met rib trpC2 tyr ura
	1A748	glgB::lacZ M15 hsd$_{RI}$R$^-$M$^+$ Km leu met
	1G13	gerG47 met pgk trpC2
	1S31	ade met spoIIA26 trpC2
	1S73	ade met Sm spo0A16 trpC2
met-14	1A344	met-14 sul thyA1 thyB1 trpC2 uvrB10
	1A345	met-14 sul thyA1 thyB1 trpC2 uvrB42
	1A488	met-14 splB1 sul thyA1 thyB1 trpC2
	1A489	met-14 splB1 sul thyA1 thyB1 trpC2 uvrB42
metA4	1A158	metA4
metA8	1A118	arg(ABCDE)1 metA8 trpC2
metA29	1A125	argF4 metA29 thiB4
metB	1A434	ala-1 leuB8 metB pur thr-5 trpC
metB2	1A234	metB2 trpC2
metB3	1A235	metB3 trpC2
	1A349	lysS2 metB3
metB4	1A261	gyrB1 metB4 recD27 trpC2
	1A335	metB4 recB2 trpC2
	1A495	metB4 recB19 trpC2
	1A496	metB4 recF15 trpC2
	1A73	metB4 recA1 trpC2
	1S7	metB4 spo0A6 trpC2
metB5	1A12	leuB8 metB5 purF6
	1A13	car-41 leuB8 metB5 purF6
	1A14	-(metB5)+ -(thr-5)+ leuB8 trnS-Lys3
	1A18	dnaA13 ilvA1 metB5
	1A19	dnaB19 ilvA1 metB5
	1A20	dnaC30 ilvA1 metB5
	1A21	dnaD23 ilvA1 metB5
	1A22	dnaE20 ilvA1 metB5
	1A23	ilvA1 metB5 polC133
	1A24	dnaN34 ilvA1 metB5
	1A25	dnaA151 ilvA1 metB5
	1A26	dnaI102 ilvA1 metB5

B. subtilis **168 Strains Indexed by Allele**

ALLELE	CODE	DESCRIPTION
metB5 (cont)	1A29	leuB8 metB5 nic-38 purA16
	1A30	ilvA64 leuB8 metB5 purA16
	1A55	aroI906 dal-1 metB5 sacA321
	1A68	leuB8 metB5 tsi-23
	1A75	ilvA1 leuB8 metB5
	1A76	ilvA1 metB5 spcB1
	1A77	ilvA1 metB5 strB3
	1A81	ilvA1 leuB8 metB5 polC12 spcB1
	1A82	ilvA1 leuB8 metB5 polC12
	1A86	ilvA1 leu leuB8 metB5 polA1443
	1A98	ilv 1 kauA1 metB5
	1A141	hisA1 hsd$_{RI}$R-M- leuB8 lys-21 metB5 nonA1 SP10^{S} thr-5 trpC2 φNR2^{S}
	1A145	leuB8 metB5 purA16
	1A146	divIB12 leuB8 metB5 purA16
	1A168	hisA1 metB5 uvrB1
	1A182	amyE(+M) amyR1 deg-9 metB5 pro(L) purF6 str trpB3
	1A197	metB5 minD1 tag-1 thyA thyB1 spo^{-}
	1A212	arg(GH)3 lys-21 metB5 pheA12 purA16 rplV1
	1A258	ile leu metB5 thyA1 thyB1
	1A276	ilvA1 metB5 polA1443 polC1
	1A277	arg(GH)3 lys-21 metB5 pheA12
	1A288	amyE dal-1 metB5 sacA321
	1A289	amyE aroI906 metB5 sacA321
	1A291	gcaD26 leuB8 metB5 purA16
	1A292	metB5 minD1 thyA1 thyB1
	1A304	metB5 SPβ- trpC2 xin-1
	1A311	amyE(+M) amyR2 deg-9 metB5 pro(L) purF6 str
	1A334	addA5 hisH2 metB5
	1A336	amm-35 leuB8 metB5 purA16
	1A338	amyE(+M) amyR1(+M) metB5 pro(L) purF6 trpB3
	1A339	amyE(+M) amyR21(+M)(H) metB5 pro(L) purF6 str trpB3
	1A340	amyE(+M) amyR1 aroI116 deg-118 metB5 pro(L) str trpB3
	1A341	amyE(+M) amyR1(+M) metB5 pro(H) purF6 str trpB3
	1A387	metB5 purE26
	1A388	metB5 purE4
	1A389	metB5 purE5
	1A412	amyE(+M) amyR2 metB5 purF6
	1A413	amyE(+N) amyR1 metB5
	1A414	amyE(+N) amyR2 metB5 purF6
	1A420	ilvA1 metB5 purA16 xhi-1479 xki-1479
	1A421	(φ105) ilvA1 metB5 purA16 xhi-1479 xki-1479
	1A445	hisA1 leuB8 lys-21 metB5 nonA1 purF6 SP10^{R} thr-5 trpC2
	1A446	hisA1 leuB8 lys-21 metB5 nonA1 SP10^{R} trpC2
	1A447	hsd$_{RI}$R- M- leuB8 metB5 SP10^{R}
	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$_{RI}$R-M- metB5 recA4
	1A701	addB72 amyE SPβ- metB5 sigB trpC2 xin-1
metB5 (cont)	1A702	addB71 amyE SPβ- metB5 sigB xin-1
	1A703	amyE SPβ- metB5 recP149 sigB trpC2 xin-1
	1A706	com-9 hisA1 leu-8 lys-21 metB5 thr-5 trpC2
	1A707	com-71 hisA1 leu-8 metB5 purF6 thr-5 trpC2
	1A708	com-30 hisA1 leu-8 lys-21 metB5 thr-5 trpC2
	1A709	com-104 hisA1 leu-8 lys-21 metB5 thr-5 trpC2
	1A710	com-31 hisA1 leu-8 lys-21 metB5 thr-5 trpC2
	1A711	com-14::Tn917 hisA1 leu-8 lys-21 metB5 purF6 thr-5 trpC2
	1A712	com-18::Tn917 hisA1 leu-8 lys-21 metB5 purF6 thr-5 trpC2
	1A713	com-44::Tn917 hisA1 leu-8 lys-21 metB5 purF6 thr-5 trpC2
	1A720	hisB leuA8 metB5 polA5 SPβ- xin-1
	1A746	Em metB5 recA260 SPβ- trpC2 xin-1
	1S2	metB5 spo0A3 thr-5
	1S3	-(metB5)+ spo0A3 sup-44 thr-5
	1S4	-(metB5)+ -(thr-5)+ spo0A3 trnS-Lys3
	1S44	argF4 hisA1 metB5 pheA12 purA16 pyrA26 spoVB91 trpC2
	1S77	metB5 spoIIA50 thr-5
	1S97	hisA1 leuA8 metB5 sinR::phl
	1S98	hisA1 leuA8 metB5 sinI::kan-50
metB10	1A35	lys-3 metB10 tagE trpC2
	1A36	aroB2 hisH2 metB10 trpC2 tyrA1
	1A37	hisA metB10 trpC2
	1A38	metB10 purF6 trpC2
	1A40	lys-3 metB10 trpC2
	1A381	cafA1 metB10 trpC2
	1A478	lys-3 metB10 spc spcD trpC2
	1A490	gltB1 leuB8 metB10
	1A719	metB10 trpC2 xylAB 1
metC	1A263	metC pfk ptsI1
metC3	1A5	glyB133 metC3 treA12 trpC2
	1A60	metC3 pyrA xin-1
	1A78	metC3 pyrA xtl-1
	1A279	-(hisA1)+ -(metC3)+ sup-22 trpC2
	1A284	metC3 pyrA xhd-1
	1A306	metC3 phoR2 tal-1
	1A376	fruC1 metC3 trpC2
	1A377	fruB22 fruC1 metC3 trpC2
	1A483	lyt-1 metC3
	1A484	lyt-2 metC3
	1S27	metC3 spoIIIJ87 tal-1
	1S42	metC3 spoIIIA(A-H)35 tal-1
	1S65	metC3 spoIVF88 tal-1
	1S66	metC3 rpoB2 spoVC285
	1S78	metC3 rpoB2 sigF63 tal-1
	1S87	metC3 spoIVG-25 tal-1
metC7	1A80	metC7 trpC2
	1A293	guaB3 metC7 purH1 trpC2
	1A294	guaA2 metC7 purH1 trpC2
	1A468	glmS2 metC7 trpC2
	1A471	pdhA1 bfmB metC7 trpC2
	1A738	iolG6 metC7 trpC2
	1A739	gntK4 metC7 trpC2
	1A740	gntP9 metC7 trpC2
	1A741	gntR1 metC7 trpC2
metC85::Tn917	1A607	(SPβc2) metC85::Tn917 trpC2
metD1	1A84	glyB133 metD1
metD4	1A482	hisH2 metD4 outA7 trpC2
	1G14	hisH2 metD4 outA7 trpC2

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ALLELE	CODE	DESCRIPTION
metD4 (cont)	1G4	hisH2 metD4 outD1 trpC2
	1G6	gsp-10 hisH2 metD4 trpC2
metD83::Tn917	1A604	(SPβc2) metD83::Tn917 trpC2
minD1	1A197	metB5 minD1 thyA thyB1 spo$^-$
	1A292	metB5 minD1 thyA1 thyB1
MLS^R	1A717	amyE::erm MLS
	1A746	metB5 MLS recA260 SPβ- trpC2 xin-1
	1A749	::Tn917lac MLS^R
	1A759	::Tn917 MLS^R
	1A760	::Tn917::pTV20 Cm MLS^R
	1A762	::Tn917::pTV20 bac-1 Cm MLS^R
	1A767	Cm MLS pheA1 phoA::pCE413 phoB::Tn917 trpC2
	1A771	amyE::erm MLS pheA1 trpC2
	1S99	MLS^R spoVK::Tn917HU8 SPβ-
motA::Tn917	1A631	(SPβc2) motA::Tn917 trpC2
mreD1	1A485	leuB8 mreD1
mth-83::Tn917	1A624	(SPβc2) mth-83::Tn917 trpC2
mth-84::Tn917	1A625	(SPβc2) mth-84::Tn917 trpC2
mtlD1	1A54	mtlD1 nasC1 sacA321
mtr-264	1A72	mtr-264
nadE47	1A647	arg nadE47 thyA thyB
nadE48	1A648	arg nadE48 thyA thyB
nadE49	1A597	arg nadE49 thyA thyB
nadE81	1G2	hisH2 nadE81 trpC2
gyrA	1A299	aroB2 hisH2 gyrA trpC2 tyrA1
narA1	1A159	deg(H)25 narA1
	1A205	narA1 trpC2 ura-1
	1A94	narA1 trpC2
nasC1	1A54	mtlD1 nasC1 sacA321
nea-1	1A194	cysE14 nea-1 spo-
nic	1A410	nic
	1A437	ade his hsd$_{RI}$R-M- met nic rib trp tyr ura
	1A438	hsd$_{RI}$R-M+ met nic rib trp tyr ura
nic-38	1A29	leuB8 metB5 nic-38 purA16
nic-82::Tn917	1A616	(SPβc2) nic-82::Tn917 trpC2
nonA1	1A141	hisA1 hsd$_{RI}$R-M- leuB8 lys-21 metB5 nonA1 SP10^S thr-5 trpC2 φNR2^S
	1A445	hisA1 leuB8 lys-21 metB5 nonA1 purF6 SP10^R thr-5 trpC2
	1A446	hisA1 leuB8 lys-21 metB5 nonA1 SP10^R trpC2
	1A448	hisA1 hsd$_{RI}$R-M- leuB8 nonA1 rpoB SP10^S thr-5
novB	1A162	ilvA1 novB thyA1
novB75	1A127	novB75 trpC2
nprB	1A274	npr
	1A751	apr bglS EV bglC 102 his npr
	1A752	apr bglS EV bglC 102 glgB::lacZ M15 his npr
odhA5	1A672	odhA5 odhA5 trpC2
	1A672	odhA5 odhA5 trpC2
odhB1	1A99	odhB1 ilvA3 trpC2
odhB17	1A673	odhB17 trpC2
ole-2	1A195	cysE14 ole-2 spo-
opp141	1S28	opp141 trpC2
outA7	1A482	hisH2 metD4 outA7 trpC2
	1G14	hisH2 metD4 outA7 trpC2
outC25	1G5	hisH2 outC25 trpC2
outD1	1G4	hisH2 metD4 outD1 trpC2
outE42	1G3	hisH2 outE42 trpC2
outF4	1G1	hisH2 outF4 trpC2
oxr-1	1A502	oxr-1 thyA thyB
oxr-2	1A503	oxr-2 thyA thyB trpC2
pabB	1A355	hisH2 pabB trpC2
pubG1	1A682	ilvA1 pubG1 sacA78 upp xpt
pbuG3	1A681	apt-6 ilvA1 pbuG3 pupA3 sacA78 upp
pdhA1	1A471	pdhA1 bfmB metC7 trpC2
pdhD22	1A70	pdhD22 trpC2
pfk	1A263	metC pfk ptsI1
pgk	1G13	gerG47 met pgk trpC2
pha-1	1A150	hpr hisA1 pha-1
	1A151	argF4 hpr hisA1 pha-1
pheA	1A254	pheA phoP
	1A492	citC met pheA trpC2
pheA1	1A57	ilvC1 pheA1 trpC2
	1A96	pheA1 trpC2
	1A174	glnA100 ilvC1 pheA1 trpC2
	1A175	dnaA13 glnA100 pheA1 trpC2
	1A176	glnA103 pheA1 trpC2
	1A224	hisH2 pheA1 trpC2
	1A225	pheA1 polA5 trpC2
	1A226	hisH2 pheA1 polA5 trpC2
	1A227	pheA1 trpC2
	1A240	glpK21 pheA1 trpC2
	1A249	ilvC1 pheA1 strC23
	1A275	pheA1
	1A698	pheA1 sfp
	1A699	pheA1 sfp srfA::Tn917
	1A737	dppE132::neo pheA1 trpC2
	1A764	flgM 80 pheA1 trpC2
	1A767	Cm MLS pheA1 phoA::pCE413 phoB::Tn917 trpC2
	1A771	amyE::erm MLS pheA1 trpC2
	1A772	amyE::cat Cm pheA1 trpC2
	1A773	Cm pheA1 thrC::cat trpC2
	1A774	pheA1 rpoC:☹His6-tag) Sp trpC2
	1S108	Cm cotT::pDE194 pheA1 trpC2
	1S16	pheA1 spo0B136 trpC2
	1S17	pheA1 spo0E11 trpC2
	1S19	pheA1 spo0F221 trpC2
	1S24	pheA1 sigH81 trpC2
	1S26	pheA1 spoIIIJ87 trpC2
	1S68	abrB23 pheA1 spo0A12 trpC2
	1S83	pheA1 spoVF1 trpC2
	1S9	pheA1 spo0A12 trpC2
	1S96	bofA::Tn917lac pheA1 trpC2
pheA12	1A66	pheA12 tolA6 trpC2
	1A67	pheA12 tolA6 trpC2 φ29^R
	1A211	arg(GH)3 pheA12 rplV1
	1A212	arg(GH)3 lys-21 metB5 pheA12 purA16 rplV1
	1A277	arg(GH)3 lys-21 metB5 pheA12
	1S44	argF4 hisA1 metB5 pheA12 purA16 pyrA26 spoVB91 trpC2
	1S46	pheA12 spoIVA178
pheA2	1A15	pheA2 trpC2
	1A119	arg(GH)2 leuA164 pheA2 trpC2
	1A121	arg(GH)2 pheA2 sdhC109 trpC2
pheA82::Tn917	1A617	(SPβc2) pheA82::Tn917 trpC2
phoA::pCE413	1A767	Cm MLS pheA1 phoA::pCE413 phoB::Tn917 trpC2
phoB::Tn917	1A767	Cm MLS pheA1 phoA::pCE413 phoB::Tn917 trpC2
phoP	1A254	pheA phoP
phoP12	1A255	phoP12
phoP22	1A256	phoP22
phoP4	1A257	phoP4
phoR2	1A306	metC3 phoR2 tal-1
phoS5	1A307	leuB8 phoS5 tal-1
polA5	1A215	polA5 thr-5 trpC2
	1A225	pheA1 polA5 trpC2
	1A226	hisH2 pheA1 polA5 trpC2
	1A720	hisB leuA8 metB5 polA5 SPβ- xin-1
polA10	1A493	citC met polA10 trpC2
polA59	1A214	polA59 thr-5 trpC2
polA1443	1A86	ilvA1 leu leuB8 metB5 polA1443
	1A276	ilvA1 metB5 polA1443 polC1

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ALLELE	CODE	DESCRIPTION
polC1	1A276	ilvA1 metB5 polA1443 polC1
polC12	1A81	ilvA1 leuB8 metB5 polC12 spcB1
	1A82	ilvA1 leuB8 metB5 polC12
	1A216	polC12 pyrA26 spcB3 strB3
polC133	1A23	ilvA1 metB5 polC133
	1A217	polC133 thr-5 trpC2
pro(AB)	1A652	pro(AB)
pro(H)	1A341	amyE(+M) amyR1(+M) metB5 pro(H) purF6 str trpB3
pro(L)	1A182	amyE(+M) amyR1 deg-9 metB5 pro(L) purF6 str trpB3
	1A311	amyE(+M) amyR2 deg-9 metB5 pro(L) purF6 str
	1A338	amyE(+M) amyR1(+M) metB5 pro(L) purF6 trpB3
	1A339	amyE(+M) amyR21(+M)(H) metB5 pro(L) purF6 str trpB3
	1A340	amyE(+M) amyR1 aroI116 deg-118 metB5 pro(L) str trpB3
pro-1	1A435	pro-1
ptm-42	1A433	ptm-42
	1A481	ptm-42
ptsI1	1A263	metC pfk ptsI1
pupA3	1A681	apt-6 ilvA1 pbuG3 pupA3 sacA78 upp
pur	1A434	ala-1 leuB8 metB pur thr-5 trpC
pur-60	1A382	hisH2 pur-60 trpC2
pur-67	1A384	pur-67 thyA1 thyB1
purA16	1A29	leuB8 metB5 nic-38 purA16
	1A30	ilvA64 leuB8 metB5 purA16
	1A51	purA16 sac(XY)46
	1A145	leuB8 metB5 purA16
	1A146	divIB12 leuB8 metB5 purA16
	1A212	arg(GH)3 lys-21 metB5 pheA12 purA16 rplV1
	1A291	gcaD26 leuB8 metB5 purA16
	1A336	amm-35 leuB8 metB5 purA16
	1A420	ilvA1 metB5 purA16 xhi-1479 xki-1479
	1A421	(φ105) ilvA1 metB5 purA16 xhi-1479 xki-1479
	1A463	ddlA1475 ilvA1 metB5 purA16
	1A662	cysE14 purA16 rpmA1 trpC2
	1A663	cysE14 purA16 rpsK2 trpC2
	1S44	argF4 hisA1 metB5 pheA12 purA16 pyrA26 spoVB91 trpC2
purA26	1A3	cysE14 purA26 trpC2
purD1	1A704	purD1
purE1	1A156	glpK21 purE1 sacA321
purE1	1A4	aroI906 dal-1 purE1 trpC2
purE4	1A388	metB5 purE4
purE5	1A389	metB5 purE5
purE6	1A320	purE6 trpC2
purE7	1A383	hisH2 purE7 trpC2
purE8	1A385	hisH2 purE8 trpC2
purE26	1A387	metB5 purE26
purF6	1A12	leuB8 metB5 purF6
	1A13	car-41 leuB8 metB5 purF6
	1A38	metB10 purF6 trpC2
	1A154	furB gutR met purF6 trpC2
	1A182	amyE(+M) amyR1 deg-9 metB5 pro(L) purF6 str trpB3
	1A311	amyE(+M) amyR2 deg-9 metB5 pro(L) purF6 str
	1A338	amyE(+M) amyR1(+M) metB5 pro(L) purF6 trpB3
	1A339	amyE(+M) amyR21(+M)(H) metB5 pro(L) purF6 str trpB3
	1A341	amyE(+M) amyR1(+M) metB5 pro(H) purF6 str trpB3
	1A412	amyE(+M) amyR2 metB5 purF6
	1A414	amyE(+N) amyR2 metB5 purF6
purF6 (cont)	1A445	hisA1 leuB8 lys-21 metB5 nonA1 purF6 SP10^{R} thr-5 trpC2
	1A707	com-71 hisA1 leu-8 metB5 purF6 thr-5 trpC2
	1A711	com-14::Tn917 hisA1 leu-8 lys-21 metB5 purF6 thr-5 trpC2
	1A712	com-18::Tn917 hisA1 leu-8 lys-21 metB5 purF6 thr-5 trpC2
	1A713	com-44::Tn917 hisA1 leu-8 lys-21 metB5 purF6 thr-5 trpC2
	1A449	car-41 leuB8 metB5 purF6 rpoC105
purH1	1A293	guaB3 metC7 purH1 trpC2
	1A294	guaA2 metC7 purH1 trpC2
	1A319	argF4 hisA1 purH4 trpC2
purH5	1A386	hisH2 purH5 thr trpC2
purM::Tn917	1A601	(SPβc2) purM::Tn917 trpC2
purM1	1A251	purM1 trpC2
pycA19	1A149	pycA19 recA1 trpC2
pyr-82::Tn917	1A609	(SPβc2) pyr-82::Tn917 trpC2
pyr-83::Tn917	1A610	(SPβc2) pyr-83::Tn917 trpC2
pyrA	1A60	metC3 pyrA xin-1
	1A78	metC3 pyrA xtl-1
	1A284	metC3 pyrA xhd-1
	1A391	arg^{S} pyrA
pyrA1	1S82	pyrA1 spoL1 trpC2
pyrA5	1A115	hisA1 pyrA5 trpC2
pyrA26	1A27	pyrA26
	1A216	polC12 pyrA26 spcB3 strB3
	1S44	argF4 hisA1 metB5 pheA12 purA16 pyrA26 spoVB91 trpC2
	1S84	argF4 cotA leu-2 pyrA26 scoA1
	1S85	argF4 kinA2 leu-2 pyrA26
pyrABC	1A402	pyrABC thyA1 thyB1 trpC2
pyrACD	1A403	pyrACD
pyrB	1A392	pyrB trpC2
	1A393	pyrB trpC3
pyrC	1A394	pyrC trpC2
	1A395	pyrC trpC2
pyrCD	1A398	pyrCD
pyrD	1A333	pyrD
	1A396	pyrD trpC2
	1A397	pyrD
pyrD1	1A6	ilvA1 pyrD1 thyA1 thyB1 trpC2
	1A466	lys-1 pyrD1 rpoB sas-1
	1A467	lys-1 pyrD1 rpoB sas-2
pyrD319	1A323	met pyrD319
pyrDF	1A399	pyrDF trpC2
pyrE270	1A321	pyrE270
pyrE305	1A322	met pyrE305
pyrF	1A400	pyrF trpC2
	1A401	pyrF trpC2
pyrR1	1A325	furB1 pyrR1 trpC2
rec-25	1A497	hisH2 rec-25 trpC2
rec-29	1A498	hisH2 rec-29 trpC2
rec-30	1A499	hisH2 rec-30 trpC2
rec-80	1A343	hisH2 rec-80 thyA1 thyB1
	1A375	rec-80 thyA1 thyB1 trpC2
recA1	1A43	recA1 trpC2
	1A73	metB4 recA1 trpC2
	1A149	pycA19 recA1 trpC2
recA4	1A46	recA4 thr-5 trpC2
	1A302	argF4 hisA1 recA4
	1A408	aroD120 recA4 trpC2
	1A409	arg(GH)15 hsd$_{RI}$R-M- leuB8 recA4
	1A422	hsd$_{RI}$R-M- leuB6 recA4
	1A423	arg(GH)15 hsd$_{RI}$R-M- leuB8 recA4 thr-5
	1A509	hisA1 hsd$_{RI}$R-M- metB5 recA4
	1A510	arg(GH)15 hsd$_{RI}$R-M- leuB8 recA4 stp thr
	1A514	hisH101 lys-21 recA4 splB1 thyA thyB uvrB10

B. subtilis 168 Strains Indexed by Allele

ALLELE	CODE	DESCRIPTION
recA4	1A575	ilvA2 recA4 spcB1 trpC2
	1A694	attSP(recA4 trpC2 zef87::Tn917
recA8	1A213	recA8 thr-5 trpC2
recA45	1A366	arg(GH)15 recA45 trpB3
recA260	1A746	Em metB5 recA260 SPβ- trpC2 xin-1
recB2	1A335	metB4 recB2 trpC2
	1A44	recB2 thr-5 trpC2
recB3	1A45	recB3 thr-5 trpC2
recB19	1A495	metB4 recB19 trpC2
recD27	1A261	gyrB1 metB4 recD27 trpC2
recD41	1A378	aroB2 hisH2 recD41 trpC2 tyrA1
recD43	1A373	arg(GH)15 recD43 trpB3
recF7	1A494	hisH2 leu met recF7
recF15	1A163	gyrB1 recF15 thr-5 trpC2
	1A262	gyrB2 recF15 thr-5 trpC2
	1A372	gyrB1 recF15 SPβ- trpC2 xin
	1A496	metB4 recF15 trpC2
recF33	1A380	aroB2 hisH2 recF33 trpC2 tyrA1
recG39	1A379	aroB2 hisH2 recG39 trpC2 tyrA1
recG40	1A103	aroB2 hisH2 recG40 trpC2 tyrA1
recH342	1A301	hisH2 recH342 trpC2
recL16	1A47	recL16 thr-5 trpC2
recM13	1A48	recM13 thr-5 trpC2
recP149	1A703	amyE SPβ- metB5 recP149 sigB trpC2 xin-1
relA	1A766	lys relA trpC2
rib	1A437	ade his hsd$_{RI}$R-M- met nic rib trp tyr ura
	1A438	hsd$_{RI}$R-M+ met nic rib trp tyr ura
	1A685	hsd$_{RI}$R-M+ rib trpC2 tyr-1 ura
	1A718	his hsd$_{RI}$R-M+ Km lacZ- M15 met rib trpC2 tyr ura
rib-2	1A210	rib-2
rna-53	1A390	hisA53 rna-53
	1A404	aroB2 hisA53 hisH2 rna-53 trpC2 tyrA1
rplA1	1A665	rplA1 rplJ1 rplL1
rplC1	1A101	rplC1 rplV1 str-2
	1A220	rplC1
rplE1	1A657	rplE1
rplE3	1A666	rplE3
rplJ1	1A665	rplA1 rplJ1 rplL1
rplK2	1A658	rplK2 rpsH2
rplK6	1A475	rplK6 thr-5 trpC2
rplL1	1A665	rplA1 rplJ1 rplL1
	1A667	rplL1
rplU1	1A670	rplU1
rplV	1A363	arg(GH)15 hsd$_{RI}$R-M- leuB8 rplV
rplV1	1A88	rplV1 sac(XY)32 trpC2
	1A101	rplC1 rplV1 str-2
	1A177	guaB1 rplV1
	1A211	arg(GH)3 pheA12 rplV1
	1A212	arg(GH)3 lys-21 metB5 pheA12 purA16 rplV1
	1A218	rplV1
	1A222	cysE14 rplV1 spo-
	1A660	rplV1
rplX2	1A669	rplX2
rpmA1	1A662	cysE14 purA16 rpmA1 trpC2
rpmD2	1A659	rpmD2
rpoA::cat	1A676	rpoA::cat trpC2
	1A677	gerD97::Tn917 rpoA::cat
rpoB	1A448	hisA1 hsd$_{RI}$R-M- leuB8 nonA1 rpoB SP10^{S} thr-5
	1A466	lys-1 pyrD1 rpoB sas-1
	1A467	lys-1 pyrD1 rpoB sas-2
rpoB1	1A500	cym-1 rpoB1
rpoB2	1S22	rpoB2 sigH17 trpC2
	1S32	rpoB2 spoIIA69 trpC2
	1S33	rpoB2 spoIID66 trpC2
	1S35	rpoB2 spoIIE64 trpC2
	1S37	rpoB2 spoIIIA(A-H)53 trpC2
	1S45	rpoB2 spoVD156 trpC2
	1S55	rpoB2 sapA6 spoIIA69
	1S56	rpoB2 sapB2 spoIIA69
	1S61	rpoB2 sigE55 trpC2
	1S64	leuB8 rpoB2 spoIIIC92 tal-1
	1S66	metC3 rpoB2 spoVC285
	1S78	metC3 rpoB2 sigF63 tal-1
rpoB18	1A308	rpoB18
rpoB500	1A248	rpoB500 trpC2
rpoC::(His6-tag)	1A774	pheA1 rpoC::(His6-tag) Sp trpC2
rpoC10	1A405	rpoC10
rpoC105	1A449	car-41 leuB8 metB5 purF6 rpoC105
rpoC121	1A450	rpoC121
rpsE2	1A219	rpsE2
	1A241	cysE14 rpsE2
rpsE302	1A668	rpsE302
rpsF1	1A664	rpsF1
rpsG3	1A661	rpsG3
rpsH2	1A658	rplK2 rpsH2
rpsH3	1A671	rpsH3
rpsI2	1A656	rpsI2
rpsK2	1A663	cysE14 purA16 rpsK2 trpC2
rpsL	1A287	rpsL tmsA1 trpC2
rpsL1	1A191	rpsL1 thr-5 trpC2 tufAA-2
	1A223	rpsL1 tmsB853
sacA78	1A142	ilvA1 sacA78 thyA112
	1A143	citB17 ilvA1 sacA78 thyB204
	1A144	ilvA1 sacA78 thyA112 thyB204
	1A681	apt-6 ilvA1 pbuG3 pupA3 sacA78 upp
	1A682	ilvA1 pubG1 sacA78 upp xpt
sacA321	1A11	ctrA1 sacA321 trpC2
	1A49	sacA321
	1A52	sacA321 treA12 trpC2
	1A54	mtlD1 nasC1 sacA321
	1A55	aroI906 dal-1 metB5 sacA321
	1A90	hisA1 sacA321 trpC2
	1A91	fruB138 sacA321 trpC2
	1A92	arg(GH)2 aroA932 bioB141 sacA321
	1A93	dnaX8132 hisA1 sacA321 thr-5
	1A126	hisH2 leuB8 sacA321 thiC5
	1A156	glpK21 purE1 sacA321
	1A160	gyrB1 sacA321
	1A201	deg-42 hisA1 sacA321 trpC2
	1A288	amyE dal-1 metB5 sacA321
	1A289	amyE aroI906 metB5 sacA321
sacB182	1A169	hisA1 sacB182 trpC2
sacP1	1A170	sacP1 trpC2
	1A171	hisH leuB8 sacP1 sac(XY)189
degQ36	1A53	ald-1 degQ36 trpC2
sacR47	1A164	sacR47
sac(XY)189	1A171	hisH leuB8 sacP1 sac(XY)189
sac(XY)32	1A88	rplV1 sac(XY)32 trpC2
sac(XY)43	1A161	sac(XY)43
sac(XY)46	1A50	sac(XY)46 trpC2
	1A51	purA16 sac(XY)46
sacT3	1A166	sacT3 trpC2
sapA6	1S55	rpoB2 sapA6 spoIIA69
sapB2	1S56	rpoB2 sapB2 spoIIA69
sas-1	1A466	lys-1 pyrD1 rpoB sas-1
sas-2	1A467	lys-1 pyrD1 rpoB sas-2
scoA1	1S84	argF4 cotA leu-2 pyrA26 scoA1
sdhA2	1A33	sdhA2 trpC2
sdhB103	1A674	leu-2 sdhB103 trpC2
sdhC109	1A121	arg(GH)2 pheA2 sdhC109 trpC2

B. subtilis 168 Strains Indexed by Allele

ALLELE	CODE	DESCRIPTION
ser	1S29	ser spoIIA2
ser-22	1A129	ser-22 trpC2
serA84::Tn917	1A614	(SPβc2) serA84::Tn917 trpC2
serC82::Tn917	1A621	(SPβc2) serC82::Tn917 trpC2
serR1	1A128	serR1 trpC2
sfp	1A698	pheA1 sfp
	1A699	pheA1 sfp srfA::Tn917
sigA1	1A579	sigA1
sigA4	1A580	sigA4
sigA47	1A581	sigA47
sigB	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
sigB::cat	1A675	furB1 sigB::cat trpC2
sigD::pLM5	1A716	Cm sigD::pLM5 trpC2
sigE55	1S61	rpoB2 sigE55 trpC2
sigF1	1S86	sigF1 trpC2
sigF63	1S78	metC3 rpoB2 sigF63 tal-1
sigH4	1S20	sigH4 str trpC2
sigH14	1S21	sigH14 trpC2
sigH17	1S22	rpoB2 sigH17 trpC2
sigH37	1S23	sigH37 trpC2
sigH81	1S24	pheA1 sigH81 trpC2
sigH116	1S25	sigH116 trpC2
sinI::kan-50	1S98	hisA1 leuA8 metB5 sinI::kan-50
sinR::phl	1S97	hisA1 leuA8 metB5 sinR::phl
Sm	1S73	ade met Sm spo0A16 trpC2
smo-1	1A138	argF4 hag-1 smo-1 trpC2
Sp	1A774	pheA1 rpoC::(His6-tag) Sp trpC2
SP10^{R}	1A445	hisA1 leuB8 lys-21 metB5 nonA1 purF6 SP10^{R} thr-5 trpC2
	1A446	hisA1 leuB8 lys-21 metB5 nonA1 SP10^{R} trpC2
	1A447	hsd$_{RI}$R- M- leuB8 metB5 SP10^{R}
SP10^{S}	1A141	hisA1 hsd$_{RI}$R-M- leuB8 lys-21 metB5 nonA1 SP10^{S} thr-5 trpC2 φNR2^{S}
	1A253	arg(GH)15 hsd$_{RI}$R-M- leuB8 SP10^{S}
	1A448	hisA1 hsd$_{RI}$R-M- leuB8 nonA1 rpoB SP10^{S} thr-5
spc	1A478	lys-3 metB10 spc spcD trpC2
spcB1	1A76	ilvA1 metB5 spcB1
	1A81	ilvA1 leuB8 metB5 polC12 spcB1
	1A575	ilvA2 recA4 spcB1 trpC2
spcB3	1A216	polC12 pyrA26 spcB3 strB3
spcD	1A478	lys-3 metB10 spc spcD trpC2
Spo^{-}	1A190	cysE14 Spo^{-} tufAA-7
	1A192	cysE14 efg-1 Spo^{-}
	1A193	kan-2 Spo^{-}
	1A194	cysE14 nea-1 Spo^{-}
	1A195	cysE14 ole-2 Spo^{-}
	1A197	metB5 minD1 tag-1 thyA thyB1
	1A222	cysE14 rplV1 Spo^{-}
	1A269	spo- thyA1 thyB1 trpC2 ts-355
	1A61	furF5 Spo^{-}
Spo^{Con}	1A508	fus Spo^{Con}
Spo^{Ts}	1A507	fus Spo^{Ts}
spo0A3	1S1	spo0A3
	1S2	metB5 spo0A3 thr-5
	1S3	-(metB5)+ spo0A3 sup-44 thr-5
	1S4	-(metB5)+ -(thr-5)+ spo0A3 trnS-Lys3
	1S5	spo0A3 trpC2
spo0A5	1S6	spo0A5
spo0A6	1S7	metB4 spo0A6 trpC2
spo0A9	1S8	spo0A9 trpC2
spo0A12	1S9	pheA1 spo0A12 trpC2
spo0A12	1S10	spo0A12 trpC2
	1S11	spo0A12 tolB24 trpC2
	1S12	spo0A12 trpF7
	1S68	abrB23 pheA1 spo0A12 trpC2
	1S69	absA6 spo0A12 trpC2
	1S70	absB24 spo0A12 trpC2
spo0A13	1S13	spo0A13 trpC2
spo0A16	1S73	ade met Sm spo0A16 trpC2
spo0A170	1S14	spo0A170 tyr
spo0A::Tn917 HU289	1S133	spo0A::Tn917 HU289
spo0A332	1S15	spo0A332 trpC2
spo0A 677	1S53	spo0A 677
	1S76	citD 29 dal-1 spo0A 677 str-76 thyA thyB uvr-1
spo0B(TS)	1S90	lys-1 spo0B(TS)
	1S91	lys-1 spo0B(TS)
spo0B12	1S54	spo0B12
spo0B136	1S16	pheA1 spo0B136 trpC2
spo0E11	1S17	pheA1 spo0E11 trpC2
spo0F221	1S19	pheA1 spo0F221 trpC2
spo0J93	1S94	spo0J93 trpC2
spo0J::Tn917 HU261	1S129	spo0J::Tn917 HU261
spo-331	1S75	spo-331 thyA1 thyB1 trpC2
spoIIA2	1S29	ser spoIIA2
spoIIA4	1S71	spoIIA4 trpC2
	1S72	spoIIA4 trpC2
spoIIA5	1S74	spoIIA5
spoIIA12	1S30	spoIIA12
spoIIA26	1S31	ade met spoIIA26 trpC2
spoIIA37	1S79	spoIIA37 trpC2
spoIIA42	1S80	spoIIA42 trpC2
spoIIA50	1S77	metB5 spoIIA50 thr-5
spoIIA69	1S32	rpoB2 spoIIA69 trpC2
	1S55	rpoB2 sapA6 spoIIA69
	1S56	rpoB2 sapB2 spoIIA69
spoIIA176	1S81	spoIIA176 trpC2
spoIIB131	1S49	spoIIB131 trpC2
spoIID66	1S33	rpoB2 spoIID66 trpC2
spoIID298	1S43	spoIID298 trpC2
spoIID::Tn917 HU8	1S115	spoIID::Tn917 HU8
spoIID::Tn917 HU298	1S135	spoIID::Tn917 HU298
spoIIE61	1S34	spoIIE61 trpC2
spoIIE64	1S35	rpoB2 spoIIE64 trpC2
spoIIE::Tn917 HU7	1S116	spoIIE::Tn917 HU7
spoIIE::Tn917 HU181	1S124	spoIIE::Tn917 HU181
spoIIG41	1S60	leuB8 spoIIG41 tal-1
spoIIG279	1S67	cysC7 furA2 spoIIG279
spoIIG::Tn917 HU325	1S138	spoIIG::Tn917 HU325
spoIIM::Tn917 HU188	1S125	spoIIM::Tn917 HU188
spoIIM::Tn917 HU287	1S132	spoIIM::Tn917 HU287
spoIIIA(A-H)7	1S36	ilvC1 spoIIIA(A-H)7 trpC2
spoIIIA(A-H)35	1S42	metC3 spoIIIA(A-H)35 tal-1
spoIIIA(A-H)53	1S37	rpoB2 spoIIIA(A-H)53 trpC2
spoIIIA(A-H)::Tn917 HU13	1S119	spoIIIA(A-H)::Tn917 HU13
spoIIIB2	1S48	spoIIIB2 trpC2
spoIIIB::Tn917 HU25	1S121	spoIIIB::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
spoIIIJ87	1S26	pheA1 spoIIIJ87 trpC2
	1S27	metC3 spoIIIJ87 tal-1
spoIVA178	1S46	pheA12 spoIVA178
spoIVA::Tn917 HU194	1S126	spoIVA::Tn917 HU194
spoIVB165	1S57	spoIVB165 trp
spoIVC133	1S47	spoIVC133 trpC2
spoIVC::Tn917 HU215	1S128	spoIVC::Tn917 HU215
spoIVD::Tn917 HU10	1S118	spoIVD::Tn917 HU10
spoIVF^{TS}	1S89	spoIVF^{TS} trpC2
	1S92	lys-1 spoIVF^{TS}
spoIVF88	1S65	metC3 spoIVF88 tal-1
spoIVF152	1S58	spoIVF152 trpC2
spoIVFA::Tn917 HU179	1S123	spoIVFA::Tn917 HU179
spoL1	1S82	pyrA1 spoL1 trpC2
spoVA89	1S50	spoVA89 trpC2
spoVA::Tn917 HU195	1S127	spoVA::Tn917 HU195
spoVA::Tn917 HU276	1S131	spoVA::Tn917 HU276
spoVM::Tn917 HU324	1S137	spoVM::Tn917 HU324
spoVB	1S93	lys-1 spoVB
spoVB91	1S44	argF4 hisA1 metB5 pheA12 purA16 pyrA26 spoVB91 trpC2
spoVC285	1S66	metC3 rpoB2 spoVC285
spoVD156	1S45	rpoB2 spoVD156 trpC2
spoVE85	1S51	spoVE85 trpC2
spoVF	1S41	spoVF trpC2
spoVF1	1S83	pheA1 spoVF1 trpC2
spoVF224	1S52	spoVF224 trpC2
spoVG::Tn917 HU265	1S130	spoVG::Tn917 HU265
spoVIA513	1S88	spoVIA513 trpC2
spoVID::Tn917	1A639	(SPβc2) spoVID::Tn917 trpC2
spoVK517	1S95	spoVK517 trpC2
spoVK::Tn917HU8	1S99	MLS^{R} spoVK::Tn917HU8 SPβ-
spoVK::Tn917HU8	1S117	spoVK::Tn917HU8
spoVK::Tn917HU178	1S122	spoVK::Tn917HU178
SPβ^{-}	1A100	SPβ^{-} trpC2
	1A304	metB5 SPβ^{-} trpC2 xin-1
	1A372	gyrB1 recF15 SPβ^{-} trpC2 xin
	1A457	ilvA2 ilvD15 SPβ^{-} thyA5 thyB5 trpC2
	1A458	ilvA2 SPβ^{-} thyA5 thyB5 trpC2
	1A459	leuB8 metB5 SPβ- thr-5 trnS-Lys3
	1A686	SPβ- trpC2 zae86::Tn917
	1A694	SPβ- recA4 trpC2 zef87::Tn917
	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
	1A747	SPβ-
	1S99	MLS^{R} spoVK::Tn917HU8 SPβ-
	1S100	bofA::cat Cm SPβ-
srfA::Tn917	1A699	pheA1 sfp srfA::Tn917
splB1	1A488	met-14 splB1 sul thyA1 thyB1 trpC2
	1A489	met-14 splB1 sul thyA1 thyB1 trpC2 uvrB42
splB1 (cont)	1A514	hisH101 lys-21 recA4 splB1 thyA thyB uvrB10
sspA	1S109	sspA
	1S111	sspA sspB
	1S112	Cm sspA sspE
	1S113	Cm sspA sspB sspE
sspB	1S110	sspB
	1S111	sspA sspB
	1S113	Cm sspA sspB sspE
sspE	1S112	Cm sspA sspE
	1S113	Cm sspA sspB sspE
	1S114	sspE
stp	1A510	arg(GH)15 hsd$_{RI}$R-M- leuB8 recA4 stp thr
str	1A182	amyE(+M) amyR1 deg-9 metB5 pro(L) purF6 str trpB3
	1A238	efg-3 str
	1A270	str sul
	1A271	hutP1 str sul
	1A272	hutH1 str sul
	1A273	hutCR1 str sul
	1A311	amyE(+M) amyR2 deg-9 metB5 pro(L) purF6 str
	1A339	amyE(+M) amyR21(+M)(H) metB5 pro(L) purF6 str trpB3
	1A340	amyE(+M) amyR1 aroI116 deg-118 metB5 pro(L) str trpB3
	1A341	amyE(+M) amyR1(+M) metB5 pro(H) purF6 str trpB3
	1S20	sigH4 str trpC2
str-2	1A101	rplC1 rplV1 str-2
str-76	1S76	citD 29 dal-1 spo0A 677 str-76 thyA thyB uvr-1
strB3	1A77	ilvA1 metB5 strB3
	1A198	strB3
	1A216	polC12 pyrA26 spcB3 strB3
strC2	1A473	bfmB1 strC2 trpC2
strC23	1A249	ilvC1 pheA1 strC23
suf-1	1A367	leuA169 suf-1 trpC2
suh-428	1A135	suh-428
sul	1A270	str sul
	1A271	hutP1 str sul
	1A272	hutH1 str sul
	1A273	hutCR1 str sul
	1A344	met-14 sul thyA1 thyB1 trpC2 uvrB10
	1A345	met-14 sul thyA1 thyB1 trpC2 uvrB42
	1A354	sul trpC2
	1A357	aecB lys-1 sul trpC2
	1A358	lysC lys-1 sul trpC2
	1A488	met-14 splB1 sul thyA1 thyB1 trpC2
sul	1A489	met-14 splB1 sul thyA1 thyB1 trpC2 uvrB42
	1A695	hisH2 sul ten trpC2
sup-1	1A477	-(hisA1)+ -(metB5)+ sup-1
sup-22	1A279	-(hisA1)+ -(metC3)+ sup-22 trpC2
sup-44	1A260	-(met)+ ile leu sup-44 thyA1 thyB1
	1A264	-(hisA1)+ sup-44 thr-5
	1S3	-(metB5)+ spo0A3 sup-44 thr-5
sup-67	1A368	leuD117 sup-67 trpC2
tag-1	1A197	metB5 minD1 tag-1 thyA thyB1 metB5 minD1 spo- thyA1 thyB1
	1A209	tag-1 thyA1 thyB1 trpC2
tagE	1A136	argF4 hag-2 tagE
	1A35	lys-3 metB10 tagE trpC2
tagF1	1A486	leuB8 tagF1
tal-1	1A306	metC3 phoR2 tal-1
	1A307	leuB8 phoS5 tal-1
	1S27	metC3 spoIIIJ87 tal-1

B. subtilis **168 Strains Indexed by Allele**

ALLELE	CODE	DESCRIPTION
tal-1 (cont)	1S42	metC3 spoIIIA(A-H)35 tal-1
	1S60	leuB8 spoIIG41 tal-1
	1S64	leuB8 rpoB2 spoIIIC92 tal-1
	1S65	metC3 spoIVF88 tal-1
	1S78	metC3 rpoB2 sigF63 tal-1
	1S87	metC3 spoIVG-25 tal-1
tem-1	1A462	leuB8 metB5 tem-1
ten	1A695	hisH2 sul ten trpC2
thiA78	1A122	glpK21 glyB133 thiA78 treA12
thiA84::Tn917	1A603	(SPβc2) thiA84::Tn917 trpC2
thiB4	1A125	argF4 metA29 thiB4
thiC5	1A126	hisH2 leuB8 sacA321 thiC5
thr	1A386	hisH2 purH5 thr trpC2
	1A510	arg(GH)15 hsd$_{RI}$R-M- leuB8 recA4 stp thr
thr-5	1A10	hisA1 thr-5 trpC2
	1A14	-(metB5)+ -(thr-5)+ leuB8 trnS-Lys3
	1A42	thr-5 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
	1A74	dnaX8132 hisA1 thr-5
	1A93	dnaX8132 hisA1 sacA321 thr-5
	1A141	hisA1 hsd$_{RI}$R-M- leuB8 lys-21 metB5 nonA1 SP10^{S} thr-5 trpC2 φNR2^{S}
	1A163	gyrB1 recF15 thr-5 trpC2
	1A191	rpsL1 thr-5 trpC2 tufAA-2
	1A213	recA8 thr-5 trpC2
	1A214	polA59 thr-5 trpC2
	1A215	polA5 thr-5 trpC2
	1A217	polC133 thr-5 trpC2
	1A242	hisA1 thr-5 trpC2
	1A262	gyrB2 recF15 thr-5 trpC2
	1A264	-(hisA1)+ sup-44 thr-5
	1A313	thr-5 trpC2
	1A314	divV32 thr-5 trpC2
	1A316	divII55 thr-5 trpC2
	1A317	divII61 thr-5 trpC2
	1A423	arg(GH)15 hsd$_{RI}$R-M- leuB8 recA4 thr-5
	1A434	ala-1 leuB8 metB pur thr-5 trpC
	1A445	hisA1 leuB8 lys-21 metB5 nonA1 purF6 SP10^{R} thr-5 trpC2
	1A448	hisA1 hsd$_{RI}$R-M- leuB8 nonA1 rpoB SP10^{S} thr-5
	1A459	leuB8 metB5 SPβ- thr-5 trnS-Lys3
	1A475	rplK6 thr-5 trpC2
thr-5	1A706	com-9 hisA1 leu-8 lys-21 metB5 thr-5 trpC2
	1A707	com-71 hisA1 leu-8 metB5 purF6 thr-5 trpC2
	1A708	com-30 hisA1 leu-8 lys-21 metB5 thr-5 trpC2
	1A709	com-104 hisA1 leu-8 lys-21 metB5 thr-5 trpC2
	1A710	com-31 hisA1 leu-8 lys-21 metB5 thr-5 trpC2
	1A711	com-14::Tn917 hisA1 leu-8 lys-21 metB5 purF6 thr-5 trpC2
	1A712	com-18::Tn917 hisA1 leu-8 lys-21 metB5 purF6 thr-5 trpC2
	1A713	com-44::Tn917 hisA1 leu-8 lys-21 metB5 purF6 thr-5 trpC2
	1A753	bmr^{R} thr-5 trpC2
	1A754	bmr::cat Cm thr-5 trpC2
	1A755	bmrR::cat Cm thr-5 trpC2
	1A756	bfmB::cat Cm thr-5 trpC2
	1G7	gerA(ABC)11 thr-5 trpC2
thr-5 (cont)	1S2	metB5 spo0A3 thr-5
	1S3	-(metB5)+ spo0A3 sup-44 thr-5
	1S4	-(metB5)+ -(thr-5)+ spo0A3 trnS-Lys3
	1S77	metB5 spoIIA50 thr-5
thrC::cat	1A773	Cm pheA1 thrC::cat trpC2
thyA	1A197	metB5 minD1 tag-1 thyA thyB1 metB5 minD1 spo- thyA1 thyB1
	1A419	thyA thyB trpC2 xhi-1479 xki-1479
	1A502	oxr-1 thyA thyB
	1A503	oxr-2 thyA thyB trpC2
	1A504	lyt-15 thyA thyB trpC2 xin-15
	1A511	lys-3 thyA thyB trpC2
	1A514	hisH101 lys-21 recA4 splB1 thyA thyB uvrB10
	1A595	arg thyA thyB tscA1
	1A596	arg thyA thyB tscA23
	1A597	arg nadE49 thyA thyB
	1A598	arg thyA thyB tscC11
	1A599	arg thyA thyB tscD14
	1A647	arg nadE47 thyA thyB
	1A648	arg nadE48 thyA thyB
	1A649	arg thyA thyB tscD14
	1S76	citD 29 dal-1 spo0A 677 str-76 thyA thyB uvr-1
thyA1	1A6	ilvA1 pyrD1 thyA1 thyB1 trpC2
	1A17	dnaB134 ilvA1 thyA1 thyB1
	1A41	dnaB1 thyA1 thyB1 trpC2
	1A162	ilvA1 novB thyA1
	1A185	thyA1 thyB1 trpC2
	1A187	ksgA618 thyA1 thyB1 trpC2
	1A188	ksgA619 thyA1 thyB1 trpC2
	1A196	divIVA1 ilvD thyA1 thyB1
	1A197	metB5 minD1 tag-1 thyA thyB1 metB5 minD1 spo- thyA1 thyB1
	1A209	tag-1 thyA1 thyB1 trpC2
	1A230	ilvD6 thyA1 trpC2
	1A243	thyA1 thyB1 trpC2
	1A258	ile leu metB5 thyA1 thyB1
	1A259	-(met)+ ile leu thyA1 thyB1 trnS-Lys3
	1A260	-(met)+ ile leu sup-44 thyA1 thyB1
	1A268	thyA1 thyB1 tmsA151 trpC2
	1A269	spo- thyA1 thyB1 trpC2 ts-355
	1A290	dnaB134 thyA1 thyB1 trpC2
	1A292	metB5 minD1 thyA1 thyB1
	1A300	glyA thyA1 thyB1 trpC2
	1A327	gltA2 ilvA8 thyA1 thyB1
	1A332	citD 1 ilvA8 thyA1 thyB1
	1A342	ebr-2 hisH2 thyA1 thyB1
	1A343	hisH2 rec-80 thyA1 thyB1
	1A344	met-14 sul thyA1 thyB1 trpC2 uvrB10
	1A345	met-14 sul thyA1 thyB1 trpC2 uvrB42
	1A346	hisH2 thyA1 thyB1 uvrC109
	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
thyA5	1A457	ilvA2 ilvD15 SPβ- thyA5 thyB5 trpC2
	1A458	ilvA2 SPβ- thyA5 thyB5 trpC2
thyA112	1A142	ilvA1 sacA78 thyA112
	1A144	ilvA1 sacA78 thyA112 thyB204
thyA	1A456	ilvD6 thyA thyB1
thyB	1A419	thyA thyB trpC2 xhi-1479 xki-1479
	1A502	oxr-1 thyA thyB
	1A503	oxr-2 thyA thyB trpC2
	1A504	lyt-15 thyA thyB trpC2 xin-15
	1A511	lys-3 thyA thyB trpC2
	1A514	hisH101 lys-21 recA4 splB1 thyA thyB uvrB10
	1A595	arg thyA thyB tscA1
	1A596	arg thyA thyB tscA23
	1A597	arg nadE49 thyA thyB
	1A598	arg thyA thyB tscC11
	1A599	arg thyA thyB tscD14
	1A647	arg nadE47 thyA thyB
	1A648	arg nadE48 thyA thyB
	1A649	arg thyA thyB tscD14
	1S76	citDΔ29 dal-1 spo0A 677 str-76 thyA thyB uvr-1
thyB1	1A6	ilvA1 pyrD1 thyA1 thyB1 trpC2
	1A17	dnaB134 ilvA1 thyA1 thyB1
	1A41	dnaB1 thyA1 thyB1 trpC2
	1A185	thyA1 thyB1 trpC2
	1A187	ksgA618 thyA1 thyB1 trpC2
	1A188	ksgA619 thyA1 thyB1 trpC2
	1A196	divIVA1 ilvD thyA1 thyB1
	1A197	metB5 minD1 tag-1 thyA thyB1 metB5 minD1 spo- thyA1 thyB1
	1A197	metB5 minD1 tag-1 thyA thyB1 metB5 minD1 spo- thyA1 thyB1
	1A209	tag-1 thyA1 thyB1 trpC2
	1A243	thyA1 thyB1 trpC2
	1A258	ile leu metB5 thyA1 thyB1
	1A259	-(met)+ ile leu thyA1 thyB1 trnS-Lys3
	1A260	-(met)+ ile leu sup-44 thyA1 thyB1
	1A268	thyA1 thyB1 tmsA151 trpC2
	1A269	spo- thyA1 thyB1 trpC2 ts-355
	1A290	dnaB134 thyA1 thyB1 trpC2
	1A292	metB5 minD1 thyA1 thyB1
	1A300	glyA thyA1 thyB1 trpC2
	1A326	citB1 gltA2 ilvA8 thyB1
	1A327	gltA2 ilvA8 thyA1 thyB1
	1A332	citD 1 ilvA8 thyA1 thyB1
	1A342	ebr-2 hisH2 thyA1 thyB1
	1A343	hisH2 rec-80 thyA1 thyB1
	1A344	met-14 sul thyA1 thyB1 trpC2 uvrB10
	1A345	met-14 sul thyA1 thyB1 trpC2 uvrB42
	1A346	hisH2 thyA1 thyB1 uvrC109
	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
	1A456	ilvD6 thyA thyB1
	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
thyB5	1A457	ilvA2 ilvD15 SPβ- thyA5 thyB5 trpC2
	1A458	ilvA2 SPβ- thyA5 thyB5 trpC2
thyB204	1A143	citB17 ilvA1 sacA78 thyB204
	1A144	ilvA1 sacA78 thyA112 thyB204
tmsA1	1A287	rpsL tmsA1 trpC2
tmsA151	1A268	thyA1 thyB1 tmsA151 trpC2
tmsB853	1A223	rpsL1 tmsB853
tolA6	1A66	pheA12 tolA6 trpC2
	1A67	pheA12 tolA6 trpC2 φ29^{R}
tolB24	1S11	spo0A12 tolB24 trpC2
treA12	1A5	glyB133 metC3 treA12 trpC2
	1A52	sacA321 treA12 trpC2
	1A122	glpK21 glyB133 thiA78 treA12
	1A167	treA12 trpC2
trnS-Lys3	1A14	-(metB5)+ -(thr-5)+ leuB8 trnS-Lys3
	1A259	-(met)+ ile leu thyA1 thyB1 trnS-Lys3
	1A459	leuB8 metB5 SPβ- thr-5 trnS-Lys3
	1S4	-(metB5)+ -(thr-5)+ spo0A3 trnS-Lys3
trp	1A437	ade his hsd$_{RI}$R-M- met nic rib trp tyr ura
	1A438	hsd$_{RI}$R-M+ met nic rib trp tyr ura
	1A506	arg trp
	1S57	spoIVB165 trp
trpA1	1A553	trpA1
trpA2	1A554	trpA2
trpA3	1A555	trpA3
trpA4	1A556	trpA4
trpA5	1A62	trpA5
trpA6	1A557	trpA6
trpA7	1A558	trpA7
trpB1	1A559	trpB1
trpB2	1A560	trpB2
trpB3	1A182	amyE(+M) amyR1 deg-9 metB5 pro(L) purF6 str trpB3
trpB3	1A338	amyE(+M) amyR1(+M) metB5 pro(L) purF6 trpB3
trpB3	1A339	amyE(+M) amyR21(+M)(H) metB5 pro(L) purF6 str trpB3
trpB3	1A340	amyE(+M) amyR1 aroI116 deg-118 metB5 pro(L) str trpB3
trpB3	1A341	amyE(+M) amyR1(+M) metB5 pro(H) purF6 str trpB3
trpB3	1A365	arg(GH)15 trpB3
trpB3	1A366	arg(GH)15 recA45 trpB3
trpB3	1A373	arg(GH)15 recD43 trpB3
trpB4	1A63	trpB4
trpB5	1A561	trpB5
trpB6	1A562	trpB6
trpB7	1A563	trpB7
trpB8	1A564	trpB8
trpB9	1A565	trpB9
trpB10	1A566	trpB10
trpB11	1A567	trpB11
trpB12	1A568	trpB12
trpB13	1A569	trpB13
trpB14	1A570	trpB14
trpB15	1A571	trpB15
trpB16	1A572	trpB16
trpC	1A434	ala-1 leuB8 metB pur thr-5 trpC
trpC1	1A543	trpC1
trpC2	1A1	trpC2
	1A3	cysE14 purA26 trpC2
	1A4	aroI906 dal-1 purE1 trpC2
	1A5	glyB133 metC3 treA12 trpC2
	1A6	ilvA1 pyrD1 thyA1 thyB1 trpC2
	1A7	gltA292 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 φ29^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	SPβ- 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 azlB101 trpC2
	1A112	azlA102 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
trpC2 (cont)	1A138	argF4 hag-1 smo-1 trpC2
	1A139	flaA4 hag-1 lys trpC2
	1A141	hisA1 hsd$_{RI}$R$^-$M$^-$ leuB8 lys-21 metB5 nonA1 SP10^S thr-5 trpC2 φNR2^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	divII55 thr-5 trpC2
	1A317	divII61 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
trpC2 (cont)	1A419	thyA thyB trpC2 xhi-1479 xki-1479
	1A428	met trpC2 ts-39-2
	1A429	aroI906 glpT6 trpC2
	1A436	hsd$_{RI}$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
trpC2 (cont)	1A619	(SPβc2) liv1-82::Tn917 trpC2
	1A620	(SPβc2) liv3-83::Tn917 trpC2
	1A621	(SPβc2) serC82::Tn917 trpC2
	1A622	(SPβc2) arg(GH)85::Tn917 trpC2
	1A623	(SPβc2) alaA84::Tn917 trpC2
	1A624	(SPβc2) mth-83::Tn917 trpC2
	1A625	(SPβc2) mth-84::Tn917 trpC2
	1A626	(SPβc2) hisA82::Tn917 trpC2
	1A627	(SPβc2) trpC2 zaa-84::Tn917
	1A628	(SPβc2) trpC2 zbj-82::Tn917;
	1A629	(SPβc2) trpC2 zca-82::Tn917
	1A630	(SPβc2) trpC2 zce-82::Tn917
	1A631	(SPβc2) motA::Tn917 trpC2
	1A632	(SPβc2) kinC::Tn917 trpC2
	1A633	(SPβc2) trpC2 zdi-82::Tn917
	1A634	(SPβc2) trpC2 zci-82::Tn917
	1A635	(SPβc2) trpC2 proJ::Tn917
	1A636	(SPβc2) cgeE::Tn917 trpC2
	1A637	(SPβc2) trpC2 yokH::Tn917
	1A638	(SPβc2) trpC2 zfg-83::Tn917
	1A639	(SPβc2) spoVID::Tn917 trpC2
	1A640	(SPβc2) trpC2 zhb-83::Tn917
	1A641	(SPβc2) trpC2 zhc-85::Tn917
	1A642	(SPβc2) trpC2 yufR::Tn917
	1A643	(SPβc2) trpC2 yvaC::Tn917
	1A644	(SPβc2) trpC2 zii-83::Tn917
	1A645	(SPβc2) trpC2 zjf-85::Tn917
	1A646	(SPβc2) trpC2 zfd-81::Tn917
	1A654	aroD120 bglS33 trpC2
	1A655	aroI906 cdr-1 trpC2
	1A662	cysE14 purA16 rpmA1 trpC2
	1A663	cysE14 purA16 rpsK2 trpC2
	1A672	odhA5 odhA5 trpC2
	1A673	odhB17 trpC2
	1A674	leu-2 sdhB103 trpC2
	1A675	furB1 sigB::cat trpC2
	1A676	rpoA::cat trpC2
	1A678	leuB8 menB325 trpC2
	1A679	ald-1 leuB8 menE312 trpC2
	1A685	hsd$_{RI}$R-M+ rib trpC2 tyr-1 ura
	1A686	SPβ- trpC2 zae86::Tn917
	1A687	(SPβc2) trpC2 zba89::Tn917
	1A688	(SPβc2) trpC2 ydaO::Tn917
	1A689	(SPβc2) trpC2 zdf88::Tn917
	1A690	(SPβc2) trpC2 zec88:Tn917
	1A691	SPβc2 trpC2 zfe86::Tn917
	1A692	(SPβc2) trpC2 zhf86::Tn917
	1A693	(SPβc2) trpC2 zhg86::Tn917
	1A694	attSP(recA4 trpC2 zef87::Tn917
	1A695	hisH2 sul ten trpC2
	1A700	trpC2
	1A701	addB72 amyE SPβ- metB5 sigB trpC2 xin-1
	1A703	amyE SPβ- metB5 recP149 sigB trpC2 xin-1
	1A706	com-9 hisA1 leu-8 lys-21 metB5 thr-5 trpC2
	1A707	com-71 hisA1 leu-8 metB5 purF6 thr-5 trpC2
	1A708	com-30 hisA1 leu-8 lys-21 metB5 thr-5 trpC2
	1A709	com-104 hisA1 leu-8 lys-21 metB5 thr-5 trpC2
	1A710	com-31 hisA1 leu-8 lys-21 metB5 thr-5 trpC2
	1A711	com-14::Tn917 hisA1 leu-8 lys-21 metB5 purF6 thr-5 trpC2
	1A712	com-18::Tn917 hisA1 leu-8 lys-21 metB5 purF6 thr-5 trpC2
	1A713	com-44::Tn917 hisA1 leu-8 lys-21 metB5 purF6 thr-5 trpC2
	1A716	Cm sigD::pLM5 trpC2
trpC2 (cont)	1A718	his hsd$_{RI}$R M Km lacZ- M15 met rib trpC2 tyr ura
	1A719	metB10 trpC2 xylAB 1
	1A721	(SPβc2) aroI86::Tn917 trpC2
	1A722	(SPβc2) bfmB84::Tn917 trpC2
	1A724	(SPβc2) trpC2 zba-88::Tn917
	1A727	(SPβc2) trpC2 zeh-82::Tn917
	1A728	(SPβc2) trpC2 zfj-83::Tn917
	1A730	(SPβc2) trpC2 zhf-83::Tn917
	1A731	(SPβc2) trpC2 zib-82::Tn917
	1A732	(SPβc2) trpC2 zjd-89::Tn917
	1A733	(SPβc2) trpC2 zjj-85:Tn917
	1A737	dppE132::neo pheA1 trpC2
	1A738	iolG6 metC7 trpC2
	1A739	gntK4 metC7 trpC2
	1A740	gntP9 metC7 trpC2
	1A741	gntR1 metC7 trpC2
	1A742	dacA::cat^{+} trpC2
	1A743	dacA^{+}::cat^{+} trpC2
	1A744	dacB^{+}::cat^{+} trpC2
	1A745	dacB::cat^{+} trpC2
	1A746	metB5 MLS recA260 SPβ^{-} trpC2 xin-1
	1A753	bmr^{R} thr-5 trpC2
	1A754	bmr::cat Cm thr-5 trpC2
	1A755	bmrR::cat Cm thr-5 trpC2
	1A756	bfmB::cat Cm thr-5 trpC2
	1A763	Cm fla/che::pLM19 trpC2
	1A764	flgM 80 pheA1 trpC2
	1A765	lys trpC2
	1A766	lys relA trpC2
	1A767	Cm MLS pheA1 phoA::pCE413 phoB::Tn917 trpC2
	1A771	amyE::erm MLS pheA1 trpC2
	1A772	amyE::cat Cm pheA1 trpC2
	1A773	Cm pheA1 thrC::cat trpC2
	1A774	pheA1 rpoC:☹His6-tag) Sp trpC2
	1G1	hisH2 outF4 trpC2
	1G2	hisH2 nadE81 trpC2
	1G3	hisH2 outE42 trpC2
	1G4	hisH2 metD4 outD1 trpC2
	1G5	hisH2 outC25 trpC2
	1G6	gsp-10 hisH2 metD4 trpC2
	1G7	gerA(ABC)11 thr-5 trpC2
	1G8	gerB(ABC)18 trpC2
	1G9	gerD19 trpC2
	1G10	gerF45 trpC2
	1G11	gerCC58 trpC2 tzm wrd
	1G13	gerG47 met pgk trpC2
	1G14	hisH2 metD4 outA7 trpC2
	1S5	spo0A3 trpC2
	1S7	metB4 spo0A6 trpC2
	1S8	spo0A9 trpC2
	1S9	pheA1 spo0A12 trpC2
	1S10	spo0A12 trpC2
	1S11	spo0A12 tolB24 trpC2
	1S13	spo0A13 trpC2
	1S15	spo0A332 trpC2
	1S16	pheA1 spo0B136 trpC2
	1S17	pheA1 spo0E11 trpC2
	1S19	pheA1 spo0F221 trpC2
	1S20	sigH4 str trpC2
	1S21	sigH14 trpC2
	1S22	rpoB2 sigH17 trpC2
	1S23	sigH37 trpC2
	1S24	pheA1 sigH81 trpC2
	1S25	sigH116 trpC2
	1S26	pheA1 spoIIIJ87 trpC2
	1S28	opp141 trpC2
	1S31	ade met spoIIA26 trpC2
	1S32	rpoB2 spoIIA69 trpC2
	1S33	rpoB2 spoIID66 trpC2

B. subtilis **168 Strains Indexed by Allele**

ALLELE	CODE	DESCRIPTION
trpC2 (cont)	1S34	spoIIE61 trpC2
	1S35	rpoB2 spoIIE64 trpC2
	1S36	ilvC1 spoIIIA(A-H)7 trpC2
	1S37	rpoB2 spoIIIA(A-H)53 trpC2
	1S38	spoIIIC94 trpC2
	1S39	spoIIID83 trpC2
	1S41	spoVF trpC2
	1S43	spoIID298 trpC2
	1S44	argF4 hisA1 metB5 pheA12 purA16 pyrA26 spoVB91 trpC2
	1S45	rpoB2 spoVD156 trpC2
	1S47	spoIVC133 trpC2
	1S48	spoIIIB2 trpC2
	1S49	spoIIB131 trpC2
	1S50	spoVA89 trpC2
	1S51	spoVE85 trpC2
	1S52	spoVF224 trpC2
	1S58	spoIVF152 trpC2
	1S59	kinA96 trpC2
	1S61	rpoB2 sigE55 trpC2
	1S63	spoIIIE36 trpC2
	1S68	abrB23 pheA1 spo0A12 trpC2
	1S69	absA6 spo0A12 trpC2
	1S70	absB24 spo0A12 trpC2
	1S71	spoIIA4 trpC2
	1S72	spoIIA4 trpC2
	1S73	ade met Sm spo0A16 trpC2
	1S75	spo-331 thyA1 thyB1 trpC2
	1S79	spoIIA37 trpC2
	1S80	spoIIA42 trpC2
	1S81	spoIIA176 trpC2
	1S82	pyrA1 spoL1 trpC2
	1S83	pheA1 spoVF1 trpC2
	1S86	sigF1 trpC2
	1S88	spoVIA513 trpC2
	1S89	spoIVF(TS) trpC2
	1S94	spo0J93 trpC2
	1S95	spoVK517 trpC2
	1S96	bofA::Tn917lac pheA1 trpC2
	1S101	Cm cotA::cat trpC2
	1S102	cotB::cat trpC2
	1S103	cotC::cat trpC2
	1S104	cotD::cat trpC2
	1S105	cotE ::cat trpC2
	1S106	cotF::cat trpC2
	1S107	cotF ::cat trpC2
	1S108	Cm cotT::pDE194 pheA1 trpC2
trpC3	1A393	pyrB trpC3
	1A544	trpC3
trpC4	1A545	trpC4
trpC5	1A546	trpC5
trpC6	1A547	trpC6
trpC7	1A548	trpC7
trpC8	1A549	trpC8
trpC9	1A550	trpC9
trpC10	1A551	trpC10
trpC11	1A552	trpC11
trpD1	1A522	trpD1
trpD2	1A64	trpD2
trpD3	1A523	trpD3
trpD4	1A524	trpD4
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
trpE26	1A65	trpE26
trpE194	1A521	trpE194
trpF1	1A531	trpF1
trpF2	1A532	trpF2
trpF3	1A533	trpF3
trpF4	1A534	trpF4
trpF5	1A535	trpF5
trpF6	1A536	trpF6
trpF7	1S12	spo0A12 trpF7
trpF8	1A537	trpF8
trpF9	1A538	trpF9
trpF10	1A539	trpF10
trpF11	1A540	trpF11
trpF12	1A541	trpF12
trpF13	1A542	trpF13
trpS1	1A102	trpC2 trpS1
	1A352	trpC2 trpS1
	1A353	trpS1
ts-2	1A461	ctrA1 ts-2
ts-355	1A269	spo- thyA1 thyB1 trpC2 ts-355
ts-39-2	1A428	met trpC2 ts-39-2
tscA1	1A595	arg thyA thyB tscA1
tscA23	1A596	arg thyA thyB tscA23
tscC11	1A598	arg thyA thyB tscC11
tscD14	1A599	arg thyA thyB tscD14
	1A649	arg thyA thyB tscD14
tsi-23	1A68	leuB8 metB5 tsi-23
tufAA-2	1A191	rpsL1 thr-5 trpC2 tufAA-2
tufAA-7	1A190	cysE14 spo- tufAA-7
tyr	1A437	ade his hsd$_{RI}$R^{-}M^{-} met nic rib trp tyr ura
	1A438	hsd$_{RI}$R^{-}M^{+} met nic rib trp tyr ura
	1A718	his hsd$_{RI}$R^{-}M^{+} Km lacZ- M15 met rib trpC2 tyr ura
	1S14	spo0A170 tyr
tyr-1	1A685	hsd$_{RI}$R^{-}M^{+} rib trpC2 tyr-1 ura
tyrA1	1A36	aroB2 hisH2 metB10 trpC2 tyrA1
	1A87	hisH2 trpC2 tyrA1
	1A103	aroB2 hisH2 recG40 trpC2 tyrA1
	1A108	hisA1 tyrA1
	1A173	hisH2 tyrA1
	1A206	trpC2 tyrA1
	1A298	aroB2 azpB80 hisH2 trpC2 tyrA1
	1A299	aroB2 hisH2 gyrA trpC2 tyrA1
	1A378	aroB2 hisH2 recD41 trpC2 tyrA1
	1A379	aroB2 hisH2 recG39 trpC2 tyrA1
	1A380	aroB2 hisH2 recF33 trpC2 tyrA1
	1A404	aroB2 hisA53 hisH2 rna-53 trpC2 tyrA1
tzm	1G11	gerCC58 trpC2 tzm wrd
upp	1A681	apt-6 ilvA1 pbuG3 pupA3 sacA78 upp
upp	1A682	ilvA1 pubG1 sacA78 upp xpt
ura	1A137	hag-3 hisA1 ura
	1A140	hag-2 hisA1 ifm-1 ura uvrB1
	1A312	argF4 flaC51 hag-1 hisA1 ura
	1A437	ade his hsd$_{RI}$R-M- met nic rib trp tyr ura
	1A438	hsd$_{RI}$R-M+ met nic rib trp tyr ura
	1A685	hsd$_{RI}$R-M+ rib trpC2 tyr-1 ura
	1A718	his hsd$_{RI}$R-M+ Km lacZ- M15 met rib trpC2 tyr ura
ura-1	1A205	narA1 trpC2 ura-1
ura-3	1A236	fruA20 ura-3
	1A237	fruB22 ura-3
	1A441	gutR1 ura-3

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
zbj-82::Tn917;	1A628	(SPβc2) trpC2 zbj-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
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
zfj-83::Tn917	1A728	(SPβc2) trpC2 zfj-83::Tn917
zhb-83::Tn917	1A640	(SPβc2) trpC2 zhb-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 hsd$_{RI}$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
abrB	(44846 ← 45136)	regulation of transition state genes (negative for *abrB, aprE, ftsAZ, kinC, motAB, nprE, pbpE, rbs, spo0H, spoVG, spo0E, tycA;* positive for *comK, hpr*)	transcriptional regulator	*cpsX*	Partial suppression of spo0 mutant phenotypes, including antibiotic sensitivity, exoenzyme secretion
addA	1139280 → 1142978	DNA repair	ATP-dependent deoxyribonuclease (subunit A)	*addA* or *addB*	sensitivity to DNA damaging agents
addB	1135793 → 1139293	DNA repair	ATP-dependent deoxyribonuclease (subunit B)		sensitivity to DNA damaging agents
aec				May be *lysC*	aminoethyl cysteine resistance (700 ìg/ml)
aecB				May be *lysC*	aminoethyl cysteine resistance (700 ìg/ml)
ahrC	(2521599 ← 2522048)	negative regulation of arginine biosynthesis; positive regulation of arginine catabolism (*roc* operons)	transcriptional regulator		arginine hydroxamate resistance (100 ìg/ml) in the presence of ornithine
ald	3277380 → 3278516	utilization of L-alanine	(EC 1.4.1.1) L-alanine dehydrogenase	*spoVN*, probably *alaA*	*ald-1*: unable to grow on L-alanine as sole carbon or nitrogen source; Tn*917* insertion additionally blocks sporulation at stage V; *alaA*: auxotrophy for L-alanine
alsR	3710555 → 3711463	regulation of the α-acetolactate operon (*alsSD*)	transcriptional regulator (LysR family)		constitutive acetolactate synthase
amm					glutamate requirement
amt					3-amino tyrosine resistance (700 ìg/ml)
amyE	327171 → 329153	starch degradation	(EC 3.2.1.1) amyA α-amylase	*amyR*	amyE^{+N}: electorphoretic variant; amyE^{H}: hyperactivity; amyR: regulation of amylase synthesis
aprE	(1103895 ← 1105040)	secreted protease	(EC 3.4.21.62) serine alkaline protease (subtilisin E)	*sprE*	reduction in extracellular protease activity
apt	(2822166 ← 2822678)	purine metabolism	adenine phosphoribosyltransferase		resistance to 2-fluoroadenine
arg(BCDJ)	1194506 → 1198731	arginine biosynthesis	operon encodes four enzymes in arginine biosynthesis pathway	originally *argO;* later *argABCDE*	requires arginine
argF	1202927 → 1203886	arginine biosynthesis	(EC 2.1.3.3) ornithine carbamoyltransferase		requires arginine or citrulline
arg(GH)	(3010823 ← 3012208)	arginine biosynthesis	operon encodes argininosuccinate synthase and argininosuccinate lyase	originally *argA*	requires arginine, ornithine, or citrulline
arg-342				probably *proAB*	requires proline, arginine, ornithine, or citrulline
arg^{s}				may be *pyrA*	sensitivity to arginine
aroA	(3044519 ← 3045595)	shikimate pathway	(EC 4.1.2.15) 3-deoxy-D-arabino-heptulosonate 7-phosphate synthase chorismate mutase-isozyme 3	*aroG*	requires phenylalanine, tyrosine, and tryptophan
aroB	(2377253 ← 2378341)	shikimate pathway	(EC 4.6.1.3) 3-dehydroquinate synthase		requires shikimic acid (or phenylalanine, tyrosine, and tryptophan)
aroC	(2411940 ← 2412707)	shikimate pathway	(EC 4.2.1.10) 3-dehydroquinate dehydratase		requires shikimic acid (or phenylalanine, tyrosine, and tryptophan)
aroD	(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
aroE	(2367195 ← 2368481)	shikimate pathway	(EC 2.5.1.19) 5-enolpyruvoylshikimate-3-phosphate synthase		requires phenylalanine, tyrosine, and tryptophan
aroF	(2378403 ← 2379509)	shikimate pathway	(EC 4.6.1.4) chorismate synthase		requires phenylalanine, tyrosine, and tryptophan
aroH	(2376873 ← 2377256)	aromatic amino acids biosynthesis	(EC 5.4.99.5) chorismate mutase (isozymes 1 and 2)		requires phenylalanine, tyrosine, and tryptophan
aroI	339597 → 340157	shikimate pathway	(EC 2.7.1.71) shikimate kinase		requires phenylalanine, tyrosine, and tryptophan
asaA			arsenate reductase?	probably *yqcM*	sensitive to sodium arsenate (1 mM); asa2 is large deletion
asaB					arsenate resistance (1 mM sodium arsenate; introduced from W23)
aspH				may be *ansR*	constitutive aspartase
aspT					deficient in high affinity aspartate transport
ath					requirement for adenine + thiamine
azc					resistance to L-azetidin-2-carboxylic acid (500 ìg/ml)
azlA				probably in *ilvBC*	4-azaleucine resistance (40 ìg/ml)
azlB	(2729022 ← 2729495)	negative regulation of the *azlBCD* operon	transcriptional regulator (Lrp/AsnC family)	*yrdG*	4-azaleucine resistance (40 ìg/ml)
azp					resistance to azopyrimidines (50 ìg/ml HPUra)
bac					reduction in bacilysin synthesis
bfmB				*bfmBAA*, *bfmBAB*, or *bfmBB*	requires branched fatty acid or valine or isoleucine
bglC	1939853 → 1941379	cellulose degradation	(EC 3.2.1.4) endo-1,4-β-glucanase	*eglS*	deficient in cellulose degradation
bglS	(4010631 ← 4011359)	lichenan degradation	(EC 3.2.1.73) endo-β-1,3-1,4 glucanase	*bgl*, *licS*	deficient in lichenan degradation
bioB	(3089563 ← 3090570)	biotin biosynthesis	biotin synthetase		biotin auxotrophy
blt	2716242 → 2717444		multidrug-efflux transporter	*acfA*, *bmr2*, *bmt*	chromosomal amplification leads to multidrug resistance via efflux
bmr	2493888 → 2495057		multidrug-efflux transporter	*bmr1*	chromosomal amplification leads to multidrug resistance via efflux
bmrR	2495130 → 2495969	positive regulation of the *bmrUR* operon	transcriptional regulator		
bofA	29770 → 30033	inhibitor of the pro-σ^K processing machinery	integral membrane protein		null allele has moderately reduce sporulation
bry					bryamycin resistance
cafA					caffeine resistance (4-8 mg/ml)
cam-2					chloramphenicol resistance (20 ìg/ml)
car					fails to grow on trehalose, maltose, or sucrose
ccpA	(3043240 ← 3044244)	carbon catabolite control; glucose regulation of several genes; mediates catabolite repression	transcriptional regulator (LacI family)	*graR*, *alsA*	loss of glucose repression for amylase and acetoin production
cdd	(2610203 ← 2610613)		(EC 3.5.4.5) cytidine/deoxycytidine deaminase		unable to grow on cytidine or deoxycytidine as sole pyrimidine source
cdr					resistance to Cd^{2+}
cer					resistance to cerulenin
cgeE	(2145256 ← 2146035)	maturation of the outermost layer of the spore		*cgeBC*	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
citB	1925935 → 1928664	citric acid cycle	(EC 4.2.1.3) aconitate hydratase		unable to grow on lactate-glutamate; autolytic, poor sporulation
citC	(2978789 ← 2980060)	citric acid cycle	(EC 1.1.1.42) isocitrate dehydrogenase		unable to grow on lactate-glutamate; autolytic, poor sporulation
citD					unable to grow on lactate-glutamate; autolytic, poor sporulation; deletion of citK and kauA
citG	(3388083 ← 3389471)	citric acid cycle	(EC 4.2.1.2) fumarate hydratase		unable to grow on lactate-glutamate; autolytic, poor sporulation
citH	(2977807 ← 2978745)	citric acid cycle	(EC 1.1.1.37) malate dehydrogenase	*mdh*	unable to grow on lactate-glutamate; autolytic, poor sporulation
com-9		competence for transformation			poorly transformable
com-14 ::Tn917		competence for transformation			poorly transformable
com-18 ::Tn917		competence for transformation			poorly transformable
com-30		competence for transformation			poorly transformable
com-31		competence for transformation			poorly transformable
com-44 ::Tn917		competence for transformation			poorly transformable
com-71		competence for transformation			poorly transformable
com-104		competence for transformation			poorly transformable
cotA	(683179 ← 684720)	protein composition of the spore coat	spore coat protein (outer)	*pig*	colonies fail to form sporulation pigment
cotB	(3713796 ← 3714938)	protein composition of the spore coat	spore coat protein (outer)		no known effect on spore morphology, resistance, or germination properties
cotC	(1904250 ← 1904606)	protein composition of the spore coat	spore coat protein (outer)		no known effect on spore morphology, resistance, or germination properties
cotD	(2332026 ← 2332253)	protein composition of the spore coat	spore coat protein (inner)		no known effect on spore morphology, resistance, or germination properties
cotE	1774435 → 1774980	outer coat assembly	morphogenic protein		spores lack outer coats; lysozyme sensitive, defective germination
cotF	4166318 → 4166800	protein composition of the spore coat	spore coat protein		no known effect on spore morphology, resistance, or germination properties
cotT	(1280096 ← 1280419)	protein composition of the spore coat	spore coat protein (inner)		slow germination on glucose, fructose, and L-asparagine
crk					resistance to fluorocytidine
crsB					sporulates in the presence of excess carbon sources
crsC					sporulates in the presence of excess carbon sources
crsD					sporulates in the presence of excess carbon sources
crsE				probably *rpoC*	sporulates in the presence of excess carbon sources
crsF					sporulates in the presence of excess carbon sources
ctrA	(3809746 ← 3811353)	pyrimidine biosynthesis	(EC 6.3.4.2) CTP synthetase		requires cytidine in the absence of NH_4^+
cym					requirement for cysteine or methionine
cysB					cysteine requirement
cysC					cysteine, methionine, sulfite, sulfide requirement
cysE	112797 → 113450	cysteine biosynthesis	(EC 2.3.1.30) serine acetyltransferase	*cysA*	cysteine requirement

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

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

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

Gene	Genome Location	Function	Gene Product	Synonyms	Mutant Phenotypes
flaC					flagellaless
flgM	(3639345 ← 3639611)	coupling late flagellar gene expression to assembly of hook-basal body complex	anti-sigma factor repressor of ó^D-dependent transcription		
fnd					fluoroindole resistance (50ìg/ml)
fruA	1508661 → 1510568	phosphotransferase system (PTS)	fructose-specific enzyme IIBC component		unable to grow on fructose as carbon source
fruB	1507735 → 1508646	fructose utilization	(EC 2.7.1.56) fructose-1-phosphate kinase		unable to grow on fructose as carbon source
fruC					unable to grow on fructose as carbon source
ftr					fluorotryptophan resistance (50 ìg/ml)
furA					5-fluoruracil resistance (1 ìg/ml)
furB					5-fluoruracil resistance (40 ìg/ml) in the presence of uracil (40 ìg/ml)
furC					5-fluoruracil resistance (40 ìg/ml) in the presence of uracil (40 ìg/ml)
furE					5-fluoruracil resistance (40 ìg/ml) in the presence of uracil (40 ìg/ml)
furF					5-fluoruracil resistance (40 ìg/ml) in the presence of uracil (40 ìg/ml)
fus	130683 → 132761		elongation factor G	*efg*	fusidic acid resistance (3 ìg/ml)
gcaD	56350 → 57720	peptidoglycan and lipopolysaccharide biosynthesis	(EC 2.7.7.23) UDP-N-acetyl-glucosamine pyrophosphorylase	*tms, tms26*	temperature-sensitive growth
gerA(ABC)	3389841 → 3391289	germination response to L-alanine and related amino acids (earliest stage)			germination defective
gerB(ABC)	3687872 → 3691553	germination response to combination of glucose, fructose, L-asparagine, and KCl			germination defective
gerCC	(2381157 ← 2382203)	menaquinone biosynthesis (germination)	(EC 2.5.1.30) heptaprenyl diphosphate synthase component II	*gerC58*	germination defective
gerD	(158514 ← 159071)	germination response to L-alanine and combination of glucose, fructose, L-asparagine, and KCl (early stage)			germination defective
gerE	(2903828 ← 2904052)	required for the expression of late spore coat genes (germination)	transcriptional regulator		germination defective
gerF					germination defective
gerG					germination defective
gerJ				*tzm*	germination defective; white on tetrazolium agar
glgB	(3168841 ← 3170724)	starch and glycogen biosynthesis	(EC 2.4.1.18) 1,4-α-glucan branching enzyme		defective glycogen synthesis
glmS	200263 → 202065		(EC 2.6.1.16) L-glutamine-D-fructose-6-phosphate amidotransferase	*gcaA, ybxD*	requires glucosamine on minimal media; spores produced with limiting glucosamine have defective cortex
glnA	1877669 → 1879003		(EC 6.3.1.2) glutamine synthetase		requires glutamine (500 µg/ml) in minimal media
glnR	1877201 → 1877608	negative regulation of the glutamine synthetase gene (glnA)	transcriptional regulator		
glpD	1004480 → 1006147	glycerol utilization	(EC 1.1.99.5) glycerol-3-phosphate dehydrogenase		inability to use glycerol as carbon source
glpK	1002849 → 1004339	glycerol utilization	(EC 2.7.1.30) glycerol kinase		inability to use glycerol as carbon source
glpP	1001249 → 1001827	control of *glpD* 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
glpT	(233983 ← 235317)	uptake of glycerol-3-phosphate	glycerol-3-phosphate permease	*ybeE*	fosfomycin resistant (200 ìg/ml)
gltA	(2009326 ← 2013888)	glutamate biosynthesis	(EC 1.4.1.13) glutamate synthase (large subunit)		requires glutamate or aspartate
gltB	(2007828 ← 2009309)	glutamate biosynthesis	(EC 1.4.1.13) glutamate synthase (small subunit)		requires glutamate or aspartate
glyA	(3788245 ← 3789492)	glycine/serine/threonine metabolism	(EC 2.1.2.1) serine hydroxymethyltransferase	*glyC*	requires glycine
glyB					requires for glycine
gntK	4113349 → 4114890	gluconate utilization	(EC 2.7.1.12) gluconate kinase		inability to utilize gluconate
gntP	4114919 → 4116265	gluconate utilization	gluconate permease		inability to utilize gluconate
gntR	4112625 → 4113356	negative regulation of gluconate operon	transcriptional regulator		constitutive expression of gnt operon
gsiB	494057 → 494428	general stress response	general stress protein		null mutant has no known phenotype
gsp-10				probably *gerA*	germination and outgrowth defective
gtaB	3664689 → 3665567	glucosylation of teichoic acid	(EC 2.7.7.9) UTP-glucose-1-phosphate uridylyltransferase		smooth colonies; resistant to ö25, ö29, SP10
gtaC					smooth colonies; resistant to ö25, ö29, SP10
guaB	15913 → 17379	GMP biosynthesis	(EC 1.1.1.205) inositol-monophosphate dehydrogenase	*guaA*	requires guanine
gutA				*may be ydjK*	inability to use sorbitol as carbon source
gutB	667183 → 668244		(EC 1.1.1.14) sorbitol dehydrogenase		inability to use sorbitol as carbon source
gutR	(664492 ← 666981)	positive regulation of the sorbitol dehydrogenase gene (gutB)	transcriptional regulator		constitutive mutation allows growth on xylitol
gyrA	6993 → 9458	initation of replication cycle and DNA elongation	(EC 5.99.1.3) DNA gyrase (subunit A)	*nalA*	resistance to naladixic acid (50 ìg/ml)
gyrB	4866 → 6782	initation of replication cycle and DNA elongation	(EC 5.99.1.3) DNA gyrase (subunit B)	*novA*	resistance to novobiocin (2 ìg/ml)
hag	(3634047 ← 3634961)	flagellar synthesis	flagellin protein		hag-1: strain 168 antigen; hag-2: strain W23 antigen; hag-3: straight filament
hemA	(2876866 ← 2878233)	porphyrin biosynthesis	(EC 1.2.1.-) glutamyl-tRNA reductase		requires heme
hemB	(2873302 ← 2874276)	porphyrin biosynthesis	(EC 4.2.1.24) δ-aminolevulinic acid dehydratase (porphobilinogen synthase)		requires heme
hemC	(2875051 ← 2875995)	hydroxymethylbilane synthesis from porphobilinogen (porphyrin biosynthesis)	(EC 4.3.1.8) porphobilinogen deaminase (hydroxymethylbilane synthase)		requires heme
hemD	(2874273 ← 2875061)	cyclisation of hydroxymethylbilane (porphyrin biosynthesis)	(EC 4.2.1.75) uroporphyrinogen III cosynthase		requires heme
hemE	1085590 → 1086651	porphyrin biosynthesis	(EC 4.1.1.37) uroporphyrinogen III decarboxylase		requires heme
hemH	1086723 → 1087655	incorporation of iron into protoporphyrin IX (porphyrin biosynthesis)	(EC 4.99.1.1) ferrochelatase	*hemF*	requires heme
hemY	1087670 → 1089082	late steps of protoheme IX synthesis (porphyrin biosynthesis)	(EC 1.3.3.4) protoporphyrinogen IX and coproporphyrinogen III oxidase	*hemG*	requires heme

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

Gene	Genome Location	Function	Gene Product	Synonyms	Mutant Phenotypes
hisA	(3583377 ← 3584114)	histidine biosynthesis	(EC 5.3.1.16) phosphoribosylformimino-5-aminoimidazole carboxamide ribotide isomerase		requires histidine
hisB	(3584750 ← 3585334)	histidine biosynthesis	(EC 4.2.1.19) imidazoleglycerol-phosphate dehydratase		requires histidine
hisH	(3584111 ← 3584749)	histidine biosynthesis	(EC 2.4.2.-) amidotransferase		requires histidine
hom	(3313886 ← 3315187)	threonine/methionine biosynthesis	(EC 1.1.1.3) homoserine dehydrogenase		requires threonine and methionine
hpr	(1072581 ← 1073192)	negative regulation of sporulation and extracellular proteases (aprE, nprE, sin)	transcriptional regulator	*catA, scoC*	hyperproduces extraceullar proteases
hsd_{BI}		restriction-modification			possesses Bsu 1247I restriction-modification system
hsd_{CI}		restriction-modification			possesses Bsu 1247II restriction-modification system
hsd_{RI}		restriction-modification			M^-: deficient in restriction methylase; R^-: deficient in restriction endonuclease
hutCR		histidine utilization			renders *hut* operon constitutive and insensitive to catabolite repression
hutH	4040840 → 4042366	histidine utilization	(EC 4.3.1.3) histidase		inability to utilize histidine
hutP	4040272 → 4040727	positive regulation of the histidine utilization operon (*hutPHUIGM*)	transcriptional regulator	*hutP1*	inability to utilize histidine
ifm					increased flagella and motility
ilvA	(2292010 ← 2293278)	isoleucine biosynthesis	(EC 4.2.1.16) threonine dehydratase		requires isoleucine
ilvB	(2894347 ← 2896071)	valine/isoleucine biosynthesis	(EC 4.1.3.18) acetolactate synthase (acetohydroxy-acid synthase) (large subunit)		requires isoleucine and valine
ilvC	(2892781 ← 2893809)	valine/isoleucine biosynthesis	(EC 1.1.1.86) ketol-acid reductoisomerase (acetohydroxy-acid isomeroreductase)		requires isoleucine and valine
ilvD	(2300003 ← 2301679)	valine/isoleucine biosynthesis	(EC 4.2.1.9) dihydroxy-acid dehydratase		requires isoleucine and valine
inh				probably *tyrA*	inhibition by histidine (50 ìg/ml)
iolG	(4074575 ← 4075609)	myo-inositol catabolism	(EC 1.1.1.18) myo-inositol 2-dehydrogenase	*iol, idh*	inability to utilize inositol
iur					inhibition by uracil
kan					kanamycin resistance (50 ìg/ml)
kauA					defective in branched-chain á-keto acid transport
kinA	1469428 → 1471248	initiation of sporulation	(EC 2.7.3.-) two-component sensor histidine kinase	*spoIIF, spoIIJ, gsiC, scoB, scoD*	null mutants cause oligosporogeny (stage 0-II) in liquid media, delayed sporulation on agar
ksgA	50638 → 51516	high level kasugamycin resistance	(EC 2.1.1.-) dimethyladenosine transferase		resistance to kasugamycin (40 ìg/ml)
lacA	(3502083 ← 3504146)		(EC 3.2.1.23) β-galactosidase	*yvfN*	null mutations eliminate endogenous â-galactosidase
lacR	(3507722 ← 3508714)	negative regulation of β-galactosidase gene (lacA)	transcriptional regulator (LacI family)	*yvfJ*	up mutations cause overproduction of â-galactosidase
leuA	(2891238 ← 2892794)	leucine biosynthesis	(EC 4.1.3.12) 2-isopropylmalate synthase		leucine auxotrophy
leuB	(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
leuD	(2888040 ← 2888639)	leucine biosynthesis	(EC 4.2.1.33) 3-isopropylmalate dehydratase (small subunit)		leucine auxotrophy
liv				deletion within *ilvBNC-leuACBD*	requires leucine, isoleucine, and valine
lmrA	(289686 ← 290252)	negative regulation of lincomycin operon	transcriptional regulator	*lin-2, yccB*	lincomycin resistance (80-100 ìg/ml)
lys	(2436179 ← 2437498)	lysine biosynthesis	(EC 4.1.1.20) diaminopimelate decarboxylase		lysine auxotrophy
lysC	(2908623 ← 2909849)	diaminopimelate/lysine biosynthesis	(EC 2.7.2.4) aspartokinase II α (aa 1-408) and β subunits (aa 246-408)	*ask, aecA*	aminoethyl cysteine resistance (700 ìg/ml)
lysS	88724 → 90223	aminoacyl-tRNA synthetase	(EC 6.1.1.6) lysyl-tRNA synthetase		temperature-sensitive growth
lyt					reduction in autolytic enzymes; cells grow as long chains
menB	(3147981 ← 3148796)	dihydroxynapthoic acid synthetase	menaquinone biosynthesis		resistance to aminoglycosides (2 ìg/ml kanamycin); menaquinone deficient; supplement with menadione
menC				probably *menD*	resistance to aminoglycosides (2 ìg/ml kanamycin); menaquinone deficient; supplement with menadione
menE	(3146430 ← 3147890)	menaquinone biosynthesis	(EC 6.2.1.26) O-succinylbenzoic acid-CoA ligase		resistance to aminoglycosides (2 ìg/ml kanamycin); menaquinone deficient; supplement with menadione
metA				possibly *yjcI*	requires methionine, cystathionine, or homocysteine
metB	2304619 → 2305293	methionine biosynthesis	(EC 2.3.1.46) homoserine O-succinyltransferase		requires methionine or homocysteine
metC	(1382784 ← 1385072)	methionine biosynthesis	(EC 2.1.1.14) cobalamin-independent methionine synthase		requires methionine
metD				possibly *yjcJ*	requires methionine
minD	(2857038 ← 2857844)	cell-division inhibition (septum placement)	ATPase activator of MinC	*divIVB1*	minicell production
motA	(1433899 ← 1434711)	flagellar motor rotation	motility protein A	*mot*	paralyzed flagella
mreD	(2858579 ← 2859097)		cell-shape determining protein	*rodB*	cell wall defective; salt dependent growth
mth				probably *thr-hom*	Requires threonine plus either methionine or homocysteine; probably deletion in thr-hom region
mtlD	451189 → 452289		(EC 1.1.1.17) mannitol-1-phosphate dehydrogenase	*mtlB*	inability to utilize mannitol as carbon source
mtr				*mtrA* or *mtrB*	5-methyl-tryptophan resistance (1 mg/ml); derepression of trp operon
nadE	337860 → 338678	NAD biosynthesis	(EC 6.3.5.1) NH3-dependent NAD+ synthetase	*outB, tscBGH, gsp-81*	temperature-sensitive growth
narA	(3771380 ← 3772405)	nitrate assimilation, anaerobic respiration		*narAB*	inability to use nitrate as nitrogen source
nasC	(357875 ← 360007)		(EC 1.7.99.4) assimilatory nitrate reductase (catalytic subunit)	*narB, nasBB*	inability to use nitrate as nitrogen source
nea					neamine resistance (10 ìg/ml)
nic				probably in *nadABC* or *nifS*	nicotinic acid requirement
nonA					permissive for infection by phages SP10 and öNR2
novB					resistance to novobiocin (2 ìg/ml)
odhA	(2108043 ← 2110856)		(EC 1.2.4.2) 2-oxoglutarate dehydrogenase (E1 subunit)	*citK*	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
odhB	(2106760 ← 2108013)		(EC 2.3.1.61) 2-oxoglutarate dehydrogenase complex (dihydrolipoamide transsuccinylase, E2 subunit)	*citM*	inability to grow on lactate-glutamate as carbon source
ole					oleandomycin resistance (200 ìg/ml)
opp(ABCDEF)	1219321 → 1224922	required for initiation of sporulation, competence development, and oligopeptide transport	oligopeptide ABC transporter (ATP-binding protein)	*spo0K*	null mutants display delayed sporulation and resistance to bialaphos
outA					temperature-sensitive outgrowth of spores
outC					temperature-sensitive outgrowth of spores
outD					temperature-sensitive outgrowth of spores
outE					temperature-sensitive outgrowth of spores
outF					temperature-sensitive outgrowth of spores
oxr					oxolinic acid resistance
pabA	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)	*trpG, trpX, gat*	Requires para-aminobenzoic acid and tryptophan
pabB	82861 → 84273	folate biosynthesis	(EC 4.1.3.-) para-aminobenzoate synthase (subunit A)	*pab*	para-aminobenzoic acid requirement
pbuG					resistance to 8-azaguanine
pdhA	1527731 → 1528846		(EC 1.2.4.1) pyruvate dehydrogenase (E1 αsubunit)	*aceA*	requires acetate
pdhD	1531275 → 1532687		(EC 1.8.1.4) dihydrolipoamide dehydrogenase E3 subunit of both pyruvate dehydrogenase and 2-oxoglutarate dehydrogenase complexes	*citL*	unable to grow on lactate-glutamate as carbon source
pfk	(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
pgk	(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
pha					resistance to phage SPO1
pheA	(2850544 ← 2851401)	phenylalanine biosynthesis	(EC 4.2.1.51) prephenate dehydratase		requires phenylalanine
phoA	(1016535 ← 1017920)	phosphorus metabolism	(EC 3.1.3.1) alkaline phosphatase A	*phoAIV*	reduction in phosphate-starvation induced APase (60-75%)
phoB	(619813 ← 621201)	phosphorus metabolism	(EC 3.1.3.1) alkaline phosphatase III	*phoAIII*	reduction in phosphate-starvation induced APase (25-40%); reduction in sporulation APase
phoP	(2976873 ← 2977595)	phosphate regulation (phoA, phoB, phoD, resABCDE)	two-component response regulator		required for starvation-induced accumulation of APase
phoR	(2975141 ← 2976880)	involved in phosphate regulation	two-component sensor histidine kinase		required for starvation-induced accumulation of APase
phoS					constitutive alkaline phosphatase production
polA	(2972255 ← 2974897)	replication and DNA repair	(EC 2.7.7.7) DNA polymerase I		sensitive to MMS (methyl methanesulphonate, 350 ìg/ml)

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

Gene	Genome Location	Function	Gene Product	Synonyms	Mutant Phenotypes
polC	1726524 → 1730837	initiation of replication cycle and DNA elongation	(EC 2.7.7.7) DNA polymerase III (α subunit)	*mut-1, dnaF, dnaP*	polC133: temperature sensitive growth; polC12: HPUra resistance (8 ìg/ml); allele1: temperature sensitive, mutator
pro(AB)	1379069 → 1380316	proline biosynthesis			proline auxotrophy
pro(H)					high production of exoproteases
pro(L)					low production of exoproteases
proJ	(2014989 ← 2016104)	proline biosynthesis	glutamate 5-kinase	*yohA*	
ptm					pyrithmine resistance
ptsI	1459117 → 1460769	general energy coupling protein of PTS; transfers phosphate from PEP to HPr	(EC 2.7.3.9) phosphotransferase system (PTS) enzyme I		no growth on phosphotransferase system sugars
pupA				*probably deoD*	adenosine phosphorylase negative
purA	(4154641 ← 4155933)	purine biosynthesis	(EC 6.3.4.4) AMP biosynthesis adenylosuccinate synthetase		adenine requirement
purB	699738 → 701033	purine biosynthesis	(EC 4.3.2.2) purine biosynthesis adenylosuccinate lyase		adenine requirement
purD	709653 → 710921	purine biosynthesis	(EC 6.3.4.13) phosphoribosylglycinamide synthetase		adenine or hypoxanthine requirement
purE	698121 → 698609	purine biosynthesis	(EC 4.1.1.21) phosphoribosyl-aminoimidazole carboxylase I	*purB33*	adenine, guanine, or hypoxanthine requirement
purF	704946 → 706376	purine biosynthesis	(EC 2.4.2.14) phosphoribosyl-pyrophosphate amidotransferase	*purB6*	adenine, guanine, or hypoxanthine requirement
purH	708099 → 709637	purine biosynthesis	(EC 2.1.2.3) phosphoribosylaminoimidazole carboxy formyl formyltransferase inosine-monophosphate cyclohydrolase	*purJ*	adenine requirement
purM	706478 → 707518	purine biosynthesis	(EC 6.3.3.1) phosphoribosylaminoimidazole synthetase		adenine and thiamine requirement
pycA	1553590 → 1557036		(EC 6.4.1.1) pyruvate carboxylase		requires citric acid cycle compounds in minimal media
pyrA	1622056 → 1623150	pyrimidine biosynthesis	(EC 6.3.5.5) carbamoyl-phosphate synthetase		arginine-sensitive growth
pyrB	1619875 → 1620789	pyrimidine biosynthesis	(EC 2.1.3.2) aspartate carbamoyltransferase		requires pyrimidine source
pyrC	1620773 → 1622059	pyrimidine biosynthesis	(EC 3.5.2.3) dihydroorotase		requires pyrimidine source
pyrD	1627117 → 1628052	pyrimidine biosynthesis	(EC 1.3.3.1) dihydroorotate dehydrogenase	*pyrX*	requires pyrimidine source
pyrE	1628719 → 1629369	pyrimidine biosynthesis	(EC 2.4.2.10) orotate phosphoribosyltransferase		requires pyrimidine source
pyrF	1628021 → 1628740	pyrimidine biosynthesis	(EC 4.1.1.23) orotidine 5'-phosphate decarboxylase		requires pyrimidine source
pyrR	1617708 → 1618253	attenuation (antitermination) of the pyrimidine operon (pyrPBCADFE) 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
rapA	**1315338 → 1316474**	**prevents sporulation by dephosphorylating Spo0F-P (and thus the phosphorelay)**	**response regulator aspartate phosphatase**	*gsiAA, spo0L*	**null mutant sporulates in the presence of excess carbon sources**
recA	**1764015 → 1765058**	**DNA repair and genetic recombination**	**multifunctional SOS repair regulator**	*recE*	**impaired in recombination and repair**
recB		**DNA repair and genetic recombination**			**impaired in recombination and repair**
recD		**DNA repair and genetic recombination**			**impaired in recombination and repair**
recF	**3437 → 4549**	**DNA repair and genetic recombination**			**impaired in recombination and repair**
recG		**DNA repair and genetic recombination**			**impaired in recombination and repair**
recH		**DNA repair and genetic recombination**			**impaired in recombination and repair**
recL		**DNA repair and genetic recombination**			**impaired in recombination and repair**
recP		**DNA repair and genetic recombination**			**impaired in recombination and repair**
recR	**28865 → 29461**	**DNA repair and genetic recombination**		*recM*	**impaired in recombination and repair**
relA	**(2819794 ← 2821998)**	**stringent response**	**(EC 2.7.6.5) GTP pyrophosphokinase**		**“relaxed” stringent response in RNA synthesis**
rib					**requirement for riboflavin**
rna-53					**temperature-sensitive RNA synthesis**
rplA	**119107 → 119805**	**ribosome, large subunit**	**ribosomal protein L1 (BL1)**		**altered electrophoretic mobility; chloramphenicol resistance (5 ìg/ml)**
rplC	**135710 → 136339**	**ribosome, large subunit**	**ribosomal protein L3 (BL3)**		**altered electrophoretic mobility; possible micrococcin resistance (50 ìg/ml)**
rplE	**141193 → 141732**	**ribosome, large subunit**	**ribosomal protein L5 (BL6)**		**altered electrophoretic mobility**
rplJ	**120057 → 120557**	**ribosome, large subunit**	**ribosomal protein L10 (BL5)**		**altered electrophoretic mobility**
rplK	**118588 → 119013**	**ribosome, large subunit**	**ribosomal protein L11 (BL11)**	*relC, tsp*	**altered electrophoretic mobility; thiostrepton resistance (1 µg/ml)**
rplL	**120604 → 120975**	**ribosome, large subunit**	**ribosomal protein L12 (BL9)**		**altered electrophoretic mobility**
rplU	**(2854779 ← 2855087)**	**ribosome, large subunit**	**ribosomal protein L21 (BL20)**		**altered electrophoretic mobility**
rplV	**138495 → 138836**	**ribosome, large subunit**	**ribosomal protein L22 (BL17)**		**altered electrophoretic mobility; erythromycin resistance (2 ìg/ml)**
rplX	**140855 → 141166**	**ribosome, large subunit**	**ribosomal protein L24 (BL23) (histone-like protein HPB12)**		**altered electrophoretic mobility**
rpmA	**(2854141 ← 2854425)**	**ribosome, large subunit**	**ribosomal protein L27 (BL24)**		**altered electrophoretic mobility**
rpmD	**143873 → 144052**	**ribosome, large subunit**	**ribosomal protein L30 (BL27)**		**altered electrophoretic mobility**
rpoA	**148929 → 149873**	**transcription**	**(EC 2.7.7.6) RNA polymerase (α subunit)**		
rpoB	**121916 → 125497**	**transcription**	**(EC 2.7.7.6) RNA polymerase (β subunit)**		**rifampin resistance (50 ìg/ml); allele 2: low rifampin resistance (2ìg/ml)**
rpoC	**125559 → 129158**	**transcription**	**(EC 2.7.7.6) RNA polymerase (β' subunit)**		**lipiarmycin (10 ìg/ml) and streptolydigin (40 ìg/ml) resistance**
rpsE	**143359 → 143859**	**ribosome, small subunit**	**ribosomal protein S5**		**altered electrophoretic mobility; spectinomycin resistance (125 ìg/ml)**
rpsF	**(4198653 ← 4198940)**	**ribosome, small subunit**	**ribosomal protein S6 (BS9)**		**altered electrophoretic mobility**
rpsG	**130159 → 130629**	**ribosome, small subunit**	**ribosomal protein S7 (BS7)**		**altered electrophoretic mobility**
rpsH	**141972 → 142370**	**ribosome, small subunit**	**ribosomal protein S8 (BS8)**		**altered electrophoretic mobility**
rpsI	**154299 → 154691**	**ribosome, small subunit**	**ribosomal protein S9**		**altered electrophoretic mobility**
rpsK	**148357 → 148752**	**ribosome, small subunit**	**ribosomal protein S11 (BS11)**		**altered electrophoretic mobility**
rpsL	**129701 → 130117**	**ribosome, small subunit**	**ribosomal protein S12 (BS12)**	*strA, fun*	**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
sacA	(3901006 ← 3902448)	sucrose metabolism	(EC 3.2.1.26) sucrase-6-phosphate hydrolase	*ipa-50d*	inability to utilize sucrose (except in a deg mutant strain)
sacB	3535072 → 3536493	sucrose metabolism	(EC 2.4.1.10) levansucrase		levanase negative
sacP	(3902445 ← 3903827)	sucrose transport	(EC 2.7.1.69) phosphotransferase system (PTS) sucrose-specific enzyme IIBC component	*ipa-49d*	inability to utilize sucrose
sacR					constitutive levansucrase and sucrase synthesis
sacT	(3904938 ← 3905768)	positive regulation of sacA and sacP	transcriptional antiterminator	*ipa-47d*	constitutive sucrase synthesis
sac(XY)	3941028 → 3943303	positive regulation of levansucrase and sucrase synthesis (sucrase regulation)		*sacS*	constitutive levansucrase and sucrase synthesis
sapA					allows synthesis of sporulation alkaline phosphatase in Spo$^-$ strains
sapB					allows synthesis of sporulation alkaline phosphatase in Spo$^-$ strains
sas				*spoIIA*	intragenic suppressor of spoIIA69
scoA					“sporulation control;” delayed sporulation, elevated protease levels
sdhA	(2905438 ← 2907198)	citric acid cycle	(EC 1.3.99.1) succinate dehydrogenase (flavoprotein subunit)	*citF*	no growth on lactate-glutamate as carbon sources; autolytic
sdhB	(2904674 ← 2905435)	citric acid cycle	(EC 1.3.99.1) succinate dehydrogenase (iron-sulfur protein)		no growth on lactate-glutamate as carbon sources; autolytic
sdhC	(2907232 ← 2907840)	citric acid cycle	succinate dehydrogenase (cytochrome b558 subunit)		no growth on lactate-glutamate as carbon sources; autolytic
serA	2410320 → 2411897	serine biosynthesis	(EC 1.1.1.95) phosphoglycerate dehydrogenase		requirement for serine or glycine
serC	(1074762 ← 1075841)	serine biosynthesis	(EC 2.6.1.52) phosphoserine aminotransferase	*yhaF*	requirement for serine
serR					resistant to serine (50 ìg/ml)
sfp	(407222 ← 407719)	surfactin production			null mutant: no surfactin synthesis
sigA	(2599490 ← 2600605)	general vegetative sigma factor	RNA polymerase major sigma factor σ^A	*rpoD, crsA*	crsA alleles: sporulate in the presence of repressing levels of glucose and other carbon sources
sigB	522413 → 523207	general stress sigma factor (class II genes)	RNA polymerase σ^B	*rpoF*	null mutant: no obvious growth or sporulation phenotype, but blocks expression of many general stress response genes
sigD	1715885 → 1716649	flagellar synthesis, motility, chemotaxis, autolysis	RNA polymerase σ^D	*flaB*	null mutant: filamentous growth; blocks flagellar synthesis, motility, chemotaxis, autolysin formation
sigE	1604166 → 1604885	early mother cell-specific gene expression	RNA polymerase sporulation-specific σ^E	*spoIIGB*	null mutations: block sporulation at stage II; two septa formed
sigF	(2442658 ← 2443425)	early forespore-specific gene expression	RNA polymerase sporulation-specific sigma factor σ^F	*spoIIAC*	null mutations: block sporulation at stage II; two septa formed
sigH	116597 → 117253	expression of vegetative and early stationary-phase genes	RNA polymerase σ^H	*spo0H*	null mutations: block sporulation before septum formation
sinI	2551722 → 2551895	prevents SinR from binding to its target sequence on aprE	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
sinR	**2551929 → 2552264**	**regulation of post-exponential-phase responses genes (positive regulation of comK; negative regulation of aprE, kinB, sigD, spo0A, spoIIA, spoIIE, spoIIG)**	**transcriptional regulator**	*sin, flaD*	**null mutations: blocks flagellar synthesis, motility, chemotaxis, autolysin formation; overexpression on plasmid: blocks sporulation**
smo					**smooth colony morphology**
SP10^R					**resistant to phage SP10**
SP10^S					**sensitive to phage SP10**
spcB					
spcD					
spl(AB)	**1461177 → 1462205**	**repair of UV radiation-induced DNA damage during spore germination**	**spore photoproduct lyase**	*spl , ssp-1*	**spores are UV-sensitive**
spo0A	**(2517301 ← 2518104)**	**central role in the initiation of sporulation (negative regulation of abrB, kinA, kinC, spo0A; positive regulation of spoIIA, spoIIE, spoIIG) (stage 0 sporulation)**	**two-component response regulator**	*spo0C, spo0G, spoIIL, sof-1*	**null mutation: blocks sporulation at stage 0; sof, rvtA: suppress null mutations in spo0B and spo0F**
spo0B	**(2853242 ← 2853820)**	**stage 0 sporulation**	**sporulation initiation phosphoprotein**	*spo0D*	**blocks sporulation at stage 0**
spo0E	**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**
spo0F	**(3808603 ← 3808977)**	**initiation of sporulation (stage 0 sporulation)**	**two-component response regulator**		**blocks sporulation at stage 0**
spo0J	**(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**	*spoCM*	**blocks sporulation at stage 0**
spoIIAA	**(2443437 ← 2444227)**	**stage II sporulation; regulation of ó^F activity**			**null mutations: block sporulation at stage II; normal septum formation**
spoIIB	**(2862555 ← 2863553)**	**endospore development (stage II sporulation)**			**null mutations: oligosporogenous; block sporulation at stage II**
spoIID	**(3775777 ← 3776808)**	**dissolution of the asymmetric septum (stage II sporulation)**		*spoIIC*	**null mutations: block sporulation at stage II; peptidoglycan layer in asymmetric septum fails to dissolve**
spoIIE	**70536 → 73019**	**dephosphorylates SpoIIAA-P and overcomes SpoIIAB-mediated inhibition of σ^F (stage II sporulation)**	**serine phosphatase**	*spoIIH, spoIIK*	**null mutations: block sporulation at stage II; asymmetric septum remains straight and thick**
spoIIG	**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**
spoIIM	**(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**
spoIIIA(A-H)	**(2531628 ← 2536889)**	**stage III sporulation**			**null mutations: block sporulation at stage III after complete engulfment**
spoIIIB			**Probably spoIIIA**		**null mutations: block sporulation at stage III**
spoIIIC	**2700607 → 2701023**	**late mother cell-specific gene expression (stage IV sporulation)**	**RNA polymerase sporulation-specific sigma factor (sigma-K) (C-terminal half)**	*sigK, spoIVD, spoIVE*	**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
spoIIID	(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
spoIIIE	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
spoIIIJ	(4213031 ← 4213816)	ó^{G} activity at stage III (stage III sporulation)		*spo0J87*	null mutations: block sporulation at stage III
spoIVA	(2385432 ← 2386910)	spore cortex formation and coat assembly (stage IV sporulation)		*spoVP*	null mutations: block sporulation at stage IV; cortex forms improperly; coat proteins accumulate as swirls in mother cell cytoplasm
spoIVB	(2518380 ← 2519657)	intercompartmental signaling of pro-ó^{K} processing in the mother-cell (stage IV sporulation)			null mutations: block sporulation at stage IV; block cortex and coat formation
spoIVC(AB)		stage IV sporulation			blocks sporulation at stage IV; phase-gray, coatless forespores with incomplete cortex
spoIVD			large deletion overlapping spoIIIC		blocks sporulation at stage IV; phase-gray, coatless forespores with incomplete cortex
spoIVF(AB)	(2855234 ← 2856887)	stage IV sporulation			blocks sporulation at stage IV; phase-gray, coatless forespores with incomplete cortex; spoIVFA mutants have temperature-sensitive sporulation
spoL					“decadent” sporulation; block of sporulation stops at heterogeneous stages in sporulation
spoVA	(2437604 ← 2442536)	stage V sporulation			blocks sporulation at stage V; phase-white spores, partially resistant to toluene and lysozyme but sensitive to CHCl$_4$ and heat; normal cortex, some coat
spoVB	2828825 → 2830381	spore cortex synthesis (stage V sporulation)		*spoIIIF*	blocks sporulation at stage V; heat-sensitive spores with defective cortex
spoVC	59502 → 60068	thermosensitive mutant blocks spore coat formation (stage V sporulation)			blocks sporulation at stage V; allele –285: at restrictive temperature, arrests coat formation
spoVD	1583616 → 1585553	spore morphogenesis (spore cortex) (stage V sporulation)	penicillin-binding protein		blocks sporulation at stage V; forms striated cortex, immature coat
spoVE	1589717 → 1590817	spore cortex synthesis (stage V sporulation)			blocks sporulation at stage V; well developed coat; no cortex
spoVF(AB)	1743758 → 1744651	stage V sporulation	dipicolinate synthase subunits		blocks sporulation at stage V; heat sensitive spores
spoVG	55864 → 56157	spore cortex synthesis (stage V sporulation)			null mutation: minicell formation during growth, oligosporogenic block of sporulation at stage V;
spoVK	1873444 → 1874412	disruption leads to the production of immature spores (stage V sporulation)		*spoVJ*	blocks sporulation at stage V; immature spores sensitive to lysozyme, organic solvents, heat
spoVM	1654845 → 1654925	spore cortex and coat synthesis (stage V sporulation)			blocks sporulation at stage V; phase gray spores with deficient cortex, thin coat
spoVIA		stage VI sporulation			blocks sporulation at stage VI; incomplete coat, lysozyme sensitive spores, slow germination
spoVID	(2870122 ← 2871849)	assembly of the spore coat (stage VI sporulation)			blocks sporulation at stage VI; defective coat, lysozyme sensitive spores, slow germination
srfA	376537 → 402697	surfactin production and competence	surfactin synthetase	*comL*	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
sspA	(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
sspB	(1049511 ← 1049714)	spore resistance properties	small acid-soluble spore protein (β-type SASP)		enhances effect of sspA mutations; no detectable phenotype alone
sspE	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
stp					reported to increase plasmid stability
strB					streptomycin resistance (200 ìg/ml)
strC					streptomycin resistance (1 mg/ml), glucose requirement
suf					suppresses leuA169 frameshift
suh					may be leaky hisH
sul	85734 → 86591	dihydrofolate biosynthesis	(EC 2.5.1.15) dihydropteroate synthase		sulfanilamide resistance (500 ìg/ml)
sup-1					nonsense suppressor
sup-22					nonsense suppressor
sup-44					nonsense suppressor
sup-67					nonsense suppressor
tagE	(3677459 ← 3679480)	teichoic acid biosynthesis	(EC 2.4.1.52) UDP-glucose:polyglycerol phosphate glucosyltransferase	*rodD, gtaA, gtaD*	cell wall defective
tagF	(3675219 ← 3677459)	teichoic acid biosynthesis	CDP-glycerol:polyglycerol phosphate glycero-phosphotransferase	*rodC*	cell wall defective
tal					â-thienylalanine resistant (100 ìg/ml)
tem					temperature-sensitive RNA and protein synthesis
ten					transfection enhancement for phage SP82 DNA
thiA	955403 → 957175	biosynthesis of the pyrimidine moiety of thiamin (thiamin biosynthesis)			thiamine requirement
thiB					thiamine requirement
thiC	(3929503 ← 3930171)	thiamine biosynthesis	(EC 2.5.1.3) thiamine-phosphate pyrophosphorylase	*ipa-26d, ywbK*	thiamine requirement
thrB	(3311902 ← 3312831)	threonine biosynthesis	(EC 2.7.1.39) homoserine kinase	*thrA*	threonine requirement
thrC	(3312828 ← 3313886)	threonine biosynthesis	(EC 4.2.99.2) threonine synthase	*thrB*	threonine requirement
thyA	1901474 → 1902313	deoxyribonucleotide biosynthesis	(EC 2.1.1.45) thymidylate synthase A		thymine requirement in conjunction with thyB mutation
thyB	(2296347 ← 2297141)	deoxyribonucleotide biosynthesis	(EC 2.1.1.45) thymidylate synthase B		thymine requirement in conjunction with thyA mutation
tmsA					temperature-sensitive growth
tmsB					temperature-sensitive growth
tolA					tolerance of bacteriophage ö29
tolB					tolerance of bacteriophage ö29
treA	851357 → 853042		(EC 3.2.1.93) trehalose-6-phosphate hydrolase	*treC*	inability to grow on trehalose
trnS-Lys3	528818 → 528893	transfer RNA	tRNA-Lys		sup-3 nonsense suppressor
trpA	(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
trpB	(2371545 ← 2372747)	tryptophan biosynthesis	(EC 4.2.1.20) tryptophan synthase (β subunit)		tryptophan requirement
trpC	(2373380 ← 2374132)	tryptophan biosynthesis	(EC 4.1.1.48) indol-3-glycerol phosphate synthase		tryptophan or indole requirement
trpD	(2374125 ← 2375138)	tryptophan biosynthesis	(EC 2.4.2.18) anthranilate phosphoribosyltransferase		tryptophan or indole requirement
trpE	(2375110 ← 2376657)	tryptophan biosynthesis	(EC 4.1.3.27) anthranilate synthase		tryptophan, indole, or anthranilate requirement
trpF	(2372728 ← 2373375)	tryptophan biosynthesis	(EC 5.3.1.24) phosphoribosyl anthranilate isomerase		tryptophan or indole requirement
trpS	(1217585 ← 1218577)	aminoacyl-tRNA synthetase	(EC 6.1.1.2) tryptophanyl-tRNA synthetase		5-fluorotryptophan resistance (50 ìg/ml)
ts-2					temperature-sensitive growth
ts-355					temperature-sensitive growth
ts-39-2					temperature-sensitive growth
tscA1					temperature-sensitive growth
tscC11					temperature-sensitive growth
tscD14					temperature-sensitive growth
tsi-23					temperature-sensitive growth
tufA	132881 → 134071		elongation factor Tu		kirromycin resistance (200 ìg/ml)
tyrA	(2368492 ← 2369607)	tyrosine biosynthesis	(EC 1.3.1.12) prephenate dehydrogenase		tyrosine requirement
upp	(3787481 ← 3788110)	pyrimidine salvage	(EC 2.4.2.9) uracil phosphoribosyltransferase	*ipc-35d*	in the absence of deoxyadenosine, 5-fluorouracil resistance (10 ìg/ml)
ura					uracil requirement
urc				*cysC-pyr region*	requirement for uracil and cysteine and methionine
urg					uracil glycosidase
urs				*carA or carB*	uracil-sensitive growth
uvr					UV sensitivity
uvrB	(3612005 ← 3613990)	excision of ultraviolet light-induced pyrimidine dimers in DNA	excinuclease ABC (subunit B)	*dinA, uvrA*	UV sensitivity
uvrC	(2910194 ← 2911990)	excision of ultraviolet light-induced pyrimidine dimers in DNA	(EC 4.1.99.3) excinuclease ABC (subunit C)	*uvrB*	UV sensitivity
uv^S					sensitive to ultraviolet radiation
virM					virginamycin M resistance (50 ìg/ml)
virS					virginamycin S resistance (13 ìg/ml)
wrd					slow growth on PGYE medium, normal on MA medium
xhd					induced PBSX phage lacks heads
xhi				*probably xre*	heat-inducible PBSX
xin				*probably xre*	induction defective PBSX
xki					PBSX particles fail to kill strain W23
xpt	(2318682 ← 2319266)	purine biosynthesis	(EC 2.4.2.7) xanthine phosphoribosyltransferase		resistance to 8-azaxanthine
xtl					induced PBSX phage lack tails
xyl(AB)	1891162 → 1894149	xylose metabolism			unable to utilize xylose
xynA	(2053853 ← 2054494)	xylan degradation	(EC 3.2.1.8) endo-1,4-β-xylanase		unable to degrade xylan
xynB	1888028 → 1889629	xylan degradation	xylan β-1,4-xylosidase	*ynaK*	unable to degrade xylan
ydaO	485985 → 487808	uknown			no known phenotype

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

yokH	**(2276762 ← 2277319)**	**uknown**	**no known phenotype**
yufR	**3243849 → 3245195**	**uknown**	**no known phenotype**
yvaC	**(3445299 ← 3447194)**	**uknown**	**no known phenotype**
zaa-zjj			**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%)**
φ29^{R}			**resistant to phage ö29**
φNR2^{S}			**sensitive to phage öNR2**