

Figure S2 Alignment of *B. anthracis* SleB_{CAT} to related proteins

Alignment Report using ClustalW

Majority	-----XXXSNVPSGYSNNNDIQLLARLVAEARGE PYEGQAVA AAVILNRVRS--PDFP--XTIAGVIYQ-PG-----AFTAV						
	130	140	150	160	170	180	190
B.anthracisSterneSleB	-SQNKGTNVPNGYSQNDIQLMANAVYGE SRGE PYLGQAVA AAVILNRVTS--ASFP--NTVSGVIFE-PR-----AFTAV						
B.cereus10987SleB	-PQNKGTVPNGYSQNDIQLMANAVYGE SRGE PYLGQAVA AAVILNRVTS--ASFP--NTVSGVIFE-PR-----AFTAV						
B.haloduransC-125SleB	-NIEKATNVPAGYSNDIQLMAQAVYGEARGE PYVGQAVA AAVILNRLNS--PTFP--DNVSGVIFE-PL-----AFTAV						
B.licheniformisATCC14580SleB	-QDAVAANMPGGFSNNNDINLLAQAVYGEARGE PYDGQAVA AAVILNRLDS--PTFP--NTVAGVIFE-PL-----AFTAV						
B.pumilusSAFR-032SleB	-PKQTAANMPGGFSNNNDIQLLSQAVYSEARGE PYEGQVAIAAVILNRLNN--STFP--NTIAGVIFE-PL-----AFTAV						
B.subtilisSleB	-QDAVAANMPGGFSNNDIRLLAQAVYGEARGE PYEGQVAIAAVILNRLNS--PLFP--NSVAGVIFE-PL-----AFTAV						
B.weihenstephanensisKSleB	-PKSTGTNVPNGYSQNDIQLMANAVYGE SRGE PYLGQAVA AAVILNRVTS--ASFP--NTVSGVIFE-PR-----AFTAV						
C.botulinumA2KyotoSleB	-IKTGASGS SSSSNQDVMLLARLINGEARGE PYEGQVAVGAVVLNRTRD--PKFP--NTIAGVIYE-PL-----AFTAI						
C.kluyveriDSM555SleB	-LAINVSGGSSGSNNQDVMLLARLINGEARGE PYEGQVAVGAVILNRTRD--PRFP--STLAGVIYQ-PG-----AFTAV						
C.tetaniE88SleB	-INVAQAQGSNTSNNQDINLLARLINGEARGE PYEGQVAVGAVILNRTRD--PRFP--NTIAGVVYQ-PL-----AFTAI						
DesulfotomaculumreducensSleB	-ATATTSRGSLPLSRQDIYDLARVHGEARGESFEGQVAVA AAVILNRVLS--GQFG--RTVQDVIFQ-PW-----AFTAV						
GeobacilluskaustophilisSleB	-AKTTASNPKGFSQNDIRLLMANAVYGEARGE PYIGQVAVA AAVILNRLEH--PSFP--DTVAGVIFQ-PG-----AFTAV						
Geobacillusthermodenitr.SleB	-AKTTASNPKGFSQNDIQLMANAVYGEARGE PYIGQVAVA AAVILNRLQH--PSFP--DTVAGVIFQ-PG-----AFTAV						
OceanobacillusihheyensisSleB	-GGTPSVNPQGYSQNDIQLMANAVYGEARGE PYEGQVAVA AAVILNRLNS--ALFP--DTVSGVIFE-PR-----AFTAV						
Thermoanaerobacterenc.SleB	DLAAYRAT-SSAGISDDDVYLLAMLINGEARGE PYIGKVAVGAVVMNRVD--PRFP--KTIPGVIFQ-PG-----AFSAV						
B.anthracisSterneCwlJ1	-----MGVIAYNEADVKLLARLMRAAEAE GEGQQGMLMVGNVGVNVRVRGNCLDFKKIIRNLRQMVYQNPNG-----GFEAT						
B.anthracisSterneCwlJ2	-----MPLI PYNESDVDLLARLIRAAEAE GEGRQGEQLVGCVVNNRVFCDCCLDFKQLRSVRDAVYQSPG-----GFEAV						
B.cereus10987CwlJ	-----MGVIAHNEEDVKLLARLMRAAEAE GEGQQGMLMVGNVGVNVRVRGNCLDFKNIRNLRQMVYQNPNG-----GFEAT						
B.licheniformisATCC14CwlJ	-----MAVVQASSKDISLLARLLRAAEAE GEGVQGMLMVGNVGINRIRANCSDFVGLRTIPQMIHQ-PH-----AFEAV						
B.pumilusSAFR-032CwlJ	-----MAVVRATSSIDLMARLLRAAEAE GEGKQGMLLVGNVGINRLRANCSDFKGLRTIPQMIYQ-EH-----AFEAV						
B.subtilisCwlJ	-----MAVVRATSADVDLMARLLRAAEAE GEGKQGMLLVGNVGINRLRANCSDFKGLRTIPQMIYQ-PH-----AFEAV						
GeobacilluskaustophilisCwlJ	--MGQIAPSIVA TEEEVKLLARLMRAAEAE GDGRGLGMLMVGNVGVNRVIACDCLDFRGIRSIRQMVQFQSPG-----GFEAV						
OceanobacillusihheyensisCwlJ	-----MAVVKHNEAEVELLARLMRAAEAE GDGLGMLMVGNNTGINRVIASCLDPNIRITNMVYQSPG-----GFEAT						
B.amyloliquefaciensFZYkvT	-EETAYQPPKKTYSRADRQLSLRVLHAEAKGE SYKGKVAVASVVLNRTEK--NGFP--DTIRGVIYQ-RN-----AFEPV						
B.anthracisSterneYkvT	YTGQHLKIN-SSI SEKEKDLMARLVTAEAGGESYKGKVAVAKVILNRVNA--KGFP--NTITGVIYE-PITYG-YAFTPV						
B.cereus10987YkvT	YTGQHLKIN-SSI SEKEKDLMARLVTAEAGGESYKGKVAVAKVILNRVNA--KGFP--NTITGVIYE-PIKYG-YAFTPV						
B.clausiiKSM-K16YkvT	EAGETLTIP-AAVSAARELLAKLVSAAEAKGE PYAGKVAVATVVLNRVN--ENYP--DTVRDVIYE-VTPSGHYAFSPV						
B.pumilusSAFR-032YkvT	-SETTNEESAKRYSNEEMELSLRVLHAEAKGE YAGKKAVASVVLNRVEH--RSFP--DSVKGVVIYQ-RN-----AFQPV						
B.subtilisYkvT	-KPDKTNDEKETYQTQSEKELLSRVLHAEAKGE SYKGKVAVASVVLNRTEK--KGFP--DTIRGVIYQ-KN-----AFEPV						
C.botulinumAHallYkvT	-INTGSSGSSSSSNQDVMLLARLINGEARGE PYEGQVAVGAVVLNRTRD--SKFP--NTIAGVIYE-PL-----AFTAI						
C.novyiNTYkvT	KVSSNTSN-TSTNNSDVMLLARLINGEARGE PYEGQVAVGAVVLNRTRD--ARFP--SSIAGVIYQ-PG-----AFTAI						
C.perfringensATCC13124YkvT	-AVFQSSNSTISLTKDDIYLMQSQVVAESKGE PFDGKIAVASVILNRRTD--SQFP--DTIHGVITQ-KN-----AFSCV						
GeobacilluskaustophilisYkvT	-PGEKLVIPDAGITAAEKDLARLVLHAEAKGE PYAGKVAVATVVLNRVDH--PDFP--DTIRAVIYE-RS-GGHYAFTPV						
OceanobacillusihheyensisYkvT	-EMIYINEETVDMTDKEKDLLERLVLHAEAKGE PYEGMVAVA VVVLNRVD--NHFP--DTVSEVINQ-DK-----QFTPV						

Majority	ADGQIYQRPXETSXKAVRDAING--WDPGGALYYFNP---DTATSWIW--SRPQIKRIGKHIFCK-----
	-----+-----+-----+-----+-----+-----+-----
	200 210 220 230 240 250
	-----+-----+-----+-----+-----+-----+-----
B.anthracisSterneSleB	ADGQIYLTPEAKKAVLDAING--WDPGNALYYFNP---DTATSKWIW--TRPQIKKIGKHIFCK
B.cereus10987SleB	ADGQIYLTPEAKKAVLDAING--WDPGNALYYFNP---DTATSKWIW--TRPQIKKIGKHIFCK
B.haloduransC-125SleB	ADGQIYMTPDETARRAVLDALNG--QDPGGATYYFNP---DTATSGWIW--SRPQIKRIGKHIFCN
B/licheniformisATCC14580SleB	ADGQIYMTPDETAKKAVLDAING--WDPSENATYYFNP---DTATSSWIW--GRPQIKRIGKHIFCE
B.pumilussAFR-032SleB	ADGQFYMSPNETAKKAVFDAING--WDPSESAVYYFNP---DTATSPWIW--GRPQIKRIGKHIFCE
B.subtilisSleB	ADGQIYMQPNETAREAVLDAING--WDPSEEALYYFNP---DTATSPWIW--GRPQIKRIGKHIFCE
B.weihenstephanensisKSleB	ADGQIYLTPEAKKAVLDAING--WDPGNALYYFNP---DTATSKWIW--TRPQIKKIGKHIFCK
C.botulinumA2KyotoSleB	ADGQINAQMQTISNAARDALNG--WDPSDGATYYFNP---ATATSSWIW--SRPLIKVIGKHRFCR
C.kluyveriDSM555SleB	VDGQVHANMEQNSINAARDALNG--WDPSEGAIYYFNP---STATSSWIW--SRPLIKIIGKHRFCR
C.tetaniE88SleB	ADGQVNAAEQSSMKAAMDAING--WDPGGAVYYFNP---ATATSSWIW--SRPLIKVIGKHRFCR
DesulfotomaculumreducensSleB	NDGQFYLQPNEASFRAVEAAIKG--WDPTRGAIYYWNP---KTATSRWIW--SRPISLKGHNHFAN
GeobacilluskaustophilisSleB	ADGQIWLTPEAKKAVLDAING--WDPGGAIYYFNP---ATATSAWIW--SRPQIKRIGNHIFCK
Geobacillusthermodenitr.SleB	ADGQIWLTPEAKKAVLDAING--WDPGGAIYYFNP---ATATSAWIW--SRPQIKRIGQHIFCK
OceanobacillusiheyensisSleB	ADGQIWLEPNDKAREAVLDAING--WDPGNALYYFNP---DTATSGWIW--TRPQIKQIGKHIFCK
Thermoanaerobactertertenc.SleB	EDGQMWLPPTESIKAIDAVSG--WDPGGALYYNA--ARVTNYWIF--TRPILTQIGRHIFAR
B.anthracisSterneCwlJ1	QKGYFYQRAREQDIALARRTIQGQRFWPANFALWFFRP--EG--PCPPTWYN--QQNSGRFKKHCFQPSGEDCPCSVY
B.anthracisSterneCwlJ2	QYGYFYQRARESEKIARKVLQGEWRWPWRALWYFRP--VG--ACPPEWYN--QPFVGQFKSHCFYEPSCNECPKLYSR
B.cereus10987CwlJ	QKGYFYQRAREQDIALARRTIQGQRFWPANFALWFFRP--EG--ACPPTWYN--QQNSGRFKKHCFQPNAGDCPSIY
B/licheniformisATCC14CwlJ	THGYFYQRARESERRLARRAVNGERLWPAFKSLWYFRP--AG--ACPAQWYN--QPHVGRFKSHCFYEPATAECENVYNTF
B.pumilussAFR-032CwlJ	THGYFYQRARETEKLARRNINGERFWPAFKSLWYFKP--PG--NCPPTWYN--QPFVARYKSHCFYQPTAETCENVYNTF
B.subtilisCwlJ	THGYFYQRARDSERALARRSINGERRWPAFKSLWYFRP--QG--DCPAQWYN--QPFVARFKSHCFYQPTAETCENVYNTF
GeobacilluskaustophilisCwlJ	QKGYFYQRAREVDIGLARQVLRGWRYHPATNALWFFKPPGQPCPPQWFG--QWNVGRYKSHCFAPTPSDCPRVYS
OceanobacillusiheyensisCwlJ	QKGYFYQRARQSEIRLARRVIQGERQHPASNSLWFFMP--EG--ACPEQWYG--QWNVGRYKAHCFYAPTAADCPEVFR
B.amyloliquefaciensFZYkvT	ANGSINQPKDKDSTIAANEALDH--PGRETNALFFYNP--KTASDHWIR--SRKIIERIGRHVFAM
B.anthracisSterneYkvT	TDGRINHPASPEAKMAVEEAIST--NGIHSWDLYFYNP--KTSTDKWIT--TRQTVAVIGNHVFAM
B.cereus10987YkvT	TDGRINQPASAEAKMAVEEAIST--NGIHSWDLYFYNP--KTSTDKWIT--TRQTVAVIGNHVFAM
B.clausiikSM-K16YkvT	LDGAINNEPDDESRRRAVTEALAF--RGQGQQSLSLYFYNP--KTATSGWVA--TREQTLVIGDHIFAK
B.pumilussAFR-032YkvT	SNGSIHKADQDSVKAVKQVVKE--HDRTTKAIYFYNP--KTATDNWIR--SRKIVERIGRHVFAM
B.subtilisYkvT	ANGSINQPKDKESIEAAEEALSS--KNRETDIAIFFYNP--KTASDNWIR--SRKIVEKIGRHVFAM
C.botulinumAHallyYkvT	ADGQINAQMQTISNAARDALNG--WDPSDGATYYFNP---ATATSSWIW--SRPLIKVIGKHRFCR
C.novyiNTYkvT	VDGQINAIEIQQSSISKAARDALNG--WDPGGAVYYFNP---DTATSGWIW--SRPLIKIIGKHRFC
C.perfringensATCC13124YkvT	RNGKIDVVPDGDSYNALKAIEG--YDPTNEALYFYNP--KIATCSWMKGVEKTGEKSIGQHVFFNVT
GeobacilluskaustophilisYkvT	ANGSIN-ERRRESYRAVEEALAF--RGLGNGLSYFYNP--KTAKSKWLR--SRPVTVVIGNHVFAM
OceanobacillusiheyensisYkvT	SNGKINKPAGKESKNAVEEALYTD--RSLVTESLYFYNP--DTATSRWLD--DKVTEVIGNHVFKD

Alignment to *B. anthracis* SleB_{CAT}. All other proteins were shortened to the same length upstream of the catalytic E residue (Red), except CwlJ proteins which are included as full-length proteins. Residue numbering corresponds to the sequence of the *B.anthracis* SleB that was examined in this study.

Yellow are SleB proteins. Identification is relatively strong, based upon direct genetic studies or on the presence of an adjacent *ypeB* gene, which is involved in stabilization of SleB in the spore.

Green are CwlJ proteins. Identification is relatively strong, based upon direct genetic studies or upon sequence similarity and genome context.

Grey are presumptive YkvT proteins. This protein is known to be expressed in vegetative *B. subtilis* cells and to have no significant effect on spore germination. Identification in other species is based solely on greater sequence similarity to *B. subtilis* YkvT than to SleB.