



Majority

	ADGQIYQRPXETSXKAVRDAING--WDPSGGALYYFNP---DTATSKWIW--SRPQIKRIGKHIFCK-----
	-----+-----+-----+-----+-----+-----+-----+-----+-----+-----
	200 210 220 230 240 250
	-----+-----+-----+-----+-----+-----+-----+-----+-----+-----
B.anthraxisSleB	ADGQIYLTTPNETAKKAVLDAING--WDPTGNALYYFNP---DTATSKWIW--TRPQIKKIGKHIFCK
B.cereus10987SleB	ADGQIYLTTPNETAKKAVLDAING--WDPTGNALYYFNP---DTATSKWIW--TRPQIKKIGKHIFCK
B.haloduransC-125SleB	ADGQIYMTDPDETARRAVLDALNG--QDPSGGATYYFNP---DTATSGWIW--SRPQIKRIGKHIFCN
B.licheniformisATCC14580SleB	ADGQIYMTDPDETAKKAVLDAING--WDPSENATYYFNP---DTATSSWIW--GRPQIKRIGKHIFCE
B.pumilusSAFR-032SleB	ADGQFYMSPNETAKKAVFDAING--WDPSESAVYYFNP---DTATSPWIW--GRPQIKRIGKHIFCE
B.subtilisSleB	ADGQIYMQPNETAREAVLDAING--WDPSEEALYYFNP---DTATSPWIW--GRPQIKRIGKHIFCE
B.weihestephanensisKSleB	ADGQIYLTTPNENAKKAVLDAING--WDPTGNALYYFNP---DTATSKWIW--TRPQIKKIGKHIFCK
C.botulinumA2KyotoSleB	ADGQINAQMQQTSINAARDALNG--WDPDSDGATYYFNP---ATATSSWIW--SRPLIKVIGKHRFCR
C.kluyveriDSM555SleB	VDGQVHANMEQNSINAARDALNG--WDPSEGAIIYYFNP---STATSSWIW--SRPLIKIIGKHRFCR
C.tetaniE88SleB	ADGQVNAAMEQSSMKAAMDAING--WDPSSGAVYYFNP---ATATSSWIW--SRPLIKVIGKHRFCR
DesulfotomaculumreducensSleB	NDGQFYLPNEASFRAVEAAIKG--WDPTRGAIYYWNP---KTATSRWIW--SRPISLKIGNHVFN
GeobacilluskaustophilisSleB	ADGQIWLTPNETAKKAVLDAING--WDPTGGAIYYFNP---ATATSAWIW--SRPQIKRIGNHIFCK
Geobacillusthermodenitr.SleB	ADGQIWLTPNETAKKAVLDAING--WDPSSGAIYYFNP---ATATSAWIW--SRPQIKRIGQHIFCK
OceanobacillusihyensisSleB	ADGQIWLPEPNDKAREAVLDAING--WDPSSGNALYYFNP---DTATSGWIW--TRPQIKQIGKHIFCK
Thermoanaerobactertenc.SleB	EDGQMWLPPTEESIKAADIVAVG--WDPTGGALYYNA---ARVTNYWIF--TRPILTQIGRHIFAR
B.anthraxisSterneCwlJ1	QKGYFYQRAREQDIALARRTIQGQRFWPANFALWFFRP-EG-PCPPTWYN---QNSGRFKKHCFQPSGEDCPSVY
B.anthraxisSterneCwlJ2	QYGYFYQRARESEKEIARKVLQGEWRWPANFALWFFRP-VG-ACPEWYN---QPFVGFQKSHCFYEPGNECPKLYSR
B.cereus10987CwlJ	QKGYFYQRAREQDIALARRTIQGQRFWPANFALWFFRP-EG-ACPPTWYN---QNSGRFKKHCFQPNAGDCPSIY
B.licheniformisATCC14CwlJ	THGYFYQRARESERLARRAVNGERLWPAKFSLWYFRP-AG-ACPAQWYN---QPHVGRFKSHCFYPTAEECENVYNTF
B.pumilusSAFR-032CwlJ	THGYFYQRARETEKTLARRNINGERFWPAKFSLWYFKP-PG-NCPPPTWYN---QPFVARYKSHCFYQPTAETCENVYNTF
B.subtilisCwlJ	THGYFYQRARDSERALARRSINGERRWPAKFSLWYFRP-QG-DCPAQWYN---QPFVARFKSHCFYQPTAETCENVYNTF
GeobacilluskaustophilisCwlJ	QKGYFYQRAREVDIGLARQVLRGWRYHPATNALWFFKPPGQPCPPQWFG---QWNVGGRYKSHCFYPTSDCPRVYS
OceanobacillusihyensisCwlJ	QKGYFYQRARQSEIRLARRVIQGERQHPASNSLWFFMP-EG-ACPEQWYG---QWNVGGRYKSHCFYPTAADCPEVFR
B.amyloliquefaciensFZYkvT	ANGSINQKPKDKSIAAANEALDH--PGRETNALFFYFNP---KTASDHWIR--SRKIIERIGRHVFAV
B.anthraxisSterneYkvT	TDGRINHPASPEAKMAVEEAIST--NGIHSDWLYFYFNP---KTSTDKWIT--TRQTVAVIGNHVFAK
B.cereus10987YkvT	TDGRINQPASAEAKMAVEEAIST--NGIHSDWLYFYFNP---KTSTDKWIT--TRQTVAVIGNHVFAK
B.clausiiKSM-K16YkvT	LDGAINNEPDESRRRAVTEALAF--RGQGQSSLYFYFNP---KTATSGWVA--TREQTLVIGDHIFAK
B.pumilusSAFR-032YkvT	SNGSIHDKADQDSVKAQVQVKE--HRTTKAIYFYFNP---KTATDNWIR--SRKIVERIGRHVFAV
B.subtilisYkvT	ANGSINQKPKDESIEAAEEALSS--KNRETDIIFYFNP---KTASDNWIR--SRKIVEKIGRHVFAV
C.botulinumAHallYkvT	ADGQINAQMQQTSINAARDALNG--WDPDSDGATYYFNP---ATATSSWIW--SRPLIKVIGKHRFCR
C.novyiNTYkvT	VDGQINAEIQSSIKAARDALNG--WDPDSDGAVYYFNP---DTATSGWIW--SRPLIKIIGKHRFCS
C.perfringensATCC13124YkvT	RNGKIDVVPDGDYSNAVLKAIEG--YDPTNEALYFYFNP---KIATCSWMMKVEKTGEKSIGQHVFFNVT
GeobacilluskaustophilisYkvT	ANGSIN-ERRRESYRAVEEALAF--RGLGNGSLYFYFNP---KTAKSKWLR--SRPVTTVIGNHVFAK
OceanobacillusihyensisYkvT	SNGKINKPAGKESKNAVEEALYTD-RSLVTEISLYFYFNP---DTATSRWLD--DKVTTEVIGNHVFKD

Alignment to *B. anthracis* SleB<sub>CAT</sub>. 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.