Supplemental Online Material Bass et al., published 22 November 2002

Materials and Methods

As in the study of the previously determined MscL structure (S1), multiple homologs of MscS [encoded by the *yggb* gene (S2)] were identified by BLAST searching of the NCBI genome database. Ten homologs from prokaryotes and Archaea were identified and subsequently cloned. The channels were subcloned into expression vectors (pET system, Novagen) and expression screening was carried out. Cells expressing sufficient channels to be identified by Western blotting were subjected to extensive detergent screening utilizing ~50 detergents (Anatrace, Sigma, Aldrich) where both the ability of the channels to be extracted out of the membrane and the ability to remain as a homo-oligomer were determined. Subsequent large-scale expressions, extraction and purification produced sufficient amounts of protein for three channels (E. coli, B. subtilis and C. tepidum) for crystallization trials. Each of these channels was produced recombinantly (vector pet28b, Novagen) in 50-liter fermenter growths in a modified Terrific Broth media containing 1% glucose and 0.4% glycerol. Protein expression was initiated by the addition of 2% lactose and 2 mM IPTG for 2-4 hours, resulting in ~1.5 kg of wet cells. To obtain phase information, selenomethionine-derivatized protein was purified from cells grown in a modified M9 media containing 50 mg/l selenomethionine, and the remaining amino acids at 40 µg/l. Extraction of the E. coli MscS was carried out using sonication and solubilization with 1% Foscholine-14. Ni-affinity chromatography, anion exchange, and size exclusion chromatography in the presence of 0.05% Foscholine-14 were used to purify the protein to homogeneity. The apparent molecular mass of the protein, as indicated by size-exclusion chromatography, was in excess of 200 kD, similar to that reported for recombinant MscS by Sukharev (S3). Crystals were obtained with 10-15 mg/ml MscS by hanging drop vapor diffusion with 100 mM pH 7.2 Hepes buffer, 150 mM Na-formate, 8% glycerol, and 16% PEG-3350 as the precipitant. Crystals grew to ~200 µm in each dimension, and were assigned to space group $P4_32_12$ (a = b = 184.7 Å, c =260.7 Å) with one MscS oligomer in the asymmetric unit (corresponding to ~71% solvent content). Only residues in the extramembrane (water-soluble) regions of MscS participated in lattice contacts.

References

S1. G. Chang, R. H. Spencer, A. T. Lee, M. T. Barclay, D. C. Rees, *Science* 282, 2220 (1998).

S2. N. Levina et al., EMBO J. 18, 1730-7 (1999).

S3. S. Sukharev, *Biophys. J.* 83, 290-8 (2002).

Figure S1

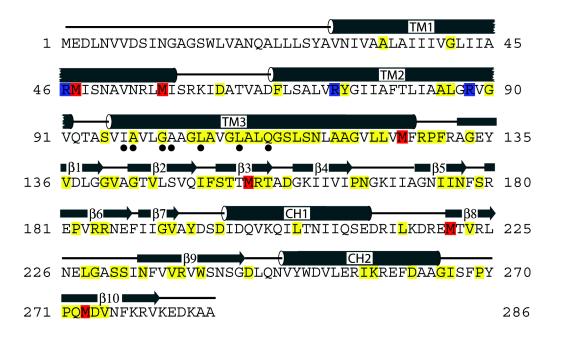


Fig. S1. Amino acid sequence of the *E. coli* MscS (S2). Residues highlighted in yellow are identical in at least 65% of the sequences of 25 yggB homologs in prokaryotes and Archaea (see Fig. S2). The red boxes indicate methionine residues located in the selenomethionine substituted protein used for phasing, while transmembrane arginine residues at positions 46, 74, and 88 are shaded blue. Cylinders above the sequence designate residues in the three transmembrane α -helices, TM1-3, and the two cytoplasmic helices, CH1 and CH2. Black circles below the sequence denote amino acids within residues 96-112 of TM3 that line the permeation pathway. Arrows above the sequence denote residues in β -strands 1-10.

Pag							
	MEDLNVVDSINGAGSWLVANQALLLSIAVNIVAALAIIIVG-						
5 typh	MEGFELFPKIKGAIKWMAEHSDSVIHFGWNVVAAIILLFIG-						
Ctep	MESTSLRDLSHVTDWLVRPLVVICHAETSIVKIVTIIL-						
	MVALDEPLPYVGVTPMQVLTAIVVLIVG-						
	MEDLNVVDSINGAGTWLVRNQALLLSYAVNIVAAIAIIIIG-						
pestis	MEELNVVEGINNASTWLANNQDLLIQYAVNIIAALLILIVG-						
Buchn	MLFIKIEIIAKTLLIINKKYTEIKMELNVVNNINHAGTWLIRNQELLLÄYTINLTSAIIILVVG-						
3d ict	MKELDVVDGIOSAGGWIVRNODLLLGYAVNLVAAVVILIIG-						
[_chol	MAGESIGVEVPIVESPÑQVNTWLTNNŠDLLIQYGVNVISAILILPIG-						
_perf	MKPDLSKMYBKLL <mark>S</mark> WITINGFKLVIGLILLYIG						
Synech	Punippinsp pppinsp						
id_aer							
/_fast	HDWTKLLSNIVS <mark>P</mark> ATVTTIHGRFDWTRIDWIHILMNLTAAAAIAILG-						
	FGLNLAAALLIFLVG -						
	DVLNYKLYGDVTVYDIIVVIVVMALATIIAK						
	MLENLLVNLBHYLPMLAGKLVAFLVICFIW-						
nanos	NFLDNDLY <mark>ST</mark> SE <mark>GP</mark> VTPADLITFVLIISFSVLLFR-						
o_tum							
	MPDVLOOYFTLDNIIOIGISLAILLVPLILRKLFTRYFFNLLFNLTNRPKTBIFKOVVLAFDKPARWFFVALGLFLAI						
	MPDILQUIFILDNIQIGISLAILLVFLILKKLFIKIFFNLLFNLINKFKIBIFNQVVLAFDKPAKWFFVALGLFLAI						
	MNMBIFG-NSISNILIFVVITLLGIFIGKIVDKIVRNYLKKIIDKTKTKFDDIILESIDLPIVLVVTLFFYFGL						
	MTITQMISEILMHNTVYNYILSLISIILFIVIGKYANALIERLADKLHKKSGIELDELLIRALSLPVAIAIILSGFYPGV						
	MQPTTQEILKAIATLIGGIVIAGLVRVWILKLSRSTKIVWVPNEDTAKLPWRFIVIVSILAALDTL 11020304050607080						
vaaB	LIIARMISNAVNRLMISRKIDATVADPLS						
yggB tvph	LIIARMISNAVNR						
tvph	KLIARLLSRGLEKLLLRROVDATIVHFFS						
typh Ctep							
typh Ctep P fur	KLIARLLSRGLEKLLLRROVDATIVHFFS						
S_typh Ctep P_fur S_ent							
E typh Ctep P fur S ent Sestis							
S_typh Ctep P_fur S_ent S_estis Buchn							
B_typh Ctep P_fur S_ent S_ent Buchn Buchn d_ict 7 chol							
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3 typh Ctep P fur S ent Buchn 3 chol Cperf 3 ynech 1 aer fast isobac chanos							
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s typh Ctep P fur S ent bestis Buchn d ictt / chol perf synech d aer / fast bisser Lisobac chanos co_tum rrobac	KLIARLISRGIEK LLIKRQUDATIVHPFS SVALIVAAKPLKR MLUGRLUSSVHDTGTR SVALIVVASFKRG KIKTKLPELVVEFLGR LIVARVISNTVNR LMRARHIDATVADPLS SIIAKVLSGMLNR VMRLRGIDVTVADPLS SIIAKVLSGMLNR VMRLRGIDVTVADPLS SIIAKVLSGMLNR VMRLRGIDVTVADPLS SIIAKVLSGMLNR VMRLRGIDVTVADPLS MFISKIISNGANQ VLITRNIDATIAGPLS SLIARGISTLIR LLKARGLDVTVVHPLA NLVVKGVAGSVAN VLKK KEDKAVVDPIH WKIINKVIKILAN IMKSRNVDPTLISPAG WWLINTLIGRVGG LLARRSVDRTLGGPVG VWSSRESKLHR ILIRAHVEITLAPPLS KWAAKRIVAVMRA AMTRAQVDATLISPLC KWAAKRIVAVMRA AMTRAQVDATLISPLC VUSSKRLSKLHR ILIRAHVEITLSPLC VUSSKRLSKD -RISKDVGEP VUTTVLRFSLKD -RISKDVGEP VUTVLRFSLKD -RISKDVGEP VUTVLRFSLKD -RISKDVGEP VITVLRFSLKD -RISKDVGEP VITVLRFSLKD -RISKDVGEP VITVLRFSLKD -RISKDVGEP						
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S typh Ctep P fur S snt Buchn d ict C perf ynech d aer fulg Isobac chanos co tum robac bermot B sub	<pre></pre>						
S typh Ctep P fur S ent S ent S chol C c	KLIARLISRGIEK LLIKRQVDATIVHPS SVALIVAAKPLKR MLVGRLVSSVHDTGTR SVALIVVASFKRG KIKTKLPELVVEFLGR LIVARVISNTVNR LMRARHIDATVADPLS SIIAKVLSGMLNR WMELRGIDVTVADPLS SIIAKVLSGMLNR VMELRGLDVTVVHPLA MFISKIISNGANQ VLITRNIDATIAGPLS SLIARGISTLIR LLKARGLDVTVVHPLA NLVVKGVAGSVAN VLKK EMDKAVVDPTH WKIIKVIKILAN IMKSRNVDPTH WWLINTLTGRVGG LLARSVDRTLGGPVG VWUSKRLSKLHR ILRARNDPLISPLC WWLINTLIGRVGG LLARRSVDATISPLC WWLINTLIGRVGG LLARSVDATLISPLC VWSSKRLSKLHR ILRANVBITLSPLC VWSKRLSKLHR ILRAHVEITLAPLE VWSSKRLSKLHR ILRAHVEITLSPLC VWSSKRLSKLHR ILRAHVEITLSPLC VWSSKRLSKLHR ILRAHVEITLSPLC VUTTVERSLKD -RISKDVGEP VITVERSLKD -RISKDVGEP VUTVERSLKN -VLTVERSLKD VUTVERSLKNALIN -VVEKLGKLQMENTIR VUTVERSLIVALLCWGLCNLTATSFIFHKVNQRPELDMDILAPFLS -VERLANFVA PFERNKTMK LLSKK - DELLANFVA						
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Figure S2 MULTIPLE SEQUENCE ALIGNMENT of yggB Page 1 of 4

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Figure S2 MULTIPLE SEQUENCE ALIGNMENT of yggB Page 2 of 4

Page 2 of 4	
yggB ALVR <mark>TGIIAFTLIAALGRVGVQT</mark> -ASVIA-VLGAAGLAVGLALQGSLSNLAAGVLLVMPRPFRAGEVVLLGGVAGTVL	146
S typh ALVRIITIAFTAVAALGRVGIET-SEIIA-VIGAAGLAIGLALGGSLENFAAGVLLVSLRPFRAGEIVOIGL-VIGTVE	146
Ctep TILQYLIVFFGILIVLQSAGIDL-S <mark>SLT</mark> V-LSGTIGLGIGFGLQNIADNFFSGLIILLERPVKVGDRIQVGEINGDVV	149
P_fur -FLSALLYVAVILLAVRALGIEV- <mark>GSVVLG</mark> LSAVI <mark>GLILGFGMQDTLTNLAAG</mark> VWIAAL <mark>RP</mark> IDI <mark>GEVVEVAG</mark> KV <mark>G</mark> KVN	134
S_ent ALVR7GVIAFTLIAALGRVGVQT-ASVIA-VLGAAGLAVGLALQGSLSNLAAGVLLVMPRPPRAGBYVDLGGVAGTVL	146
Y pestis AMVRISILAFTIVAVLGRLGVQT-ASVIA-VIGAAGLAVGLALOGSLSNFAAGVLLVAPRPFKAGEVVLLGGVAGTVV Buchn ALMRIIIITFTFIAALGRIGVQT-TSVIA-ILGAAGMAIGLALOGSLSNFAAGVLLVTLRPLKTEEVVLLGSVSGTVL	146 170
Editin Alinkiilli FIFIALGIIVU - ISVIA - LEGANGLAVGLAVGLAVGLAVILVLFRPPRAGEVULGG- VGGVU	146
V chol GLVRYTLFIIVLIAALSRIGVOT-ASVVA-VIGAAGLAVGLALOGSLENPAAGVLIVAPRPFKSGDYVEIGGVAGSVD	152
C perf AFSEVSLKVLLVITLMSYVGFDI-AGLAA-LIASAGLAVGLALOGSLSNFAGGVIIILLRPFRVNDFIBASGYSGTVE	138
Synech NISYYLLLVVFFVLCLAQL <mark>GIQT</mark> -S <mark>S</mark> LVA-LLGASTLAIGLAL <mark>QG</mark> SLANVAGGILLVLFNYFRVGERIEVAGIEGIVE	152
Pseud_aer SLVSIVLKILLVVSVASMIGIQT-TSFVA-AIGAAGLAIGLALQGSLANFAGGVLILLFRPFKVGDWIEAQGVAGTVD	141
Xy_fast NIAYALLLIVVSVSVLQRLGVPA-TSLAA-VVGATGLAVGLALKDSLSNIAAGVMLIVLGPVRSGDHVVIAGQEGIID	152
Neisser NVANTGLILUVITAALGELGVST TSVTA-LIGGAGLAVALSLEDGLSNFAAGALIILPEPFKVGDFIRVGGPEGYVR	146
A fulg KVIYFGIIIVAFIAVLPALGLDLSGLLVAGGITGIVLGFASOSVVANLVSGIFLISEKPIKIGDQVNIDGVAGFVE Fusobac SLIKTIMYIILAFILVGILGVRA-TSLVT-ILGTAGVAVGLALOGSLSNLASGILILFFKQVSKGDFVSSLDKNIEGTVQ	135 137
Methanos KLIYIGSLVIVPIAALPLIGLN-PSGLLLAGGITGIILGPASONIVGNLVSGPFLMVERPIKIGDQVEINGTAGTVŤ	143
Agro tum GGIRIVVLILVIVMVLGOFGVOT-ASILA-ALGAAGLAIGLALGCTLONIAAGIMLLVLRPFRVGEVIETSTVSGTII	146
Pyrobac KFIRISILILASVIALASLGFDITGALVAGGFLGLVIGLAAGTSISNFISGVLLMFERPFSLGDVIHIGDVVGAVV	128
Thermot FFLGLIISVIAVMIILDIWDLSLA <mark>P</mark> LLAGVGIGGLVIGLALQEPLANFFSGLFLLVSRAVKEGEALEAGGVS <mark>GT</mark> VE	120
B_sub_KLLRFVIIALSVSVIAQEFNYDVNGFVAGLGLGGLAFALAAKDTISNFPGGIIIITEKPFTIGDWVETSTVTGSVE	214
Helico QVIPILLIITTIIALSTLGVOT-TSIIT-VLGTVGIAVALALKDVLSSIAGGIILIILHPFKKGDIIEISGLEGKVE	135
Mjan1 KVVKIL <mark>T</mark> ILLGILTALSSVGYDITALLAGLGVGGLALALAMODTIKNFIAGILILIDKPFSLGHWVKVKGAEGIVE Mjan2 KLVRLVVWVVGLLLILSNLGYDIKTLLAGLGIGGLAVALASONLV SN LIAGLIILTDKPFKIGNWITFSGGSGIVE	211 218
P hor KLFYITLITLAFFLALNVAGFTGKLTTIVAAAGTTGIVLGFSAOTVISNLISGIFMYPDKPLEIGDFIEVAGVSGVVH	192
ruler	
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	219
: *: : ** yggB SVQIP <mark>STIMRTADG</mark> KIIVIPNGKIIAGNIINPSRE-PVRRNEFIIGVAYDSDIDQVKQILTNIQSEDRILKDR S typh KVHIP <mark>STILLTAD</mark> SKEVVIPNGKIIADNIINYSRH-PYRRIDLIIGVDIQSRIADVKNVIHRIIEQDHRIDKTR	219 219
yggB SVQIPSTTMRTADGKIIVIPNGKIIAGNIINPSRE-PVRRNEFIIGVAVDSDIDQVKQILTNIQSEDRILKDR S typh KVHIPSTTLLTADSKEVVIPNGKIIADNIINYSRH-PYRRIDLIIGVDTQSRIADVKNVIHRIIEQDHRIDKTR Ctep RIAIRSTTLLTNDNINIIIPNSEPVSKQVINNSHNDRSLRVSVPVGVATGSDPEQVKHVLLGVAENHPDILTKP	219 223
yggB SVQIPSTTMRTADGKIIVIPNGKIIAGNIINPSRE-PVRRNEFIIGVAYDSDIDQVKQILTNIIQSEDRILKDR S typh kvhipsttlitadskevvipngkiiadniinysku-pyrkidliigvDgSsRiadvknviikiigohhridktR Ctep RiairsttlitndniniiipnsepvSkqvinwshndrslrvSvPvGVaygSDPDQVkhvLlgVaenhPDIItkP P fur AvGINSTELLTADNVLITIPN-KLVWGNVITNYITMPTRRVDVNVGVAYGSDLDKAKVAMELMONHPKVLKDP	219 223 207
yggB SVQIPSTTRRIADGKIIVIPNGKIIAGNIINPSRE-PVRRNEFIIGVAIDSDIDQVKQILTNIIQSEDRILKDR S_typh KVHIPSTTLLTADSKEVVIPNGKIIADNIINYSRH-PYRRIDLIIGVDYQSRIADVKNVIHRIIEQDHRIDKTR Ctep RIARSTTLLTNDNINIIPNSFVSKQVINWSHNDRSLEVSVPVGVAIGSDEPQVKHVLLGVARNHPDILTKP P_fur AVGIMSTELLTADNVLITIPN-KLVWGNVITNYTRMPTRVDVNVGVAIGTDLDKAIKVAMELMQNHPKVLKDP S_ent NVQIPSTTRRAVDGKIIVIPNGKIIAGNIINYSRE-PVRRNEFIIGVAIDSDIDQVKQLLTIIESDDRILKDP	219 223 207 219
yggB SVQIPSTTRRTADGKIIVIPNGKIIAGNIINPSRE-PVRRNEFIIGVAYDSDIDQVKQILTNIIQSEDRILKDR S_typh KVHIPSTTLLTADSKEVVIPNGKIIADNIINYSRH-PYRRIDLIIGVDYQSRIADVKNVIHRIIEQDHRIDKTR Ctep RIARSTTLLTNDNINIIPNSEVSKQVINWSHNDRSLRVSVEVGVAYGSDEQVKHVLGVARNHPDIITKP P_fur AVGIMSTELLTADNVLITIPN-KLVWGNVITNYTRMPTRRVDVNVGVAYGTDLDKAIKVAMELMQNHPKVLKDP S_ent NVQIPSTTMRAVDGKIIVIPNGKIIAGNIINYSRE-PVRNEFIIGVAYDSDDQVKQLLTTIIESDDRILKDR Y_pestis QVQIPSTTRRVDGKIIVIPNGKIIAGNIINTSRE-PNRRTDMIVGVAYDADIDVVKKVLGDIIAADSRIHEK	219 223 207 219 219
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yggB SVQIPSTTRRTADGKIIVIPNGKIIAGNIINPSRE-PVRRNEFIIGVAYDSDIDQVKQILTNIIQSEDRILKDR S_typh KVHIPSTTLLTADSKEVVIPNGKIIADNIINYSRH-PYRRIDLIIGVDYQSRIADVKNVIHRIIEQDHRIDKTR Ctep RIARSTTLLTNDNINIIPNSEVSKQVINWSHNDRSLRVSVEVGVAYGSDEQVKHVLGVARNHPDIITKP P_fur AVGIMSTELLTADNVLITIPN-KLVWGNVITNYTRMPTRRVDVNVGVAYGTDLDKAIKVAMELMQNHPKVLKDP S_ent NVQIPSTTMRAVDGKIIVIPNGKIIAGNIINYSRE-PVRNEFIIGVAYDSDDQVKQLLTTIIESDDRILKDR Y_pestis QVQIPSTTRRVDGKIIVIPNGKIIAGNIINTSRE-PNRRTDMIVGVAYDADIDVVKKVLGDIIAADSRIHEK	219 223 207 219 219
<pre>yggB SVQIPSTTRRIADGKIIVIPNGKIIAGNIINPSRE-PVRENEFIIGVAIDSDIDQVKQILTNIIQSEDRILKDR S typh kVHIPSTTLLTADSKEVVIPNGKIIADNIINYSRH-PYRRIDLIIGVDVGSRIADVKNVIRNIEDHRIDKTR Ctep RIAIRSTLLTADNVLITIPNSEVSKQVINWSHNDRSLRVSVPVGVAIGSDPBQVKHVLLGVAENHPDILTKP P fur AVGIMSTELLTADNVLITIPN-KLVWGNVITNYTRMPTRRVDVNVGVAIGSDIDQVKKULGVAENHPDILTKP S_ent NVQIPSTTRRAVDGKIIVIPNGKIIAGNIINYSRE-PVRENEFIIGVAIDSDIDQVKQLLTTIIESDDRILKDR Y pestis QVQIPSTTRRIVDGKIIVVPNGKIIAGNIINYSRE-PARRDEFIISVSVNSDIDVVKKULGDIAADSRIHEK Buchn NHHPYTTLRTLDGKIVVVPNGKIIAGNIINYSRE-PARRDEFIISVSVNSDIDLVIKILRSVIEKBERVIKDK Ed ict EVQIPSTLATADNKVIVVPNGKIIAGNIINYSRE-PARRDEFIISVSVNSDIDVVKKVLGDIAADSRIHEK</pre>	219 223 207 219 219 243 219
<pre>yggB SVQIPSTTRRIADGKIIVIPNGKIIAGNIINPSRE-PVRRNEFIIGVAIDSDIDQVKQLLTNIIQSEDRILKDR S typh kVHIPSTTLLTADSKEVVIPNGKIIAGNIINPSRH-PYRRIDLIIGVDVGSDIDQVKNVLLGVAENHPDILTKR Ctep RIAIRSTTLLTADSNLVIPNGKIIAONIINYSRH-PYRRIDLIIGVDVGVAIGSDPGQVKNVLLGVAENHPDILTKP P fur AVGINSTELLTADVLITIPN-KLVWGNVITNYTRMPTRRVDVNVGVAIGSDIDQVKLVLLGVAENHPDILTKP S ent NVQIPSTTRRAVDGKIIVIPNGKIIAGNIINYSRE-PVRRNEFIIGVAIDSDIDQVKQLLTTIIESDDRILKDR J pestis QVQIPSTLRTVDDKLIVVPNGKIIAGNIINYSRE-PVRRNEFIIGVAIDSDIDQVKKVLGDIIAADSRIHEK Buchn NiHIPYTTLRTUDGKIVVVPNKIISGNIINYSRE-PARRIDBIISVSVNSDIDQVKKVLGDVIRABKREFKEDK Ed ict EVQIPSTLATADNKVIVVPNGKIIAGNIINPSRE-PKRRIDIIVGVAIDADIDVVKKVLGDVVAADTRILHDD V chol SIQIPGTVLKSPDNKMVVVPNSAVIGGAIINYSRE-PKRRIDIIVGVAIDADIDVVKRVLGDVVAADTRILHDD Synech SIGIPGTVLKSPDNKMVVVPNSAVIGGAIINYSRE-PKRVDMVIGVSVSDLQKWKKVLRETLEKDPRIKDF Synech SIGILSTTCTVDRVLVTPNKQILENNINHVGK-PRRKIDLVIGVSUSDDIKVKNVLWDIINKNELIKKTP Synech SIGILSTTCTVDRVVTNPNKQILENNINHVGK-PRRKIDLVIGVGEEDIDVVKSUGVUDQNSSUCTE</pre>	219 223 207 219 243 219 225 211 225
<pre>yggB SVQIPSTTRRIADGKIIVIPNGKIIAGNIINPSRE-PVRRNEFIIGVAIDSDIDQVKQLLTNIIQSEDRILKDR S typh KVHIPSTLLTADSKEVVIPNGKIIAGNIINPSRH-PYRRIDLIIGVDVGSRIADVKNVIRKIIEQDHRIDKTR Ctep RIAIRSTLLTADSVLUTIPNSEVSKQVINWSHNDRSLRVSVPVGVAIGSDPBQVKHVLLGVARNHPDIITKP P fur AvGIMSTELLTADNVLUTIPN-KLVGVNITNYTRMPTRVDVNVGVAIGSDIDQVKLULGVARNHPDILKKDP S_ent NVQIPSTTRAVDGKIIVIPNGKIIAGNIINPSRE-PVRRNEFIIGVAVDSDIDQVKLULGUIAADSRIHEK Buchn NIHIFYTTLRIDGKIVVVPNKIIAGNIINPSRE-PVRRNEFIISVSVNSDIDVVKKULGDIIAADSRIHEK Buchn NIHIFYTTLRIDGKIVVVPNKIIAGNIINPSRE-PKRRIDIIVGVAZDADIDVVKKULGDUIAADSRIHEK Ed ict EVQIPSTLATADNKVIVVPNKIIAGNIINPSRE-PKRRIDIIVGVAZDADIDVVKKULGDUAADTRIHEK Chol SIQIPGTVLKSPDNKMVVVPNSAVIGGAITNYSRH-ETRRVDMVIGVSVKSDLQKTKRVLRETLEKDPRILKDP C _perf RITVFYTHLVTPDNKELLPNGLANGSLINYSSK-DKRVDLVFSVGUDDDIKVKNVLGDUAADTRILKTP Synech SIELISTTICTUDNKLUTPNKQIIENNINHVGK-PERRUDLVGVGUDEDIKVKNSSLOWVIDONSEVCTEP Pseud_aer SILIFFTURSGOKKRIVVPNGALSNGTVTNYSAR-PVRKVIPOVGUDDADIKVKNSLOWVILLAMADDFRVLKDP CKLSS</pre>	219 223 207 219 243 219 225 211 225 211
<pre>yggB SVQFPSTTRRTADGKIIVIPNGKIIAGNIINFSRE-PVRRNEFIIGVAYDSDIDQVKQLLTNIQSEDRILKDR S typh KVHIPSTTLLTADSREVVIPNGKIIAGNIINFSRE-PVRRIDLIGVDQSDEQVKHVLLGVAENHPDILKKR Ctep RIARSTTLLTADSREVVIPNGKIIAONIINTSRE-PVRRIDLIGVDQSDEQVKHVLLGVAENHPDILKKP p fur AVGINSTELLTADNVLITIPN-KLVWGNVITNYTRMPTRRVDVNVGVAYGSDEQVKHVLLGVAENHPDILKKP S ent NVQIPSTTMRAVDGKIIVIPNGKIIAGNIINTSRE-PVRRNEFIIGVAYDSDIDQVKGVLTTIESDDRILKDR Buchn NHIFFTTLRTVDDKIIVVPNGKIIAGNIINTSRE-PKRNEFIIGVAYDADIDVVKKVLGDVAADSRIHEK Buchn NHIFFTTLRTLDGKIVVVPNGKIIAGNIINTSRE-PKRNEFIIGVAXDSDIDQVKKVLGDVAADSRIHEK Ed ict EVQIPSTTLATADNKVIVVPNGKIIAGNIINTSRE-PKRNEFIIGVAXDADIDVVKKVLGDVAADTRILKDP C _perf RITVFTHATDDKVIVVPNGKIIAGNIINTSRE-PKRNIDIIVGVAXDADIDVVKKVLGDVAADTRILHDD V _chol SIQIPSTTLATADNKVIVVPNGKIIAGNIINTSRE-PKRNIDIIVGVAXDADIDVVKKVLGDVAADTRILHDP C _perf RITVFTHLVTPDNKELLIPNGTLANGSLINYSSL-DKRVDLVFSVGIDDDIKVKNVLGDVIANDVFNKLKTP Synech SIELISTIGTVDNKLVIVPNGKIIANGSLINYSSL-DKRVDLVFSVGIDDDIKVKNVLGDVAADAP Xy fast EILIPTVRSGDNKRIVVPNGALSNGTVTNYSAE-PKRVIPVGGVGVGVGCDDIKVKNUDADINNELLKTP Xy fast EILIPTTRFVDRGLNSTTTVPINALSTIPTNEN</pre>	219 223 207 219 243 219 225 211 225 211 225 213
<pre>yggB SVQFPSTTRRIADGKIIVIPNGKIIAGNIINFSRE-PVRRNEFIIGVAIDSDIDQVKQLLTNIQSEDRILKDR S typh KVHIPSTLLTADSREVVIPNGKIIAGNIINFSRH-PYRRIDLIIGVDQSDEVQVKHVLLGVAENHPDHIDKTR Ctep RIAIRSTLLTADNINIIIPNSEVSKQVINWSHNDRSLRVSVPVGVAIGSDPEQVKHVLLGVAENHPDIITKP P fur AVGIMSTELLTADNULITPN-KLVWGNVITNYTRMPTRRVDVNVGVAIGTDIDQVKHVLLGVAENHPDIITKP S ent NVQIPSTTMRAVDGKIIVIPNGKIIAGNIINFSRE-PVRRNEFIIGVANDGARGTDIDQVKKVLGDIAADSRIHEK Buch NHHPYTTLRTUDGKIVVVPNKIISGNIINFSRE-PVRRNEFIISVSNDSDIDQVKKVLGDIAADSRIHEK Bd ict EVQIPSTTAAADNKVIVVPNKKIIAGNIINFSRE-PKRRIDIIVGVAIDADIDVVKKVLGDVVAADTRILHDD V chol SIQIPGTUKSPDNKMVVVPNSKIIAGNIINFSRE-PKRRIDIIVGVAIDADIDVVKKVLGDVVAADTRILHD</pre>	219 223 207 219 243 219 225 211 225 213 225 213
<pre>yggB SVQIPSTTRRIADGKIIVIPNGKIIAGNIINPSRE-PVRRNEFIIGVAIDSDIDQVKQLLTNIIQSEDRILKDR S typh kVHIPSTTLLTADSKEVVIPNGKIIAGNIINPSRH-PYRRIDLIIGVDVGSDIDQVKVULGVAENHPDILKKR Ctep RIALRSTLLTADNVLITIPN-KLVWGNVITNYTRMPTRVDVNVGVAGSDPBQVKHVLLGVAENHPDILKKP P fur AVGIMSTELLTADNVLITIPN-KLVWGNVITNYTRMPTRVDVNVGVAGSDIDQVKKULGVAENHPDILKKP S_ent NVQIPSTTRRAVDGKIIVIPNGKIIAGNIINPSRE-PVRRNEFIIGVAYDSDIDQVKKULGDIIAADSRIHEK Buchn NHHPYTTLRIDGKIVVVPNKIISGNIINPSRE-PKRRIDHIVGVADADIDVVKKUGDIIAADSRIHEK Buchn NHHPYTTLRIDGKIVVVPNKIISGNIINPSRE-PKRRIDHIVGVADADIDVVKKUGDUIAADSRIHEK Bd ict EVQIPSTLRIVDVNVNKIISGNIINPSRE-PKRRIDHIVGVADADIDVVKKULGUVAADTRIHDD V chol SIQIPGTUKSPDNKMVVVPNSAVIGGAINNPSRE-PKRRIDHIVGVADADIDVVKKULETLEKDPRILKDP C_perf RITVPYTHLVTPDNKELIPNGLIAGSLINPSK-DTRVDLVPSVGVDDDIKVKNVLWDIINKNELIKTP Synech SIELISTTCTUDNKLVIPNKQIIENNIINFSRE-PKRVDVVIGVSVGVDDDIKVKNVLWDINKNELIKTP Synech SIELISTTCTUDNKLVIPNKQIENNINTSR-PKRVDLVPSVGVDDDIKVKNVLWDINKNELIKTP Synech SIELISTTCTUDNKLVIPNKQIENNINTSR-PKRVDLVVSVGVDDDIKVKNVLRDINKNELIKTP Neisser EIKMVQTSLRTFDQRIITPNKQIENNINTITVPINSTL-PTRIETTVGVSVGVDDLKVARAVLKAAVERPLKDP Kaf BILFPTTLRFDDRUSVLPNSVVGNSVNGNSIVNSTL-PLCRAQVIVGVDINCDLKVARAVLKAAVERPLKDP NeIsser EIKMVQTSLRTFDDRUITPNKQIENNINTPTRIETTVGVGVDINCDLKVARAVLKAAVERPLSVQNBE NEISSER EIKMVQTSLRTTDNEKVLPNSVLMSSINT-PLCRAQVIVGVDINCDLKVARAVLKAAVERPLSVQNBE A fulg DVNILSTIRTVDEVLVRIPNEKVFTSNITNYRAH-LARRFEVVGNGTSDDLKVARAVLKAAVERPLSVQNBE A</pre>	219 223 207 219 243 219 225 211 225 213 225 221 208
<pre>yggB SVQFPSTTRRTADGKIIVIPNGKIIAGNIINFSRE-PVRRNEFIIGVAYDSDIDQVKQLLTNIQSEDRILKDR S typh KVHIPSTTLLTADSREVVIPNGKIIAGNIINFSRE-PVRRIDLIGVDQSDEQVKHVLLGVAENHPDILKKR Ctep RIARSTTLLTADSREVVIPNGKIIAGNIINFSRE-PVRRIDLIGVDQSDEQVKHVLLGVAENHPDILKKP p fur AVGINSTELLTADNVLITIPN-KLVWGNVITNFTRMPTRVDVNVGVAFGSDEQVKHVLLGVAENHPDILKKP S ent NVQIPSTTMRAVDGKIIVIPNGKIIAGNIINFSRE-PVRRNEFIIGVAYDSDIDQVKCVLGUITTIESDDRILKDR U pestis QVQIPSTTLRTVDDKIIVVPNGKIIAGNIINFSRE-PKRNEFIIGVAYDADIDVVKKVLGDVIAADSRIIHEK Buchn NHHFYTTLRTLDGKIVVVPNGKIIAGNIINFSRE-PKRNEFIIGVAYDADIDVVKKVLGDVVAADTRILHDD V Chol SIQIPSTTLATADNKVIVVPNGKIIAGNIINFSRE-PKRNIDIIVGVAYDADIDVVKKVLGDVVAADTRILHDD S perf RITVFYTHAVDFNVVPNGKIIAGNIINFSRE-PKRNIDIVGVSYGSDIDLVKKVLGDVVAADTRILHDD V Chol SIQIPSTTLATADNKVIVVPNGKIIAGNIINFSRE-PKRNIDIVGVSYGSDIDVVKKVLGDVVAADTRILHDD Synech SIELISTIGTVDNKKILIPNGTLANGSLINYSSL-DTRVDMVIGVSYGSDIDVVKRVLGDVVAADTRILHDP Synech SIELISTIGTVDNKKILPNGTLSNITNYSRH-BTRVDMVIGVSYGSDIDVVKRVLGDVVAADDPRVLKTP Neisser EIKHVQTSLKTTDNKUVVPNGALSNGTVTNYSAE-PVRVIPDGIDDDIKVAANDIINKNELLKTP Neisser EIKHVQTSLKTTDNEVUPNGALSNGTVTNYSAE-PVRVIPDGVSGDDDLKVAACAVLKAAVEHPLSVQNEEP Neisser EIKHVQTSLKTTDNEVUPNSTITVPNINFSTPRRIEITVGVSSGDNLKAAQELLKKARSNPKILDDP Neisser SIHLIFTTDREVVLPNSVUMGNSIVNSTI</pre>	219 223 207 219 243 219 225 211 225 213 225 213
<pre>yggB SVQIPSTTRRIADGKIIVIPNGKIIAGNIINPSRE-PVRRNEFIIGVAIDSDIDQVKQLLTNIIQSEDRILKDR S typh kVHIPSTTLLTADSKEVVIPNGKIIAGNIINPSRH-PYRRIDLIIGVDVGSDIDQVKVULGVAENHPDILKKR Ctep RIALRSTLLTADNVLITIPN-KLVWGNVITNYTRMPTRVDVNVGVAGSDPBQVKHVLLGVAENHPDILKKP P fur AVGIMSTELLTADNVLITIPN-KLVWGNVITNYTRMPTRVDVNVGVAGSDIDQVKKULGVAENHPDILKKP S_ent NVQIPSTTRRAVDGKIIVIPNGKIIAGNIINPSRE-PVRRNEFIIGVAYDSDIDQVKKULGDIIAADSRIHEK Buchn NHHPYTTLRIDGKIVVVPNKIISGNIINPSRE-PKRRIDHIVGVADADIDVVKKUGDIIAADSRIHEK Buchn NHHPYTTLRIDGKIVVVPNKIISGNIINPSRE-PKRRIDHIVGVADADIDVVKKUGDUIAADSRIHEK Bd ict EVQIPSTLRIVDVNVNKIISGNIINPSRE-PKRRIDHIVGVADADIDVVKKULGUVAADTRIHDD V chol SIQIPGTUKSPDNKMVVVPNSAVIGGAINNPSRE-PKRRIDHIVGVADADIDVVKKULETLEKDPRILKDP C_perf RITVPYTHLVTPDNKELIPNGLIAGSLINPSK-DTRVDLVPSVGVDDDIKVKNVLWDIINKNELIKTP Synech SIELISTTCTUDNKLVIPNKQIIENNIINFSRE-PKRVDVVIGVSVGVDDDIKVKNVLWDINKNELIKTP Synech SIELISTTCTUDNKLVIPNKQIENNINTSR-PKRVDLVPSVGVDDDIKVKNVLWDINKNELIKTP Synech SIELISTTCTUDNKLVIPNKQIENNINTSR-PKRVDLVVSVGVDDDIKVKNVLRDINKNELIKTP Neisser EIKMVQTSLRTFDQRIITPNKQIENNINTITVPINSTL-PTRIETTVGVSVGVDDLKVARAVLKAAVERPLKDP Kaf BILFPTTLRFDDRUSVLPNSVVGNSVNGNSIVNSTL-PLCRAQVIVGVDINCDLKVARAVLKAAVERPLKDP NeIsser EIKMVQTSLRTFDDRUITPNKQIENNINTPTRIETTVGVGVDINCDLKVARAVLKAAVERPLSVQNBE NEISSER EIKMVQTSLRTTDNEKVLPNSVLMSSINT-PLCRAQVIVGVDINCDLKVARAVLKAAVERPLSVQNBE A fulg DVNILSTIRTVDEVLVRIPNEKVFTSNITNYRAH-LARRFEVVGNGTSDDLKVARAVLKAAVERPLSVQNBE A</pre>	219 223 207 219 243 219 225 211 225 213 225 221 208 213
<pre>yggB SVQFPSTTRRTADGKIIVIPNGKIIAGNIINFSRE-PVRRNEFIIGVAYDSDIDQVKQLLTNIQSEDRILKDR S typh KVHIPSTTLLTADSREVVIPNGKIIAGNIINFSRE-PVRRIDLIGVDQSDEQVKHVLLGVAENHPDILKKR Ctep RIARSTTLLTADSREVVIPNGKIIAGNIINFSRE-PKRIDLIGVDQSDEQVKHVLLGVAENHPDILKKP p fur AVGINSTELLTADNVLITIPN-KLVWGNVITNFTRPTRRVDVNVGVAYGSDEQVKHVLLGVAENHPDILKKP S ent NVQIPSTTMRAVDGKIIVIPNGKIIAGNIINFSRE-PKRNEFIIGVAYDSDIDQVKCVLGUITTIESDDRILKDR Buchn NHHFYTTLRTVDDKIIVVPNGKIIAGNIINFSRE-PKRNEFIIGVAYDADIDVVKKVLGDVIAADSRIHEK Buchn NHHFYTTLRTLDGKIVVVPNGKIIAGNIINFSRE-PKRNEFIIGVAYDADIDVVKKVLGDVVAADTRILHEK Ed ict EVQIPSTTLATADNKVIVVPNGKIIAGNIINFSRE-PKRNEFIIGVAYDADIDVVKKVLGDVVAADTRILHED V Ghol SIQIPGTVLKSPDNKMVVVPNGKIIAGNIINFSRE-PKRNIDIIVGVAYDADIDVVKKVLGDVVAADTRILHED Synech SIELISTIGTVDNKLIIPNGTLANGSLINFSS-DKRVDLVFSVGIDDDIKVKNVLGDVVAADTRILHEP Synech SIELISTIGTVDNKKIIVPNGKIIANGSLINFSR-PKRNIDIIVGVAYDADIDVVKKVLGDVVAADTRILHEP Neisser EIKHVQTSLKTTDNKKIIVPNGALSNUTVTNFAR-PKRVIPDVGUDYDADIKVAKVLGDVVAADPRVLKDP Neisser EIKHVQTSLKTTDNKVIVPNGALSNUTVTNFAR-PKRVIPDVGUDYDADIKVAKVLGDVVAADPRVLKDP Neisser EIKHVQTSLKTTDNEVVLPNSTITVPINFAR-PKRVIPDVGUDYDADIKVAKEAUKAAVEHPLSVQNEE-R A fulg DVNILSTIRTYDGLVVIPNSTITVPINFAR-PKRVIPDVGUDYDADKKNAQNILLAMAD-DPRVLKDP Psuda cillfTTDNEVVLPNSVVMGNSIVNSTI-PTRRIEITVGVSSGDNLKVAQELLKKARNPKILDDP Neisser EIKHVQTSLKTTDNEVVLPNSVVMGNSIVNSTI-PFRRIEITVGVSSGDDKVKNIENHENGUVENEPFNLKNP Pusobac SIHILYTIGGLVRIPNEVVPNSNITNYKN-PFRREVVVGIRVSDDAKANENKKIEBHPFALKNP Prusobac SIHILYTIGGVVRVPNSUVMGNSINNSTI-PFRREPFYTGIRVSD</pre>	219 223 207 219 243 219 225 211 225 211 225 211 208 213 216 213 219 201
<pre>yggB SVQFPSTTRRTADGKIIVIPNGKIIAGNIINFSRE-PVRRNEFIIGVAIDS DIDQVKQLLTNIIQSEDRILKDR S typh KVHIPSTTLLTADSREVVIPNGKIIAGNIINFSRH-PYRRIDLIIGVDQS DEDQVKHVLLGVAENHPDLIKTR "Ctep RIAIRSTTLLTADSREVVIPNGKIIAGNIINFSRH-PYRRIDLIIGVDQS DEDQVKHVLLGVAENHPDLIKKP p fur AVGIMSTELLTADNVLITPN-KLVWGNVITNYTRMPTRRVDVNVGVAIGS DEDQVKHVLLGVAENHPDLIKKP S ent NVQIPSTTMRAVDGKIIVIPNGKIIAGNIINFSRE-PVRRNEFIIGVAVDS DIDQVKKVLGDUAADSRIHEK Buchn NHIPYTTRTDDKLIVVPNGKIIAGNIINFSRE-PKRNEFIIGVAVDA DIDQVKKVLGDUAADSRIHEK Ed ict EVQIPSTTLATADNKVIVVPNGKIIAGNIINFSRE-PKRNEFIIGVAVDA DIDVVKKVLGDUAADSRIHEK Ed ict EVQIPSTTLATADNKVIVVPNGKIIAGNIINFSRE-PKRNEFIIGVAXDA DIDVVKKVLGDUAADSRIHEK Ed ict EVQIPSTTLATADNKVIVVPNGKIIAGNIINFSRE-PKRRIDIIVGVAXDA DIDVVKKVLGDUVAADTRIHEDD V chol SIQIPQTVLKSPDNKMVVVPNSAVIGGAITNYSRE-PKRRIDIIVGVAXDA DIDVVKKVLGDVVAADTRIHEDD Synech SIELLSTTICTVDNRLVIPNGKIIAGSLINYSSE-DTRRVDMVIGVSKS DLQKIKKVLRETLEKDPRILKDP Synech SIELLSTTICTVDNRLVIPNGUIENNIINFVR-ETRRVDMVIGVSKS</pre>	219 223 207 219 243 219 225 211 225 213 225 221 208 213 216 219 201 193
<pre>yggB SVQFPSTTRRIADGKIIVIPNGKIIAGNIINFSRE-PVRRNEFIIGVAIDSDIDQVKQLLTNIQSEDRILKDR S typh KVHIPSTTLTADSREVVIPNGKIIAGNIINFSRH-PYRRIDLIIGVDVQSRIADVKNVIRNIEDHRIDKTR Ctep RIAIRSTLLTADSNEVVIPNGKIIAGNIINFSRH-PYRRIDLIIGVDVQSDEQVKHVLLGVAENHPDIITKP P fur AVGIMSTELLTADVLIITPN-KLVWGNVITNYTRMPTRRVDVNVGVAIGSDEQVKHVLLGVAENHPDII S-ent NVQIPSTTRRAVDGKIIVIPNGKIIAGNIINFSRE-PVRRNEFIIGVAIDSDIDQVKQLLTTIIESDDRILKDR J pestis QVQIPSTTLRTVDDKIIVVPNGKIIAGNIINFSRE-PVRRNEFIIGVAIDSDIDQVKQLLTTIIESDDRILKD</pre>	219 223 207 219 243 219 225 211 225 213 225 213 208 213 208 213 216 219 201 193 289
<pre>yggB SVQFPSTTRRTADGKIIVIPNGKIIAGNIINFSRE-PVRRNEFIIGVAVDSDIDQVKQLLTNIQSEDRILKDR S typh KVHIPSTTLLTADSREVVIPNGKIIAGNIINFSRE-PVRRIDLIGVDQSDEADVKNVLRIIEODHRIDKTR Ctep RIALRSTTLLTADSREVVIPNGKIIAGNIINTSRE-PVRRIDLIGVDQSDEQVKHVLLGVAENHPDILKKP p fur AVGINSTELLTADNVLITIPN-KLVWGNVITNYTRMPTRVDVNVGVAYGSDEQVKHVLLGVAENHPDILKKP S ent NVQIPSTTMRAVDGKIIVIPNGKIIAGNIINTSRE-PVRRNEFIIGVAYDSDIDQVKQLITTIESDDRILKD R Deuch NHIFFYTLRTVDDKIIVVPNGKIIAGNIINTSRE-PVRRNEFIIGVAYDSDIDQVKQLGUITTIESDDRILKD B ent NVQIPSTTMRAVDGKIIVVPNGKIIAGNIINTSRE-PKRNEFIIGVAYDSDIDQVKKVLGDVIAADSRIHEK Buchn NHIFFYTLRTVDDKIIVVPNGKIIAGNIINTSRE-PKRNEFIIGVAYDADIDVVKKVLGDVIAADSRIHEK Bd ict EVQIPSTTLATADNKVIVVPNGKIIAGNIINTSRE-PKRNIDIIVGVAYDADIDVVKKVLGDVVAADTRILHED V Ghol SIQIPGTVLKSPDNKMVVVPNSAVIGGAINYSRE-PKRNIDIIVGVAYDADIDVVKKVLGDVVAADTRILHED Synech SIELISTIGTVDNKKIIVVPNGKIIANGSINYSS-DTRRVDLVGVSYGSDIGKVKRVLGEVVAADTRILHED Synech SIELISTIGTVDNKKIUVPNGKIIANGSINYSS-DTRRVDLVGVSYGSDIKVKRVLGDVVAAD-DPRVLKDP NeIsser EIKMVQTSLKTTDNKUVVPNGALSNGTVTNYSAE-PKRNIDIIVGVSVGDDIKVAKVLGDVVAAD-DPRVLKDP NeIsser EIKMVQTSLKTTDNKEVVLPNSVVMGNSIVNSTI</pre>	219 223 207 219 249 243 225 211 225 213 225 221 208 213 219 201 193 289 208
<pre>yggB SVQFPSTTRTADGKLIVIPNGKILAGNIINFSRE-PVRRNEFIGVATDSDIDQVKQLLTNIQSEDRILKDR S typh KVHIPSTTLLTADSREVVIPNGKILAGNIINFSRH-PYRRIDLIGVDQSDEQVKHVLLGVAENHPDLIKKR Ctep RIALRSTTLLTADSKEVVIPNGKILAGNIINTSRH-PYRRIDLIGVDQSDEQVKHVLLGVAENHPDLIKKR Fut AVGIMSTELLTADVLITIPN-KLVWGNVITNYTRMPTRRVDVNVGVATGSDEQVKHVLLGVAENHPDLIKKP S ent NVQIPSTTMRAVGGILVIPNGKILAGNIINTSRE-PVRNEFIIGVAYDADIDVVKKVLGDILAADSRIHEK Buchn NHIPYTTRTDDKLIVVPNGKILAGNIINTSRE-PVRNEFIIGVAYDADIDVVKKVLGDUVAADSRIHEK Buchn NHIPYTTLTDGKIVVVVPNGKILAGNIINTSRE-PARRNEFIISVSINSDIDVVKKVLGDVVAADTRIHEK Bd ict EVQIPSTTLATADNKVIVVPNGKILAGNIINTSRE-PARRNEFIISVSINSDIDVVKKVLGDVVAADTRIHEK Bd ict EVQIPSTTLATADNKVIVVPNGKILAGNIINTSRE-PARRNEFIISVSINSDIDVVKKVLGDVVAADTRIHEF Bd ict EVQIPSTTLATADNKVIVVPNGKILAGNIINTSRE-PARRNEFIISVSINSDIDVVKKVLGDVVAADTRIHEF Bd ict EVQIPSTLATADNKVIVVPNGKILAGNIINTSRE-PARRVDMVIGVSKSDIDVVKKVLGDVVAADTRIHEF Bd ict EVQIPSTLATADNKVIVVPNGKILAGNINFSRE-PARRVDMVIGVSKSDIDVVKKVLGDVVAADTRIHEDF V chol SIQIPQTVLKSPDNKMVVVPNSAVIGAITNISRE-FKRVDMVIGVSKSDIDVVKKVLGDVVAADTRIHEDF Synech SIELLSTTICTYDNRLVIIPNGLIENNIINFSRE-FKRVDMVIGVSKGVF</pre>	219 223 207 219 225 211 225 211 208 213 216 219 201 219 201 193 289 208 285
<pre>yggB SVQPPSTTRRTADGKIIVIPNGKIIAGNIINFSRE-PVRRNEFIIGVAYDSDIDQVKQLLTNIQSEDRILKDR S typh KVHIPSTTLLTADSREVVIPNGKIIAGNIINFSRE-PVRRIDLIGVDQSDEQVKHVLLGVAENHPDLIKKR Ctep RIALRSTTLLTADSKEVVIPNGKIIAONIINTSRE-PKRIDLIGVDQSDEQVKHVLLGVAENHPDLIKKP P fur AVGIMSTELLTADNVLITIPN-KLVWGNVITNYTRMPTRVDVNVGVAYGSDEQVKHVLLGVAENHPDLIKKP S ent NVQIPSTTMRAVDGKIIVIPNGKIIAGNIINTSRE-PVRRNEFIIGVAYDSDIDQVKQLITTIIESDDRILKD K pestis QVQIPSTTLRTVDDKIIVVPNGKIIAGNIINTSRE-PVRRNEFIIGVAYDSDIDQVKKVLGDUHAADSRIIHEK Buchn NHHFYTTLRTLDGKIVVVPNGKIIAGNIINTSRE-PARRNEFIIGVAYDADIDVVKKVLGDUHAADSRIIHEK Bd ict EVQIPSTTLATADNKVIVVPNGKIIAGNIINTSRE-PKRIDIIVGVAYDADIDVVKKVLGDUHAADSRIIHEK Bd ict EVQIPSTTLATADNKVIVVPNGKIIAGNIINTSRE-PKRIDIIVGVAYDADIDVVKKVLGDUHAADSRIIHEF P Seuch NHHFYTTLRTLDGKIVVVPNGKIIAGNIINTSRE-PKRIDIIVGVAYDADIDVVKKVLGDUHAADSRIIHEF Bd ict EVQIPSTLATADNKVIVVPNGKIIAGNINTSRE-PKRIDIIVGVAYDADIDVVKKVLGDUHAADTRILHDD V_Ghol SIQIFQTVLKSPDNKMVVVPNSAVIGGAITNYSRE-PKRIDIIVGVAYDADIKVKVLGDUWAADTRILHDD Synech SIELISTICTYDNKEVIPNGALSNGVTNYSR-PKRIDIVGVSVKSDIKVKRVLGDUHAAD-DPKUKDP Synech SIELISTICTYDNKEVIPNGALSNGVTNYSR-PKRIDLVGVSVGDDDIKVAKVLGDUHAAD-DPFVLKDP Neisser EIKMVQTSLFTTDNEVVLPNSVVMGNSIVNRSTL-PLCRAVVIPVGIDYDADIKVAKEAVLKAAVENPLSVQNBE-R A_fulg DVNILSTIRTYDGLVRIPNSVVMGNSIVNRSTL-PLCRAVVIFVGIRVSDDAKAAIEHIKKIIEBHPFALKNP Pusobac SIHLISTIITYDGLVRIPNSVVMGNSINNSTNIPPREVITGIRVSDDAKAIEHIKKIEBHPFALKNP Physobac SIHLISTIITYDGLVRIPNSVVMDVITNYSR-PSRHELSLTVKNDEDANAAIWLIKDLIDKEPFALQNP MAFtanos DIRIISTLIRTYDGLVRIPNSVVMDNXINNSTNINPPREVENTGIRVSDDANAAIWLIKDLIDKEPFALQNP Magro_tum EIGLPATELKYSDGLVRLPNSVVMDNXINNNNNNPFTACREFEVINTIGINVSAFDLRKVVEFFXALEBETVEKDP B sub DITFRTRRTAQGALVTVPNSTLSMANTINNTN-ACREFEVVGUPYSADLRKVVEFYKALEBETVEKDP Fhermat VVNLNHTVIRTWDGRRVMIPNKAVNNNKIINFN-KRGEITVGVPTSA</pre>	219 223 207 219 249 243 225 211 225 213 225 221 208 213 219 201 193 289 208
<pre>yggB SVQFPSTTRTADGKLIVIPNGKILAGNIINFSRE-PVRRNEFIGVATDSDIDQVKQLLTNIQSEDRILKDR S typh KVHIPSTTLLTADSREVVIPNGKILAGNIINFSRH-PYRRIDLIGVDQSDEQVKHVLLGVAENHPDLIKKR Ctep RIALRSTTLLTADSKEVVIPNGKILAGNIINTSRH-PYRRIDLIGVDQSDEQVKHVLLGVAENHPDLIKKP P fur AVGIMSTELLTADNVLITPN-KLVWGNVITNYTRMPTRRVDVNVGVATGSDEQVKHVLLGVAENHPDLIKKP S ent NVQIPSTTMRAVGGILVIPNGKILAGNIINTSRE-PVRNEFIIGVAYDADIDVVKKVLGDILAADSRIHEK Buchn NHIPYTTRTDDKLIVVPNGKILAGNIINTSRE-PVRNEFIIGVAYDADIDVVKKVLGDUKAADSRIHEK Buchn NHIPYTTLTDGKIVVVVPNGKILAGNIINTSRE-PARRNEFIISVSINSDIDVVKKVLGDVVAADTRILHDD V chol SIQIPQTVLKSPDNKMVVVPNSKILAGNIINFSRE-PKRRIDIIVGVAYDADIDVVKKVLGDVVAADTRILHDD V chol SIQIPQTVLKSPDNKMVVVPNSKILAGNIINFSRE-PKRRIDIIVGVAYDADIDVVKKVLGDVVAADTRILHDD V great sigtefitigtingstrifterformedications for the state of the sta</pre>	219 223 207 219 243 225 211 225 213 225 213 225 221 208 213 208 216 219 201 193 289 208 285 293
<pre>yggB SVQPPSTTRTADGKIIVIPNGKIIAGNIINFSRE-PVRRNEFIIGVAVDSDIDQVKQLLTNIQSEDRILKDR S typh KVHIPSTTLLTADSREVVIPNGKIIAGNIINFSRE-PVRRIDLIGVDQSPEQVHVLLGVAENHPDITKR Ctep FAIRSTTLLTADNINIIIPNSEFVSKQVINWSHNDRSLPVSVQVAXGSDEQVHVLLGVAENHPDITKP P fur AVGIMSTELLTADNVLITIPN-KLVWGNVITNTTRMPTRVDVNVGVAGSDEQVHVLLGVAENHPDITKP S ent NVQIPSTTRAVDGKIIVVPNGKIIAGNIINFSRE-PVRRNEFIIGVADSDIDQVKCVLGUITTIESDDRILKDR U pestis QVQIPSTTRAVDGKIIVVPNGKIIAGNIINFSRE-PNRRPEFIIGVADSDIDQVKCVLGUITADSRIHEK Buchn NHIPYTTRTLDGKIVVVPNGKIIAGNIINFSRE-PNRRPEFIIGVADS</pre>	219 223 207 219 243 225 211 225 213 225 213 225 221 208 213 208 216 219 201 193 289 208 285 293
<pre>yggB SVQPPSTTRTADGKIIVIPNGKIIAGNIINFSRE-PVRRNEFIIGVAVDSDIDQVKQLLTNIQSEDRILKDR S typh KVHIPSTTLLTADSREVVIPNGKIIAGNIINFSRE-PVRRIDLIGVDQSPEQVHVLLGVAENHPDITKR Ctep FAIRSTTLLTADNINIIIPNSEFVSKQVINWSHNDRSLPVSVQVAXGSDEQVHVLLGVAENHPDITKP P fur AVGIMSTELLTADNVLITIPN-KLVWGNVITNTTRMPTRVDVNVGVAGSDEQVHVLLGVAENHPDITKP S ent NVQIPSTTRAVDGKIIVVPNGKIIAGNIINFSRE-PVRRNEFIIGVADSDIDQVKCVLGUITTIESDDRILKDR U pestis QVQIPSTTRAVDGKIIVVPNGKIIAGNIINFSRE-PNRRPEFIIGVADSDIDQVKCVLGUITADSRIHEK Buchn NHIPYTTRTLDGKIVVVPNGKIIAGNIINFSRE-PNRRPEFIIGVADS</pre>	219 223 207 219 243 225 211 225 213 225 213 225 221 208 213 208 216 219 201 193 289 208 285 293
<pre>yggB SVQPPSTTRRTADGKIIVIPNGKIIAGNIINFSRE-PVRRNEFIIGVAYDSDIDQVKQLLTNIQSEDRILKDR S typh KVHIPSTTLLTADSREVVIPNGKIIAGNIINFSRE-PVRRIDLIGVDQSDEQVKHVLLGVAENHPDLIKKR Ctep RIALRSTTLLTADSKEVVIPNGKIIAGNIINTSRE-PKRIDLIGVDQSDEQVKHVLLGVAENHPDLIKKP P fur AVGIMSTELLTADNVLITIPN-KLVWGNVITNYTRMPTRVDVNVGVAFGSDEQVKHVLLGVAENHPDLIKKP S ent NVQIPSTTMRAVDGKIIVIPNGKIIAGNIINTSRE-PVRRNEFIIGVAYDSDIDQVKQLTTIIESDDRILKD K pestis QVQIPSTTLRTVDDKIIVVPNGKIIAGNIINTSRE-PVRRNEFIIGVAYDSDIDQVKKVLGDUAADSRIHEK Buchn NHHFYTTLRTLDGKIVVVPNGKIIAGNIINTSRE-PARRNEFIIGVAYDADIDVVKKVLGDUAADSRIHEK Bd ict EVQIPSTTLATADNKVIVVPNGKIIAGNIINTSRE-PKRIDIIVGVAYDADIDVVKKVLGDUAADSRIHEK Bd ict EVQIPSTLATADNKVIVVPNGKIIAGNIINTSRE-PKRIDIIVGVAYDADIDVVKKVLGDUAADTRILHDD V_Ghol SIQIPQTVLKSPDNKMVVVPNSAVIGGAITNYSRE-PKRIDIIVGVAYDADIDVVKKVLGDVVAADTRILHDD Synech SIELISTICTYDNKELUIPNGKIIAGNIINTSRE-PKRIDIIVGVAYDADILKVKVLGDVVAADTRILHDD Synech SIELISTICTYDNKEVIPNSAVIGGAITNYSRE-PKRIDIVGVSVGDDDIKVKVLGDVVAADTRILHDP Synech SIELISTICTYDNKEVIPNSAVIGAISNYSK-DTRRVDLVFSVGUDDDIKVAKVLGDVVAAD-DPRVLKDP Neisser EIKMVQTSLRTTDNEWVLPNSAVIGNINTNYSR-PKRIDLVGVSVGDDDIKVAKVLGDVDAD-DPRVLKDP Neisser EIKMVQTSLRTTDNEVVLPNSVVMGNSIVNRSTL-PLCRAVVIPONSSUCDLKVAKEAVLKAAVENPLSVQNEB-R A_fulg DVNILSTIRTYDGLVVRIPNSVVMGNSIVNRSTL-PLCRAVVIPONSSDDDNKVNSVLGVIDQNEBERVLKAAVENPLSVQNEB-R A_fulg DVNILSTIRTYDGLVVRIPNSVVMGNSINNRSTN-PRRELSLTVKNDEDAAAAWLKALKAVENPLSVQNEB-R A_fulg DVNILSTIRTYDGLVVRIPNQVPTTNINVGH-PVRKVIPNGINSSDANAAIWLKDLIDENEPFIACNP Phusobac SIHLIFTINGULVRLPNQVVTINNSTNN-PFRELSLTVKNDEDAAAAWLKALKDVENEPFALQNP Neisser EIKMVQTSLRTDNGKVTINSTNNNTNN-PRRELSLTVKNDE</pre>	219 223 207 219 243 225 211 225 213 225 213 225 221 208 213 208 216 219 201 193 289 208 285 293

Figure S2 MULTIPLE SEQUENCE ALIGNMENT of yggB Page 3 of 4

Tag	, , , ,	•	
yggB	EMTVRLNELGASSINFVVRVW	SNS <mark>GD-LONVYWDVLERIK</mark> REFDAA <mark>GISFPYPOMDVNF</mark> KRVKEDKAA	286
		VPNAQ-YWSTYYDLLENIKEAMDENGINIPYPRMDVRVENVKSITP	285
		TETRIQTPRFLRSELNYRIFDAFRKNGIEIPFPOTDLHIRSSDIPLWEPRERKNP	299
		AKTBDYWTVKFDLTKGIYEAYRREGIEIPFPOLDVHIKEMPK	270
		SKSSD-LONVYWDVLERIKREFDAAGISFPYPOMDVNFKRVKDNAAE	286
		TINGD-AQEVFWDLTENFKRALDAHKIGIPYPQMDVHLHQVAKABABKPB	289
		ISKNHD-LNTVYWDLMAKFKKELDKNNINIPFPOLDVHVYKKK	
			305
		GNNAD-YWAIYFDLMENFKRALDANNIGIPFPQMDVHLYQAVKARAB	286
		CKTSD-YWAVYFDSMQAIKEALDANGIEIPFPQMDVHLNKIN	287
		TKQBD-YWKVHFSLLEEVKLRFDEENITIPYPQMDVTLTK	271
		WKSED-YFRLKLQLTEAIKRKLDEENISIPFPQRDVHLIQPETKELDIKAA	296
Pseud aer	APVAVVSNLGESAI TLSLRVW	VKNAD-YWDVMFMFNEKARDALGKEGIGIPFPQRVVKVVQGAMAD	278
Xy fast	APLVYVNNLGESSVDLLLLAY	TONDN-FNPAKSELLEOIHNOLPENGLNIPYPORDLHLYHHDTNNRKIASLLLP	299
Neisser	QAAAYITALGDNAIEITLWAW	ANEAD-RWTLOCDLNBOVVENLRKVNINIPFPORDIHIINS	282
A fulg	EPVVFVDNLGDSSVNIVVRIW	APSTEWYNVKMELLWKIKTELEKNGIEIPFPORVVWFANELR	271
		WRKBDYVDTMLDCNIN-VKKFFDKNGIEIPYNKLDLYMKNNLDIDNKQ	281
		APVSEWFGLKTRLLWDIKCTLEENGIEVPFPORVLHIKNNSGKKPOEFEGLKE	290
		WRSDN-YFVTTRDVTKAMRLAFDERKAEVNAOPA	273
		TAGVTWFNLYSSLATLVKRALDEAGIEIPYPORVVWFATPLP	264
		WNRDNFFEGVKRLAFRIKDYLEKEGIYIPFOLDVHFDEEFIRVWKHEGSENK	264
		TKTT VWAENLNI REDINYKI I BILGAEGVQ FAYPGQMVVVKQKHESDQFQVNLNKE	366
		AKIBDGIFNVRSELIERIKNALDANRIEIPFNKLDISINKQDSSKZ	275
		VRNMGFDYYLNAVDBINLKIKEBFEKEGIEMAFPTYTVYLEKDN	350
		IKN <mark>SRYNG</mark> YQKYISTINEVNLKIKEEFDRKGIEFAFPTYTLYLKRDD	361
		A <mark>P</mark> SBKWFDVRIEILKKVKKALDEA <mark>GIEIPFPQH</mark> VNWFABBLK	328
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S_typh Ctep		286	
S_typh Ctep P fur	T <mark>G</mark> Z	286 285	
S_typh Ctep P fur	T <mark>G</mark> Z	286 285 302	
S_typh Ctep P_fur S_ent	T <mark>G</mark> Z	286 285 302 270	
S_typh Ctep P_fur S_ent Y_pestis Buchn	T@Z	286 285 302 270 286	
S_typh Ctep P_fur S_ent Y_pestis Buchn	T@Z	286 285 302 270 286 289	
S_typh Ctep P_fur S_ent Y_pestis Buchn Ed ict	T@2	286 285 302 270 286 289 305 286	
S_typh Ctep P_fur S_ent Y_pestis Buchn Ed_ict V chol	T <mark>G</mark> Z	286 285 302 270 286 289 305 286 287	
S_typh Ctep P_fur S_ent Y_pestis Buchn Ed_ict V_chol C_perf	TCZ	286 285 302 270 286 289 305 286 287 271	
S_typh Ctep P_fur S_ent Y pestis Buchn Ed_ict V_chol C_perf Synech	T G 2	286 285 302 270 286 289 305 286 287 271 271	
S_typh Ctep P_fur S_ent Y_pestis Buchn Ed_ict V_chol C_perf Synech Pseud aer	T <mark>@</mark> Z	286 285 302 270 286 289 305 286 287 271 296	
S_typh Ctep P_fur S_ent Y_pestis Buchn Ed_ict V_chol C_perf Synech Pseud_aer Xy fast	TGZ	286 285 302 270 286 289 305 286 287 271 296 278 305	
S_typh Ctep P_fur S_ent Y_pestis Buchn Ed_ict V_chol C_perf Synech Pseud_aer Xy_fast Neisser	DVADES	286 285 302 270 286 289 305 286 287 271 296 278 305 282	
S_typh Ctep P_fur S_ent Y_pestis Buchn Ed_ict V_chol C_perf Synech Pseud_aer Xy_fast Neisser A fulg	TG2	286 285 302 270 286 289 305 286 287 271 296 278 305 298	
S_typh Ctep P_fur S_ent V_pestis Buchn Ed_ict V_chol C_perf Synech Pseud_aer Xy fast Neisser A_fulg Fusobac	TGZ DVADES ANVEGKEERRQA-	286 285 302 270 286 289 305 286 287 271 296 278 305 282 282 283	
S_typh Ctep P_fur S_ent Y_pestis Buchn Ed_ict V_chol C_perf Synech Pseud_aer Xy_fast Neisser A_fulg Fusobac Methanos	TGZ DVADES ANVEGKEBRRQA- GHPEGNEGVINPEGRGVN	286 285 302 270 286 289 305 286 287 271 296 278 305 282 283 283	
S_typh Ctep P_fur S_ent Y_pestis Buchn Ed_ict V_choll C_perf Synech Pseud_aer Xy_fast Neisser A_fulg Fusobac Methanos Agro_tum	TGZ	286 285 302 270 286 289 305 286 287 271 296 296 278 305 292 298 293 283 283	
S_typh Ctep P_fur S_ent V_pestis Buchn Ed_ict V_chol C_perf Synech Pseud_aer Xy fast Neisser A_fulg Fusobac Methanos Agro_tum Pyrobac	TGZ DVADES ANVEGKEERRQA- GHPEGNEGVLNPEGRGVN ANLKA	286 285 302 270 286 289 305 286 287 271 296 278 305 282 283 282 283 281 308 273	
S_typh Ctep P_fur S_ent Y_pestis Buchn Ed_ict V_chol C_perf Synech Pseud_aer Xy_fast Neisser A_fulg Fusobac Methanos Agro_tum Pyrobac Thermot	TGZ DVADES ANVEGKEERRQA- GHPEGNEGVLNPEGRGVN ANLKA	286 285 302 270 286 289 305 286 287 271 296 278 305 282 283 282 283 283 283	
S_typh Ctep P_fur S_ent V_pestis Buchn Ed_ict V_chol C_perf Synech Pseud_aer Xy_fast Neisser A_fulg Fusobac Methanos Agro_tum Pyrobac Thermot B_sub	TG2 TG2 DVADES ANVEGKE	286 285 302 270 286 289 305 286 287 271 296 278 305 282 293 283 281 308 273 269 268 371	
S_typh Ctep P_fur S_ent Ed_ict V_chol C_perf Synech Pseud_aer Xy_far Neisser A_fulg Fusobac Methanos Agro_tum Pyrobac Thermot B_sub He_lico	TGZ DVADES ANVEGKE ANVEGKE GHPEGNEGVLNPEGRGVN ANLKA S	286 285 302 270 286 289 305 286 287 271 296 278 305 282 283 283 281 308 273 269 269 268 371	
S_typh Ctep P_fur S_ent Y_pestis Buchn Ed_ict V_chol C_perf Synech Pseud_aer Xy_fast Neisser A_fulg Fusobac Methanos Agro_tum Pyrobac Thermot B_sub Helico Mjanl	TGZ DVADES DVADES ANVEGKEERRQA GHPEGNEGVLNPEGRGVN ANLKA SERRQA	286 285 302 270 286 289 305 286 287 271 296 278 305 282 283 283 283 281 308 273 269 269 269 269 269 278 305 282 283 281 305 282 283 281 305 285 305 285 305 285 305 285 305 286 305 286 305 286 305 286 296 271 296 271 296 271 296 287 287 287 287 296 271 296 287 287 296 287 296 278 305 282 283 283 283 281 305 282 283 283 281 305 282 283 283 283 283 281 305 282 283 283 283 283 283 283 283	
S_typh Ctep P_fur S_ent Y_pestis Buchn Ed_ict V_chol C_perf Synech Pseud_aer Xy_fast Neisser A_fulg Fusobac Methanos Agro_tum Pyrobac Thermot B_sub Helico Mjan1 Mjan2	TG2 DVADES ANVEGKE ERRQA GHPEGNEGVLNPEGRGM ANLKA S EKERA	286 285 302 270 286 289 305 286 287 271 296 278 305 282 283 281 308 273 269 268 371 275 350 350	
S typh Ctep P fur S ent V pestis Buchn Ed ict V chol C perf Synech Pseud aer Xy fast Neisser A fulg Fusbac Methanos Agro_tum Pyrobac Thermot B sub Helico Mjan1 P hor	TG2 	286 285 302 270 286 289 305 286 287 271 296 278 305 282 283 283 283 281 308 273 269 269 269 269 268 371 308	
S typh Ctep P fur S ent V pestis Buchn Ed ict V chol C perf Synech Pseud aer Xy fast Neisser A fulg Fusbac Methanos Agro_tum Pyrobac Thermot B sub Helico Mjan1 P hor	TG2 DVADES ANVEGKE ERRQA GHPEGNEGVLNPEGRGM ANLKA S EKERA	286 285 302 270 286 289 305 286 287 271 296 278 305 282 283 281 308 273 269 268 371 275 350 350	

Figure S2 MULTIPLE SEQUENCE ALIGNMENT of yggB Page 4 of 4

Abbreviation	Species	Ge	nbank ID
yggb S_typh Ctep P_fur M_tub S_ent Y_pestis Buchn Ed_ict V_chol C_perf Synech Pseud_aer Xy_fast Neisser A_fulg Fusobac Methanos Agro_tum Pyrobac Thermot B_sub Helico Mjan2 Mjan1	E. coli Salmonella typhimurium Chlorobium tepidum Pyrococcus furiosus Mycobacterium tuberculosis Salmonella enterica Yersinia pestis Buchnera sp. Edwardsiella ictaluri Vibrio cholerae Clostridium perfringens Synechocystis sp. Pseudomonas aeruginosa Xylella fastidiosa Neisseria meningitidis Archaeoglobus fulgidus Fusobacterium nucleatum Methanosarcina acetivorans Agrobacterium tumefaciens Pyrobaculum aerophilum Thermotoga maritima Bacillus subtilis Helicobacter pylori Methanococcus jannaschii		16130825 16767368 21648046 18977188 15609571 16761848 16121224 15617051 2708660 15640507 18309195 16331560 15599590 15837859 15793305 11499141 19703954 20090570 15888392 18313911 15644311 2633299 4155504 1591775 1590923
P_hor	Pyrococcus horikoshii	gi	3256727

Fig. S2. Sequence alignment of MscS homologs. This figure was prepared using ClustalX.