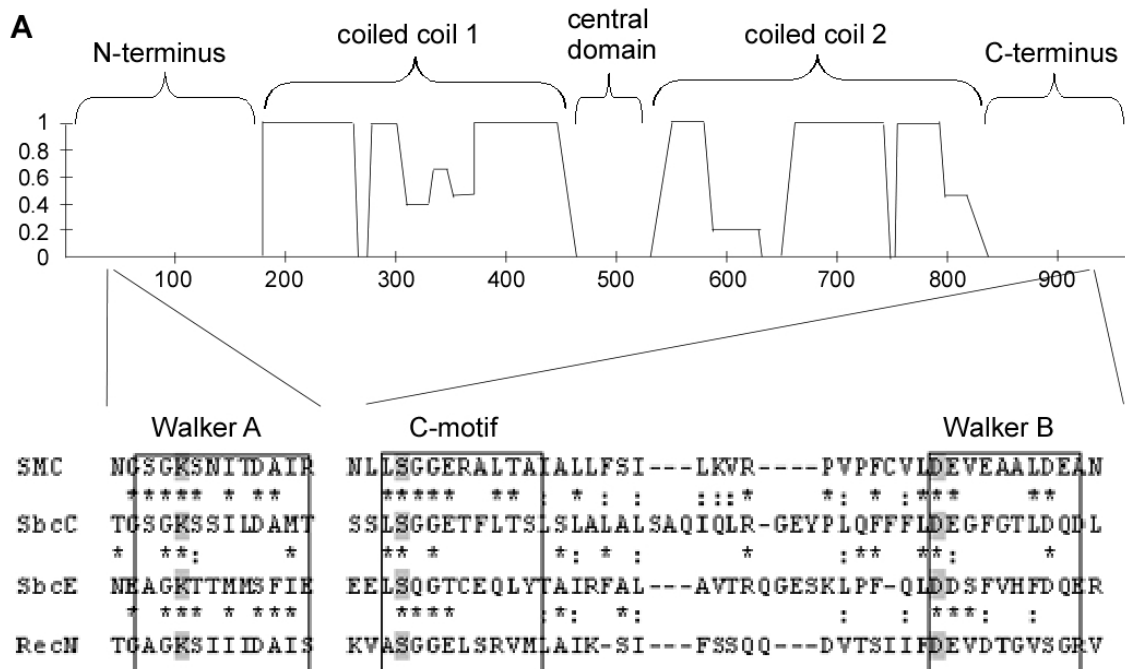


Supplementary material

Suppl. FigureS 1



B

central domain:

470

GMLFIVLFLSLQQWIPAI SFGAALIVYWLVS GKSSSRNSRETRQPM TDISPAEAEMLRREAL

++ SL P + + V +++ S ++ + + + E +

Fig. 1 A) Structure of SbcE according to sequence analysis. Coiled coil prediction shows the two extended heptad repeat regions that are separated by a central domain of unknown function. Sequence alignment (stars indicate identical residues between SMC and the other 3 SMC-like proteins from *B. subtilis*, colon indicates similar residues) indicating Walker A motif in the N-terminus and Walker B motif and the C-motif (boxed) within the C-terminus. Grey shaded residues have been shown to be essential for ATP binding and/or hydrolysis in SMC proteins. B) Sequence of the central (non-coiled coil) domain, conserved positions are indicated by "+" and highly conserved residues by the corresponding letter. The invariant proline is written in bold.