
STRUCTURAL
BIOLOGY

**Volume 75 (2019)**

**Supporting information for article:**

# Crystal structures of the *Bacillus subtilis* prophage lytic cassette proteins XepA and YomS

**Stefanie Freitag-Pohl, Andrius Jasilionis, Maria Håkansson, L. Anders Svensson, Rebeka Kovačič, Martin Welin, Hildegard Watzlawick, Lei Wang, Josef Altenbuchner, Magdalena Płotka, Anna Karina Kaczorowska, Tadeusz Kaczorowski, Eva Nordberg Karlsson, Salam Al-Karadaghi, Björn Walse, Arnthór Aevarsson and Ehmke Pohl**

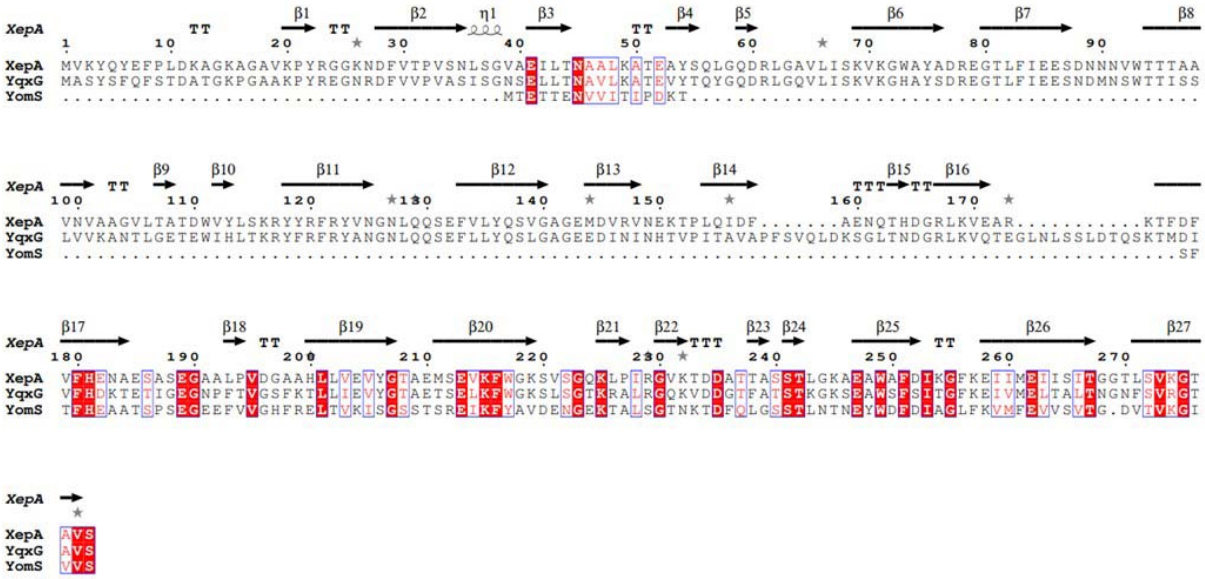


**Figure S1** Sequence alignment of the putative lysins XepA, YomS and YqxG. The secondary structure annotation in the top line is based on the crystal structure of XepA presented here.

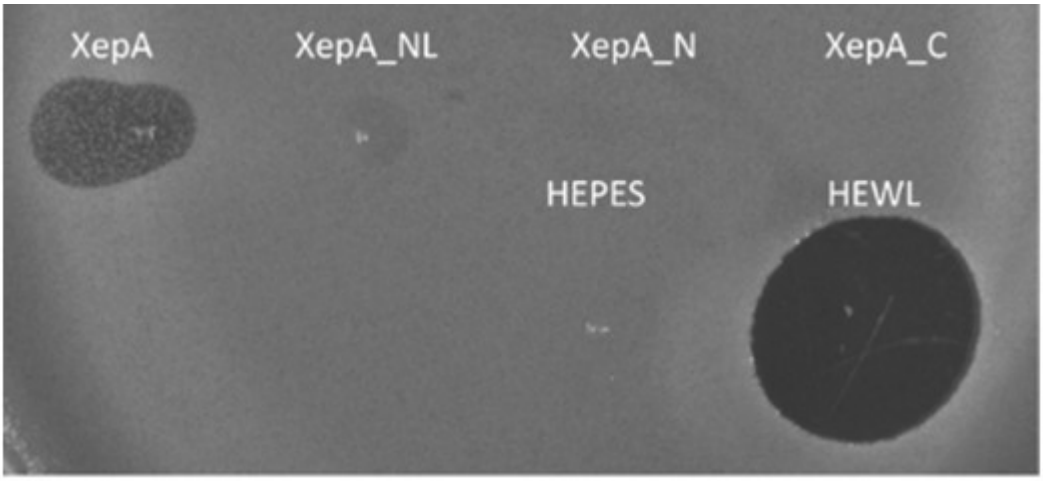


**Figure S2** Cytotoxicity of XepA truncated variants. *In vivo* assays of XepA truncated variants XepA_NL, XepA_N and XepA_C on *Bacillus megaterium* ATCC 14581. Wild-type XepA and HEWL served as positive controls, HEPES buffer (20 mM, pH 7.4) was used as a negative control. Out of three truncated XepA variants tested, only XepA_NL shows minimal activity.

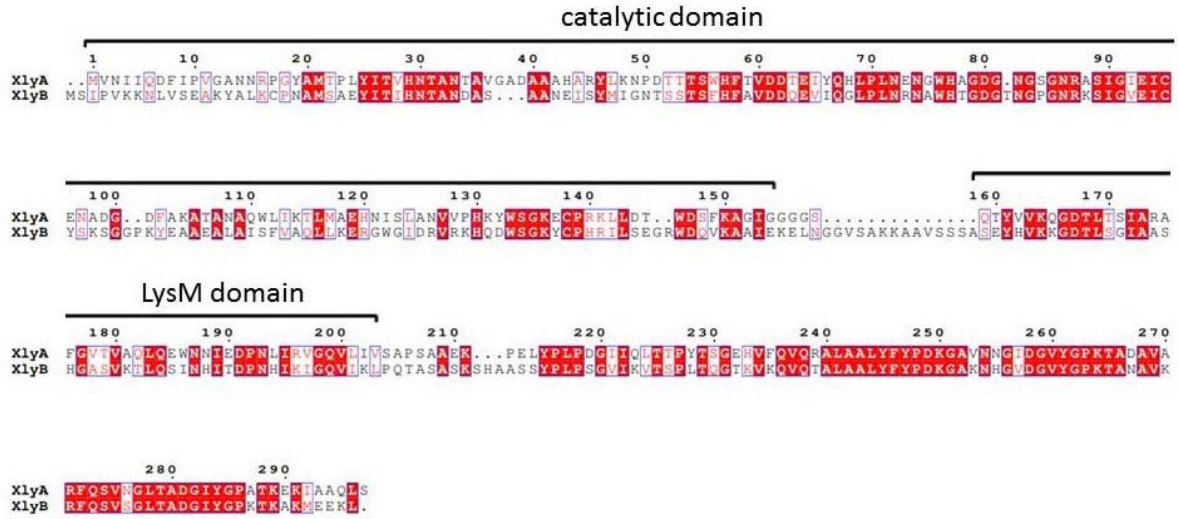


**Figure S3** Sequence alignment of the lysins XlyA and XlyB with ClustalW (Larkin et al. 2007) and ESPript (Robert & Gouet, 2014). The residues corresponding to the cell wall binding LysM domain are 159 to 203 (XlyA) and 177 to 222 (XlyB).

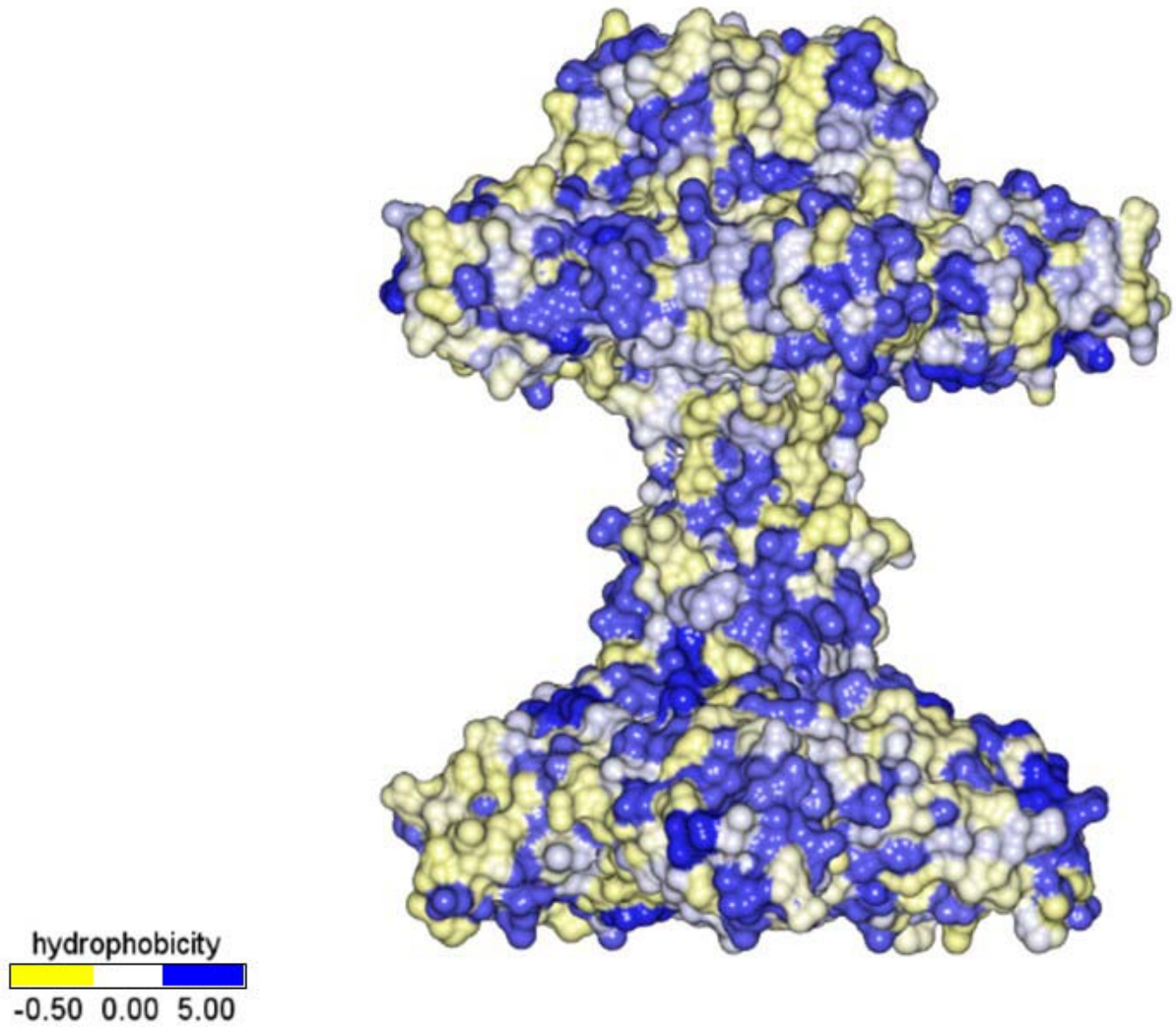


**Figure S4** Surface representation of hydrophobicity of the XepA pentamer for its side view (CCP4mg) shows that the linker region is not entirely hydrophobic and thus does not resemble a trans-membrane region.