Identification of the first endolysin Cell Binding Domain (CBD) targeting Paenibacillus larvae

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Fig. S1 Colour-coded scheme for amino acid conservation of the multiple sequence alignment of all the *Paenibacillus* phage lysins (15 lysins from 25 proteomes) using Praline ¹⁸. The scoring scheme works from 0 for the least conserved alignment position, up to 10 for the most conserved alignment position.