

## Supplementary material

Figure S1

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                                     1   5   10  15  20   25  30  35
KMV45                               MNKPLRGAALAAALAGLVALEGGSETTAYRDIAGVPT
21 endolysin                       MPPSLRKAVAAAIGGGAIASVLTGTPSGNDGLEGVSYIPYKDIVGVWT
P1 endolysin                        MKGKTAAGGGAICAIIVMITIVMGNGNVRTNQAGLELIGNAEGCRRDPYMCPPAGVWT
ERA103 endolysin                   MSVKKALAGGACSLALVTASFFGIVTDKVRISQEGLEHLIDCEGCKRQAYKDGGAGVPT
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### Sequence alignment of the N-termini of KMV45, phage 21, phage P1 and phage ERA103 endolysin.

The N- and H-region of the signal-arrest-release (SAR) domain are colored red and blue, respectively. Catalytic residues are highlighted in yellow. The cysteine residues in the SAR domain which are involved in the disulfide isomerization (P1 endolysin) or disulfide caging (ERA103 endolysin) upon membrane release are underlined. Five other endolysins encoded by the taxonomic group of the “phiKMV-like” phages (LUZ19, LKD16, phiKF77, PT2 and PT5) have an identical terminus as KMV45 and have an overall protein sequence identity above 95%.