

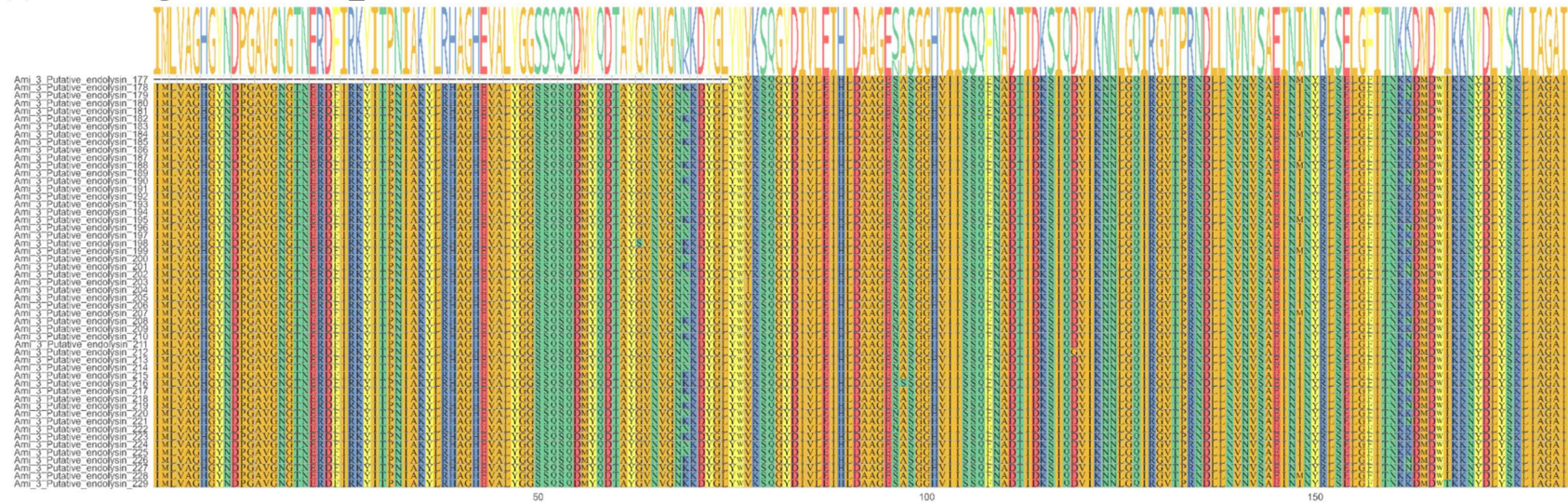
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Sequence logo and sequence alignment for the endoysin protein family. The sequence logo at the top shows the conservation of residues across the 100 amino acid positions. Below it, a sequence alignment of 72 putative endoysin sequences is shown, with residues color-coded to match the sequence logo. The sequences are numbered 1 to 72 on the left. The alignment shows high conservation across most positions, with some variations in the C-terminal region.

Figure S1. Multi-alignment of putative endolysins belonging to group 1 based on amino acids.

(a) Multi-alignment of the cysteine, histidine-dependent amidohydrolases/peptidases domain (Accession: pfam05257 and sequence identity: 83.5%). (b) Multi-alignment of the Ami_2 domain (Accession: smart00644 and sequence identity: 82.4%). (c) Multi-alignment of the SH3_5 domain (Accession: pfam08460 and sequence identity: 75.8%).

(a) Multi-alignment of Ami_3 domain



(b) Multi-alignment of SH3b domain

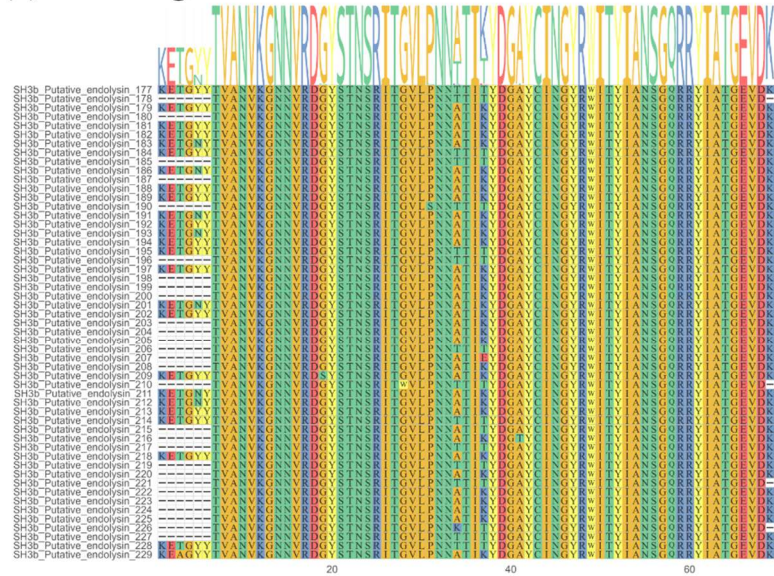


Figure S2. Multi-alignment of putative endolysins belonging to group 3 based on amino acids. (a) Multi-alignment of the Ami_3 domain (Accession: pfam01520 and sequence identity: 95.1%). (b) Multi-alignment of the SH3_b domain (Accession: smart00287 and sequence identity: 88.4%).

(a) NCCP 16830



(b) NCCP 14567



(c) NCCP 14754



(d) KVCC-BA0500624



Figure S3. Antibiotic susceptibility test of *Staphylococcus aureus* strains. Cells of each *S. aureus* strain were spread on Mueller-Hinton agar, and antibiotic discs were placed on the plates. FOX, cefoxitin, 30 μ g; OX, oxacillin, 1 μ g; P, penicillin, 10 μ g; E, erythromycin, 15 μ g; DA, clindamycin, 2 μ g; Chloramphenicol, 30 μ g.