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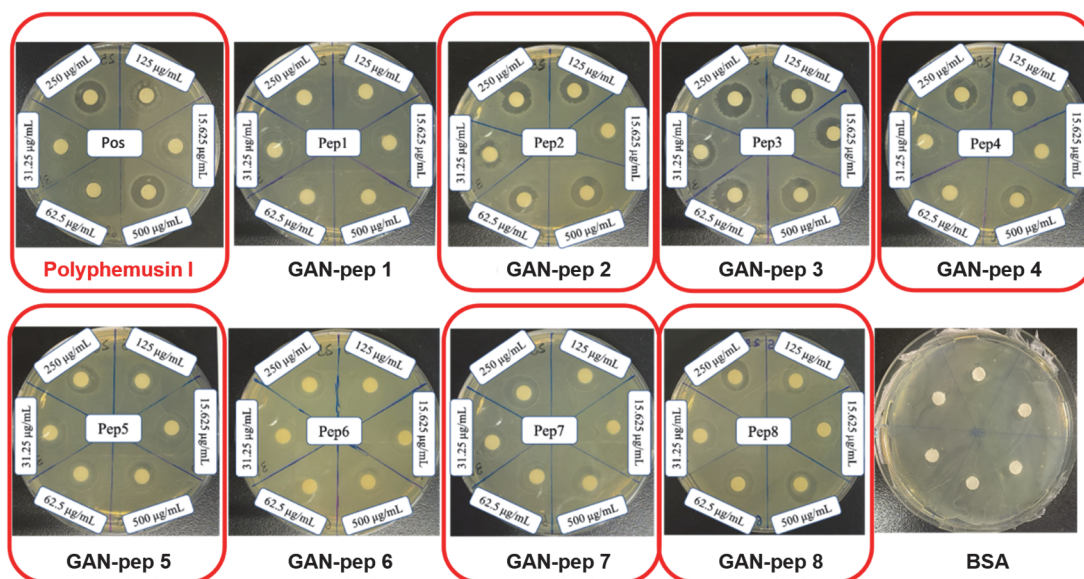


Figure S1. Growth inhibition test against *E. coli* with peptides at different concentrations. Peptides are highlighted with red rectangles if inhibition zones occur around the disks. Here, polyphemus I is a known AMP with broad-spectrum activity against various microorganisms as a positive control.

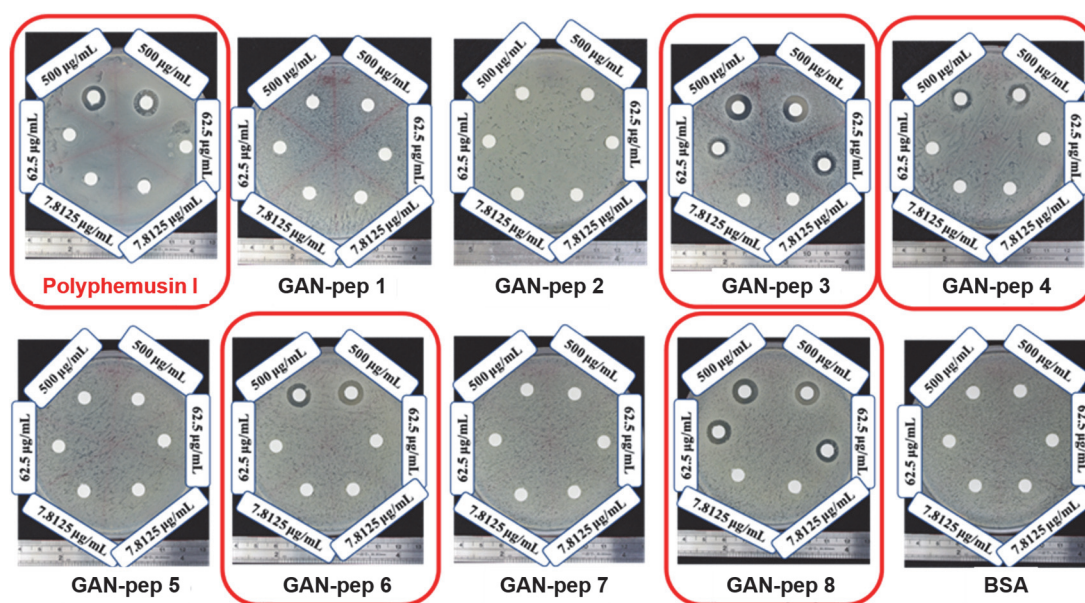


Figure S2. Growth inhibition test against methicillin-susceptible *S. aureus* (MSSA) with peptides at different concentrations. Peptides are highlighted with red rectangles if inhibition zones occur around the disks. Here, polyphemusin I is a known AMP with broad-spectrum activity against various microorganisms as a positive control.

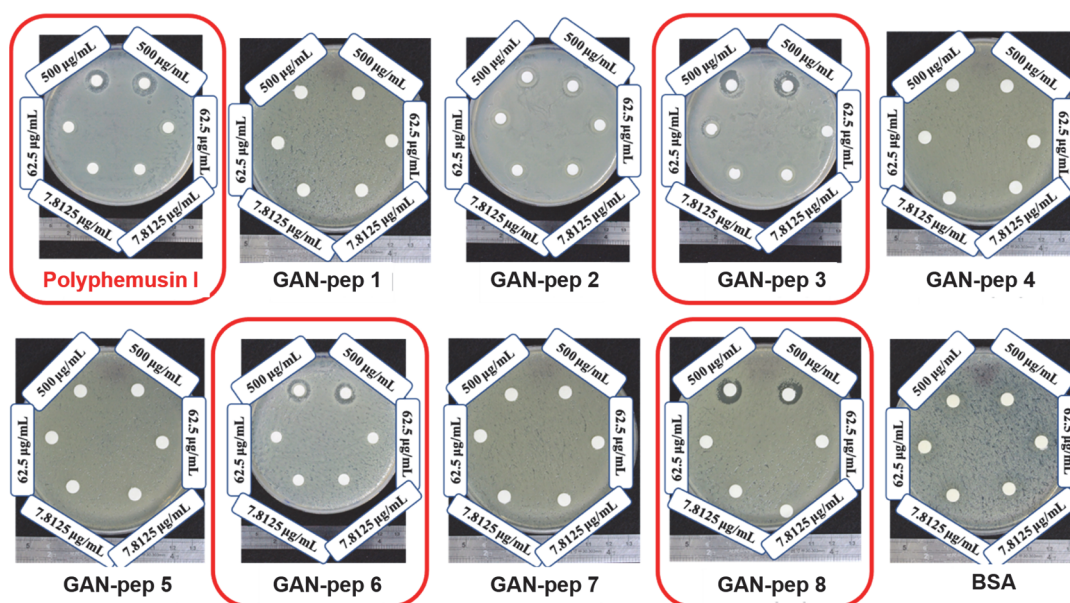


Figure S3. Growth inhibition test against methicillin-resistant *S. aureus* (MRSA) with peptides at different concentrations. Peptides are highlighted with red rectangles if inhibition zones occur around the disks. Here, polyphemusin I is a known AMP with broad-spectrum activity against various microorganisms as a positive control.

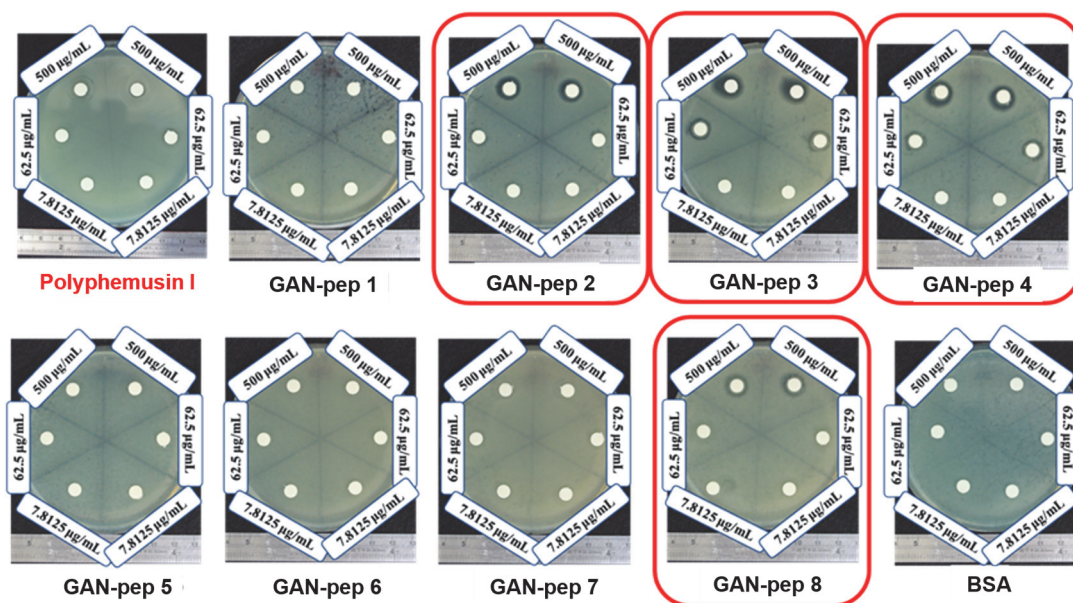


Figure S4. Growth inhibition test against carbapenem-susceptible *P. aeruginosa* with peptides at different concentrations. Peptides are highlighted with red rectangles if inhibition zones occur around the disks. Here, polyphemusin I is a known AMP with broad-spectrum activity against various microorganisms.

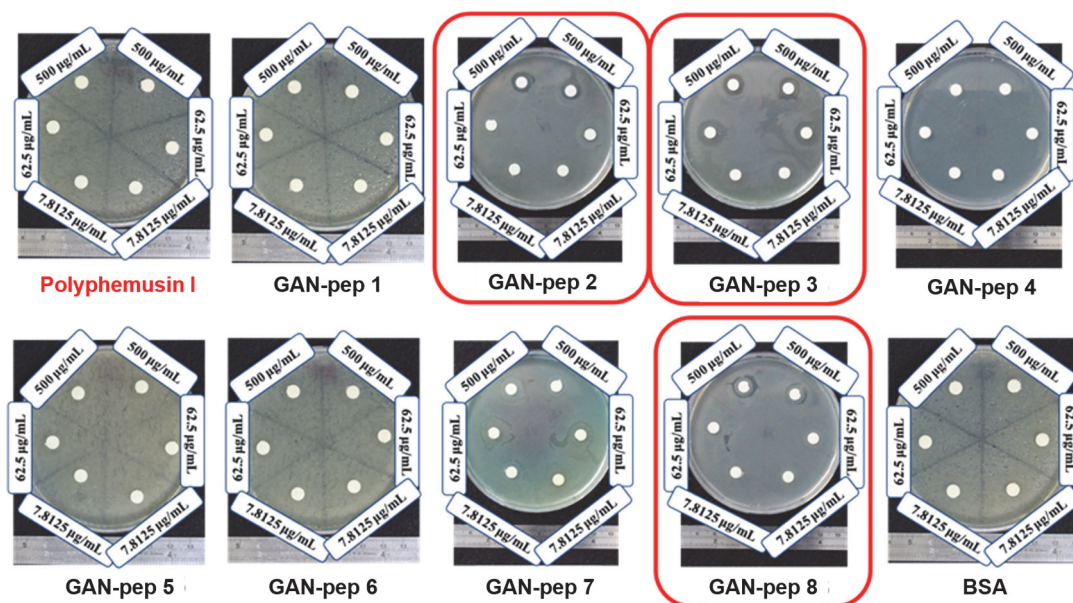


Figure S5. Growth inhibition test against carbapenem-resistant *P. aeruginosa* with peptides at different concentrations. Peptides are highlighted with red rectangles if inhibition zones occur around the disks. Here, polyphemusin I is a known AMP with broad-spectrum activity against various microorganisms.

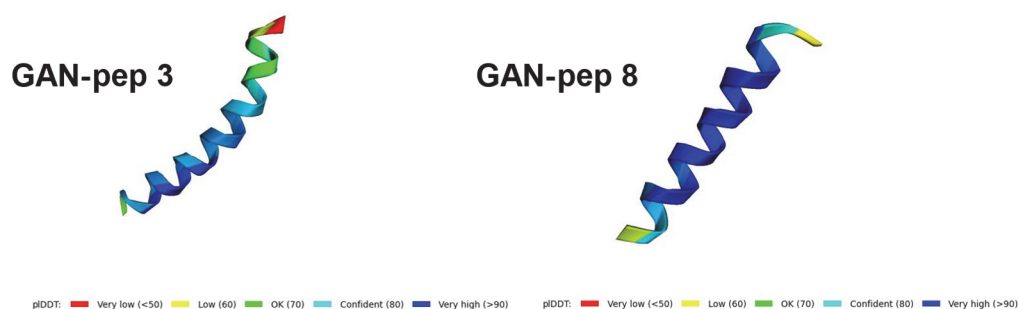


Figure S6. The structure prediction in alphafold2 and GAN-pep 3 and 8 show the helix structures. pLDDT stands for predicted local distance difference test score in AlphaFold2. It is a measure used to evaluate the accuracy and reliability of protein structure predictions generated by deep learning models. pLDDT scores range from 0 to 100, with higher scores represented in cyan and blue, indicating better model accuracy.