

Title: DeepQSP: Identification of Quorum Sensing Peptides Through Neural Network Model

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Abstract: [Quorum Sensing](#) Peptides (QSP) are [small molecules](#) crucial for microbial communication, enabling bacterial populations to coordinate behaviors such as [biofilm](#) formation and virulence. The identification of QSP is vital for understanding these [biological processes](#). While existing clinical and lab-based methods are available, they can be costly and time-consuming. This study introduces DeepQSP, a novel technique for QSP identification, which combines Latent Semantic Analysis (LSA), a word embedding feature extraction method, with classical amino acid-based extraction Pseudo [Amino Acid Composition](#) (PAAC), and a convolutional [neural network](#) (CNN) classifier. The DeepQSP model was evaluated using a dataset of 440 [peptide sequences](#), achieving impressive performance metrics: 0.9697 accuracy, 0.9655 sensitivity, 0.9730 specificity, and a Matthews [correlation coefficient](#) (MCC) of 0.9385. The LSA combined with PAAC improves peptide sequence representation, while the CNN effectively captures complex patterns, leading to accurate QSP identification. These quantified results demonstrate the effectiveness of the DeepQSP method, offering a powerful tool for advancing the study of [microbial interaction](#) and quorum sensing. The enhanced identification of QSPs is critical for microbiology and [bioengineering](#), aiding in the understanding of cell-to-cell communication in [microorganisms](#).

Key words: Quorum sensing peptide Convolutional neural network Latent semantic analysis Microorganisms Bioengineering

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