

## Hybrid Transformer and Neural Network Configuration for Protein Classification Using Amino Acids

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**Abstract :** This study introduces a hybrid machine learning model for classifying proteins, developed to address the complexities of protein sequence and structural analysis. Utilizing an architecture that combines a lightweight transformer with a concurrent neural network, the hybrid model leverages both sequential and intrinsic physical properties of proteins. Trained on a comprehensive dataset from the Research Collaboratory for Structural Bioinformatics Protein Data Bank, the model demonstrates a classification accuracy of 95%, outperforming existing methods by at least 15%. The high accuracy achieved demonstrates the potential of this approach to innovate protein classification, facilitating advancements in drug discovery and the development of personalized medicine. By enabling precise protein function prediction, the hybrid model allows for specialized strategies in therapeutic targeting and the exploration of protein dynamics in biological systems. Future work will focus on enhancing the model's generalizability across diverse datasets and exploring the integration of more machine learning techniques to refine predictive capabilities further. The implications of this research offer potential breakthroughs in biomedical research and the broader field of protein engineering.

**Keywords :** amino acids, deep learning, enzymes, neural networks, protein classification, proteins, transformers

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