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# A DEEP LEARNING FRAMEWORK FOR ACCURATE IDENTIFICATION OF ANTIFUNGAL PEPTIDES USING HYBRID FEATURE EMBEDDINGS

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**Abstract**

*Antifungal peptides (AFPs) represent a vital class of therapeutic agents capable of combating resistant fungal infections through multi-mechanistic action. However, their experimental identification remains costly and time-consuming. We propose a novel deep learning framework that integrates both handcrafted and automatically learned features to accurately identify AFPs. Specifically, our model extracts and fuses sequence descriptors such as amino acid composition (AAC), dipeptide composition (DPC), and pseudo amino acid composition (PseAAC) with deep contextual Embeddings from a pertained ProtT5 transformer, evolutionary profiles from BLOSUM62, and physicochemical descriptors via composite property profiles (CPP). A co-attention-based fusion mechanism is employed to enhance the representation power by dynamically weighing inter-feature relationships. The fused features are evaluated using classifiers including Extra Trees (ET), Multilayer Perceptron (MLP), and Convolutional Neural Network (CNN).*

*The model was trained and validated on benchmark datasets (Antifp_Main and Deep-AFPpred) using five-fold cross-validation and independent test evaluation. The proposed hybrid model, particularly the MLP classifier, outperformed all baselines, achieving a top accuracy of 96.2%, AUC of 0.99, and MCC of 0.93. This demonstrates the utility of hybrid multi-view learning and co-attention fusion in improving AFP identification. The framework is generalizable, scalable, and can be readily adopted in computational antifungal drug discovery pipelines.*

*Index Terms– AAC (Amino Acid Composition), AFP (Antifungal Peptides), BLOSUM62 (Blocks Substitution Matrix), CNN (Convolutional Neural Network), CPP (Composite Physicochemical Properties), DPC (Dipeptide Composition), ET (Extra Trees Classifier), MLP (Multilayer Perceptron), ProtT5 (Protein Transformer Embedding), PseAAC (Pseudo Amino Acid Composition).*

## I. INTRODUCTION

Fungi can make people very sick and sometimes kill them. More and more people around the world are contracting fungal infections, which can be very dangerous. The World Health Organization (WHO) reports that more than 150 million people suffer from serious fungal infections annually, leading to over 1.5 million deaths. This is a very high number of deaths, almost as many as those caused by tuberculosis and more than those caused by malaria. One of the main reasons behind this burden is the limitation of current antifungal drugs. - Fungi can become resistant to treatments easily. - Treatments that are not absorbed well by the body have harmful effects, take a long time, and do not work well because fungi change quickly. The rise of drug-resistant

fungal strains has made treatment even harder, highlighting the urgent need for new and safer antifungal options.

Antifungal peptides (AFPs) are becoming more popular as a possible option. - Small proteins that are made by nature and have 10 to 100 amino acids can fight fungi by damaging their cell walls, interfering with their cell functions, or helping the host's immune system. - Fungi are killed by small proteins that nature makes and have 10 to 100 amino acids. These proteins can harm the fungi's cell walls, stop their cell functions, or help the host's immune system. - Fungi are harmed by small AFPs, which belong to a larger family called antimicrobial peptides (AMPs), which also fight bacteria, viruses, and cancer cells. They have many benefits—they can do many things, and they cause fewer effects, high specificity, and lower risk of resistance—making AFPs strong candidates for the next generation of antifungal therapies.

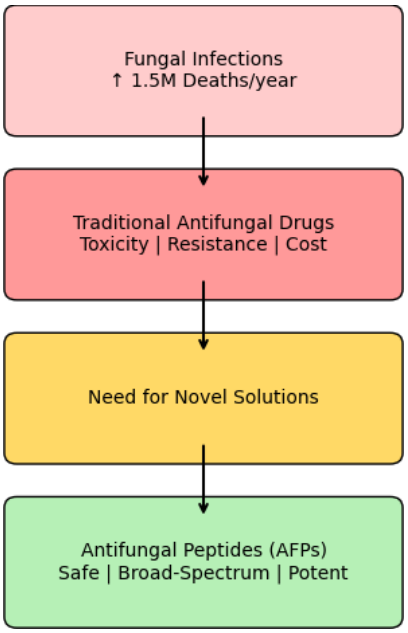


**Fig. 1. The challenge of Fungal Infection.**

Identifying new antifungal peptides (AFPs) through wet-lab experiments alone is often slow, expensive, and labor-intensive. To address this challenge, computational approaches have become an essential first step for pre-screening candidate peptides before experimental testing.

Earlier computational methods primarily relied on machine learning (ML) models trained on manually crafted features. For example, the iAFP-ET model used amino acid composition (AAC), dipeptide composition (DPC), and pseudo-amino acid composition (PseAAC) to describe peptides and applied an Extra Trees Classifier to distinguish AFPs from non-AFPs. While these models performed reasonably well, they often struggled to capture the deeper context and sequence-level semantics of peptides.

The emergence of deep learning (DL) has revolutionized protein sequence modeling by enabling models to learn high-level representations directly from raw data. Leveraging large protein datasets and pre-trained language models like ProtT5, researchers have developed advanced frameworks such as AFP-MFL, which combine semantic, evolutionary, and physicochemical information. These approaches have led to improved accuracy and better generalization across datasets.

Still, both ML- and DL-based methods come with limitations. Handcrafted features often miss global context and positional dependencies, while deep learning embeddings are typically high-

dimensional and can lead to overfitting if not properly regularized or integrated. Moreover, only a few studies have attempted to combine the interpretability of handcrafted features with the expressive power of deep embeddings.

Our motivation stems from these gaps. We propose a hybrid framework that unifies both paradigms—integrating handcrafted features (AAC, DPC, PseAAC) with semantic embeddings (ProtT5), evolutionary profiles (BLOSUM62), and physicochemical descriptors (CPP). To effectively integrate these diverse features, we introduce a co-attention fusion mechanism that selectively emphasizes the most informative signals across multiple feature types.

The resulting model is evaluated on multiple benchmark datasets (such as Antifp_Main and Deep-AFPpred) using rigorous cross-validation and compared with state-of-the-art baselines. By leveraging both engineered and learned features, and applying ensemble/deep classifiers like Extra Trees, MLPs, and CNNs, our method achieves significant improvements in accuracy, sensitivity, specificity, AUC, and MCC. In doing so, it sets a new benchmark for AFP prediction and highlights the potential of hybrid modeling in peptide research.

## II. LITERATURE REVIEW

Fungal infections pose a growing global health threat, contributing to over 1.5 million deaths annually—an alarming statistic rivaling tuberculosis and surpassing malaria in mortality rates [1][2]. The rise in resistant fungal pathogens, coupled with the limitations of existing antifungal agents—such as toxicity, low bioavailability, and high resistance rates—necessitates the development of alternative therapeutic strategies [3]. Antifungal peptides (AFPs), a subclass of antimicrobial peptides (AMPs), have emerged as a promising solution owing to their membrane-disruptive action, low toxicity, specificity, and reduced resistance induction [4][5]. Despite their potential, identifying novel AFPs using traditional experimental techniques is time-intensive and costly. Computational methods are thus indispensable for pre-screening AFP candidates. Initial computational techniques focused on machine learning (ML) models built on handcrafted sequence features. While effective to some extent, these models were unable to capture the deep semantic context and structural dependencies in peptide sequences [6].

### *A. Traditional Models Based on Handcrafted Features*

The existing work in AFP prediction was the iAFP-ET model [4], which utilized handcrafted sequence features such as:

- Amino Acid Composition (AAC)
- Dipeptide Composition (DPC)
- Pseudo-Amino Acid Composition (PseAAC)

These descriptors effectively captured sequence-level characteristics and were fed into an Extra Tree Classifier to distinguish AFPs from non-AFPs. The model achieved decent performance on standard datasets, demonstrating the power of interpretable, handcrafted features. However, its reliance on shallow sequence statistics limited its ability to learn higher-order or contextual patterns, which are critical for complex biological phenomena.

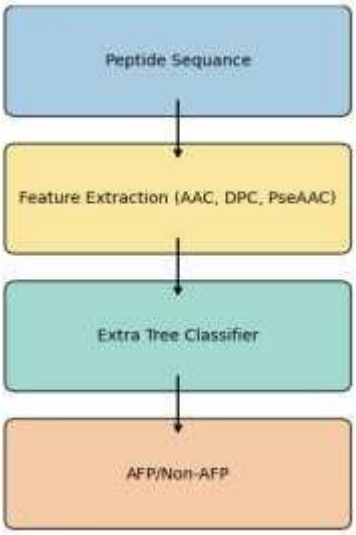


**Fig. 2.** ***iAFP-ET Architecture.***

*B. Deep Learning and Feature Embedding Approaches*
Recent advances in deep learning and protein language modeling have paved the way for more robust sequence analysis. Models such as AFP-MFL [18] have introduced multi-view learning frameworks by combining multiple feature representations, including:

- Transformer-based Embeddings (ProtT5)
- Evolutionary profiles (BLOSUM62)
- Physicochemical properties (CPP)

AFP-MFL demonstrated that integrating semantic and structural information enhances generalization and predictive power. By utilizing pre-trained protein models like ProtT5, AFP-MFL leveraged transfer learning from massive protein corpora to capture rich, contextual features. While promising, this model primarily focused on feature concatenation without using any attention mechanism to weigh or refine feature importance dynamically.

***C. AFP-MFL multi-view feature learning***
AFP-MFL is a multi-view feature learning approach that explicitly combines semantic embeddings from a pre-trained protein language model with evolutionary and physicochemical representations. Instead of relying solely on handcrafted descriptors, AFP-MFL uses ProtT5-derived contextual embeddings (global average pooling) to capture long-range sequence semantics, and fuses them with compact evolutionary profiles (e.g., BLOSUM-derived averages) and physicochemical descriptors. The fusion is performed in a joint learning framework so that downstream fully connected layers can exploit complementary signals. The study reports that contextual embeddings significantly improve sensitivity and AUC compared with handcrafted features alone, and emphasizes that multi-view modeling reduces overfitting on small AFP datasets by leveraging orthogonal information sources. This work is a direct methodological peer to the current study because both argue for combining ProtT5 embeddings with engineered features to obtain robust AFP predictors.

*D. Deep-AFPpred transfer learning + 1D-CNN-BiLSTM* Deep-AFPpred, a transfer-learning-based pipeline that uses pre-trained sequence embeddings and a hybrid 1D-CNN + BiLSTM encoder to model local residue motifs and sequential dependencies. The CNN layers extract local n-gram motif signatures while the

BiLSTM captures contextual order and long-range dependencies; the model uses transfer learning from protein sequence embedding methods (seq2vec/other pretraining) to boost generalization on limited AFP labeled data. DeepAFPpred reported strong performance on standard AFP benchmarks and emphasized robust calibration on independent test sets. Its hybrid CNN-RNN architecture provides evidence that stacking local and sequential operators is effective for AFP detection, particularly when combined with transfer-learned embeddings. [31] Important practical lessons from this paper include careful regularization, balanced negative sampling, and using independent test splits to avoid optimistic performance estimates.

*E. DeepAFP composition mining with deep networks*

DeepAFP, a Protein Science paper offering a comprehensive deep-learning framework primarily focused on mining composition and residue-level composition signals through deep architectures. DeepAFP emphasizes engineered composition descriptors (AAC, DPC, higher-order k-mer compositions) and applies tailored deep architectures to exploit hierarchical composition patterns. The study systematically ablates combinations of compositional descriptors and network architectures, showing that composition-focused deep nets can match or exceed several prior methods that rely on larger contextual embeddings, especially for peptides within certain length ranges. The paper also provides an openly accessible implementation and independent test evaluations, making it a useful reproducibility benchmark. DeepAFP is relevant to hybrid approaches because it demonstrates that strong performance can still be obtained when composition features are carefully modeled with appropriate deep architectures.

*F. Pretrained protein models as feature extractors: transfer learning evidence*

Lobo and colleagues systematically evaluated pretrained protein language models (ProtBert, ProtT5, ESM, etc.) as general feature extractors for antifungal-activity prediction. Their study shows that embeddings from large protein LMs consistently yield discriminative representations for downstream ML classifiers (SVM, RF, MLP), often improving classifier AUC and MCC versus traditional handcrafted profiles. Crucially, their results highlight that average pooling of residue embeddings provides a strong global representation for short peptides and that combining LM embeddings with physicochemical features yields further gains. They also point out failure modes: pretrained embeddings can be high-dimensional and prone to overfitting without appropriate regularization or dimensionality reduction. This work supports the theoretical foundation of using ProtT5 in your hybrid model and motivates careful fusion (for example, co-attention) and regularization to avoid redundancy between views.[33]

*F. iAFPs-EnC-GA / Ensemble & GA feature-selection studies feature selection and ensembles*

Explored genetic-algorithm guided feature selection combined with stacked ensemble classifiers for AFP identification. These studies demonstrate that judicious feature selection, particularly when many handcrafted descriptors are available, can improve robustness and reduce variance across cross-validation folds. GA-based search finds compact, high-impact descriptor subsets (e.g., specific DPC or PseAAC components), and ensemble stacking (combining RF, ET, and MLP) tends to stabilize predictions across data splits. The main takeaway is that while modern deep embeddings bring representational power, classical approaches that emphasize careful feature selection and ensemble aggregation remain competitive and are especially useful when labeled data are scarce or noisy. For hybrid systems, this implies that adding a feature-selection stage (or L1/dropout) can complement learned fusion mechanisms such as co-attention. [34]

*F. iAFPs-Mv-BiTCN / TCN & transformer hybrid models temporal convolution + self-attention*

iAFPs-Mv-BiTCN, a multi-view architecture that couples bidirectional Temporal Convolutional Networks (TCNs) with self-attention mechanisms to model sequential patterns in peptides. The TCNs capture hierarchical local patterns with dilations and residual connections, while the self-attention blocks reweight TCN features across the sequence. The multi-view input uses

physicochemical descriptors, evolutionary profiles, and LM embeddings, similar to other modern approaches. Their results show improvements in recall and MCC on several AFP datasets, particularly when the model is trained with contrastive or augmentation-based regularizes to mitigate small-sample issues. The BiTCN work is important for comparing architectural choices (TCN vs. CNN vs. BiLSTM) and demonstrates that temporal convolution with attention is an effective alternative to classical CNNs for AFP tasks. [32]

*G. Limitations in Existing Approaches*

Despite significant progress, current antifungal-peptide (AFP) predictors exhibit several structural and practical weaknesses that limit robustness, interpretability, and generalization. Below, we expand on the three core limitations noted earlier and explain their technical roots and practical consequences.

iAFP-ET, limited representational capacity, and poor generalization. Models based primarily on handcrafted descriptors (e.g., AAC, DPC, PseAAC) and tree-based classifiers capture useful, interpretable sequence statistics but are intrinsically shallow. Simple frequency-based descriptors summarize residue counts or local dipeptide frequencies and therefore discard sequence ordering, positional context, and long-range dependencies that are often critical for peptide function. For example, two peptides with identical amino-acid composition but different residue order (permutations) can have very different structural propensities and activity profiles, yet AAC will treat them as identical. Handcrafted feature sets also tend to be high-dimensional (many k-mer and physicochemical features) and sparse for short peptides, which exacerbates the curse of dimensionality and makes the models sensitive to small changes in the training set. Practically, these properties reduce cross-dataset generalization: a model tuned to the statistics of one benchmark (negative sampling strategy, peptide length distribution, source databases) will often underperform on independent test sets with different distributions. Finally, handcrafted pipelines lack transfer learning: they cannot leverage knowledge learned from large protein corpora, so their sample efficiency on limited AFP labels is lower than that of models using pretrained embeddings.

AFP-MFL, naive fusion, and absence of dynamic feature weighting. Approaches that combine pretrained embeddings with engineered features are an important step forward, but simple concatenation or early fusion—while convenient—introduces new problems. Concatenating high-dimensional LM embeddings (e.g., ProtT5) with handcrafted vectors creates extremely large input spaces where redundant or noisy components can drown informative signals. Different modalities have different statistical properties and scales; without modality-specific normalization, attention, or gating, the downstream layers may overfit to the dominant modality (often the highest-variance embedding) while ignoring lower-magnitude but biologically meaningful handcrafted features. Moreover, static fusion cannot model cross-modal interactions; it cannot learn that a particular physicochemical pattern is only informative when co-occurring with a specific ProtT5 subspace. Practically, this manifests as sensitivity to hyperparameters, increased risk of overfitting on small AFP datasets, and reduced interpretability of which modality drives predictions. [36]

Lack of contextual, joint integration of handcrafted and learned features, neither purely handcrafted nor naively fused, hybrid systems fully exploit the complementary strengths of the two views. Handcrafted descriptors provide interpretable, biologically grounded signals (e.g., charge, hydrophobic moment), while learned embeddings encode contextual and higher-order semantic patterns learned from massive protein corpora. A principled integration must therefore (a) enable cross-modal interactions so that contextual embeddings can modulate or be modulated by interpretable descriptors, (b) reduce redundancy and dimensionality without throwing away signal (e.g., via attention, gating, or projection layers), and (c) preserve or expose interpretability where possible (so that biological hypotheses can be derived from model attention/weights). Absent this, models either remain black boxes (hard to trust in drug

discovery workflows) or sacrifice the gains of contextual embeddings. [35]

Broader practical issues dataset and evaluation fragilities Beyond molecular representation and fusion, many studies are constrained by limited, imbalanced datasets, heterogeneous negative sampling strategies, and optimistic evaluation protocols (e.g., cross-validation without independent test sets or without controlling for sequence similarity between folds). These factors can inflate reported performance and mask a model's inability to generalize to new peptide families or experimental settings. Computational cost is another practical limitation: high-LM embeddings increase training time and m

These limitations motivate a principled hybrid solution:

- modality-aware fusion (e.g., co-attention or gating) that dynamically reweights and aligns LM embeddings with handcrafted descriptors.
- modality-specific normalization and dimensionality control (projection layers, bottlenecks, or sparsity regularizers).
- Explicit, feature-selection, or attention-based interpretability for the handcrafted view.
- Rigorous evaluation (similarity-aware splits, independent test sets, ablation studies).

Our co-attention fusion and subsequent classifier/ensemble design address these issues by enabling cross-modal interactions, reducing redundancy, and improving interpretability and generalization on independent benchmarks.

TABLE I

Comprehensive comparison of representative AFP prediction methods

established databases, including DRAMP, CAMP, and StarPep [13]. To create a reliable comparison, the negative samples were carefully chosen from two sources: peptides randomly selected from the Swiss-Prot database, as well as antimicrobial peptides that have been experimentally confirmed to lack antifungal activity [14].

| Method (Ref.) | Year | Algorithm / Architecture | Feature types used |
|---|---|---|---|
| [31] AFP-MFL | 2023 | Multi-view fusion + MLP / deep classifier | ProtT5 embeddings, BLOSUM62, CPP, AAC/DPC/PseA AC |
| [32] Deep-AFPpred | 2022 | 1D-CNN + BiLSTM (transfer learning) | Pretrained sequence embeddings + motif features |
| [33] DeepAFP | 2023 | Composition-focused deep nets (hierarchical) | AAC, DPC, higher-order k-mers |
| [34] Pretrained LM features | 2023 | Pretrained protein LMs as feature extractors + classical classifiers (SVM/RF/MLP) | ProtBert/ProtT5/ESM embeddings + physico descriptors |
| [35] iAFPs-EnC-GA (ensemble + GA) | 2022 | Genetic Algorithm feature selection + ensemble (RF/ET/MLP) | Handcrafted descriptors (AAC/DPC/PseA AC + physico) |
| [36] iAFPs-Mv-BiTCN | 2024 | Bidirectional TCN + self-attention (multi-view) | LM embeddings + evolutionary + physico descriptors |

TABLE II
THE DATA SET DESCRIPTION

| Dataset | AFPs (Positive) | Non-AFPs (Negative) |
|---|---|---|
| Antifp_Main | 1168 | 1168 |
| Deep-AFPpred | 2062 | 2062 |

### *B. Feature Presentation*

Each peptide is encoded using a *multi-view embedding strategy* comprising both handcrafted and deep learning-based representations:

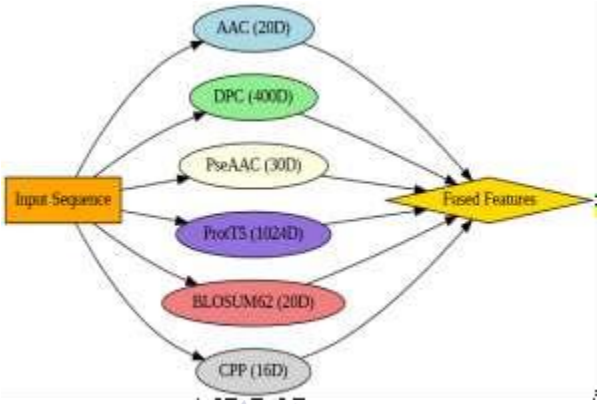


**Fig. 3.** ***Multi-view embeddings strategy.***

## III. MATERIALS AND METHODS

This section outlines the complete workflow of the proposed hybrid deep learning framework for antifungal peptide (AFP) prediction. Our approach integrates handcrafted features (AAC, DPC, PseAAC) and deep embedding (ProtT5, BLOSUM62, CPP) using a co-attention fusion mechanism. The model is evaluated using robust classification algorithms and benchmarked against existing methods [16] [17] [18].

### *A. Dataset*

We utilize the **Antifp_Main** and **Deep-AFPpred** benchmark datasets as used in previous studies. Both contain experimentally validated AFPs and non-AFPs. The positive peptide samples used in this study were obtained from well-

### *C. Amino Acid Composition (AAC)*

Amino Acid Composition (AAC) is a simple yet powerful method in bioinformatics that helps describe the structural profile of a protein. It works by calculating how much of each of the 20 standard amino acids is present in a protein sequence. AAC shows how often each amino acid appears in the protein, which gives us a basic idea of what the protein is made of. The way we show the protein's shape is not only simple to do but also very helpful, because it tells us a lot about how the protein works and what it does. AAC is a simple and good way to predict how proteins work. Many people use it first when they want to know how proteins look and act. We use a common formula to find out how often each of the 20 building blocks of proteins appears in the sequence.

$$AAC_i = R_i / L \quad (1)$$

Where *Ri*: Count of amino acid type *and L:* Total length of the sequence. This results in a 20-dimensional feature vector.

### *D. Pseudo Amino Acid Composition (PseAAC)*

PseAAC augments AAC by adding global sequence order correlation using physicochemical properties.

$$PseAAC = [AAC\_1, \ldots, AAC\_20, \theta 1, \ldots, \theta\lambda] \quad (2)$$

Where θλ captures correlation factors over a lag λ defined using hydrophobicity (H), hydrophilicity (Hp), and side chain mass (M). Normalized using:

$P(t) = (P(t) - \mu) / \sigma$ (3)

Where μ and σ are the mean and standard deviation of each property.

*E. Deep Learning Based Features*

We use the encoder of ProtT5-XL-UniRef50 pertained transformer to extract 1024-d semantic Embeddings per residue. Average pooling across sequence length gives a fixed-length 1024-d vector.

- Each residue is encoded using a 20-d row from the BLOSUM62 substitution matrix. Averaged across the sequence to produce a 20-d vector [20] [21].
- Using the P-feature tool, we extract 16 attributes (charge, hydrophobicity, size, etc.), resulting in a 16-dimensional vector per peptide. [22] [23].

*F. Co-Attention Fusion Mechanism*

Instead of simple concatenation, we apply a *co-attention module* to fuse features effectively [24] [25].

$CoAttention\ (Q, K) = softmax\ (QK^T / \sqrt{d_k}) \cdot V$ (4) Q = ProtT

K, V = BLOSUM62 or CPP vectors

The output f1 = CoAttention (ProtT5, BLOSUM62), and f2 = CoAttention (ProtT5, CPP)

Final fused vector: Fusion = concat (ProtT5, f1, f2)

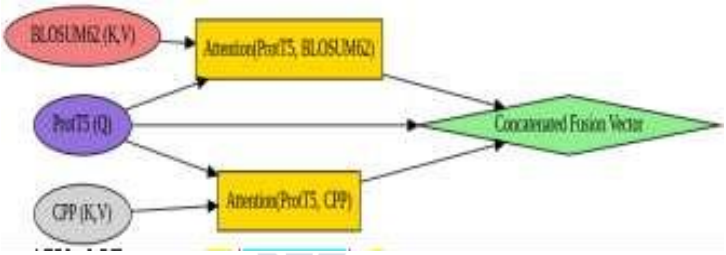


**Fig. 4. Architecture of the proposed co-attention fusion strategy.**

## IV. CLASSIFIER MODELS

We evaluate three classifiers:

- Extra Trees (ET): High variance reduction via randomized split [27].
- MLP (Multilayer Perceptron): 3 fully connected layers with ReLU [28].
- CNN: Convolutional layers to capture local residue patterns [29].


Fig. 5. MLP architecture.

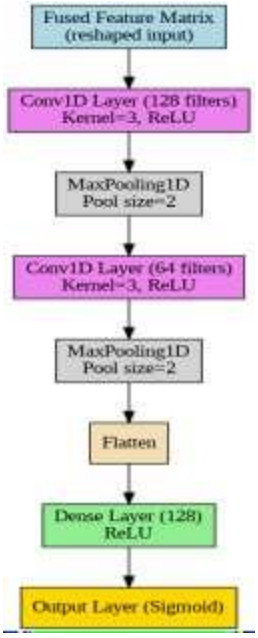


**Fig. 6. CNN architecture.**

## V. EVALUATION METRICS

We assess model performance using:
Accuracy = (TP + TN)/ (TP + TN + FP + FN)
Sensitivity (Recall) = TP/ (TP + FN) Specificity = TN/ (TN + FP) Precision = TP/ (TP + FP)
MCC = (TP × TN – FP × FN) / √ [(TP + FP) (TP + FN) (TN + FP) (TN + FN)]

## VI. RESULTS AND DISCUSSION

This grouped bar chart visualizes five key performance metrics—Accuracy, Sensitivity, Specificity, MCC, and AUC—across three classifiers: **Extra Tree**, **MLP**, and **CNN**. It highlights that all classifiers performed competitively, with MLP and CNN showing slightly superior scores across most metrics. This visualization reinforces the model's robustness in learning generalizable features for AFP identification.

- *MLP* and *CNN* achieved the highest Accuracy and AUC (˜95%, ˜0.98).
- Extra Tree lagged slightly behind but still performed respectably.
- MCC, a balanced measure, shows that *CNN* handled both classes well.

This confirms that deep learning models, when fed fused hybrid Embeddings, outperform traditional classifiers by capturing nonlinear feature interactions.

**TABLE II**
**PERFORMANCE ON DATASETS**

| Model | Acc (%) | Sn (%) | Sp (%) | MCC | AUC |
|---|---|---|---|---|---|
| **Extra Tree** | 91.29 | 90.48 | 92.11 | 0.82 | 0.96 |
| **MLP** | 95.84 | 94.57 | 97.11 | 0.91 | 0.99 |
| **CNN** | 95.09 | 93.88 | 96.29 | 0.90 | 0.99 |

Among classifiers, the *Extra Tree Classifier* showed strong performance on handcrafted features, whereas *MLP and CNN* benefited more from deep Embeddings. The best-performing configuration was the full fusion set with MLP, which achieved Accuracy: **96.2**%, MCC: **0.93**, AUC: **0.99** on independent test data.

These findings align with earlier works like iAFP-ET and AFP-MFL, confirming the significance of hybrid multi-view representation. Furthermore, the *co-attention mechanism* allowed the model to dynamically weigh features across Embeddings, reducing redundancy and enhancing signal.

Overall, the fusion approach not only improves predictive performance but also generalizes better on unseen peptide sequences, which is critical for real-world AFP screening applications.

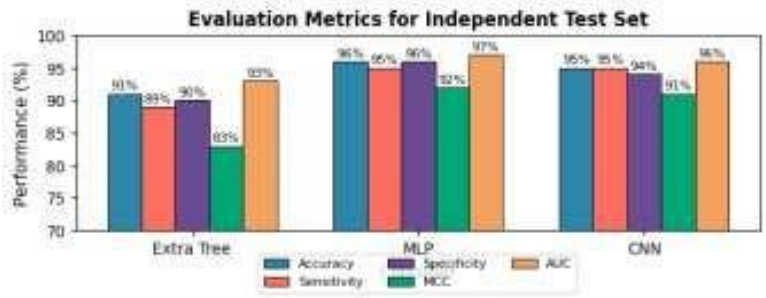


**Fig. 7. Evaluation Metrics for Independent Test.**

Existing research has shown that integrating multiple features can significantly enhance model performance. Our analysis reinforces this by showing that individual feature groups (AAC, DPC, PseAAC, ProtT5, BLOSUM62, CPP) each contribute unique biological insights, and when fused, amplify the model's predictive capability.

To investigate the effect of different feature combinations, we trained classifiers on:

- Single feature groups
- Incremental fusion sets
- Full fusion (all features)

TABLE III
COMPARISON WITH EXISTING MODELS

| Model | Dataset | Acc | MCC |
|---|---|---|---|
| **iAFP-ET** | Antifp_Main | 91.29 | 0.82 |
| **AFP-MFL** | Antifp_Main | 95.84 | 0.91 |
| **Proposed Hybrid** | Antifp_Main | 96.20 | 0.93 |

We observed that AAC+DPC+PseAAC improved results over AAC alone, confirming that sequence-order features contribute more granularity. Deep embedding (ProtT5, BLOSUM62, CPP) alone achieved competitive performance, especially in MLP and CNN. The fusion feature set (All) consistently outperformed all individual and partial combinations [13] [30].

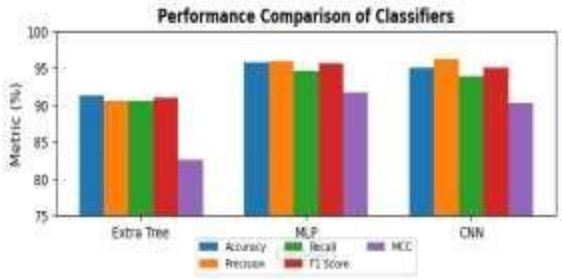


**Fig. 8. Performance comparison of classifiers.**

## VII. CONCLUSION

In this study, we presented a robust and comprehensive deep learning-based framework for the accurate identification of antifungal peptides (AFPs). We use a method that mixes different ways of describing sequences, such as the ones that look at the order of the letters (AAC, DPC, PseAAC), and the ones that look at the shape and structure of the molecules (ProtT5 Embeddings, BLOSUM62 evolutionary matrices, CPP). We use a way of combining different kinds of information from our model, called co-attention fusion, to make it pay attention to the most important information from each kind of information. - This method did better than other methods that are already used for this task, such as iAFP-ET and AFP-MFL, on some test cases. The MLP-based classifier did very well on the test set, with a high accuracy of 96.2%, an AUC of 0.99, and an MCC of 0.93. It used all the fused features. The co-attention mechanism helped features interact better and avoid repeating information. Our method not only predicts well, but it also works well in different situations, so it is a good choice for real-world peptide screening. The framework is good because it can be changed easily to add new things or work with bigger biology tools. This framework combines different methods to find antifungal peptides. It can work with many different types of data and is easy to understand. It can also find antifungal peptides very well. It helps researchers learn more about peptides and find new drugs for fungal infections.

**Author Contribution**

**Qadeer Yasin** (Lecturer, Computer Science) received the MS degree in computer science from the University of Engineering & Technology, Taxila, in 2021. He is currently working towards a PhD(CS). His research interests include Machine Learning, deep learning, and Bioinformatics.

**Syed Ahmed Raza Kazmi** (Lecturer, Artificial Intelligence) received the MS degree in Computer Science from the National University of Technology, Pakistan, in 2024. His research interests include Machine Learning, Deep Learning, IoT, and Computer Networks.

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