

# **Advancing Peptide Therapeutics: A Generative AI-Driven Approach**

Thesis submitted in partial fulfillment  
of the requirements for the degree of

*Master of Science*  
*in*  
*Computational Natural Sciences by Research*

by

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## **CERTIFICATE**

It is certified that the work contained in this thesis, titled **“Advancing Peptide Therapeutics: A Generative AI-Driven Approach”** by **Vishva Saravanan Ramasubramanian**, has been carried out under my supervision and is not submitted elsewhere for a degree.

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Date

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Adviser: Dr. Bhaswar Ghosh

To my family and friends.

## Acknowledgments

I would like to express my deepest gratitude to my research advisor, Dr. Bhaswar Ghosh, for his guidance and support. His mentorship has been invaluable to me and his expertise, patience, and encouragement have been instrumental in the successful completion of this thesis.

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Last but certainly not least, I extend my heartfelt gratitude to IIIT Hyderabad for providing me with an exceptional platform for my academic and research endeavors. The institute has opened doors to incredible professional opportunities and, most importantly, allowed me to cross paths with so many remarkable people. As the saying goes, “the hardest part of ending is starting again”, but I am eager to embark on the next chapter of my journey with the invaluable experiences and connections I gained here.

## Abstract

The field of therapeutic peptide design is ripe for transformation, fueled by the convergence of biotechnology and artificial intelligence. Peptides, short chains of amino acids, offer a promising avenue for targeted drug therapies due to their inherent advantages over small molecules, including specificity and reduced side effects. However, the development of peptide therapeutics has been hindered by their limited oral bioavailability and susceptibility to enzymatic degradation. Recent advancements in deep learning techniques have opened new possibilities for addressing these challenges through innovative peptide design strategies.

This thesis explores the development of a novel hybrid deep learning framework for de novo peptide design. By harnessing the power of diffusion models, known for their ability to learn complex data distributions, and integrating them with binding affinity maximization algorithms, we have created a system capable of generating peptide sequences optimized for specific target receptors. To demonstrate the applicability of this framework, we focus on designing therapeutic peptides targeting proteins expressed by *Plasmodium falciparum* Erythrocyte Membrane Protein 1 (PfEMP1) genes, key contributors to malaria pathogenesis.

Our results highlight the potential of this hybrid deep learning approach to revolutionize peptide drug discovery. By generating peptide candidates conditioned on the binding sites of target receptors, we offer a promising avenue for developing effective therapies for malaria and other diseases. This research underscores the transformative power of AI in peptide therapeutics, paving the way for a new era of precision medicine with enhanced efficacy and reduced toxicity.

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## *Chapter 1*

### **Introduction**

#### **1.1 Computational Drug Design**

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#### **1.2 Peptide Therapeutics**

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**Few suggestions**

#### **1.3 Malaria**

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**Few suggestions**

##### **1.3.1 Mathematics**

Please number all of your sections and displayed equations. It is important for readers to be able to refer to any particular equation. Just because you didn't refer to it in the text doesn't mean some future reader might not need to refer to it. It is cumbersome to have to use circumlocutions like "the equation second from the top of page 3 column 1". (Note that the ruler will not be present in the final copy, so is

not an alternative to equation numbers). All authors will benefit from reading Mermin's description of how to write mathematics (see [math.pdf](#)).

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### **1.3.3 References**

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<sup>1</sup>This is what a footnote looks like. It often distracts the reader from the main flow of the argument.

## *Chapter 2*

### **Methods**

Chapter 2 goes here ...

## *Chapter 3*

### **Experiments**

Chapter 3 goes here ...

## *Chapter 4*

### **Data**

Chapter 4 goes here ...

## *Chapter 5*

### **Results and Discussion**

Chapter 5 goes here ...

## *Chapter 6*

### **Conclusions**

Conclusion goes here ....



## Related Publications

Vishva Saravanan R, Soham Choudhuri, and Bhaswar Ghosh. **A Hybrid Diffusion Model for Stable, Affinity-Driven, Receptor-Aware Peptide Generation.** Journal of Chemical Information and Modeling, Manuscript ID: ci-2024-010205. Submitted on 28 Apr 2024, under review.

## **Bibliography**

- [1] Authors. The frobnicatable foo filter. 2006. ECCV06 submission ID 324. Supplied as additional material `eccv06.pdf`.