

Protein interactions with various molecules are crucial for their function and, consequently, for the overall functioning of organisms. Studying these interactions is important across many scientific fields, including medicine, where it is essential for drug development. Protein-ligand binding is a key type of these interactions, and a significant goal in bioinformatics is to develop reliable models for binding site prediction. The recent surge in the collection of protein structures, combined with the immense power of modern GPUs, has allowed the development of many machine-learning models. Notably protein language models, inspired by their counterparts in natural language processing, have been successfully applied throughout bioinformatics. In this thesis, we fine-tuned a protein language model for binding site prediction and sought to enhance its performance by incorporating various three-dimensional features of proteins.