

Nikša Praljak

Ph.D. Candidate in Biophysics at the University of Chicago

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PraljakReps

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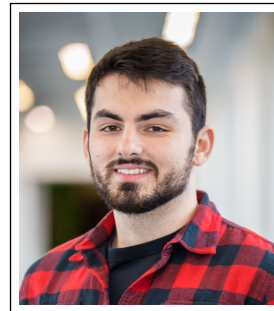
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🌐 Personal Website

🎓 Google Scholar Profile

🏛️ University of Chicago Website

🌐 X (formerly Twitter)



Professional Summary

PhD candidate in Biophysics developing deep generative models and multimodal approaches for protein design, focused on bridging the gap between *in silico* performance and wet-lab success in AI-driven drug discovery.

Education

Note: Words highlighted in [blue](#) are clickable links.

University of Chicago

Autumn 2020 - Present

Chicago, Illinois

PhD Student: Biophysical Sciences Graduate Program (NSF Graduate Research Fellow)

Thesis: Molecular Dialogues: Guiding Protein Design through Natural Language Prompts

PhD co-advisors: Professors [Rama Ranganathan](#) and [Andrew Ferguson](#)

1. Developed **BioM3**, a multimodal protein language model, enabling novel protein sequence generation directly from natural language prompts.
 - Implemented a multi-GPU pretraining workflow (PyTorch, DeepSpeed) aligning protein and biomedical language models via contrastive learning.
 - Created a conditional diffusion model for text-prompted protein design; experimentally confirmed model-generated proteins were functional *in vivo* and *in vitro*.
 - Deployed an interactive demo on [Hugging Face Spaces](#).
2. Developed and applied novel Variational Autoencoder (VAE) architectures for generative protein design:
 - Engineered synthetic SH3 signaling domain orthologs using an information-maximizing VAE; experimentally validated designs and analyzed novelty. (Co-first author publication featured in *Patterns*).
 - Created ProtWave-VAE, integrating autoregressive sampling with VAE latent inference for alignment-free design, enabling property guidance via latent conditioning. (Work featured in *ACS Synthetic Biology* special issue).
3. Actively developing novel deep learning methods for protein prediction and design, focusing on large-scale model post-training (DPO for mutation effects, scaling laws) and improved text-to-protein generation (discrete flow matching, frontier model integration).

Case Western Reserve University

Autumn 2018 - Summer 2020

Cleveland, Ohio

Department of Physics: Visiting Student and Researcher

GPA: 4.0

Research: Integrating computer vision with protein adhesion-based microfluidic assays for sickle cell patient diagnostics

Advisors: Drs. Michael Hinczewski (Theoretical Biophysics Research Group) and Umut Gurkan (CASE Biomanufacturing and Microfabrication Laboratory)

Cleveland State University

Autumn 2016 - Spring 2020

Cleveland, Ohio

Undergraduate Majors: Honors Mathematics and Honors Physics

Publications

These are selected publications. For a complete list, please see my [Google Scholar profile](#). * Denotes co-first authors

1. **N Praljak**, H Yeh, M Moore, M Socolich, R Ranganathan, A L Ferguson (2024). Natural Language Prompts Guide the Design of Novel Functional Protein Sequences. *bioRxiv*, doi:10.1101/2024.11.11.622734.
 - Presented in AIDrugX workshop at NeurIPS 2024.
 - [BioM3-app](#): Deployed text-to-protein generation demo.
2. X Lian*, **N Praljak***, SK Subramanian*, S Wasinger, R Ranganathan, ... (2024). Deep-learning-based design of synthetic orthologs of SH3 signaling domains. *Cell Systems*, 15(8), 725-737.
 - Featured in: Fu X. How deep can we decipher protein evolution with deep learning models. *Patterns*, Volume 5, Issue 8, 9 August 2024, 101043. This preview highlights our work on applying deep learning to protein evolution and design.
3. **N Praljak**, X Lian, R Ranganathan, AL Ferguson. (2023). ProtWave-VAE: Integrating autoregressive sampling with latent-based inference for data-driven protein design. *ACS Synthetic Biology*, 12(12), 3544-3561.
 - Featured in: Martín García H, Mazurenko S, Zhao H. Special Issue on Artificial Intelligence for Synthetic Biology. *ACS Synth. Biol.* 2024, 13, 2, 408–410. This special issue highlights and features our work on integrating AI with synthetic biology.

Patents

- **Techniques for Artificial Intelligence (AI) Based Protein Engineering Using Natural Language Prompting.** Inventors: A. Ferguson, **N. Praljak**, R. Ranganathan. (Application Submitted)
- **Classification of Blood Cells.** Inventors: **N. Praljak**, I. Shamreen, U. Goreke, M. Hinczewski, et al. US App. No. 17/928,976.
- Additional patents ([link](#)).

Talks & Presentations

1. **Praljak N.** "Natural language prompts guide the design of novel functional protein sequences" Invited/Nominated talk, PhD Student Research Day, Data Science Institute, Univ. of Chicago, Dec 2024. ([Link](#))
2. **Praljak N.**, "A multimodal generative model with natural language for protein design" Oral presentation, Multimodal AI Workshop, Toyota Tech Institute at Chicago (TTIC), Jan 2024. ([Link](#))

Honors & Awards

- 2023 UChicago DSI AI+Science Grant (\$10k) for project: "[Discovering Design Rules...](#)"
- 2021 Finalist, Grier Prize for Innovative Research in Biophysics; UChicago Duchossois Family Institute Fellow
- 2020 [NSF Graduate Research Fellowship](#); [COSHP Valedictorian](#)

Technical Skills

Programming Python, C++, R, MATLAB

ML Software PyTorch, DeepSpeed, HuggingFace, Jax, TensorFlow, Scikit-learn

Data Science NumPy, Pandas, Matplotlib, Seaborn, SciPy, Dask, TensorBoard, HDF5

Tools Git, Linux, HPC Environments, PBS, SLURM, bash