BENJAMIN FRY

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EDUCATION

Harvard University
Biophysics PhD Program **Expected May 2027**
GPA: 3.90 out of 4.0

Johns Hopkins University
Biophysics Major, Computer Science Minor **Awarded May 2022**
GPA: 3.92 out of 4.0

AWARDS

Marci and Martin Karplus Family Foundation Biophysics Prize Fellowship	February 2026
Rosetta Commons Mini Grant	October 2025
National Science Foundation Graduate Research Fellowship (GRFP)	April 2024
Harvard Graduate School of Arts and Sciences Prize Fellowship	March 2022

RESEARCH INTERESTS

Functional Protein Design, Biotechnology & Therapeutic Development, Geometric Deep Learning

RESEARCH EXPERIENCE

Deep Learning Guided Design of Small-Molecule Binding Proteins with Nick Polizzi at Harvard Medical School
PhD Candidate **Sept. 2022 – Present**

- Developed a geometric deep learning algorithm “LASErMPNN” which generates protein sequences conditioned on 3D atomic structure released freely under MIT license.
- Identified a binder optimization protocol (Neural Iterative Selection and Expansion) which leverages protein-ligand co-structure prediction neural networks (RoseTTAFold-All Atom, Boltz, AlphaFold3) in conjunction with LASErMPNN to jointly optimize designed protein sequence and structure.
- Implemented a structural bioinformatics informed filtering and ranking pipeline to select LASErMPNN designs achieving unprecedented experimentally determined success rates and affinities over a range of small molecule targets.

Independent Research Project with Dr. Jeffrey Gray at Johns Hopkins University
Undergraduate Researcher **Sept. 2021 – May 2022**

- Continued work on “Cloaking with Glycans” algorithm from REU in collaboration with Kulp Lab.
- Improving combinatorial selection algorithm using clustering and benchmarking against natural glycosylation patterns to optimize computational performance metrics.

Rosetta Commons Research Experience for Undergraduates (REU) with Dr. Daniel Kulp at the Wistar Institute
Summer Intern **June 2021 – Aug. 2021**

- Implemented novel “Cloaking with Glycans” protocol which scans protein structure for N-linked glycosylation sites away from sites of interest to guide neutralizing antibody development.
- Parallelized PyRosetta functions to comprehensively introduce independent N-linked glycosylation sequon mutations throughout protein sequence and screen them for stability in parallel.

- Designed a custom data structure for representing 3D space as voxels of arbitrary size used to screen glycan configurations for overlap with eachother and structures of interest.
- Created novel visualization protocol for inspecting designed voxel data structure in PyMol.

GENERAL SKILLS

Deep Learning Model Engineering (PyTorch, PyTorch Geometric, PyTorch Distributed), **Software Development** (Python, C/C++, Java, MATLAB, Bash), **Physics-Based Protein Design** (PyRosetta & Rosetta Scripts)**, Molecular Dynamics Simulations** (OpenMM), **Collaborative Development** (Git & GitHub)

PRESENTATIONS

“Leveraging Deep Learning Model Embeddings for Protein Property Prediction and Design”

November 19th, 2025

- Presented at Broad Institute Models, Inference, and Algorithms talk series discussing recent advances in learning and applying protein embeddings for property prediction and design.
- Demonstrated how model representations can be used to build accurate predictors of protein properties with the goal of introducing concepts necessary to understand the AF2Bind model.
- Link to Recording: https://www.youtube.com/watch?v=Cjby1HQg9zw

“Zero-shot design of drug-binding proteins via neural selection-expansion”

August 5th, 2025

- 10-minute talk at Summer RosettaCON comparing the LASErMPNN neural network to LigandMPNN, explaining our Neural Iterative Selection and Expansion (NISE) protein design optimization loop, and experimental results for high affinity binders to the cancer therapeutics exatecan and duocarmycin.

“Design of small molecule binding proteins using deep learning”

January 15th, 2025

- 30-minute talk at Boston Protein Design and Modeling club on the LASErMPNN neural network, our Neural Iterative Selection and Expansion (NISE) protein design optimization loop, and experimental results for binders targeting Exatecan ligand.
- Work was also presented at Winter RosettaCON in February 2025.
- Link to Recording: https://www.youtube.com/watch?v=IgFgAYQrke4&t=1s

“Ligand-Aware Protein Sequence Design Using Protein Self-Contacts”

December 15th, 2022

- Presented poster at NeurIPS MLSB Workshop on tool developed during rotation project which decomposes small molecule ligands into fragments derived from amino acids and predicts protein sequence using simple neural networks trained on van der Mer (vdM) databases.
- Work was also presented at Molecular Machine Learning (MoML) Conference in October 2022.

“A Novel Computational Pipeline for Glycoprotein Immunofocusing Utilizing Distributed PyRosetta”

August 9-13th, 2021

- Presented poster at Summer RosettaCON detailing work on algorithm for automated N-linked glycosylation motif design to guide immune recognition.

PUBLICATIONS

Zero-shot design of drug-binding proteins via neural selection-expansion
Nature Jun. 2026
Benjamin Fry, Kaia Slaw, Nicholas Polizzi

Molecular basis of mitochondrial leucine transport by human Sideroflexin 1
bioRxiv Jun. 2026
Fiona M Fitzpatrick, Daniel T. D. Jones, Hannah Aguirre, Benjamin Fry, Elena T. Kaemmerer, Sijie Tan, Luise E. Veelken, Wen Han Tong, Samuel Block, Ali Aghvami, Edmund R.S. Kunji, Nicholas Polizzi, Stephen Blacklow, Nora Kory

Deep confident steps to new pockets: Strategies for docking generalization
International Conference on Learning Representations (ICLR) Feb. 2024
Gabriele Corso, Arthur Deng, Benjamin Fry, Nicholas Polizzi, Regina Barzilay, Tommi Jaakkola

Ligand-Aware Protein Sequence Design Using Protein Self-Contacts
Neural Information Processing Systems (NeurIPS) Machine Learning in Structural Biology (MLSB) Workshop Dec. 2022
Jody Mou, Benjamin Fry, Nicholas Polizzi

Nucleic acid delivery of immune-focused SARS-CoV-2 nanoparticles drives rapid and potent immunogenicity capable of single-dose protection
Cell Reports Feb. 2022
Kylie M. Konrath, Kevin Liaw, Yuanhan Wu, Xizhou Zhu, Susanne N. Walker, Ziyang Xu, Katherine Schultheis, Neethu Chokkalingam, Himanshi Chawla, Jianqiu Du, Nicholas J. Tursi, Alan Moore, Jared Adolf-Bryfogle, Mansi Purwar, Emma L. Reuschel, Drew Frase, Matthew Sullivan, Benjamin Fry, Igor Maricic, Viviane M. Andrade, Christel Iffland, Max Crispin, Kate E. Broderick, Laurent M.P.F. Humeau, Ami Patel, Trevor R.F. Smith, Jesper Pallesen, David B. Weiner, Daniel W. Kulp