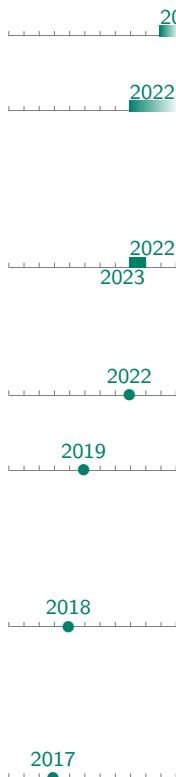


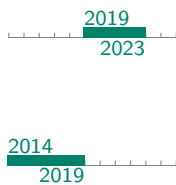
# Jeffrey Ruffolo, PhD

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## Professional

- 
- 2024 **Profluent Bio, Head of Protein Design**
- Building and leading team of protein design scientists.
- 2022 **Profluent Bio, Machine Learning Scientist**
- Contributed to OpenCRISPR initiative, aimed at designing a novel Cas9-like nuclease protein for genome editing applications.
  - Developed structure-conditioned language model (proseLM) for usage across diverse design projects.
- 2022 **Ably Bio, Founder and CEO**
- Co-founded company to apply machine learning methods to therapeutic antibody design.
  - Won Microsoft Innovation Acceleration Award.
  - Accepted into Microsoft for Startups program.
- 2022 **Generate:Biomedicines, Machine Learning Scientist Intern**
- Developed diffusion models for protein complex prediction.
- 2019 **Microsoft, Software Engineer Intern**
- Developed efficient process for migrating large quantities of user metadata for the Microsoft Teams product.
  - Reworked architecture of globally-distributed metadata storage service to reduce load in high-traffic regions and increase resiliency to bursts of increased demand.
- 2018 **Microsoft, Software Engineer Intern**
- Developed initial implementation of GraphQL service layer, providing backend service abstraction for Microsoft Teams product.
  - Built representative metrics for analyzing performance impact resulting from additional layer between client and distributed services.
- 2017 **IBM, Software Developer Intern**
- Performed exploratory analysis of Spring web framework and its compatibility with IBM Cloud platform.
  - Published ten articles on official IBM Cloud blog, aimed at providing support for Spring community and establishing IBM Cloud as a preferred choice for enterprise Java development.

## Education

- 
- 2019 **Doctor of Philosophy, Johns Hopkins University, Baltimore, MD**
- **Program** Molecular Biophysics
  - Advised by Prof. Jeffrey Gray and Prof. Jeremias Sulam
  - Johns Hopkins-AstraZeneca Scholar
- 2014 **Bachelor of Science, University of Missouri, Columbia, MO**
- **Majors** Biochemistry, Computer Science
  - Minor in Mathematics
  - Summa Cum Laude (GPA 3.979)

## Research

2020  
2023

### Graduate Student, Johns Hopkins University

- **Adviser** Prof. Jeffrey Gray
- Developed first deep learning methods for antibody  $F_V$  structure prediction (DeepH3, DeepAb), which significantly improved performance on the critical CDR H3 loop over prior approaches.
- Developed antibody-specific language models for representation learning and synthetic library design.
- Developed fast, accurate method for antibody structure prediction (IgFold), leveraging 558M natural antibody sequences.

2020  
2023

### Graduate Student, Johns Hopkins University

- **Adviser** Prof. Jeremias Sulam
- Applied protein language models and weakly supervised learning to identify specific antibodies within immune repertoires.

2021  
2023

### Johns Hopkins-AstraZeneca Scholar, AstraZeneca

- **Adviser** Dr. Gilad Kaplan
- Experimentally validated designed antibodies and received industry mentorship as part of joint training program between Johns Hopkins and AstraZeneca.

2018  
2019

### Undergraduate Researcher, University of Missouri

- **Adviser** Prof. Yi Shang
- Developed TPCref, a method for refinement of protein contact-map predictions using the results of predictions by the same method on template structures.

2015  
2019

### Undergraduate Researcher, University of Missouri

- **Adviser** Prof. Andrew McClellan
- Used parallel dual-annealing exploration strategy to demonstrate that diverse combinations of parameters can produce realistic neuronal behavior for a multi-compartmental neuron model.

## Publications

2025

Sai Pooja Mahajan, Fátima A Davila-Hernandez, **Jeffrey A Ruffolo**, and Jeffrey J Gray. “How well do contextual protein encodings learn structure, function, and evolutionary context?” *Cell Systems* (2025)

2024

Jason Yang, Aadyot Bhatnagar, **Jeffrey A Ruffolo**, and Ali Madani. “Conditional enzyme generation using protein language models with adapters”. *arXiv* (2024)

2024

**Jeffrey A Ruffolo**, Aadyot Bhatnagar, Joel Beazer, Stephen Nayfach, Jordan Russ, Emily Hill, Riffat Hussain, Joseph Gallagher, and Ali Madani. “Adapting protein language models for structure-conditioned design”. *bioRxiv* (2024)

2024

**Jeffrey A Ruffolo\***, Stephen Nayfach\*, Joseph Gallagher\*, Aadyot Bhatnagar\*, Joel Beazer, Riffat Hussain, Jordan Russ, Jennifer Yip, Emily Hill, Martin Pacesa, Alexander J Meeske, Peter Cameron, and Ali Madani. “Design of highly functional genome editors by modeling the universe of CRISPR-Cas sequences”. *bioRxiv* (2024)

2024

**Jeffrey A Ruffolo** and Ali Madani. “Designing proteins with language models”. *Nature Biotechnology* (2024)

2024

Lee-Shin Chu, **Ruffolo, Jeffrey A**, Ameya Harmalkar, and Jeffrey J Gray. “Flexible protein–protein docking with a multitask iterative transformer”. *Protein Science* (2024)

2023

Mark Hutchinson\*, **Jeffrey A Ruffolo\***, Nantaporn Haskins, Michael Iannotti, Giuliana Voza, Tony Pham, Nurjahan Mehzabeen, Harini Shandilya, Keith Rickert, Rebecca Croasdale-Wood, Melissa Damschroder, Ying Fu, Andrew Dippel, Jeffrey J. Gray, and Gilad Kaplan. “Enhancement of antibody thermostability and affinity by computational design in the absence of antigen”. *bioRxiv* (2023)

2023

Alex Morehead, **Jeffrey A Ruffolo**, Aadyot Bhatnagar, and Ali Madani. “Towards Joint Sequence-Structure Generation of Nucleic Acid and Protein Complexes with SE(3)-Discrete Diffusion”. *Arxiv* (2023)



2023 Michael F Chungyoun, **Jeffrey A Ruffolo**, and Jeffrey J. Gray. "FLAB: Benchmarking deep learning methods for antibody fitness prediction". *bioRxiv* (2023)

2023 Erik Nijkamp\*, **Jeffrey A Ruffolo\***, Eli N. Weinstein, Nikhil Naik, and Ali Madani. "ProGen2: Exploring the Boundaries of Protein Language Models". *Cell Systems* (2023)

2023 Richard W. Shuai\*, **Jeffrey A Ruffolo\***, and Jeffrey J. Gray. "IgLM: infilling language modeling for antibody sequence design". *Cell Systems* (2023)

2023 **Jeffrey A Ruffolo**, Lee-Shin Chu, Sai Pooja Mahajan, and Jeffrey J. Gray. "Fast, accurate antibody structure from deep learning on massive set of natural antibodies". *Nature Communications* (2023)

2022 Sai Pooja Mahajan, **Jeffrey A Ruffolo**, Rahel Frick, and Jeffrey J. Gray. "Hallucinating structure-conditioned antibody libraries for target-specific binders". *Frontiers in Immunology* (2022)

2022 Seth D. Ludwig\*, Zachart J. Bernstein\*, Christian Agatemor, Kris Dammen-Brower, **Jeffrey Ruffolo**, Jonah M. Rosas, Jeremy D. Post, Robert N. Cole, Kevin J. Yarema, and Jamie B. Spangler. "A versatile design platform for glycoengineering therapeutic antibodies". *mAbs* (2022)

2022 Deniz Akpinaroglu, **Jeffrey A Ruffolo**, Sai Pooja Mahajan, and Jeffrey J. Gray. "Simultaneous prediction of antibody backbone and side-chain conformations with deep learning". *PLOS One* (2022)

2022 **Jeffrey A Ruffolo**, Jeremias Sulam, and Jeffrey J. Gray. "Antibody structure prediction using interpretable deep learning". *Patterns* (2022)

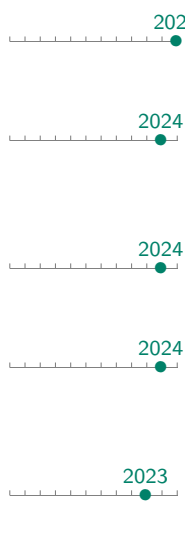
2021 **Jeffrey A Ruffolo**, Jeffrey J. Gray, and Jeremias Sulam. "Deciphering antibody affinity maturation with language models and weakly supervised learning". *arXiv* (2021)

2020 **Jeffrey A Ruffolo** and Andrew D. McClellan. "Modeling of lamprey reticulospinal neurons: multiple distinct parameter sets yield realistic simulations". *Journal of Neurophysiology* (2020)

2020 **Jeffrey A Ruffolo**, Carlos Guerra, Sai Pooja Mahajan, Jeremias Sulam, and Jeffrey J. Gray. "Geometric potentials from deep learning improve prediction of CDR H3 loop structures". *Bioinformatics* (2020)

2019 **Jeffrey A Ruffolo**, Zhaoyu Li, and Yi Shang. "MUFold-Contact and TPCref: New Methods for Protein Structure Contact Prediction and Refinement". *IEEE International Conference on Bioinformatics and Biomedicine* (2019)

## Invited Talks



2025 **BioLogic Summit, San Diego, CA, USA**

- "Steering protein language models for functional protein design"
- January 14, 2025

2024 **Stanford AI + Biomedicine Seminar, San Diego, CA, USA**

- "OpenCRISPR: Design of highly functional genome editors by modeling the universe of CRISPR-Cas sequences"
- July 23, 2024

2024 **PEGS Boston, Boston, MA, USA**

- "Design of highly functional genome editors by modeling the universe of CRISPR-Cas proteins"
- May 17, 2024

2024 **ML Protein Engineering Seminar Series, Virtual**

- "Design of highly functional genome editors by modeling the universe of CRISPR-Cas proteins"
- May 7, 2024
- Video recording

2023 **PEGS Europe, Lisbon, Portugal**

- "Generative modeling for functional protein design"
- November 15, 2023

2023

#### **GSK Seminar, Virtual**

- “Harnessing immune repertoire data for antibody understanding and design”
- February 28, 2023

2022

#### **iReceptor+ Seminar Series, Virtual**

- “Language models for protein generation and fitness prediction”
- September 22, 2022
- Video recording

2022

#### **Absci Invites, Virtual**

- “Fast, accurate antibody structure prediction from deep learning on massive set of natural antibodies”
- May 26, 2022
- Video recording

2022

#### **Boston Protein Modeling and Design Club, Virtual**

- “Learning from natural antibodies for sequence generation and fast structure prediction”
- March 2, 2022
- Video recording

## **Presentations**

2024

#### **RosettaCon, Oral**

- “Steering protein language models for functional protein design”
- **Jeffrey A. Ruffolo**

2023

#### **Computational Design and Modeling of Biomolecules, Poster**

- “Harnessing immune repertoire data for antibody understanding and design”
- **Jeffrey A. Ruffolo**, Richard W. Shuai, Jeremias Sulam, Jeffrey J. Gray

2022

#### **RosettaCon, Oral**

- “Language models for protein generation and fitness prediction”
- **Jeffrey A. Ruffolo**

2022

#### **Biophysical Society Annual Meeting, Oral**

- “Fast, accurate antibody structure prediction from deep learning on massive set of natural antibodies”
- **Jeffrey A. Ruffolo** and Jeffrey J. Gray

2021

#### **Antibody Engineering & Therapeutics (The Antibody Society), Poster**

- “Antibody structure prediction using interpretable deep learning”
- **Jeffrey A. Ruffolo**, Jeremias Sulam, and Jeffrey J. Gray

2021

#### **Machine Learning for Structural Biology (NeurIPS workshop), Oral**

- “Deciphering antibody affinity maturation with language models and weakly supervised learning”
- **Jeffrey A. Ruffolo**, Jeffrey J. Gray, and Jeremias Sulam
- Video recording

2021

#### **Machine Learning for Structural Biology (NeurIPS workshop), Poster**

- “Generative language modeling for antibody design”
- Richard Shuai, **Jeffrey A. Ruffolo**, and Jeffrey J. Gray

2021

#### **Winter RosettaCon, Poster**

- “Improved antibody structure prediction using repertoire sequence data and neural attention”
- **Jeffrey A. Ruffolo**, Jeremias Sulam, and Jeffrey J. Gray

2020

#### **Computational Drug Discovery & Development for Biologics Summit, Poster**

- “Deep learning improves prediction of antibody CDR H3 loop structures”
- **Jeffrey A. Ruffolo**, Sai Pooja Mahajan, Jeremias Sulam, and Jeffrey J. Gray

2020

#### **RosettaCon, Oral**

- “Geometric potentials from deep learning improve prediction of CDR H3 Loop structures”
- **Jeffrey A. Ruffolo**, Carlos Guerra, Sai Pooja Mahajan, Jeremias Sulam, and Jeffrey J. Gray

2020

#### **Intelligent Systems for Molecular Biology, Oral**

- “Geometric potentials from deep learning improve prediction of CDR H3 Loop structures”
- **Jeffrey A. Ruffolo**, Carlos Guerra, Sai Pooja Mahajan, Jeremias Sulam, and Jeffrey J. Gray

2017

**MU Undergraduate Research Forum, *Poster***

- “Computer model of reticulospinal neurons in the lamprey”
- **Jeffrey A. Ruffolo** and Andrew D. McClellan

2016

**MU Undergraduate Research Forum, *Poster***

- “User-friendly computer model of reticulospinal neurons in the lamprey”
- **Jeffrey A. Ruffolo** and Andrew D. McClellan