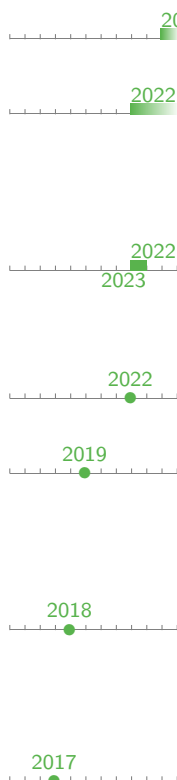


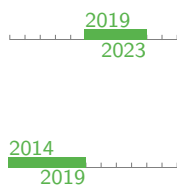
Jeffrey Ruffolo

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jeffreyruffolo.com
github.com/jeffreyruffolo
linkedin.com/in/jeffreyruffolo

Professional

- 
- A horizontal timeline for the Professional section. It features a series of vertical tick marks. Green bars of varying lengths are placed above the timeline to represent the duration of each role. The years 2017, 2018, 2019, 2022, 2023, and 2024 are marked with green dots and labels above the timeline.
- 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.
 - Rewrote 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

- 
- A horizontal timeline for the Education section. It features a series of vertical tick marks. Green bars of varying lengths are placed above the timeline to represent the duration of each degree. The years 2014, 2019, and 2023 are marked with green dots and labels above the timeline.
- 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
 - Utilized highly-parallelized dual-annealing exploration strategy to demonstrate that diverse combinations of parameters can produce realistic neuronal behavior for a multi-compartmental neuron model.

Publications

- 2024
- Jason Yang, Aadyot Bhatnagar, **Jeffrey A Ruffolo**, and Ali Madani. “Conditional enzyme generation using protein language models with adapters”. In: *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”. In: *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”. In: *bioRxiv* (2024)
- 2024
- Jeffrey A Ruffolo** and Ali Madani. “Designing proteins with language models”. In: *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”. In: *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”. In: *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”. In: *Arxiv* (2023)
- 2023
- Michael F Chungyoun, **Jeffrey A Ruffolo**, and Jeffrey J. Gray. “FLAb: Benchmarking deep learning methods for antibody fitness prediction”. In: *bioRxiv* (2023)
- 2023
- Sai Pooja Mahajan, **Jeffrey A Ruffolo**, and Jeffrey J Gray. “Contextual protein and antibody encodings from equivariant graph transformers”. In: *bioRxiv* (2023)

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

2023 Richard W. Shuai*, **Jeffrey A Ruffolo***, and Jeffrey J. Gray. "IgLM: infilling language modeling for antibody sequence design". In: *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". In: *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". In: *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". In: *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". In: *PLOS One* (2022)

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

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

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

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

Invited Talks

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

- 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
- **Summer Rosetta Conference, 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 Rosetta Conference, 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
- **Summer Rosetta Conference, 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

Software

- 2022
- **IgFold**
 - Fast, accurate antibody structure prediction from deep learning on massive set of natural antibodies.
 - <https://github.com/Graylab/IgFold>



AntiBERTy

- Masked language model for natural antibody sequences.
- <https://github.com/jeffreyruffolo/AntiBERTy>



IgLM

- Infilling language model for antibody sequence generation.
- <https://github.com/Graylab/IgLM>



DeepAb

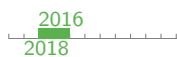
- Deep learning models and structure realization scripts for the DeepAb antibody structure prediction method.
- <https://github.com/RosettaCommons/DeepAb>

Honors and Awards



Johns Hopkins-AstraZeneca Scholar

- Funded joint PhD training program by JHU and AstraZeneca



Life Sciences Undergraduate Research Opportunity Program

- Fellowship at the University of Missouri providing funding for research in the life sciences and an opportunity to present findings in a poster session, with twenty participants chosen each year.



Discovery Fellow

- Funded research fellowship in the Honors College at the University of Missouri, with participants nominated by the dean of their college, with twenty-three participants chosen each year.



Engineering Entrepreneur Award

- Scholarship for aspiring entrepreneurs within the University of Missouri College of Engineering, with two recipients chosen.



Show-Me Scholar

- Award for high-achieving students entering the University of Missouri as freshmen, with thirty scholars chosen each year.

Service and Outreach



Manuscript Review

- Nature Biotechnology, Nature Machine Intelligence, PNAS, Bioinformatics, PLoS Computational Biology, PROTEINS



Phi Beta Kappa, *Member*

- Alpha of Missouri Chapter



Mizzou Computing Association, *President*

- Served as President of largest computer science student organization at the University of Missouri, with over 100 members



Upsilon Pi Epsilon, *Community Outreach Leader*

- Gamma Chapter