


# Samuel Sledzieski

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## RESEARCH

### Flatiron Institute

Flatiron Research Fellow, Center for Computational Biology

New York, NY

Sep 2024 – Present

### Princeton University

Visiting Research Collaborator, Lewis-Sigler Institute for Integrative Genomics

Princeton, NJ

Sep 2024 – Present

### Massachusetts Institute of Technology

Research Assistant, Computation and Biology Group

Cambridge, MA

Feb 2020 – Aug 2024

### Centre Scientifique de Monaco

Visiting Researcher

Monaco

Jan 2024 – Feb 2024

### Serinus Biosciences

Consultant

Cambridge, MA

Feb 2023 – Dec 2023

### Microsoft Research

Research Intern, AI For Good Lab

Redmond, WA

May 2023 – Oct 2023

### Cellarity

Machine Learning Intern, Perturbation Biology Group

Cambridge, MA

May 2021 – Aug 2021

### MIT Lincoln Laboratory

Summer Research Program, Advanced Lasercom Systems Group

Lexington, MA

May 2019 – Aug 2019

### University of Connecticut

Undergraduate Research Assistant, Computational Biology Lab

Storrs, CT

Jan 2017 – May 2019

Software Developer, Jackson Laboratory for Genomic Medicine

Aug 2018 – May 2019

Undergraduate Research Assistant, Nelson Lab

Oct 2015 – Dec 2016

## EDUCATION

### Massachusetts Institute of Technology

PhD, Computer Science

Cambridge, MA

2019 – 2024

- Minor in Biological Engineering
- Concentration: Protein language models, protein and drug interactions, protein structure
- Advisor: Dr. Bonnie Berger

SM, Electrical Engineering and Computer Science

2019 – 2021

### University of Connecticut

BS, Computer Science

Storrs, CT

2015 – 2019

- Minor in Molecular and Cellular Biology
- Concentration: Bioinformatics, Data Science
- Advisor: Dr. Mukul Bansal
- Magna Cum Laude, Honors Scholar

## TEACHING

### Massachusetts Institute of Technology

Teaching Assistant, Intro to Deep Learning (6.S191)

Cambridge, MA

Winter 2021, 2022, 2023

Teaching Assistant, Machine Learning in Genomics (6.878)

Fall 2021

### University of Connecticut

Teaching Assistant, Theory of Computation

Storrs, CT

Spring 2018

**JOURNAL**

- [9] Kshirsagar, Meller, Humphreys, **Sledzieski**, Xu, Dodhia, Horvitz, Berger, Bowman, Lavista Ferres, Baker, Baek, “Rapid and accurate prediction of protein homo-oligomer symmetry,” *Nature Communications*, 16(2017), 2025.
  - [8] Singh, Im, Qiu, Macnkess, Gupta, Sorenson, **Sledzieski**, Erlach, Wendt, Nanfack, Bryson, Berger, “Learning the Language of Antibody Hypervariability,” *Proceedings of the National Academy of Sciences*, 122(1):e2418918121, 2024.
  - [7] **Sledzieski**, Kshirsagar, Baek, Berger, Dodhia, Lavista Ferres, “Democratizing Protein Language Models with Parameter-Efficient Fine-Tuning,” *Proceedings of the National Academy of Sciences*, 121(26):e2405840121, 2024.
  - [6] **Sledzieski\***, Devkota\*, Singh, Cowen, Berger, “TT3D: Leveraging Pre-Computed Protein Sequence Models to Predict Protein-Protein Interactions,” *Bioinformatics*, 39(11):btad663, 2023.
  - [5] Singh\*, **Sledzieski\***, Bryson, Cowen, Berger, “Contrastive learning in protein language space predicts interactions between drugs and protein targets,” *Proceedings of the National Academy of Sciences*, 120(24):e2220778120, 2023.
  - [4] Kumar, Brenner, **Sledzieski**, Olaosebikan, Lynn-Goin, Putnam, Yang, Lewinski, Singh, Daniels, Cowen, Klein-Seetharaman, “Transfer of knowledge from model organisms to evolutionarily distant non-model organisms: The coral *Pocillopora damicornis* membrane signaling receptome,” *Plos one*, 18(2):e0270965, 2023.
  - [3] Zaman\*, **Sledzieski\***, Wu, Bansal, “virDTL: Viral recombination analysis through phylogenetic reconciliation and its application to sarbecoviruses and SARS-CoV-2,” *J Comput Biol*, 30(1):3–20, 2023.
  - [2] Singh\*, Devkota\*, **Sledzieski**, Berger, Cowen, “Topsy-Turvy: integrating a global view into sequence-based PPI prediction,” *Bioinformatics*, 38(Supplement 1):i264-i272, 2022.
  - [1] **Sledzieski\***, Singh\*, Cowen, Berger, “D-SCRIPT translates genome to phenome with sequence-based, structure-aware, genome-scale predictions of protein-protein interactions,” *Cell Systems*, 12(10):969-982, 2021.
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**CONFERENCE AND WORKSHOPS**

- [6] **Sledzieski**, Versavel, Singh, Ocitti, Devkota, Kumar, Shhpilker, Roger, Yang, Lewinski, Putnam, Berger, Klein-Seetharaman, Cowen, “Decoding the Functional Interactome of Non-Model Organisms with PHILHARMONIC,” *Conference on Research in Computational Molecular Biology (RECOMB)*, 2025.
  - [5] **Sledzieski**, Kshirsagar, Baek, Berger, Dodhia, Lavista Ferres, “Parameter-Efficient Fine-Tuning of Protein Language Models Improves Prediction of Protein-Protein Interactions,” *Machine Learning for Structural Biology Workshop at NeurIPS*, 2023.
  - [4] **Sledzieski\***, Singh\*, Cowen, Berger, “Contrasting drugs from decoys,” *Machine Learning for Structural Biology Workshop at NeurIPS*, 2022.
  - [3] **Sledzieski\***, Singh\*, Cowen, Berger, “Adapting Protein Language Models for Rapid Drug-Target Interaction Prediction,” *Machine Learning for Structural Biology Workshop at NeurIPS*, 2021.
  - [2] **Sledzieski\***, Singh\*, Cowen, Berger, “Sequence-based prediction of protein-protein interactions: a structure-aware interpretable deep learning model,” *Conference on Research in Computational Molecular Biology (RECOMB)*, 2021.
  - [1] **Sledzieski\***, Zhang, Mandoiu, Bansal, “TreeFix-TP: Phylogenetic Error Correction for Accurate Reconstruction of Viral Transmission Networks,” *Pacific Symposium on Biocomputing (PSB)*, 2021.
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**PREPRINTS**

- [4] **Sledzieski**, Hanson, “RocketSHP: Ultra-fast Proteome-scale Prediction of Protein Dynamics,” *bioRxiv*, 2025. 10.1101/2025.06.12.659353.
- [3] Ullanat, Jing, **Sledzieski**, Berger, “Learning the language of protein-protein interactions,” *bioRxiv*, 2025. 10.1101/2025.03.09.642188v1.
- [2] Vizgaudis, Kumar, Olaosebikan, Roger, Brenner, **Sledzieski**, Yang, Lewinski, Singh, Daniels, Cowen, Klein-Seetharaman, “Insulin Signaling and Pharmacology in Corals,” *Authorea Preprints*, 2024. 10.22541/au.170666200.07483513/v1.

- [1] Kousi, Boix, Park, Mathys, **Sledzieski**, Peng, Bennett, Tsai, Kellis, “Single-cell mosaicism analysis reveals cell-type-specific somatic mutational burden in Alzheimers Dementia,” *bioRxiv*, 2022. 10.1101/2022.04.21.489103.

<b>PRESENTATIONS</b>	Cold Spring Harbor Laboratory Meeting on Network Biology	Mar 2021, Mar 2023, Mar 2025
	Biophysical Society Annual Meeting (BPS)	Jan 2025
	Intelligent Systems for Molecular Biology (ISMB)	Jul 2022, Jul 2023, Jul 2024
	Machine Learning in Structural Biology (MLSB) Workshop at NeurIPS	Dec 2021, Dec 2022, Dec 2023
	Research on Computational Molecular Biology (RECOMB)	Apr 2019, May 2022, Apr 2025
	Pacific Symposium on Biocomputing (PSB)	Jan 2021
	IEEE ICCABS Workshop on Computational Advances for Next Generation Sequencing	Oct 2018
	UConn Fall Frontiers in Undergraduate Research	Oct 2018
	University of Connecticut Bioinformatics Seminar	Mar 2018, Oct 2018
<b>AWARDS &amp; FELLOWSHIPS</b>	Flatiron Postdoctoral Research Fellowship	2024 - 2026
	National Science Foundation (NSF) Graduate Research Fellowship	2021 - 2024
	First Place, MIT Intro to Deep Learning Final Project Competition	2020
	New England Scholar, University of Connecticut	2017 – 2019
	Dean’s List, College of Liberal Arts and Sciences, School of Engineering	2015 – 2019
	Academic Excellence Scholarship, University of Connecticut	2015 – 2019
	National Merit Scholarship Finalist	2014
<b>SOFTWARE</b>	<b>D-SCRIPT</b>	<a href="https://github.com/samsledje/D-SCRIPT">https://github.com/samsledje/D-SCRIPT</a>
	58k+ PyPI downloads	
	<b>ConPLex</b>	<a href="https://github.com/samsledje/ConPLex">https://github.com/samsledje/ConPLex</a>
	24k+ PyPI downloads	
	<b>PHILHARMONIC</b>	<a href="https://github.com/samsledje/philharmonic">https://github.com/samsledje/philharmonic</a>
	5k+ PyPI downloads	
	<b>virDTL</b>	<a href="https://github.com/suz11001/virDTL">https://github.com/suz11001/virDTL</a>
	<b>TreeFix-TP</b>	<a href="https://github.com/samsledje/TreeFix-TP">https://github.com/samsledje/TreeFix-TP</a>
<b>MENTORING</b>	MIT Undergraduate Research Opportunities Program (UROP) Advisor	2021 – 2024
	MIT Research Summer Institute (RSI) Advisor	2022 – 2023
	HackMIT Mentor	2019 – 2022
<b>PEER REVIEW</b>	<i>Nature, Nature Methods, Nature Communications, Nature Biotechnology, Current Opinions in Structural Biology, Bioinformatics, Genome Biology, Journal of Computational Biology, PLOS Computational Biology, IEEE Transactions on Artificial Intelligence, NeurIPS, Machine Learning in Structural Biology (MLSB), RECOMB, ISMB</i>	
<b>MEMBERSHIPS &amp; ACTIVITIES</b>	International Society for Computational Biology (ISCB)	
	Institute of Electronics Engineers (IEEE)	
	Association for Computing Machinery (ACM)	
	Tau Beta Pi, Engineering Honor Society (TBII)	
	Eta Kappa Nu (IEEE-HKN)	
	Upsilon Pi Epsilon, Computer Science Honor Society (UPE)	

[CV compiled on 2025-09-10]

