JEFFREY M LOTTHAMMER

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SUMMARY

- Computational Systems Biology PhD Candidate with over 7 years of academic research experience.
- Experienced deep learning researcher with a proven track record of building and deploying models in biology.

EDUCATION

Washington University in St. Louis   August 2020 - Present
PhD Candidate in Computational Systems Biology
Department of Biochemistry and Molecular Biophysics
Thesis: Mapping Sequence Determinants of Disordered Protein Function

The Ohio State University   2016 - 2020
B.S. *with Honors Research Distinction* in Biochemistry   *Magna Cum Laude*
Thesis: Molecular Dynamics Simulations of the Inner-Ear Hair-Cell Mechanotransduction Apparatus

KEY SKILLS

Programming / SWE:	Python; Cython; Git/GitHub; testing; packaging; APIs
Deep Learning:	PyTorch; sequence models; generative models; model evaluation
Protein Design:	IDR-focused generative modeling; sequence-to-ensemble prediction; design-build-test loops
Bioinformatics:	Sequence analysis; feature engineering; dataset curation/QC
MLOps / Infra:	Slurm/HPC; Docker/Apptainer; W&B; k3s/Kubernetes (basic); profiling
Collaboration:	Cross-functional communication; scientific writing; presentations to mixed audiences

SOFTWARE / OPEN SOURCE

SPARROW (Python / PyTorch)   github.com/idptools/sparrow
Lead developer; extensible protein sequence analysis framework with built-in sequence-to-annotation inference.

RAVEN (Python / PyTorch)   private
Lead developer; generative modeling library for disordered protein sequences (training/inference pipelines).

STARLING (Python / PyTorch)   github.com/idptools/starling
Core developer; IDR sequence-to-ensemble generative model shipped as a Python package + CLI (CPU/GPU)

GOOSE (Python)   github.com/idptools/goose
Contributor; rational IDR design via composition and patterning targets (FCR, NCPR, κ).

FINCHES (Python)   github.com/idptools/finches
Contributor; Cython-optimized core algorithm for IDR interaction prediction ($\sim 50\times$ faster).

metapredict (Python)   github.com/idptools/metapredict
Contributor; accelerated disorder prediction pipeline (PyTorch / Cython; $\sim 100\times$ faster vs prior release).

SPARROW Online (Python / JavaScript)   sparrow-online.com
Sole developer; deployed web app for interactive IDP analysis.

RESEARCH EXPERIENCE

Washington University in St. Louis   Jul 2022 – Mar 2026 (expected)

Graduate Research Fellow (Advisor: Dr. Alex S. Holehouse)   St. Louis, MO

Washington University in St. Louis   Mar 2021 – Jun 2022

Graduate Student (Advisor: Dr. Gregory R. Bowman)   St. Louis, MO

The Ohio State University   2018 – Aug 2020

Undergraduate Research Fellow (Advisor: Dr. Marcos Sotomayor)   Columbus, OH

PUBLICATIONS

* indicates co-first authors

(1) Novak, B.*; **Lotthammer**, **J. M.***; Emenecker, R. J.; Holehouse, A. S. Accurate predictions of disordered protein ensembles with STARLING. *Nature* **2026**, 1–11.

(2) Ginell, G. M.; Emenecker, R. J.; **Lotthammer**, **J. M.**; Keeley, A. T.; Plassmeyer, S. P.; Razo, N.; Usher, E. T.; Pelham, J. F.; Holehouse, A. S. Sequence-based prediction of intermolecular interactions driven by disordered regions. *Science* **2025**, *388*, eadq8381.

(3) Romero-Pérez, P. S.; Moran, H. M.; Cordone Jr, D. P.; Horani, A.; Truong, A.; Manriquez-Sandoval, E.; Ramirez, J. F.; Martinez, A.; Gollub, E.; Hunter, K.; Kolamunna, K. C.; **Lotthammer**, **J. M.**; Emenecker, R. J.; Liu, H.; Iwasa, J. H.; Boothby, T. C.; Holehouse, A. S.; Fried, S. D.; Sukenik, S. Protein surface chemistry encodes an adaptive tolerance to desiccation. *Cell Syst.* **2025**, *16*, 101407.

(4) **Lotthammer**, **J. M.**; Holehouse, A. S. Disentangling folding from energetic traps in simulations of disordered proteins. *J. Chem. Inf. Model.* **2025**, *65*, 2897–2910.

(5) Giese, A. P. J.; Weng, W.-H.; Kindt, K. S.; Chang, H. H. V.; Montgomery, J. S.; Ratzan, E. M.; Beirl, A. J.; Aponte Rivera, R.; **Lotthammer**, **J. M.**; Walujkar, S.; Foster, M. P.; Zobeiri, O. A.; Holt, J. R.; Riazuddin, S.; Cullen, K. E.; Sotomayor, M.; Ahmed, Z. M. Complexes of vertebrate TMC1/2 and CIB2/3 proteins form hair-cell mechanotransduction cation channels. *Elife* **2025**, *12*.

(6) **Lotthammer**, **J. M.**; Hernández-García, J.; Griffith, D.; Weijers, D.; Holehouse, A. S.; Emenecker, R. J. Metapredict enables accurate disorder prediction across the Tree of Life. *bioRxiv* **2024**, 2024.11. 05.622168.

(7) DelRosso, N.; Suzuki, P. H.; Griffith, D.; **Lotthammer**, **J. M.**; Novak, B.; Kocalar, S.; Sheth, M. U.; Holehouse, A. S.; Bintu, L.; Fordyce, P. High-throughput affinity measurements of direct interactions between activation domains and co-activators. *bioRxiv* **2024**.

(8) Keeley, A. T.; **Lotthammer**, **J. M.**; Pelham, J. F. Rhythmidia: A modern tool for circadian period analysis of filamentous fungi. *PLoS Comput. Biol.* **2024**, *20*, e1012167.

(9) **Lotthammer**, **J. M.***; Ginell, G. M.*; Griffith, D.*; Emenecker, R. J.; Holehouse, A. S. Direct prediction of intrinsically disordered protein conformational properties from sequence. *Nat. Methods* **2024**, *21*, 465–476.

(10) Lehman, S. J.; Meller, A.; Solieva, S. O.; **Lotthammer**, **J. M.**; Greenberg, L.; Langer, S. J.; Greenberg, M. J.; Tardiff, J. C.; Bowman, G. R.; Leinwand, L. Divergent Molecular Phenotypes in Point Mutations at the Same Residue in Beta-Myosin Heavy Chain Lead to Distinct Cardiomyopathies. *bioRxiv* **2023**.

(11) Meller, A.; Ward, M.; Borowsky, J.; Kshirsagar, M.; **Lotthammer**, **J. M.**; Oviedo, F.; Ferres, J. L.; Bowman, G. R. Predicting locations of cryptic pockets from single protein structures using the PocketMiner graph neural network. *Nat. Commun.* **2023**, *14*, 1–15.

(12) Lee, L. A.; Barrick, S. K.; Meller, A.; Walklate, J.; **Lotthammer**, **J. M.**; Tay, J. W.; Stump, W. T.; Bowman, G.; Geeves, M. A.; Greenberg, M. J.; Leinwand, L. A. Functional divergence of the sarcomeric myosin, MYH7b, supports species-specific biological roles. *J. Biol. Chem.* **2023**, *299*, 102657.

(13) Meller, A.; **Lotthammer**, **J. M.**; Smith, L. G.; Novak, B.; Lee, L. A.; Kuhn, C. C.; Greenberg, L.; Leinwand, L. A.; Greenberg, M. J.; Bowman, G. R. Drug specificity and affinity are encoded in the probability of cryptic pocket opening in myosin motor domains. *Elife* **2023**, *12*, e83602.

(14) Walujkar, S.; **Lotthammer**, **J. M.**; Nisler, C. R.; Sudar, J. C.; Ballesteros, A.; Sotomayor, M. In Silico Electrophysiology of Inner-Ear Mechanotransduction Channel TMC1 Models. *bioRxiv* **2021**, 2021.09.17.460860.

SCHOLARSHIPS AND AWARDS

Spencer T. and Ann W. Olin Medical Science Fellow — March 9, 2026
Washington University in St. Louis

Travel Award — September 2024
Fellows Biophysical Research Conference at the NIH

Best Poster Award — June 2024
Biophysics and Biology of Intrinsically Disordered Proteins Gordon Research Conference

Frontera Computational Science Fellowship — April 2024
Texas Advanced Computing Center (TACC)

D.E. Shaw Research Fellowship — March 2024
D.E. Shaw Research

Student Research Achievement Award — February 2024
The Biophysical Society

68th Annual Biophysical Society Meeting Travel Award — November 2023
The Biophysical Society

BMB Professional Development Grant — November 2023
WUSTL Dept. of Biochemistry & Molecular Biophysics

NSF Graduate Research Fellowship — April 2022
The National Science Foundation

Student Research Achievement Award — February 2020
The Biophysical Society

64th Annual Biophysical Society Meeting Travel Award — February 2020
The Biophysical Society

Undergraduate Research Scholarship — August 2019 – May 2020
College of Arts and Sciences: Honors Program

The Gary Booth Scholarship Fund — August 2019 – May 2020
Department of Chemistry and Biochemistry

The Charles W. Medick Scholarship — August 2019 – May 2020
The Ohio State University

Mayer's Summer Research Fellowship — May 2019 – August 2019
College of Arts and Sciences: Natural and Mathematical Sciences

Mayer's Summer Research Fellowship — May 2018 – August 2018
College of Arts and Sciences: Natural and Mathematical Sciences

Maximus Scholarship — August 2016 – May 2020
The Ohio State University

ORAL PRESENTATIONS

70th Biophysical Society Annual Meeting   San Francisco, CA
Probabilistic Deep Learning Enables the Data-Driven Design of Disordered Proteins

Benzon Symposium 69 — Protein Structure Prediction & Design   Copenhagen, Denmark
Bayesian Deep Learning Enables the Data-Driven Design of Disordered Proteins

38th Gibbs Conference on Biothermodynamics   Carbondale, IL
Disentangling folding from energetic traps in simulations of disordered proteins

MGG/CSB/HSG/BIDS Retreat 2023   Grafton, IL
Direct Prediction of Intrinsically Disordered Protein Conformational Properties from Sequence

Chodera Lab Group Meeting — MSKCC   Manhattan, NY
Direct Prediction of Intrinsically Disordered Protein Conformational Properties from Sequence

SMBp Group Meeting — Flatiron Institute   Manhattan, NY
Direct Prediction of Intrinsically Disordered Protein Conformational Properties from Sequence

Biochemistry and Molecular Biophysics Science Friday   St. Louis, MO
Adaptive Sampling of the Actomyosin Mechanochemical Cycle

Autumn Undergraduate Research Festival   Columbus, OH
A Molecular Movie of Auditory Transduction in Inner-Ear Hair Cells

POSTERS

70th Biophysical Society Annual Meeting   San Francisco, CA — Feb 2026
Probabilistic Deep Learning Enables the Data-Driven Design of Disordered Proteins

69th Annual Biophysical Society National Conference   Los Angeles, CA — Feb 2025
A Flock of Computational Methods for Investigating Disordered Protein Regions

Intrinsically Disordered Protein Gordon Conference   Les Diablerets, Switzerland — June 2024
Direct Prediction of Intrinsically Disordered Protein Conformational Properties from Sequence

68th Annual Biophysical Society National Conference   Philadelphia, PA — Feb 2024
Direct Prediction of Intrinsically Disordered Protein Conformational Properties from Sequence

MOLSSI: Machine Learning and Chemistry – Are We There Yet?   College Park, MD — May 2023
Direct Prediction of Intrinsically Disordered Protein Conformational Properties from Sequence

67th Annual Biophysical Society National Conference   San Diego, CA — Feb 2023
Quantifying Local Conformational Heterogeneity in Simulations of Disordered Proteins

66th Annual Biophysical Society National Conference   San Francisco, CA — Feb 2022
Exploring the Myosin Active/Auto-inhibited State Equilibrium by Markov State Modeling

64th Annual Biophysical Society National Conference   San Diego, CA — Feb 2020
In-Silico Electrophysiology of Inner-Ear Mechanotransduction Channel TMC1 Models

63rd Annual Biophysical Society National Conference   Baltimore, MD — Mar 2019
Ion Permeation in Molecular Dynamics Simulations of TMEM16-based TMC1 Homology Models

TEACHING EXPERIENCE

Structural Bioinformatics of Proteins   August 2022 - Spring 2024
Assistant in Instruction for Dr. Craig Smith

Chemistry and Physics of Biomolecules   August 2021 - December 2021
Assistant in Instruction for Dr. Jay Ponder

COMMUNITY OUTREACH

Washington University in St. Louis   St. Louis, Missouri — March 2023 - Present
Summer Undergraduate Research Group Experience Committee

Washington University in St. Louis   St. Louis, Missouri — March 2023 - Present
Diversity, Equity and Inclusion Committee

Washington University in St. Louis   St. Louis, Missouri — May 2021 - August 2021
Young Scientists Program

The Ohio State University   Columbus, Ohio — August 2019 - May 2020
Undergraduate Research Ambassador

The Ohio State University   Columbus, Ohio — March 2019 - May 2020
College of Arts and Sciences: Honors Student Peer Mentor

The Ohio State University   Columbus, Ohio — March 2018 - May 2020
BuckeyeThon Liaison

SeriousFun Children's Network   Columbus, Ohio — September 2017 - May 2020
Student Volunteer