

Samuel M. D. Seaver, PhD

Computational Biologist: Finding signals in noisy systems — connecting data and tools in networks of every kind: molecular, metabolic, regulatory, social

Skokie, IL 60076 · samseaver@gmail.com · 773-655-3316

ORCID: <https://orcid.org/0000-0002-7674-5194>

Google Scholar: <https://scholar.google.com/citations?user=DMSBiAAAAAJ>

GitHub: <https://github.com/samseaver>

LinkedIn: <https://www.linkedin.com/in/sam-seaver/>

Professional summary

Computational biologist who connects across systems — integrating data and tools at every scale to turn complex biology into solvable problems. 20+ years spanning molecular biology, bioinformatics, and quantitative analysis, and a decade building the open-source resources for metabolic reconstruction in the plant- and microbial-systems-biology community: first or senior author of the **ModelSEED Biochemistry Database** and **PlantSEED**, and a core member of DOE's **KBase** plants team building the apps and data integration for the analysis of plant metabolism. Most recently adopting **machine learning** as a tool to simulate predictive fluxes from transcriptomics data — physics-informed, mass-balance-constrained optimization. Seeking a staff-scientist role with the research independence to build the next generation of predictive, mission-driven plant science.

Research interests

Genome-scale metabolic modeling · constraint-based reconstruction & analysis · biochemistry database curation & thermodynamics · physics-informed / mechanistic machine learning · multi-omics integration · plant & microbial systems biology.

Education

- **PhD, Biological Sciences**, Northwestern University, 2011. Dissertation: *Modeling of gene regulation and metabolism in microbial organisms* (Under Luís Amaral).
- **Postdoctoral Fellow**, Argonne National Laboratory, 2011–2015. Plant genomics & metabolic reconstruction.
- **MS, Molecular Modeling & Bioinformatics**, Birkbeck College, University of London, UK, 2001.
- **BS, Molecular Biology & Biochemistry**, Durham University, UK, 2000.

Appointments

- **Computational Scientist**, Argonne National Laboratory, Data Science & Learning Division, 2019–present.
 - **Senior Scientist at-large**, University of Chicago, 2025–present.
 - **Assistant Computational Scientist**, Argonne National Laboratory, 2015–2019.
 - Scientist at-large, University of Chicago, Consortium for Advanced Science & Engineering, 2013–2025.
 - Earlier: Intern, Integrated Genomics (2008); Research Technician (2002–2004) & Junior Bioinformatician (2001–2002), Northwestern University; Intern, European Bioinformatics Institute (EBI), Hinxton, UK (2000).
-

Selected accomplishments (impact highlights)

- **Reference community resources.** Led development of the ModelSEED Biochemistry Database (*NAR* 2021) and PlantSEED (*PNAS* 2014; *Plant Journal* 2018) — the resources labs use to reconstruct and compare genome-scale metabolic models — and, as a core member of the KBase plants team, built the apps for integrating data with, and simulation of, plant metabolic reconstructions in DOE's KBase (*Nature Biotechnology* 2018).
 - **Machine learning in metabolic simulation.** Senior-authored a flexible neural-mechanistic hybrid that simulates the iron-deficiency response in plant plastidial metabolism (bioRxiv 2026) — physics-informed neural-network solver machinery coupled to a mechanistic model.
 - **Biochemical curation.** Led "structure and formula curation across a ~56K-reaction / ~45K-compound biochemistry database, with 37K compounds carrying resolved structures and ~39K reactions carrying thermodynamics data integrated from multiple sources.
 - **Spatiotemporal integration of multi-omics datasets.** Built and tested pipelines integrating transcriptomics, proteomics, and dual-provider metabolomics across a four-species × two-tissue circadian time-course, mapped onto genome-scale metabolic networks.
 - **Protein contacts web server.** Wrote and released **MONSTER**, a web server that infers non-covalent interactions between peptide chains in macromolecular structures directly from atomic coordinates (*Nucleic Acids Research* 2004) — the first of many community tools built across the career.
-

Grants & funding

Amounts are total anticipated project value; role noted per award. Source: DOE Current & Pending Support (certified 2025-03-18).

As Principal Investigator

- **Integration of computational tools to explore the diversity of temporal regulation in plant specialized metabolism.** DOE Office of Science (BER, Genomic Science Program), PRJ1011480. **PI.** 2023–2026. **\$1,041,228.** Collaboration with K. Greenham (Univ. of Minnesota); develops integrative modeling approach incorporating multi-omics data with a metabolic reconstruction to predict metabolite abundances from enzyme abundances.
- **Quantitative Plant Science Initiative (QPSI) — Argonne computational subaward.** DOE BER Science Focus Area led by C. Blaby-Haas, Brookhaven National Laboratory. **PI of Argonne subaward, \$450,000, 2022–2023.** Led the metabolic-reconstruction and simulation aim on Fe/Zn metal-stress response in poplar and sorghum, within the multi-institution QPSI SFA.

As Senior Personnel (funded)

- **KBase: An Integrated Knowledgebase for Predictive Biology and Environmental Research.** DOE, PRJ1003559. Senior personnel. 2021–2026. \$16,420,000.
 - **Unlocking the Molecular Basis of Plant-Pathogen Interactions to Create Resilient Bioenergy Crops.** DOE, PRJ1011481. Senior personnel. 2023–2026. \$1,080,000.
-

Publications

Metrics: **2,914 citations** · **h-index 13** · **i10-index 16** (Google Scholar, Aug 2026). † first author · ‡ senior/corresponding author.

Reference resources & infrastructure

1. **Seaver SMD**†, Liu F, Zhang Q, Jeffries J, Faria JP, Edirisinghe JN, Mundy M, Chia N, Noor E, Beber ME, Best AA, DeJongh M, Kimbrel JA, D'haeseleer P, McCorkle SR, Bolton JR, Pearson E, Canon S, Wood-Charlson EM, Cottingham RW, Arkin AP, Henry CS. The ModelSEED Biochemistry Database for the integration of metabolic annotations and the reconstruction, comparison and analysis of metabolic models for plants, fungi and microbes.

Nucleic Acids Research 49(D1):D575–D588 (2021). 336 citations.

2. Arkin AP, Cottingham RW, Henry CS, Harris NL, Stevens RL, Maslov S, ... **Seaver SMD**, ... Yu D. KBase: The United States Department of Energy Systems Biology Knowledgebase. *Nature Biotechnology* 36(7):566–569 (2018). 1,917 citations. (KBase consortium, ~70 authors.)
3. **Seaver SMD**†, Gerdes S, Frelin O, Lerma-Ortiz C, Bradbury LM, Zallot R, Hasnain G, Niehaus TD, El Yacoubi B, Pasternak S, Olson R, Pusch G, Overbeek R, Stevens R, de Crécy-Lagard V, Ware D, Hanson AD, Henry CS. High-throughput comparison, functional annotation, and metabolic modeling of plant genomes using the PlantSEED resource. *PNAS* 111(26):9645–9650 (2014). 101 citations.
4. **Seaver SMD**†, Lerma-Ortiz C, Conrad N, Mikaili A, Sreedasyam A, Hanson AD, Henry CS. PlantSEED enables automated annotation and reconstruction of plant primary metabolism with improved compartmentalization and comparative consistency. *The Plant Journal* 95(6) (2018). 49 citations.
5. **Seaver SMD**†, Bradbury LM, Frelin O, Zarecki R, Rupp E, Hanson AD, Henry CS. Improved evidence-based genome-scale metabolic models for maize leaf, embryo, and endosperm. *Frontiers in Plant Science* 6 (2015). 75 citations.
6. Wood-Charlson EM, Henry CS, Dehal PS, Mahmud G, Allen BH, Beilsmith K, ... **Seaver SMD**, ... Arkin AP. KBase: Open-source platform for collaborative biological data analysis and publication. *Journal of Molecular Biology* 438(18):169676 (2026). (KBase consortium, ~42 authors.)

Machine learning & high-throughput reconstruction

7. El Alaoui S, Henry CS, Blaby-Haas CE, Paape T, Xie M, **Seaver SMD**‡. Simulating Iron Deficiency in Plant Plastidial Metabolism With a Flexible Neural-Mechanistic Hybrid Approach. *bioRxiv* 2025.06.10.658179v2 (2026). 1 citation.
8. Faria JP, Liu F, Edirisinghe JN, Gupta N, **Seaver SMD**, Freiburger AP, et al. ModelSEED v2: High-throughput genome-scale metabolic model reconstruction with enhanced energy biosynthesis pathway prediction. *bioRxiv* (2023). 35 citations.

Applied metabolic analysis & multi-omics

9. Mishra A, Bhat A, Kumari S, Sharma R, Braynen J, Tadesse D, El Alaoui S, **Seaver SMD**, Grosjean N, Ware D, Xie M, Paape T. Time-series multi-omics analysis of micronutrient stress in *Sorghum bicolor* reveals iron and zinc crosstalk and regulatory network conservation. *Plant Biology (Stuttg)* (2025). PMID 40402192. 4 citations.
10. Beilsmith K, Henry CS, **Seaver SMD**‡. Genome-scale modeling of the primary–specialized metabolism interface. *Current Opinion in Plant Biology* 68 (2022). 12 citations.
11. **Seaver SMD**†. Systems-level analysis of the plasticity of the maize metabolic network reveals novel hypotheses in the nitrogen-use efficiency of maize roots. *Journal of Experimental Botany* 73(1) (2022). Invited editorial. 2 citations.
12. Kumari S, Kumar V, Beilsmith K, **Seaver SMD**, Canon S, Dehal P, Gu T, Joachimiak M, Lerma-Ortiz C, Liu F, Lu Z, Pearson E, Ranjan P, Riel W, Henry C, Arkin A, Ware D. A KBase case study on genome-wide transcriptomics and plant primary metabolism in response to drought stress in Sorghum. *Current Plant Biology* 28:100229 (2021). 11 citations.
13. Jeffries JG, **Seaver SMD**, Faria JP, Henry CS. A pathway for every product? Tools to discover and design plant metabolism. *Plant Science* 273 (2018). 27 citations.
14. Noutsos C, Perera AM, Nikolau BJ, **Seaver SMD**, Ware DH. Metabolomic profiling of the nectars of *Aquilegia pubescens* and *A. canadensis*. *PLoS One* 10(5) (2015). 26 citations.
15. Töpfer N, **Seaver SMD**, Aharoni A. Integration of plant metabolomics data with metabolic networks: progresses and challenges. *Plant Metabolomics: Methods and Protocols (Methods Mol Biol)* (2018). 17 citations.
16. Faria JP, Khazaei T, Edirisinghe JN, Weisenhorn P, **Seaver SMD**, et al. Constructing and analyzing metabolic flux models of microbial communities. *Hydrocarbon and Lipid Microbiology Protocols* (2016). 18 citations.
17. Colasanti R, Edirisinghe JN, Khazaei T, Faria JP, **Seaver SMD**, Xia F, et al. Tapping the Wealth of Microbial Data in High-Throughput Metabolic Model Reconstruction. *Metabolic Flux Analysis: Methods and Protocols* (2014).

Foundational reviews & early quantitative work

18. Gerdes S, Lerma-Ortiz C, Frelin O, **Seaver SMD**, Henry CS, de Crécy-Lagard V, Hanson AD. Plant B vitamin

pathways and their compartmentation: a guide for the perplexed. *Journal of Experimental Botany* 63(15) (2012). 122 citations.

19. **Seaver SMD**[†], Henry CS, Hanson AD. Frontiers in metabolic reconstruction and modeling of plant genomes. *Journal of Experimental Botany* 63(6):2247–2258 (2012). 92 citations.
20. **Seaver SMD**[†], Sales-Pardo M, Guimerà R, Amaral LA. Phenomenological model for predicting the catabolic potential of an arbitrary nutrient. *PLoS Computational Biology* 8(11):e1002762 (2012). 2 citations.
21. **Seaver SMD**[†], Moreira AA, Sales-Pardo M, Malmgren RD, Diermeier D, Amaral LA. Micro-bias and macro-performance. *European Physical Journal B* 67(3):369–375 (2009). 10 citations.
22. Salerno WJ, **Seaver SMD**, Armstrong BR, Radhakrishnan I. MONSTER: inferring non-covalent interactions in macromolecular structures from atomic coordinate data. *Nucleic Acids Research* 32(Web Server):W566–W568 (2004). 47 citations.
23. **Seaver SMD**[†]. Modeling of gene regulation and metabolism in microbial organisms. PhD dissertation, Northwestern University (2011).

Software & scientific resources

- **ModelSEED Biochemistry Database** — reference biochemistry DB (compounds, reactions, structures, thermodynamics, mass/charge balancing); ongoing curation lead.
- **PlantSEED** — automated plant-metabolism annotation & genome-scale reconstruction; integrated in KBase; leading a v3 refactor.
- **KBase (plants team)** — built plant metabolic-modeling apps and integrated plant data on DOE's Systems Biology Knowledgebase.
- **BioFlux — neural-mechanistic hybrid optimization** — biochemistry-informed mechanistic gradient optimization with mass-balance constraints (PINN solver machinery; no trained weights).

Mentoring & leadership

Have trained **10+ interns, graduate students, and postdocs** over ~15 years, leading by growing people into new capabilities and building the shared tools and teams that let them do their best work. Recent examples: senior-authored the flagship ML preprint led by a mentee (S. El Alaoui); supervised graduate and intern researchers on the structure-validation and thermodynamics pipelines.

Selected collaborations

KBase consortium (DOE, multi-lab) · Greenham lab (circadian multi-omics) · DOE Joint Genome Institute (plant genomics/metabolomics) · Hanson lab (plant biochemistry).

Invited talks & seminars

- **Invited talk (2026)** — *Interpreting metabolic imbalance in hybrid ML–constraint-based models* — 10th Conference on Constraint-Based Reconstruction and Analysis (COBRA), Potsdam, Germany.
- **Invited talk (2025)** — *Science, Unmuted* (accessibility & inclusion in science) — University of Tennessee, Knoxville (REU program).
- **Invited departmental seminar (2024)** — *Predicting metabolic fluxes in plant tissues* — University of Minnesota, Dept. of Plant & Microbial Biology.
- **Invited talk (2019)** — *Plant Informatics in DOE Systems Biology KnowledgeBase* — IPK Gatersleben, Germany.
- **Invited seminar (2018)** — *PlantSEED Enables Automated Reconstruction of Plant Primary Metabolism...* — Charles University, Prague.
- **Invited seminar (2016)** — *The key evidence underlying the construction and analysis of plant-microbial metabolic*

models — Plant Systems Biology Group, Oak Ridge National Laboratory.

- **Invited workshop talk (2016)** — *Plant Workflows in Persistent KBase Narratives* — Multi-scale Plant Modeling Workshop, EMSL, Pacific Northwest National Laboratory.
- **Invited European seminar series (2015)** — "*The key evidence underlying the top-down construction, propagation and analysis of genome-scale plant metabolic models*" — presented at the Max Planck Institute of Molecular Plant Physiology (Potsdam), CEPLAS / Cluster of Excellence on Plant Science (Düsseldorf), Institut Jean-Pierre Bourgin (Versailles), Vrije Universiteit Amsterdam, Oxford Brookes University, and Universitat Rovira i Virgili (Tarragona).
- **Invited talk (2013)** — *Modeling Angiosperm Metabolism in silico: a History, Applications, and the Future* — Symposium on Plant Science & Agricultural Biotechnology, NC State University.

Contributed conference talks

- Selected oral presentation — *plant metabolic networks* — ICAR 2018 (Int'l Conference on Arabidopsis Research), Turku, Finland (abstract selected for oral).
- *Enabling the Systemic Inter-specific Comparison of Predicted Metabolic Responses...* — Plant Biology 2016, Austin, TX.
- *When Biologists and Modelers Meet in KBase: Modeling Plant–Microbe Metabolic Interactions* (with D. Weston) — Plant & Animal Genome (PAG) XXIV, San Diego (2016).
- *Metabolic Modeling of Plant–Microbe Interactions in KBase and The PlantSEED Resource for Functional Annotation and Cross-Kingdom Comparative Genomics* — PAG XXIII, San Diego (2015).
- *Refinement of Maize Genome-scale Metabolic Models for Leaf, Embryo, and Endosperm* — Plant Biology 2015, Minneapolis, MN.
- *Metabolic Reconstruction in KBase* — PAG XXII, San Diego (2014).
- *Comparative Genomics and Systems Approaches to Primary Metabolism in Magnoliophyta* — Plant Biology 2013, Providence, RI.

Workshops & symposia organized

- **Metabolic Reconstruction and Flux Modelling** — workshop co-led with N. Töpfer, German Conference on Bioinformatics (GCB), online (2021).
- **KBase & metabolic-modeling workshop** — ASPB Plant Biology (online, 2021), co-led with K. Beilsmith.
- **Metabolic Networks Symposia/Workshops** — ICAR 2018 (Turku, Finland), Plant Biology 2016 (Austin), and Plant Biology 2013 (Providence).
- **PlantSEED Workshops** — Northwestern University (2016, 2018) and University of Florida (2015, 2017).

Professional service & activities

- Community workshops: Nitrogen Economy "Big Idea" Workshop, ORNL (2016); iPASS Multiscale Plant Modeling Workshop, PNNL (2016); Software Carpentry instructor, Plant Biology 2014 (Portland).
- Member, American Society of Plant Biology (2011–2015).
- **Journal peer review** (ad hoc referee): *The Plant Journal* (2018, 2022) · *New Phytologist* (2022) · *Plant Physiology* · *Plant Biology* (2024–2025) · *in silico Plants* (2024) · *GigaScience* (2016) · *BMC Systems Biology* (2018) · *Phycological Research* (2021) · *Standards in Genomic Sciences* (2015) · *3 Biotech* (Springer, 2012–2015).
- **Conference program committee**: NetSci 2025 (International School & Conference on Network Science).

Honors & awards

- NIH Predoctoral Biotechnology Training Grant (T32), 2006–2008.
- Student Poster Award, Northwestern Institute for Complex Systems, 2006.