

Payman Tohidifar

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SUMMARY

Computational biologist and biomolecular engineer with 14+ years of experience spanning molecular biology, computational science, and AI to solve complex biological problems. Hands-on experience spans bioinformatics, software development and AI, from conventional ML to modern architectures and foundation models, on the computational side, and molecular biology, genetics, and biosynthesis on the experimental side. A collaborative team player and independent, innovative problem-solver (6 patents filed), comfortable navigating shifting project scope across computational, wet-lab, and engineering domains. Passionate about applying AI to advance biological discovery.

TECHNICAL SKILLS

Programming/Scripting: Python, R, Bash, C++

Deep Learning Frameworks: PyTorch, JAX/Flax, TensorFlow/Keras (familiar)

Data Science & Computing: NumPy, SciPy, Pandas, Scikit-learn, Seaborn, Jupyter Lab, HPC/Slurm

SWE Tools: VS Code, Claude Code, Pixi/Conda, uv/pip, Docker, Git, CI/CD (GitLab CI, GitHub Actions)

CompBio & Bioinformatics: DESeq2, HMMER, BLAST, fastp, SeqKit, Bowtie2, Samtools, bedtools, IGV, EPI2ME, MEME Suite, Nextflow;
Databases: NCBI, Ensembl, UniProt, AlphaFold, PDB, KEGG, GO

MolBio & Genetics: Protein engineering/expression, CRISPR editing, ONT sequencing, Flow cytometry, Genetic assembly

EXPERIENCE

Scientist

Feb 2022 – Present

BP (Biosciences, Technology and Innovation)

San Diego, CA

- Engineered and deployed an end-to-end, ML-assisted low-N protein engineering pipeline, combining unsupervised (VAE, transformer) feature extraction with supervised fitness models, to improve industrial enzyme activity and thermostability.
- Built statistical and ML pipelines to analyze complex, multi-dimensional biorefinery data, directly informing key business decisions.
- Built a full-stack GUI for ingestion, consolidation, statistical analytics, and visualization of multi-modal biological data across projects; selected as a top-3 platform for executive leadership review (see a *demo prototype*).
- Co-developed a semi-automated HTP directed-evolution and protein-expression pipeline that cut turnaround time from 6 weeks to 2 weeks, accelerating the DBTL cycle.
- Developed an HTP platform (a novel FACS + 2A-peptide co-translation method) to boost protein production in an industrial fungal host, identifying multiple enzyme hyperproducers for scaled testing and cutting discovery time from 1+ year to 3 months.
- Standardized in-house Oxford Nanopore long-read sequencing and de novo genome assembly SOPs (EPI2ME, Nextflow).
- Led a 7-person cross-functional project on biosynthesis of value-added small molecules, resulting in publication of 6+ patent applications within 3 years.
- Built a CRISPR-MAD7 platform for single-nucleotide-resolution genetic engineering, enabling construction of 50+ bacterial cell lines and replacing a technology costing over \$10K/yr.

Postdoctoral Research Associate

Aug 2019 – Feb 2022

Institute for Genomic Biology, UIUC

Urbana, IL

- Co-developed a modular genetic toolkit for multi-gene expression and CRISPR-Cas9 chromosomal editing in two non-model oleaginous yeasts, enabling biosynthesis of value-added small molecules (2 publications, 1 conference paper).

Graduate Research Assistant

Jan 2012 – May 2019

Department of Chemical & Biomolecular Engineering

Urbana, IL

- Co-developed a modular C++ framework for multiscale simulation of cellular population behavior in response to complex spatiotemporal chemical gradients (see *here* for details).
- Led three independent projects elucidating molecular mechanisms of unconventional chemoreceptor sensing in bacteria, bidirectional pH, alcohol, and toxic aromatic molecule sensing, spanning protein engineering, genetic engineering, bioinformatics, structural biology, and MD simulations; resulted in 3 journal publications and multiple conference presentations.
- Led discovery and characterization of an unconventional DNA-sensing receptor in *B. subtilis* using in vivo/in vitro assays and in silico motif-discovery analysis; presented at multiple conferences and awarded Best Presentation (see *here* for details).

VOLUNTARY PROJECTS

Deep Learning for Protein Function Prediction | [GitHub Repo](#)

June 2026 – July 2026

- Built a modular deep learning platform (PyTorch, JAX/Flax) on the CAFA benchmark to predict multi-label protein function across 291 Gene Ontology terms from sequence alone, integrating ESM-2 transformer embeddings into an extensible framework for rapid experimentation with custom architectures, loss functions, and metrics.

Production ready GPT-2 Text Classifier From Scratch | [GitHub Repo](#)

April 2026 – May 2026

- Built a GPT-2 architecture from scratch in PyTorch for text classification, with a configuration-driven pipeline that ingests multi-source, two-column datasets with zero code changes.
- Scaled training across multiple GPUs via Distributed Data Parallel (DDP) with real-time tracking in Weights & Biases (WandB), and built an end-to-end evaluation suite for benchmarking and iterative experimentation.

Lung Cancer Bulk RNA-Seq Data Analysis Pipeline | [GitHub Repo](#)

Feb 2026 – April 2026

- Built an end-to-end Python/R pipeline for CCLE bulk RNA-seq data – count processing, PCA, hierarchical clustering, differential expression, and pathway enrichment.

PUBLICATIONS

Co-first authors are denoted with asterisks.

8. Koh, HG.*, **Tohidifar, P.***, Oh, H., Ye, Q., Jung, SC., Rao, CV., Jin, YS. (2025) RT-EZ: A Golden Gate Assembly Toolkit for Streamlined Genetic Engineering of *Rhodotorula toruloides*. ACS Synth. Biol.
7. Hamed, S., Emara, M., **Tohidifar, P.**, Rao, CV. (2025) N-Acetyl Cysteine Exhibits Antimicrobial and Anti-Virulence Activity Against *Salmonella enterica*. PLoS One.
6. Yook, S., Deewan, A., Ziolkowski, L., Lane, S., **Tohidifar, P.**, Cheng, M., Singh, V., Stasiewicz, MJ., Rao, CV., Jin, YS. (2025) Engineering and Evolution of *Yarrowia lipolytica* for Producing Lipids from Lignocellulosic Hydrolysates. Bioresource Technology.
5. Bodhankar, GA., **Tohidifar, P.**, Foust, ZL., Ordal, GW., Rao, CV. (2022) Characterization of Opposing Responses to Phenol by *Bacillus subtilis* Chemoreceptors. J Bacteriol.
4. Joseph, E.*, **Tohidifar, P.***, Sarver, CT., Mackie, RI., Rao, CV. (2022) Fundamentals of Polymer Biodegradation Mechanisms. Wiley (Book chapter).
3. **Tohidifar, P.**, Bodhankar, GA.*, Pei, S.*, Cassidy, CK., Walukiewicz, HE., Ordal, GW., Stansfeld, PJ., Rao, CV. (2020) The Unconventional Cytoplasmic Sensing Mechanism for Ethanol Chemotaxis in *Bacillus subtilis*. mBio.
2. **Tohidifar, P.**, Plutz, MJ., Ordal, GW., Rao, CV. (2020) The Mechanism of Bidirectional pH Taxis in *Bacillus subtilis*. J Bacteriol.
1. Walukiewicz, HE., **Tohidifar, P.**, Ordal, GW., Rao, CV. (2014) Three Adaptation Systems of *B. subtilis* Chemotaxis. Molecular Microbiology.

PATENTS

4. "Recombinant microorganisms for beta-myrecene and nerol production." Valle, F., Vu, HNN., **Tohidifar, P.** Patent Application Pub. No. WO/2026/122843 A1, published June 11, 2026.
 3. "Engineered dxp pathway for improved isoprenoid production in *E. coli*." Valle, F., **Tohidifar, P.**, Najdi, T., Vu, HNN. Patent Application Pub. No. WO/2025/155822 A1, published July 24, 2025.
 2. "Recombinant microorganisms with increased accumulation and/or flux of cytidine triphosphate (CTP)." Valle, F., **Tohidifar, P.**, Najdi, T. Patent Application Pub. No. WO/2025/111429 A1, published May 30, 2025.
 1. "Gluconate-regulated expression systems." Valle, F., **Tohidifar, P.** Patent Application Pub. No. WO/2025/059030 A1, published March 20, 2025.
- Co-invented 2 provisional patent applications with colleagues, covering novel enzymes and metabolic pathways for the biosynthesis of value-added small molecules (filed Feb 2 and Feb 19, 2026).

EDUCATION

University of Illinois at Urbana-Champaign (UIUC)

Urbana, IL

Ph.D. in Chemical & Biomolecular Engineering

2019

- Computational Science & Engineering Certificate, 2019
- Dissertation: *Non-canonical sensing mechanisms in bacteria*

Sharif University of Technology

Tehran, Iran

B.S. in Chemical Engineering

2011

COURSEWORK & CERTIFICATIONS

- Self-Study: *Deep Learning for Biology*, C. Ravarani and N. Latysheva (O'Reilly Media, 2025) – in progress (*Notes*)
- *Claude Code: A Highly Agentic Coding Assistant*, DeepLearning.AI (2026)
- Deep Learning Specialization, Coursera (2026) (*Credential, Notes*)
- Self-Study: *Build a Large Language Model (From Scratch)*, S. Raschka (Manning Publications, 2024) – completed 2026 (*Notes*)
- Machine Learning Specialization, Coursera (2025) (*Credential, Notes*)
- Mathematics for Machine Learning and Data Science Specialization, Coursera (2025) (*Credential*)
- bp Data Science Intermediate Bootcamp, Pragmatic Institute (2024) (*Credential*)
- Computational Science & Engineering Certificate, UIUC (2019) – Numerical Analysis (CS450), Numerical Methods for PDEs (CS555), Introduction to Optimization (CSE441), Nonlinear Dynamics (PHYS510)
- ChIP-Seq Analysis Hands-On Training, High-Performance Biological Computing, UIUC (2017)

SELECTED CONFERENCE TALKS

- **Tohidifar, P.**, Kimura, Y., Rao, CV. (2015) A modular computational framework for multi-scale simulation of chemotaxis in complex environments. AIChE, Salt Lake City, UT.
- **Tohidifar, P.**, Walukiewicz, HE., Ordal, GW., Rao, CV. (2016) DNA taxis in *Bacillus subtilis*. Receptor Fest 19th Annual Meeting, Santa Barbara, CA.
- **Tohidifar, P.**, Walukiewicz, HE., Ordal, GW., Rao, CV. (2017) DNA sensing in *Bacillus subtilis*. BLAST XIV, New Orleans, LA.

HONORS & AWARDS

- Nucleic Acids Research Award for an Outstanding Poster/Oral Presentation by a Young Investigator, BLAST XIV, New Orleans, LA, 2017.
- Graduate College Conference Travel Award, UIUC, 2016.
- Graduated with honors (ranked 2nd/120), Department of Chemical Engineering, Sharif University of Technology, Iran, 2011.
- Singapore International Pre-Graduate Award, ICES, A*STAR, Singapore, 2010.

PROFESSIONAL SERVICE

- Reviewer for PLoS Computational Biology and PLoS One, 2018 – present.