Stanford



Brian Hie

Assistant Professor of Chemical Engineering

Curriculum Vitae available Online

Bio

BIO

I am an Assistant Professor of Chemical Engineering at Stanford University, the Dieter Schwarz Foundation Stanford Data Science Faculty Fellow, and an Innovation Investigator at Arc Institute. I supervise the Laboratory of Evolutionary Design, where we conduct research at the intersection of biology and machine learning.

I was previously a Stanford Science Fellow in the Stanford University School of Medicine and a Visiting Researcher at Meta AI. I completed my Ph.D. at MIT CSAIL and was an undergraduate at Stanford University.

ACADEMIC APPOINTMENTS

- Assistant Professor, Chemical Engineering
- Member, Bio-X
- Affiliate, Institute for Human-Centered Artificial Intelligence (HAI)
- Faculty Fellow, Sarafan ChEM-H
- The Dieter Schwarz Foundation SDS Faculty Fellow, Stanford Data Science

HONORS AND AWARDS

- AI2050 Early Career Fellow, Schmidt Sciences (2025)
- Innovation Investigator, Arc Institute (2024)
- Stanford Science Fellow, Stanford University (2021)
- National Defense Science and Engineering Graduate Fellowship Program, US Department of Defense (2019)

BOARDS, ADVISORY COMMITTEES, PROFESSIONAL ORGANIZATIONS

- Board of Reviewing Editors, Science Magazine (2025 - present)

PROFESSIONAL EDUCATION

- Ph.D., Massachusetts Institute of Technology , Electrical Engineering and Computer Science (2021)
- M.S., Massachusetts Institute of Technology , Electrical Engineering and Computer Science (2019)
- B.S.H., Stanford University , Computer Science (2016)

PATENTS

- Anupama Thubagere Jagadeesh, Brian Hie. "United States Patent 11,532,400 Hyperspectral scanning to determine skin health", Dec 20, 2022

- Brian Hie, Bonnie Berger, Hyunghoon Cho. "United States Patent 11,450,439 Realizing private and practical pharmacological collaboration using a neural network architecture configured for reduced computation overhead", Sep 20, 2022
- Brian Hie, Bryan Bryson, Bonnie Berger. "United States Patent 11,011,253 Escape profiling for therapeutic and vaccine development", May 18, 2021

LINKS

- Lab site: https://evodesign.org/
- Personal site: http://brianhie.com/
- Twitter: https://twitter.com/BrianHie
- GitHub: https://github.com/brianhie/

Teaching

COURSES

2026-27

- Colloquium: CHEMENG 699 (Aut, Spr)
- Data Science and Machine Learning Approaches in Chemical and Materials Engineering: CHEMENG 177, CHEMENG 277, MATSCI 166, MATSCI 176 (Win)

2025-26

- Colloquium: CHEMENG 699 (Aut, Spr)
- Data Science and Machine Learning Approaches in Chemical and Materials Engineering: CHEMENG 177, CHEMENG 277, MATSCI 166, MATSCI 176 (Win)
- Data Science for Computational Molecular Biology: DATASCI 194B, DATASCI 294B (Spr)

2024-25

- Colloquium: CHEMENG 699 (Aut, Win, Spr)
- Data Science and Machine Learning Approaches in Chemical and Materials Engineering: CHEMENG 177, CHEMENG 277, MATSCI 166, MATSCI 176 (Win)
- Data Science for Computational Molecular Biology: DATASCI 194B, DATASCI 294B (Spr)

STANFORD ADVISEES

Doctoral Dissertation Reader (AC)

Chiho Im, Tianyu Lu, Richard Shuai, Sebastian Somolinos Cedeno, Alp Tartici

Postdoctoral Faculty Sponsor

Alex Hao, Lily Taylor

Doctoral Dissertation Advisor (AC)

Brandon Ameglio, Garyk Brixi, Daniel Chang, Brian Kang, Samuel King, Aditi Merchant, Soyoon Park, Talal Widatalla

Doctoral Dissertation Co-Advisor (AC)

Mia Grahn, Ivan Specht, Chloe Wen, Chang M. Yun

Doctoral (Program)

Matthew Liu, Divya Nori

Publications

PUBLICATIONS

- **Machine learning-assisted directed evolution of plant Rubisco.** *Science advances*
  McDonald, J. L., Lin, J., Zhao, Y., Hie, B. L., Birch, R., Gehring, M., Bryson, B. D., Whitney, S. M., Shoulders, M. D., Wilson, R. H.
  2026; 12 (41): eaeh3246

- **Aligning protein-generative models to experimental fitness with ProteinDPO.** *Nature methods*
  Widatalla, T., Borah, A. A., King, S. H., Driscoll, C. L., Rafailov, R., Hie, B. L.
  2026

- **Alignment with experimental data improves protein generative modeling** *NATURE METHODS*
  Widatalla, T., Hie, B. L.
  2026

- **Generative design of bacteriophages with genome language models.** *Science (New York, N.Y.)*
  King, S. H., Driscoll, C. L., Li, D. B., Guo, D., Merchant, A. T., Brixi, G., Wilkinson, M. E., Hie, B. L.
  2026; 393 (6811): eaec2657

- **Efficient generation of epitope-targeted antibodies with Germinal.** *Nature biotechnology*
  Mille-Fragoso, L. S., Driscoll, C. L., Wang, J. N., Dai, H., Widatalla, T., Zhang, J. L., Zhang, X., Rao, B., Feng, L., Hie, B. L., Gao, X. J.
  2026

- **Genome modelling and design across all domains of life with Evo 2.** *Nature*
  Brixi, G., Durrant, M. G., Ku, J., Naghipourfar, M., Poli, M., Sun, G., Brockman, G., Chang, D., Fanton, A., Gonzalez, G. A., King, S. H., Li, D. B., Merchant, et al
  2026

- **Rapid directed evolution guided by protein language models and epistatic interactions.** *Science (New York, N.Y.)*
  Tran, V. Q., Nemeth, M., Bartie, L. J., Chandrasekaran, S. S., Fanton, A., Moon, H. C., Hie, B. L., Konermann, S., Hsu, P. D.
  2026: eaea1820

- **Semantic design of functional de novo genes from a genomic language model.** *Nature*
  Merchant, A. T., King, S. H., Nguyen, E., Hie, B. L.
  2025

- **Efficient generation of epitope-targetedde novoantibodies with Germinal.** *bioRxiv : the preprint server for biology*
  Mille-Fragoso, L. S., Wang, J. N., Driscoll, C. L., Dai, H., Widatalla, T., Zhang, X., Hie, B. L., Gao, X. J.
  2025

- **Sidechain conditioning and modeling for full-atom protein sequence design with FAMPNN.** *Proceedings of machine learning research*
  Widatalla, T., Shuai, R. W., Hie, B. L., Huang, P. S.
  2025; 267: 66746-66771

- **Sidechain conditioning and modeling for full-atom protein sequence design with FAMPNN.** *Proceedings of machine learning research*
  Widatalla, T., Shuai, R. W., Hie, B. L., Huang, P.
  2025; 267: 66746-66771

- **Utilizing Machine Learning to Improve Neutralization Potency of an HIV-1 Antibody Targeting the gp41 N-Heptad Repeat.** *ACS chemical biology*
  Filsinger Interrante, M. V., Tang, S., Kim, S., Shanker, V. R., Hie, B. L., Bruun, T. U., Wu, W., Pak, J. E., Fernandez, D., Kim, P. S.
  2025

- **Sidechain conditioning and modeling for full-atom protein sequence design with FAMPNN**
  Widatalla, T., Shuai, R. W., Hie, B. L., Huang, P.
  edited by Singh, A., Fazel, M., Hsu, D., Lacoste-Julien, S., Berkenkamp, F., Maharaj, T., Wagstaff, K., Zhu, J.
  JMLR-JOURNAL MACHINE LEARNING RESEARCH.2025: 66746-66771

- **Sequence modeling and design from molecular to genome scale with Evo.** *Science (New York, N.Y.)*
  Nguyen, E., Poli, M., Durrant, M. G., Kang, B., Katrekar, D., Li, D. B., Bartie, L. J., Thomas, A. W., King, S. H., Brixi, G., Sullivan, J., Ng, M. Y., Lewis, et al
  2024; 386 (6723): eado9336
- **Unsupervised evolution of protein and antibody complexes with a structure-informed language model.** *Science (New York, N.Y.)*
  Shanker, V. R., Bruun, T. U., Hie, B. L., Kim, P. S.
  2024; 385 (6704): 46-53
- **Scanorama: integrating large and diverse single-cell transcriptomic datasets.** *Nature protocols*
  Hie, B. L., Kim, S., Rando, T. A., Bryson, B., Berger, B.
  2024
- **Generative artificial intelligence for de novo protein design.** *Current opinion in structural biology*
  Winnifrith, A., Outeiral, C., Hie, B. L.
  2024; 86: 102794
- **Inverse folding of protein complexes with a structure-informed language model enables unsupervised antibody evolution.** *bioRxiv : the preprint server for biology*
  Shanker, V. R., Bruun, T. U., Hie, B. L., Kim, P. S.
  2023
- **Machine Learning for Protein Engineering.** *ArXiv*
  Johnston, K. E., Fannjiang, C., Wittmann, B. J., Hie, B. L., Yang, K. K., Wu, Z.
  2023
- **Efficient evolution of human antibodies from general protein language models.** *Nature biotechnology*
  Hie, B. L., Shanker, V. R., Xu, D., Bruun, T. U., Weidenbacher, P. A., Tang, S., Wu, W., Pak, J. E., Kim, P. S.
  2023
- **Evolutionary-scale prediction of atomic-level protein structure with a language model.** *Science (New York, N.Y.)*
  Lin, Z., Akin, H., Rao, R., Hie, B., Zhu, Z., Lu, W., Smetanin, N., Verkuil, R., Kabeli, O., Shmueli, Y., Dos Santos Costa, A., Fazel-Zarandi, M., Sercu, et al
  2023; 379 (6637): 1123-1130
- **Evolutionary velocity with protein language models predicts evolutionary dynamics of diverse proteins.** *Cell systems*
  Hie, B. L., Yang, K. K., Kim, P. S.
  2022
- **Predicting the mutational drivers of future SARS-CoV-2 variants of concern.** *Science translational medicine*
  Maher, M. C., Bartha, I., Weaver, S., di Iulio, J., Ferri, E., Soriaga, L., Lempp, F. A., Hie, B. L., Bryson, B., Berger, B., Robertson, D. L., Snell, G., Corti, et al
  1800: eabk3445
- **Adaptive machine learning for protein engineering.** *Current opinion in structural biology*
  Hie, B. L., Yang, K. K.
  1800; 72: 145-152
- **Schema: metric learning enables interpretable synthesis of heterogeneous single-cell modalities** *GENOME BIOLOGY*
  Singh, R., Hie, B. L., Narayan, A., Berger, B.
  2021; 22 (1): 131
- **Learning the language of viral evolution and escape** *SCIENCE*
  Hie, B., Zhong, E. D., Berger, B., Bryson, B.
  2021; 371 (6526): 284-+
- **Leveraging Uncertainty in Machine Learning Accelerates Biological Discovery and Design** *CELL SYSTEMS*
  Hie, B., Bryson, B. D., Berger, B.
  2020; 11 (5): 461-+

- **Computational Methods for Single-Cell RNA Sequencing** *ANNUAL REVIEW OF BIOMEDICAL DATA SCIENCE, VOL 3, 2020*
  Hie, B., Peters, J., Nyquist, S. K., Shalek, A. K., Berger, B., Bryson, B. D.
  edited by Altman, R. B.
  2020; 3: 339-364
- **Geometric Sketching Compactly Summarizes the Single-Cell Transcriptomic Landscape** *CELL SYSTEMS*
  Hie, B., Cho, H., DeMeo, B., Bryson, B., Berger, B.
  2019; 8 (6): 483-+
- **Efficient integration of heterogeneous single-cell transcriptomes using Scanorama** *NATURE BIOTECHNOLOGY*
  Hie, B., Bryson, B., Berger, B.
  2019; 37 (6): 685-+
- **Fine-mapping cis-regulatory variants in diverse human populations** *ELIFE*
  Tehranchi, A., Hie, B., Dacre, M., Kaplow, I., Pettie, K., Combs, P., Fraser, H. B.
  2019; 8
- **Realizing private and practical pharmacological collaboration** *SCIENCE*
  Hie, B., Cho, H., Berger, B.
  2018; 362 (6412): 347-350
- **Pooled ChIP-Seq Links Variation in Transcription Factor Binding to Complex Disease Risk** *CELL*
  Tehranchi, A. K., Myrthil, M., Martin, T., Hie, B. L., Golan, D., Fraser, H. B.
  2016; 165 (3): 730-741