



## Brian Hie

Assistant Professor of Chemical Engineering

 Curriculum Vitae available Online

### Bio

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#### 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

- Personal site: <http://brianhie.com/>
- Twitter: <https://twitter.com/BrianHie>
- GitHub: <https://github.com/brianhie/>

## Teaching

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### COURSES

#### 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)

Tianyu Lu, Alp Tartici

#### Orals Chair

Izumi de los Rios Kobara

#### Postdoctoral Faculty Sponsor

Alex Hao

#### Doctoral Dissertation Advisor (AC)

Brandon Ameglio, Garyk Brix, Daniel Chang, Brian Kang, Samuel King, Aditi Merchant, Talal Widatalla

#### Doctoral Dissertation Co-Advisor (AC)

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

#### Doctoral (Program)

Divya Nori

## Publications

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### PUBLICATIONS

- **Genome modelling and design across all domains of life with Evo 2.** *Nature*  
Brix, 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

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- **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-targeted de novo antibodies 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
  - **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., Bixi, 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*  
Winnifrieth, 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