

# Stanford

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## 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
- Faculty Fellow, Sarafan ChEM-H
- The Dieter Schwarz Foundation SDS Faculty Fellow, Stanford Data Science

#### HONORS AND AWARDS

- Stanford Science Fellow, Stanford University (2021)
- National Defense Science and Engineering Graduate Fellowship Program, US Department of Defense (2019)

#### PROFESSIONAL EDUCATION

- Ph.D., Massachusetts Institute of Technology, Electrical Engineering and Computer Science (2021)

#### PATENTS

- Brian Hie, Bryan Bryson, Bonnie Berger. "United States Patent 11,011,253 Escape profiling for therapeutic and vaccine development"

#### LINKS

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

## Teaching

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### COURSES

#### 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)

Eric Nguyen, Alp Tartici

#### Postdoctoral Faculty Sponsor

Claudia Driscoll

#### Doctoral Dissertation Advisor (AC)

Brandon Ameglio, Garyk Brixli, Brian Kang, Samuel King, Aditi Merchant, Talal Widatalla

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

Mia Grahn, Chloe Wen, Chang M. Yun

## Publications

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### PUBLICATIONS

- **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., 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