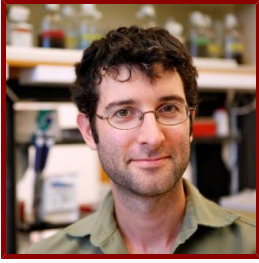


# Stanford

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## Hunter Fraser

Associate Professor of Biology

 Curriculum Vitae available Online

### Bio

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#### ACADEMIC APPOINTMENTS

- Associate Professor, Biology
- Member, Bio-X
- Member, Maternal & Child Health Research Institute (MCHRI)
- Member, Stanford Cancer Institute

#### LINKS

- Fraser Lab: <https://web.stanford.edu/group/fraserlab/>

### Research & Scholarship

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#### CURRENT RESEARCH AND SCHOLARLY INTERESTS

We study the evolution of complex traits by developing new experimental and computational methods.

Our work brings together quantitative genetics, genomics, epigenetics, and evolutionary biology to achieve a deeper understanding of how genetic variation shapes the phenotypic diversity of life. Our main focus is on the evolution of gene expression, which is the primary fuel for natural selection. Our long-term goal is to be able to introduce complex traits into new species via genome editing.

### Teaching

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#### COURSES

##### 2020-21

- Evolutionary Genomics: BIO 332 (Spr)
- Problem solving in infectious disease: BIO 60 (Sum)

##### 2018-19

- Evolutionary Genomics: BIO 332 (Win)
- Problem solving in infectious disease: BIO 60 (Win)

##### 2017-18

- Evolutionary Genomics: BIO 332 (Win)
- Introduction to Problem Solving in Biology: BIO 60 (Win)

## STANFORD ADVISEES

### Postdoctoral Faculty Sponsor

David Gokhman, Sur Herrera Paredes, Katya Mack, Ban Wang, Bin Zhao

### Doctoral Dissertation Advisor (AC)

Roy Ang, Shi-An Chen, Alex Kern, Kade Pettie

### Doctoral Dissertation Co-Advisor (AC)

Thomas Silvers

### Doctoral (Program)

Mark Berger, Shi-An Chen, Kade Pettie

### Postdoctoral Research Mentor

Bin Zhao

## GRADUATE AND FELLOWSHIP PROGRAM AFFILIATIONS

- Biology (School of Humanities and Sciences) (Phd Program)
- Biomedical Informatics (Phd Program)

## Publications

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### PUBLICATIONS

- **Detecting selection with a genetic cross.** *Proceedings of the National Academy of Sciences of the United States of America*  
Fraser, H. B.  
2020
- **The somatic mutation landscape of the human body.** *Genome biology*  
Garcia-Nieto, P. E., Morrison, A. J., Fraser, H. B.  
2019; 20 (1): 298
- **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
- **Tissue-Specific cis-Regulatory Divergence Implicates *eloF* in Inhibiting Interspecies Mating in *Drosophila*.** *Current biology : CB*  
Combs, P. A., Krupp, J. J., Khosla, N. M., Bua, D., Petrov, D. A., Levine, J. D., Fraser, H. B.  
2018
- **Functional Genetic Variants Revealed by Massively Parallel Precise Genome Editing.** *Cell*  
Sharon, E., Chen, S. A., Khosla, N. M., Smith, J. D., Pritchard, J. K., Fraser, H. B.  
2018
- **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
- **Dissecting the Genetic Basis of a Complex cis-Regulatory Adaptation.** *PLoS genetics*  
Naranjo, S., Smith, J. D., Artieri, C. G., Zhang, M., Zhou, Y., Palmer, M. E., Fraser, H. B.  
2015; 11 (12)
- **Genetic conflict reflected in tissue-specific maps of genomic imprinting in human and mouse.** *Nature genetics*  
Babak, T., Deveale, B., Tsang, E. K., Zhou, Y., Li, X., Smith, K. S., Kukurba, K. R., Zhang, R., Li, J. B., van der Kooy, D., Montgomery, S. B., Fraser, H. B.  
2015; 47 (5): 544-549

- **Gene expression drives local adaptation in humans** *GENOME RESEARCH*  
Fraser, H. B.  
2013; 23 (7): 1089-1096
- **Polygenic cis-regulatory adaptaion in the evolution of yeast pathogenicity** *GENOME RESEARCH*  
Fraser, H. B., Levy, S., Chavan, A., Shah, H. B., Perez, J. C., Zhou, Y., Siegal, M. L., Sinha, H.  
2012; 22 (10): 1930-1939
- **Harnessing novel gene expression analyses to identify drivers of regenerative ear wound healing in MRL mice**  
desJardins-Park, H. E., Mack, K. L., Davitt, M. F., Griffin, M., Fraser, H. B., Longaker, M. T.  
WILEY.2020: S25
- **Molecular mechanisms of coronary disease revealed using quantitative trait loci for TCF21 binding, chromatin accessibility, and chromosomal looping.** *Genome biology*  
Zhao, Q., Dacre, M., Nguyen, T., Pjanic, M., Liu, B., Iyer, D., Cheng, P., Wirka, R., Kim, J. B., Fraser, H. B., Quertermous, T.  
2020; 21 (1): 135
- **Comparative expression profiling reveals widespread coordinated evolution of gene expression across eukaryotes** *NATURE COMMUNICATIONS*  
Martin, T., Fraser, H. B.  
2018; 9
- **Comparative expression profiling reveals widespread coordinated evolution of gene expression across eukaryotes.** *Nature communications*  
Martin, T., Fraser, H. B.  
2018; 9 (1): 4963
- **Behavior-dependent cis regulation reveals genes and pathways associated with bower building in cichlid fishes.** *Proceedings of the National Academy of Sciences of the United States of America*  
York, R. A., Patil, C., Abdilleh, K., Johnson, Z. V., Conte, M. A., Genner, M. J., McGrath, P. T., Fraser, H. B., Fernald, R. D., Strelman, J. T.  
2018
- **Spatially varying cis-regulatory divergence in Drosophila embryos elucidates cis-regulatory logic.** *PLoS genetics*  
Combs, P. A., Fraser, H. B.  
2018; 14 (11): e1007631
- **Improving Estimates of Compensatory cis-trans Regulatory Divergence.** *Trends in genetics : TIG*  
Fraser, H. B.  
2018
- **High-resolution mapping of cis-regulatory variation in budding yeast** *PROCEEDINGS OF THE NATIONAL ACADEMY OF SCIENCES OF THE UNITED STATES OF AMERICA*  
Kita, R., Venkataram, S., Zhou, Y., Fraser, H. B.  
2017; 114 (50): E10736–E10744
- **Worldwide patterns of human epigenetic variation** *NATURE ECOLOGY & EVOLUTION*  
Carja, O., MacIsaac, J. L., Mah, S. M., Henn, B. M., Kobor, M. S., Feldman, M. W., Fraser, H. B.  
2017; 1 (10): 1577–83
- **Cis-regulatory evolution in prokaryotes revealed by interspecific archaeal hybrids** *SCIENTIFIC REPORTS*  
Artieri, C. G., Naor, A., Turgeman-Grott, I., Zhou, Y., York, R., Gophna, U., Fraser, H. B.  
2017; 7: 3986
- **Worldwide patterns of human epigenetic variation.** *Nature ecology & evolution*  
Carja, O., MacIsaac, J. L., Mah, S. M., Henn, B. M., Kobor, M. S., Feldman, M. W., Fraser, H. B.  
2017; 1 (10): 1577–83
- **Local Adaptation of Sun-Exposure-Dependent Gene Expression Regulation in Human Skin.** *PLoS genetics*  
Kita, R., Fraser, H. B.  
2016; 12 (10)
- **Genetic variation in MHC proteins is associated with T cell receptor expression biases.** *Nature genetics*

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- Sharon, E., Sibener, L. V., Battle, A., Fraser, H. B., Garcia, K. C., Pritchard, J. K.  
2016; 48 (9): 995-1002
- **Disentangling Sources of Selection on Exonic Transcriptional Enhancers.** *Molecular biology and evolution*  
Agoglia, R. M., Fraser, H. B.  
2016; 33 (2): 585-590
  - **A pooling-based approach to mapping genetic variants associated with DNA methylation** *GENOME RESEARCH*  
Kaplow, I. M., MacIsaac, J. L., Mah, S. M., McEwen, L. M., Kobor, M. S., Fraser, H. B.  
2015; 25 (6): 907-917
  - **Common variants spanning PLK4 are associated with mitotic-origin aneuploidy in human embryos** *SCIENCE*  
McCoy, R. C., Demko, Z., Ryan, A., Banjevic, M., Hill, M., Sigurjonsson, S., Rabinowitz, M., Fraser, H. B., Petrov, D. A.  
2015; 348 (6231): 235-238
  - **Discordance of DNA Methylation Variance Between two Accessible Human Tissues.** *Scientific reports*  
Jiang, R., Jones, M. J., Chen, E., Neumann, S. M., Fraser, H. B., Miller, G. E., Kobor, M. S.  
2015; 5: 8257-?
  - **Accounting for biases in riboprofiling data indicates a major role for proline in stalling translation** *GENOME RESEARCH*  
Artieri, C. G., Fraser, H. B.  
2014; 24 (12): 2011-2021
  - **Transcript Length Mediates Developmental Timing of Gene Expression Across Drosophila** *MOLECULAR BIOLOGY AND EVOLUTION*  
Artieri, C. G., Fraser, H. B.  
2014; 31 (11): 2879-2889
  - **Transcript length mediates developmental timing of gene expression across Drosophila.** *Molecular biology and evolution*  
Artieri, C. G., Fraser, H. B.  
2014; 31 (11): 2879-2889
  - **Evolution at two levels of gene expression in yeast.** *Genome research*  
Artieri, C. G., Fraser, H. B.  
2014; 24 (3): 411-421
  - **A Novel Test for Selection on cis-Regulatory Elements Reveals Positive and Negative Selection Acting on Mammalian Transcriptional Enhancers.** *Molecular biology and evolution*  
Smith, J. D., McManus, K. F., Fraser, H. B.  
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  - **Ancient cis-regulatory constraints and the evolution of genome architecture** *TRENDS IN GENETICS*  
Irimia, M., Maeso, I., Roy, S. W., Fraser, H. B.  
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  - **The molecular mechanism of a cis-regulatory adaptation in yeast.** *PLoS genetics*  
Chang, J., Zhou, Y., Hu, X., Lam, L., Henry, C., Green, E. M., Kita, R., Kobor, M. S., Fraser, H. B.  
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2013; 9 (9)
  - **Cell-cycle regulated transcription associates with DNA replication timing in yeast and human** *GENOME BIOLOGY*  
Fraser, H. B.  
2013; 14 (10)
  - **Differences in enhancer activity in mouse and zebrafish reporter assays are often associated with changes in gene expression** *BMC GENOMICS*  
Ariza-Cosano, A., Visel, A., Pennacchio, L. A., Fraser, H. B., Luis Gomez-Skarmeta, J., Irimia, M., Bessa, J.  
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- **Extensive conservation of ancient microsynteny across metazoans due to cis-regulatory constraints** *GENOME RESEARCH*  
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2012; 109: 17253-17260
- **Population-specificity of human DNA methylation** *GENOME BIOLOGY*  
Fraser, H. B., Lam, L. L., Neumann, S. M., Kobor, M. S.  
2012; 13 (2)
- **Genome-wide approaches to the study of adaptive gene expression evolution** *Systematic studies of evolutionary adaptations involving gene expression will allow many fundamental questions in evolutionary biology to be addressed* *BIOESSAYS*  
Fraser, H. B.  
2011; 33 (6): 469-477
- **Systematic Detection of Polygenic cis-Regulatory Evolution** *PLOS GENETICS*  
Fraser, H. B., Babak, T., Tsang, J., Zhou, Y., Zhang, B., Mehrabian, M., Schadt, E. E.  
2011; 7 (3)
- **Genetic validation of whole-transcriptome sequencing for mapping expression affected by cis-regulatory variation** *BMC GENOMICS*  
Babak, T., Garrett-Engele, P., Armour, C. D., Raymond, C. K., Keller, M. P., Chen, R., Rohl, C. A., Johnson, J. M., Attie, A. D., Fraser, H. B., Schadt, E. E.  
2010; 11
- **Evidence for widespread adaptive evolution of gene expression in budding yeast** *PROCEEDINGS OF THE NATIONAL ACADEMY OF SCIENCES OF THE UNITED STATES OF AMERICA*  
Fraser, H. B., Moses, A. M., Schadt, E. E.  
2010; 107 (7): 2977-2982
- **The Quantitative Genetics of Phenotypic Robustness** *PLOS ONE*  
Fraser, H. B., Schadt, E. E.  
2010; 5 (1)
- **Common polymorphic transcript variation in human disease** *GENOME RESEARCH*  
Fraser, H. B., Xie, X.  
2009; 19 (4): 567-575
- **Ab initio construction of a eukaryotic transcriptome by massively parallel mRNA sequencing** *PROCEEDINGS OF THE NATIONAL ACADEMY OF SCIENCES OF THE UNITED STATES OF AMERICA*  
Yassour, M., Kapan, T., Fraser, H. B., Levin, J. Z., Pfiffner, J., Adiconis, X., Schroth, G., Luo, S., Khrebtkova, I., Gnirke, A., Nusbaum, C., Thompson, D., Friedman, et al  
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- **Confirmation of organized modularity in the yeast interactome** *PLOS BIOLOGY*  
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- **Assessing the determinants of evolutionary rates in the presence of noise** *MOLECULAR BIOLOGY AND EVOLUTION*  
Plotkin, J. B., Fraser, H. B.  
2007; 24 (5): 1113-1121
- **Using protein complexes to predict phenotypic effects of gene mutation** *GENOME BIOLOGY*  
Fraser, H. B., Plotkin, J. B.  
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- **Coevolution, modularity and human disease** *CURRENT OPINION IN GENETICS & DEVELOPMENT*  
Fraser, H. B.  
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- **Codon usage and selection on proteins** *JOURNAL OF MOLECULAR EVOLUTION*  
Plotkin, J. B., Dushoff, J., Desai, M. M., Fraser, H. B.  
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- **Estimating selection pressures from limited comparative data** *MOLECULAR BIOLOGY AND EVOLUTION*  
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- **Aging and gene expression in the primate brain** *PLOS BIOLOGY*  
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- **Sum1p, the origin recognition complex, and the spreading of a promoter-specific repressor in *Saccharomyces cerevisiae*** *MOLECULAR AND CELLULAR BIOLOGY*  
Lynch, P. J., Fraser, H. B., Sevastopoulos, E., Rine, J., Rusche, L. N.  
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- **Functional genomic analysis of the rates of protein evolution** *PROCEEDINGS OF THE NATIONAL ACADEMY OF SCIENCES OF THE UNITED STATES OF AMERICA*  
Wall, D. P., Hirsh, A. E., Fraser, H. B., Kumm, J., Giaever, G., Eisen, M. B., Feldman, M. W.  
2005; 102 (15): 5483-5488
- **Modularity and evolutionary constraint on proteins** *NATURE GENETICS*  
Fraser, H. B.  
2005; 37 (4): 351-352
- **Adjusting for selection on synonymous sites in estimates of evolutionary distance** *MOLECULAR BIOLOGY AND EVOLUTION*  
Hirsh, A. E., Fraser, H. B., Wall, D. P.  
2005; 22 (1): 174-177
- **Conservation and evolution of cis-regulatory systems in ascomycete fungi** *PLOS BIOLOGY*  
Gasch, A. P., Moses, A. M., Chiang, D. Y., Fraser, H. B., Berardini, M., Eisen, M. B.  
2004; 2 (12): 2202-2219
- **Coevolution of gene expression among interacting proteins** *PROCEEDINGS OF THE NATIONAL ACADEMY OF SCIENCES OF THE UNITED STATES OF AMERICA*  
Fraser, H. B., Hirsh, A. E., Wall, D. P., Eisen, M. B.  
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- **Noise minimization in eukaryotic gene expression** *PLOS BIOLOGY*  
Fraser, H. B., Hirsh, A. E., Giaever, G., Kumm, J., Eisen, M. B.  
2004; 2 (6): 834-838
- **Evolutionary rate depends on number of protein-protein interactions independently of gene expression level** *BMC EVOLUTIONARY BIOLOGY*  
Fraser, H. B., Hirsh, A. E.  
2004; 4
- **Detecting selection using a single genome sequence of *M-tuberculosis* and *P-falciparum*** *NATURE*  
Plotkin, J. B., Dushoff, J., Fraser, H. B.  
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- **Detecting putative orthologs** *BIOINFORMATICS*  
Wall, D. P., Fraser, H. B., Hirsh, A. E.  
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- **A simple dependence between protein evolution rate and the number of protein-protein interactions** *BMC EVOLUTIONARY BIOLOGY*  
Fraser, H. B., Wall, D. P., Hirsh, A. E.  
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- **Evolutionary rate in the protein interaction network** *SCIENCE*

Fraser, H. B., Hirsh, A. E., Steinmetz, L. M., Scharfe, C., Feldman, M. W.  
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● **Explaining mortality rate plateaus** *PROCEEDINGS OF THE NATIONAL ACADEMY OF SCIENCES OF THE UNITED STATES OF AMERICA*

Weitz, J. S., Fraser, H. B.  
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● **Protein dispensability and rate of evolution** *NATURE*

Hirsh, A. E., Fraser, H. B.  
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