

# HUNTER FRASER

## EDUCATION

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- 1997 – 2001                      M.I.T.    Cambridge, MA  
*B.S., Biology*
- 2001 – 2005                      U.C. Berkeley    Berkeley, CA  
*Ph.D., Molecular and Cell Biology*

## RESEARCH EXPERIENCE

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- 1996 – 1997                      Harvard Medical School    Boston, MA  
• Worked in Fred Alt's lab on DNA knockout vectors which led to successful knockout mice.
- 1998 – 1999                      M.I.T.    Cambridge, MA  
• Worked in Leonard Guarente's lab on gene expression and aging in yeast.
- 1999                                      Santa Fe Institute    Santa Fe, NM  
• Worked for one summer on computational analysis of non-Mendelian inheritance in inbred mice.
- 2000                                      Stanford University    Stanford, CA  
• Worked in Marcus Feldman's lab, on yeast functional genomics and evolution.
- 2000 – 2001                      M.I.T.    Cambridge, MA  
• Worked in Daniel Rothman's lab on mathematical models of aging and ecosystems.
- 2001 – 2005                      U.C. Berkeley    Berkeley, CA  
• Ph.D. work in Michael Eisen's lab on functional and evolutionary genomics.
- 2004                                      Max Planck Institute    Leipzig, Germany  
• Worked for one month in Svante Pääbo's lab on aging and gene expression in the primate brain.
- 2005                                      Khao Chong Research Station    Khao Chong, Thailand  
• Worked for one month at a field station in the Khao Chong rainforest, collecting and analyzing local caterpillars and butterflies as part of a biodiversity project led by Naomi Pierce.
- 2006 – 2007                      Broad Institute of MIT and Harvard    Cambridge, MA  
• Studied the population genetics of polymorphic mRNA splicing in humans: its extent, and its impact on common disease.
- 2008 – 2009                      Rosetta Inpharmatics    Seattle, WA  
• Worked with Eric Schadt to analyze the effects of genetic polymorphisms on gene expression in mouse and yeast.
- 2009 – present                      Stanford University    Stanford, CA  
• Currently an Assistant Professor in the Department of Biology.

## PUBLICATIONS

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- A.E. Hirsh and **H.B. Fraser**. Protein dispensability and rate of evolution. *Nature* 411: 1046 (2001).
- J.S. Weitz and **H.B. Fraser**. Explaining mortality rate plateaus. *PNAS* 98: 15383 (2001).
- S.B. Snapper, F. Takeshima, I. Anton, C.H. Liu, S.M. Thomas, D. Nguyen, D. Dudley, **H. Fraser**, D. Purich, M. Lopez-Illasaca, C. Klein, L. Davidson, R. Bronson, R.C. Mulligan, F. Southwick, R. Geha, M.B. Goldberg, F.S. Rosen, J.H. Hartwig, and F.W. Alt. N-WASP deficiency reveals distinct pathways for cell surface projections and microbial actin-based motility. *Nature Cell Biology* 3: 897 (2001).
- **H.B. Fraser**, A.E. Hirsh, L.M. Steinmetz, C. Scharfe, and M. Feldman. Evolutionary rate in the protein interaction network. *Science* 296: 750 (2002).
- A.E. Hirsh and **H.B. Fraser**. Genomic function: Rate of evolution and gene dispensability. *Nature* 421: 497 (2003).
- A.E. Hirsh, **H.B. Fraser**, and D.P. Wall. Detecting putative orthologs. *Bioinformatics* 19: 1710 (2003).
- **H.B. Fraser**, D.P. Wall, and A.E. Hirsh. A simple dependence between protein evolution rate and the number of protein-protein interactions. *BMC Evolutionary Biology* 3: 11 (2003).
- J.B. Plotkin, J.S. Dushoff, and **H.B. Fraser**. Detecting selection using a single genome sequence of *M. tuberculosis* and *P. falciparum*. *Nature* 428: 942 (2004).
- **H.B. Fraser**, A.E. Hirsh, G. Giaever, J. Kumm, and M.B. Eisen. Noise minimization in eukaryotic gene expression. *PLoS Biology* 2: 824 (2004).
- **H.B. Fraser** and A.E. Hirsh. Evolutionary rate depends on number of protein-protein interactions independently of gene expression level. *BMC Evolutionary Biology* 4: 13 (2004).
- **H.B. Fraser**, A.E. Hirsh, D.P. Wall, and M.B. Eisen. Coevolution of gene expression among interacting proteins. *PNAS* 101: 9033 (2004).
- A.P. Gasch, A.M. Moses, D.Y. Chiang, **H.B. Fraser**, M. Berardini, M.B. Eisen. Conservation and evolution of *cis*-regulatory systems in ascomycete fungi. *PLoS Biology* 2: e398 (2004).
- A.E. Hirsh, **H.B. Fraser**, and D.P. Wall. Adjusting for selection on synonymous sites in estimates of evolutionary distance. *Molecular Biology and Evolution* 22: 174 (2005).
- P.J. Lynch, **H.B. Fraser**, E. Sevastopoulos, J. Rine, and L.N. Rusche. A single amino acid substitution enhances the spreading ability of the promoter-specific repressor Sum1p from *S. cerevisiae*. *Molecular and Cellular Biology* 25: 5920 (2005).
- D.P. Wall, A.E. Hirsh, **H.B. Fraser**, J. Kumm, G. Giaever, M.B. Eisen, and M.W. Feldman. Functional genomic analysis of the rates of protein evolution. *PNAS* 102: 5483 (2005).
- **H.B. Fraser**, P. Khaitovich, J.B. Plotkin, S. Paabo, and M.B. Eisen. Aging and gene expression in the primate brain. *PLoS Biology* 3: 274 (2005).
- **H.B. Fraser**. Modularity and evolutionary constraint on proteins.

*Nature Genetics* 37: 351 (2005).

- J.B. Plotkin, J. Dushoff, M.M. Desai, and **H.B. Fraser**. Estimating selection pressures from limited comparative data.  
*Molecular Biology and Evolution*. 23: 1457 (2006).
- J.B. Plotkin, J. Dushoff, M.M. Desai, and **H.B. Fraser**. Codon usage and selection on proteins.  
*Journal of Molecular Evolution*, 63: 635 (2006).
- N. Bertin, N. Simonis, D. Dupuy, M.E. Cusick, J.D. Han, **H.B. Fraser**, F.P. Roth, and M. Vidal. Confirmation of organized modularity in the yeast interactome.  
*PLoS Biology* 5: e153 (2007).
- J.B. Plotkin and **H.B. Fraser**. Assessing the determinants of evolutionary rates in the presence of noise.  
*Molecular Biology and Evolution*, 24: 1113 (2007).
- **H.B. Fraser** and J.B. Plotkin. Using protein complexes to predict phenotypic effects of gene mutation.  
*Genome Biology*, 8: R252 (2007).
- M. Yassour, T. Kaplan, **H.B. Fraser**, J. Levin, J. Pfiffner, X. Adiconis, G. Schroth, S. Luo, I. Khrebtkova, A. Gnirke, C. Nusbaum, D. Thompson, N. Friedman, and A. Regev. *Ab initio* construction of a eukaryotic transcriptome by massively parallel mRNA sequencing.  
*PNAS* 106: 3264 (2009).
- **H.B. Fraser** and X. Xie. Common polymorphic transcript variation in human disease.  
*Genome Research* 19: 567 (2009).
- **H.B. Fraser** and E.E. Schadt. The quantitative genetics of phenotypic robustness.  
*PLoS ONE* 5: e8635 (2010).
- **H.B. Fraser**, A. Moses, and E.E. Schadt. Evidence for widespread adaptive evolution of gene expression in budding yeast.  
*PNAS* 107: 2997 (2010).
- T. Babak, P. Garrett-Engle, C. Armour, C. Raymond, M. Keller, R. Chen, C. Rohl, J. Johnson, A. Attie, **H.B. Fraser\***, and E.E. Schadt\* (\*equal contribution and corresponding authorship). Genetic validation of whole-transcriptome sequencing for mapping expression affected by *cis*-regulatory variation.  
*BMC Genomics* 11: 473 (2010).
- Lamb JR, Zhang C, Xie T, Wang K, Zhang B, Hao K, Chudin E, **H.B. Fraser**, Millstein J, Ferguson M, Suver C, Ivanovska I, Scott M, Philippar U, Bansal D, Zhang Z, Burchard J, Smith R, Greenawalt D, Cleary M, Derry J, Loboda A, Watters J, Poon RT, Fan ST, Yeung C, Lee NP, Guinney J, Molony C, Emilsson V, Buser-Doepner C, Zhu J, Friend S, Mao M, Shaw PM, Dai H, Luk JM, and Schadt EE. Predictive genes in adjacent normal tissue are preferentially altered by sCNV during tumorigenesis in liver cancer and may be rate limiting.  
*PLoS One* 6: e20090 (2011).
- **H.B. Fraser**, T. Babak, J. Tsang, Y. Zhou, M. Mehrabian, and E.E. Schadt. Systematic detection of polygenic *cis*-regulatory evolution.  
*PLoS Genetics* 7: e1002023 (2011).
- **H.B. Fraser**, L. Lam, S. Neumann, and M.S. Kobor. Population-specificity of human DNA methylation.  
*Genome Biology*, 13: R8 (2012).
- L. Lam, E. Emberly, **H.B. Fraser**, S. Neumann, E. Chen, G. Miller, and M.S. Kobor. Factors Underlying Variable DNA Methylation in a Human Community Cohort.  
*PNAS*, 109 Suppl 2: 17253 (2012).
- **H.B. Fraser**, S. Levy, A. Chavan, H.B. Shah, S. Kowli, J.C. Perez, Y. Zhou, M.L. Siegal, and H. Sinha. Polygenic *cis*-regulatory adaptation in the evolution of yeast pathogenicity.  
*Genome Research*, 22: 1930 (2012).
- M. Irimia, J.J. Tena, M.S. Alexis, A. Fernandez-Minan, I. Maeso, O. Bogdanovic, E. de la Calle-Mustienes, S.W. Roy, J.L. Gómez-Skarmeta, and **H.B. Fraser**. Extensive conservation of ancient microsynteny across metazoans due to *cis*-regulatory constraint.  
*Genome Research*, 22: 2356 (2012).

- A. Ariza-Cosano, A. Visel, L.A. Pennacchio, **H.B. Fraser**, J.L. Gómez-Skarmeta, M. Irimia, and J. Bessa. Differences in enhancer activity in mouse and zebrafish reporter assays are often associated with changes in gene expression. *BMC Genomics*, 13: 713 (2012).
- **H.B. Fraser**. Gene expression drives local adaptation in humans. *Genome Research*, 23: 1089 (2013).
- J. Chang, Y. Zhou, X. Hu, C. Henry, E.M. Green, R. Kita, and **H.B. Fraser**. The molecular mechanism of a *cis*-regulatory adaptation in yeast. *PLoS Genetics*, in press.
- J.D. Smith, K. McManus, and **H.B. Fraser**. A novel test for selection on *cis*-regulatory elements reveals positive and negative selection acting on mammalian transcriptional enhancers. *Molecular Biology and Evolution*, in press.
- C.G. Artieri and **H.B. Fraser**. Transcript length mediates developmental timing of gene expression across *Drosophila*. *Submitted*.
- **H.B. Fraser**. Cell-cycle regulated transcription associates with DNA replication timing in yeast and human. *Submitted*.
- C.G. Artieri and **H.B. Fraser**. Evolution at two levels of gene expression in yeast. *Submitted*.
- R. Kita, Y. Zhou, and **H.B. Fraser**. Heritability of gene expression reveals natural selection on gene expression variance. *Submitted*.

#### Review articles

- **H.B. Fraser**. Coevolution, modularity, and human disease. *Current Opinion in Genetics & Development*, 16: 637 (2006).
- **H.B. Fraser**. Genome-wide approaches to the study of adaptive gene expression evolution. *Bioessays* 33: 469 (2011).
- M. Irimia, I. Maeso, S.W. Roy, and **H.B. Fraser**. Ancient *cis*-regulatory constraints and the evolution of genome architecture. *Trends in Genetics*, in press.

#### AWARDS RECEIVED

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- NIH New Innovator Award (2011)
- Pew Scholar in the Biomedical Sciences (2011)
- Alfred P. Sloan Fellowship (2010)
- Frederick E. Terman Fellowship (2009)
- Life Science Research Foundation Postdoctoral Fellowship (2007)
- Merck/MIT Computational Systems Biology Initiative Postdoctoral Fellowship (2006)
- Belling Prize, awarded to the most outstanding Ph.D. graduate of the previous five years in Genetics at UC Berkeley (2005)
- National Science Foundation Predoctoral Fellowship (2002)
- Massachusetts Biotechnology Council Scholarship (1997)

#### FUNDING

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- Alfred P. Sloan Foundation Fellowship BR-5128                      9/15/10 – 9/15/12                      \$50,000  
Title: Genome-wide scans for adaptive *cis*-regulatory evolution                      Role: PI

- Pew Foundation Scholar in the Biomedical Sciences      7/01/11 – 6/30/16      \$240,000  
Title: Systematically pinpointing casual polymorphisms underlying complex diseases      Role: PI
- NIH R21HG005240-01A      9/18/10 – 7/31/12      \$276,500  
Title: Genome-wide discovery of allele-specific gene expression and chromatin states      Role: PI
- DoD Pilot Award OC100097      4/01/11 – 4/30/13      \$294,017  
Title: Systematic characterization of oncogenes and tumor suppressors in ovarian cancer      Role: PI
- NIH 1R21HG005750-01A      6/02/11 – 2/28/13      \$275,000  
Title: High-throughput characterization of *cis*-acting polymorphisms in the human genome      Role: PI
- NIH 1DP2OD008456-01      9/30/11 – 7/30/16      \$1,500,000  
Title: Systematic functional annotation of human *cis*-regulatory genetic variation      Role: PI
- NIH 1R01GM097171-01A1      2/05/12 – 1/31/16      \$760,000  
Title: Yeast as a model for understanding gene expression adaptation      Role: PI
- Hellman Faculty Scholars Fund      9/01/12 – 8/31/13      \$40,000  
Title: Pinpointing Targets of Natural Selection in Ovarian Cancer Progression      Role: PI

## SEMINARS

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2013:

- Department of Organismal and Evolutionary Biology, Harvard University, Cambridge, MA
- Center for Comparative and Population Genomics, Cornell University, Ithaca, NY
- Society of Molecular Biology and Evolution conference, Chicago, IL
- Department of Biomolecular Engineering, University of California, Santa Cruz, CA
- Quantitative Genetics and Genomics Gordon Conference, Galveston, TX
- Tokyo Medical and Dental University, Tokyo, Japan

2012:

- Department of Systems Biology, Harvard Medical School, Boston, MA
- Society of Molecular Biology and Evolution conference, Dublin, Ireland
- International Conference on Quantitative Genetics, Edinburgh, Scotland
- Channing Division of Network Medicine, Harvard Medical School, Boston, MA

2010:

- Biomolecular Interaction Networks and Disease (Keystone Conference), Quebec City, Quebec, Canada
- Department of Biology, Georgia Institute of Technology, Atlanta, GA
- Hopkins Marine Station, Stanford University, Monterey, CA
- Symposium on Evolutionary Genomics, Stanford University, Stanford CA

2009:

- Quantitative Genetics and Genomics Gordon Conference, Galveston, TX
- Dahlem Colloquium, Max Planck Institute for Molecular Genetics, Berlin, Germany
- Center for Molecular Medicine and Therapeutics, Vancouver, Canada
- Center for Computational Biology and Bioinformatics, Columbia University, New York, NY

2008:

- Department of Ecology and Evolution, University of Chicago, Chicago, IL
- Stowers Institute for Biomedical Research, Kansas City, MO
- Department of Biology, Stanford University, Palo Alto, CA
- Department of Biology, California Institute of Technology, Pasadena, CA
- Human Genetics Institute, University of California, San Francisco, CA

2007:

- Bioinformatics Gordon Conference, Colby, NH
- Physical and Chemical Foundations of Bioinformatics conference, Dresden, Germany
- Max Planck Institute for Evolutionary Anthropology, Leipzig, Germany
- ORFeomes and Systems conference, Boston, MA
- Memorial Sloan-Kettering Cancer Center, New York, NY

2006:

- Department of Human Genetics, University of Chicago, Chicago, IL
- Cold Spring Harbor Lab/Wellcome Trust Interactome Networks conference, Hinxton, UK
- Shanghai Institute of Biological Sciences, Shanghai, China
- Shanghai Center for Bioinformation Technology, Shanghai, China

2005:

- Rockefeller University Center for Studies in Physics and Biology, New York, NY
- Whitehead Institute for Biomedical Research, Cambridge, MA
- Structural, Functional, and Evolutionary Genomics Gordon Conference, NH
- Center for Molecular Medicine and Therapeutics, Vancouver, Canada
- Program in Evolutionary Dynamics, Harvard University, Cambridge, MA
- Banting and Best Department of Medical Research, University of Toronto, Toronto, Canada
- Integrative Program in Quantitative Biology, University of California, San Francisco, CA
- Division of Medical Genetics, University of Washington, Seattle, WA

2004:

- Beckman Research Institute, Duarte, CA
- Structural Approaches to Sequence Evolution conference, Dresden, Germany
- Max Planck Institute for Evolutionary Anthropology, Leipzig, Germany
- Max Planck Institute for Infection Biology, Berlin, Germany
- Functional Genomics conference, Gothenburg, Sweden
- National Center for Biotechnology Information, Bethesda, MD
- Harvard University Bauer Center for Genomic Research, Cambridge, MA

## TEACHING

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- Personalized Genomic Medicine (Bio 4N): Fall 2010, 2011, 2012
- Evolution (Bio 43): Spring 2012, 2013