Jenny Chen, PhD

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CURRENT

NIH MOSAIC K99/R00 Postdoctoral Fellow, Harvard University, Cambridge, MA
Postdoctoral fellow investigating the genetic basis of innate reproductive behaviors using comparative genomics, single-cell transcriptomics, and computational methodologies.
<u>Faculty advisors:</u> Profs. Hopi Hoekstra and Sean Eddy

EDUCATION

2011 – 2018   PhD, Bioinformatics and Integrative Genomics, Division of Health Sciences and Technology (HST), MIT
<u>Thesis</u>: Evolutionary signatures for unearthing functional elements in the human transcriptome
<u>Faculty advisor</u>: Prof. Aviv Regev

2006 – 2011   BS/MS (with distinction), Biomedical Computation, Stanford University
<u>Thesis</u>: Analysis of Transcription Factor ChIP-Seq Datasets
<u>Faculty advisor</u>: Prof. Gill Bejerano

FELLOWSHIPS AND GRANTS

2022 – now   MOSAIC K99/R00 Postdoctoral Career Transition Award to Promote Diversity, NIH
2018 – 2021   Harvard Data Science Postdoctoral Fellowship, Harvard University
2013 – 2014   Jan and Ruby Krouwer Fund, Massachusetts Institute of Technology
2011 – 2013   National Human Genome Research Institute Training Grant, NIH
2011   Vice Provost Undergraduate Education Award, Stanford University
2010   CS Undergraduate Research Grant, Stanford University

AWARDS

2017   Division of Health Sciences and Technology Director's Award
2017   MIT Graduate Women of Excellence Award and invited speaker for award ceremony
2014   3rd Place (of 246 entries), MIT Big Data Challenge
2013   IDEA^2 Award for Best Research Proposal, HST, MIT

KEY PUBLICATIONS

1. **Chen J**, Richardson PR, Kirby C, Eddy SR, and HE Hoekstra. Cellular evolution of the hypothalamic preoptic area of behaviorally divergent deer mice. *bioRxiv*. doi: 10.1101/2024.08.22.608850. Under review at *eLife*.
2. Kautt A*, **Chen J***, Lewarch CL, Hu C, Turner K, Lassance JM, Baier F, Bedford NL, Bendesky A, and HE Hoekstra. Evolution of gene expression across brain regions in behaviorally divergent deer mice and their hybrids. *Molecular Ecology*. 2024; e17270. *Contributed equally.

ADDITIONAL PUBLICATIONS

3. **Chen J**, Swofford R, Johnson J, Cummings BB, Rogel N, Lindblad-Toh K, Haerty W, di Palma F, and A Regev. A quantitative model for characterizing the evolutionary history of mammalian gene expression. *Genome research*. 2019; 29: 53-63.
4. **Chen J**, Shishkin A, Zhu X, Kadri S, Hanna J, Regev A, and M Garber. Evolutionary analysis across mammals reveals distinct classes of long noncoding RNAs. *Genome biology*. 2016; 17: 19.
5. Dixit A*, Parnas O*, Li B, **Chen J**, Fulco CP, Jerby-Arnon L, Marjanovic ND, Dionne D, Burks T, Raychowdhury R, Adamson B, Norman TM, Lander ES, Weissman JS, Friedman N, and A Regev. Perturb-seq: dissecting molecular circuits with scalable single-cell RNA profiling of pooled genetic screens. *Cell*. 2016; 167: 1853-1866.
6. Schiebinger G*, Shu J*, Tabaka M*, Cleary B*, Subramanian V, Solomon A, Liu S, Lin S, Berube P, Lee L, **Chen J,** Brumbaugh J, Rigollet P, Hochedlinger K, Jaenisch R, Regev A, and ES Lander. Optimal-transport analysis of single-cell gene expression identifies developmental trajectories in reprogramming. *Cell*. 2019; 176: 928-943.
7. Munschauer M, Nguyen CT, Sirokman K, Hartigan CR, Hogstrom L, Engreitz JM, Ulirsch JC, Fulco CP, Subramanian V, **Chen J**, Schenone M, Guttman M, Carr SA, and ES Lander. The NORAD lncRNA assembles a topoisomerase complex critical for genome stability. *Nature*. 2018; 561: 132.
8. Engreitz JM, Haines JE, Perez EM, Munson G, **Chen J**, Kane M, McDonel PE, Guttman M, and ES Lander. Local regulation of gene expression by lncRNA promoters, transcription and splicing. *Nature*. 2016; 539: 452.
9. Ye CJ*, **Chen J***, Villani AC, Subramaniam M, Gate RE, Bhangale T, Lee MN, Raj T, Raychowdhury R, Li W, Rogel N, Imboywa SH, Chipendo PI, McCabe C, Lee MH, Frohlich IY, Stranger Be, De Jager PL, Regev A, Behrens T, and N Hacohen. Genetic analysis of isoform usage in the human antiviral response reveals influenza-specific regulation of ERAP2 transcripts under balancing selection. *Genome research*. 2018; 28: 1812-1826. *Contributed equally.
10. Shishkin AA, Giannoukos G, Ciulla D, Busby M, Surka C, **Chen J**, Bhattacharrya RP, Patel MM, Hun DT, Gnirke A, Guttman M, and J Livny. Simultaneous generation of large numbers of strand-specific RNA-Seq cDNA libraries in a single reaction. *Nature methods*. 2015; 12: 323.
11. Bochkis I, Przybylski D, **Chen J**, and A Regev. Changes in nucleosome occupancy associated with metabolic alterations in aged mammalian liver. *Cell reports*. 2014; 9: 996-1006.
12. Camp JG, Frank CL, Lickwar CR, Guturu H, Rube T, Wenger AM, **Chen J**, Bejerano G, Crawford GE, and JF Rawls. Microbiota modulate transcription in the intestinal epithelium without remodeling the accessible chromatin landscape. *Genome research*. 2014; 24: 1504-1516.
13. Tuteja G, Moreira KB, Chung T, **Chen J**, Wenger AM, and G Bejerano. Automated Discovery of Tissue-Targeting Enhancers and Transcription Factors from Binding Motif and Gene Function Data. *PLoS computational biology*. 2014; 10: e1003449.
14. Wenger AM, Clarke SL, Guturu H, **Chen J**, Schaar BT, McLean CY, and G Bejerano. PRISM offers a comprehensive genomic approach to transcription factor function prediction. *Genome research*. 2013; 23: 889-904.

INVITED TALKS

A model for expression evolution across the mammalian lineage. Ecological & Evolutionary Genomics, Gordon Research Conference. July 2017.

A model for expression evolution across the mammalian lineage. Biology of Genomes, Cold Spring Harbor, NY. May 2017.

POSTER PRESENTATIONS

The genetic control of neuron number and behavior. Neuropeptide Signaling: Bridging Cell Biology, Neurophysiology and Behavior. HHMI, Janelia Research Campus, VA. April 2023.

Using wild mice to study the molecular control of a sexually dimorphic behavior. EMBO | EMBL Symposium: The Molecular Basis and Evolution of Sexual Dimorphism. Virtual, September 2020.

Evolutionary analysis across mammals reveals distinct classes of long noncoding RNAs. Genome Informatics, Cold Spring Harbor, NY. October 2015.

Comparative analysis of computational pipelines for RNA sequencing in genomic studies. American Society of Human Genetics 2014 Annual Meeting, San Diego, CA. October 2014.

Analysis of Transcription Factor ChIP-Seq Data Sets. Stanford Computer Science Undergraduate Research Presentations, Stanford, CA. August 2011.

TEACHING EXPERIENCE

Instructor (G) / Teaching Assistant, Molecular Biology and Genetics in Modern Medicine, MIT/Harvard Medical School (2013 – 2016)

Developed curriculum, created problem sets and exams, organized guest lectures and patient visits, lectured, and led discussion sections for 60 first-year MD and PhD students.

MENTORING AND OUTREACH EXPERIENCE

Research Mentor, Harvard University (2020 – 2024)

Research mentor for four undergraduates and two research technicians, all who come from underrepresented groups in biomedical research. Oversaw one computational neuroscience senior thesis. Mentee achievements including NSF Rising Scientist Award for Minoritized Students (2023).

Outreach Educator, Broad Institute (2016 – 2018)

Taught genetics and evolution to local middle school students.

Research Mentor, Broad Summer Research Program (2015)

Research mentor for intensive nine-week summer research program designed for undergraduates from underrepresented backgrounds. Mentee won Poster Award at the National Biomedical Research Conference for Minority Students (2015)

PROFESSIONAL EXPERIENCE

Reviewer Services: Nature ecology & evolution, Nature communications, Molecular Ecology, National Science Foundation, Harvard Data Science Initiative

Professional Memberships: American Society for Cellular Biology (ASCB)

Board Membership: Field Projects International

Community Services: Presidential Advisory Cabinet, MIT (2017); Committee on Student Life, MIT (2016); Women's Advisory Group to the Office of the President, MIT (2015); Graduate Resident Tutor, Baker House, MIT (2015-2018); Public Service Director, HST, MIT (2012-2014)