Jesse Engreitz, Ph.D.

Curriculum Vitae

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Education

2010–2016	**Massachusetts Institute of Technology**, Doctor of Philosophy	*Cambridge, MA*

Ph.D. in Health Sciences and Technology: Bioinformatics and Integrative Genomics
Thesis: *Genome regulation by long noncoding RNAs.* Advisor: Eric Lander.

2009–2010	**Stanford University**, Master of Science	*Stanford, CA*

M.S. Bioengineering. Advisors: Russ Altman and Michael Clarke.

2005–2010	**Stanford University**, Bachelor of Science	*Stanford, CA*

B.S. Engineering - Biomedical Computation (with Honors, with Distinction).
Thesis: *Independent component analysis: Mining microarray data for fundamental human gene expression modules.* Advisor: Russ Altman.

Research Positions

2011–present	**Eric Lander Laboratory**, Broad Institute of MIT and Harvard	*Cambridge, MA*

Functions of long noncoding RNAs (lncRNAs) in transcriptional regulation.

2009–2010	**Michael Clarke and Max Diehn Labs**, Stanford University	*Stanford, CA*

Epigenetic regulation of self-renewal in cancer stem cells.

2010	**Atul Butte Laboratory**, Stanford University	*Stanford, CA*

Mining public gene expression databases based on patterns of differential expression.

2008–2010	**Russ Altman Laboratory**, Stanford University	*Stanford, CA*

Statistical methods to identify differentially regulated gene pathways.

Honors and Awards

2011–2016	Fannie and John Hertz Foundation Fellowship
2011–2014	National Defense Science and Engineering Graduate Fellowship
2011	National Science Foundation Graduate Research Fellowship (declined)
2010	Phi Beta Kappa Society
2009	Frederick Emmons Terman Engineering Scholastic Award, Stanford University
2008	Bio-X Undergraduate Research Award, Stanford University
2008	Tau Beta Pi Engineering Honors Society
2006	Introductory Studies Award, Stanford University
2006	President's Award for Freshman Academic Excellence, Stanford University
2005–2008	Robert C. Byrd Honors Scholarship

Publications

Engreitz JM*, Ollikainen N*, and Guttman M. Long non-coding RNAs (lncRNAs) as spatial amplifiers that control nuclear architecture and gene expression. *Nat Rev Mol Cell Biol*, Oct 2016.

Engreitz JM, Haines JE, Munson G, Chen J, Perez EM, Kane M, McDonel PE, Guttman M, and Lander ES. Local regulation of gene expression by lncRNA promoters, transcription, and splicing. *Nature*, Oct 2016.

Moynihan KD*, Opel CF*, Szeto GL, Tzeng A, Zhu ER, **Engreitz JM**, Williams RT, Rakhra K, Zhang

MH, Rothschilds AM, Kumari S, Kelly RL, Kwan BH, Abraham W, Hu K, Mehta NK, Kauke MJ, Suh H, Cochran JR, Lauffenburger DA, Wittrup KD, and Irvine DJ. Eradication of large established tumors by combination immunotherapy engaging innate and adaptive immunity. *Nat Med*, Oct 2016.

Fulco CP, Munschauer M, Anyoha R, Munson G, Grossman SR, Perez EM, Kane M, Cleary B, and Lander ES*, **Engreitz JM***. Systematic mapping of functional enhancer-promoter connections with CRISPR interference. *Science*, 10.1126/science.aag2445, Sep 2016.

Engreitz JM, Lander ES*, and Guttman M*. RNA antisense purification (RAP) for mapping RNA interactions with chromatin. *Methods Mol Biol*, 1262:183-197, Jan 2015.

Engreitz JM, Sirokman K, McDonel P, Shishkin A, Surka C, Russell P, Grossman SR, Chow AY, Guttman M*, and Lander ES*. RNA-RNA interactions enable specific targeting of noncoding RNAs to nascent pre-mRNAs and chromatin sites. *Cell*, 159(1):188-199, Sep 2014.

Schwartz S, Bernstein DA, Mumbach MR, Jovanovic M, Herbst RH, Leon-Ricardo BX, **Engreitz JM**, Guttman M, Satija R, Lander ES*, Fink G*, and Regev A*. Transcriptome-wide mapping reveals widespread dynamic regulated pseudouridylation of ncRNA and mRNA. *Cell*, 159(1):148-162, Sep 2014.

Hacisuleyman E, Goff LA, Trapnell C, Williams A, Henao-Mejia J, Sun L, McClanahan P, Hendrickson DG, Sauvageau M, Kelley DR, Morse M, **Engreitz J**, Lander ES, Guttman M, Lodish HF, Flavell R, Raj A, and Rinn JL. Topological organization of multi-chromosomal regions by *Firre*. *Nat Struct Mol Bio*, 21(2):198-206, Feb 2014.

Lee CY, Lin Y, Bratman S, Feng W, Kuo A, Scheeren F, **Engreitz JM**, Varma S, West R, and Diehn M. Neuregulin autocrine signaling promotes self-renewal of breast tumor-initiating cells by triggering HER2/HER3 activation. *Cancer Res*, 74(1):341–352, Oct 2013.

Engreitz JM, Pandya-Jones A, McDonel P, Shishkin A, Surka C, Sirokman K, Kadri S, Xing J, Goren A, Lander ES*, Plath K*, and Guttman M*. The Xist lncRNA exploits three-dimensional genome architecture to spread across the X chromosome. *Science*, 341: 1237973, Jul 2013.

Engreitz JM*, Agarwala V*, and Mirny LA. Three dimensional genome architecture influences partner selection for chromosomal translocations in human disease. *PLOS ONE*, 7(9): e44196, Sep 2012.

Engreitz JM, Chen R, Morgan AA, Dudley JT, Mallelwar R, and Butte AJ. Profilechaser: searching microarray repositories based on genome-wide patterns of differential expression. *Bioinformatics*, Oct 2011.

Zhu H, Shyh-Chang N, Segrè AV, Shinoda G, Shah SP, Einhorn WS, Takeuchi A, **Engreitz JM**, Hagan JP, Kharas MG, Urbach A, Thornton JE, Triboulet R, Gregory RI, DIAGRAM Consortium, MAGIC Investigators, Altshuler D, and Daley GQ. The lin28/let-7 axis regulates glucose metabolism. *Cell*, 147(1):81–94, Sep 2011.

Engreitz JM, Morgan AA, Dudley JT, Chen R, Thathoo R, Altman RB, and Butte AJ. Content-based microarray search using differential expression profiles. *BMC Bioinformatics*, 11(1):603, Dec 2010.

Engreitz JM, Daigle BJ Jr, Marshall JJ, and Altman RB. Independent component analysis: Mining microarray data for fundamental human gene expression modules. *J Biomed Inform*, 43(6):932–944, Jul 2010.

Selected Talks

Engreitz JM, Haines JE, Munson G, Kane M, McDonel P, Guttman M, and Lander ES. Many promoters of lncRNAs and mRNAs act as enhancers in local gene regulatory networks. Selected talk at *Systems Biology: Global Regulation of Gene Expression*, Cold Spring Harbor, NY. Mar 2016.

Engreitz JM, Haines JE, Munson G, Kane M, McDonel P, Guttman M, and Lander ES. Mechanisms for regulatory crosstalk between neighboring genes in mammals. Selected talk at *Noncoding RNAs in Health and Disease*, Santa Fe, NM. Feb 2016.

Engreitz JM, Haines JE, Munson G, Kane M, McDonel P, Guttman M, and Lander ES. Many promoters of lncRNAs and mRNAs act as enhancers in local gene regulatory networks. Selected talk at *Epigenomics 2016*, Puerto Rico. Jan 2016.

Engreitz JM, Haines JE, McDonel P, Sirokman K, Munson M, Fulco C, Munschauer M, Russell P, Guttman M, and Lander ES. Many nuclear-localized lincRNAs directly regulate gene expression in *cis*. Selected talk at *Long Noncoding RNAs: From Evolution to Function*, Keystone, CO. March 2015.

Engreitz JM, Pandya-Jones A, McDonel P, Shishkin A, Surka C, Sirokman K, Kadri S, Plath K, Lander ES*, and Guttman M*. Large noncoding RNAs can localize to regulatory DNA targets by exploiting the three-dimensional architecture of the genome. Selected talk at *Chromatin Structure & Function*, Grand Cayman. Oct 2013.

Engreitz JM, Pandya-Jones A, McDonel P, Shishkin A, Surka C, Sirokman K, Kadri S, Plath K, Lander ES*, and Guttman M*. Large noncoding RNAs can localize to regulatory DNA targets by exploiting the three-dimensional architecture of the genome. Selected talk at *The Biology of Genomes*, Cold Spring Harbor, NY. May 2013.

Engreitz JM, McDonel P, Shishkin A, Surka C, Sirokman K, Lander ES, and Guttman M. RNA Antisense Purification (RAP) identifies novel mechanisms of lncRNA localization to chromatin. Selected talk at *Epigenetics & Chromatin*, Boston, MA. March 2013.

Engreitz JM, Daigle BJ Jr, Marshall JJ, and Altman RB. Independent component analysis of large microarray data compendium identifies fundamental modules of human biology. Selected talk at *Biomedical Computation at Stanford*, Stanford, CA. Nov 2009.

Patents

US 20160040218 A1, Guttman M, **Engreitz J**, and Lander ES.
Selective purification of RNA and RNA-bound molecular complexes

Teaching and Service

2014–2015	**Guest Instructor**, Harvard Medical School	*Boston, MA*

Molecular Biology and Genetics in Modern Medicine. Developed and led classroom sessions on "Personal Genomics" and "Cancer Genetics".

2013–2015	**Teaching Assistant**, Harvard Medical School	*Boston, MA*

Human Genetics (Profs Joel Hirschhorn, David Altshuler, Sekar Katherisan)

2011–2013	**Teaching Assistant**, Harvard Medical School	*Boston, MA*

Molecular Biology and Genetics in Modern Medicine (Profs David Housman, Anne Giersch)

2012	**Guest Instructor**, MIT	*Cambridge, MA*

Quantitative Genomics (Prof Leonid Mirny). Developed and led classroom session. Topic: "Personal Genomics: Disease Diagnosis and Risk Prediction"

2010–2015	**Joint Council**, Harvard-MIT Health Sciences and Technology	*Cambridge, MA*

PhD Representative to the MD Curriculum Committee for the Division of Health Science and Technology and HST-IMES Committee on Academic Programs. Evaluated Harvard Medical School courses with a committee of faculty and students. Discussed implementation and vision for curriculum. Represented HST.160 teaching team. Contributed to organizational policy.

2010–2013	**Committee Member**, MIT Colleges Against Cancer	*Cambridge, MA*

Helped to organize Relay For Life of MIT, a fundraiser to benefit the American Cancer Society.

2010	**Mentor**, Stanford Medical Youth Science Program	*Stanford, CA*

Mentored and tutored high school students as part of an intensive summer program. Explored with students possible educational and career opportunities in biomedical science.

2009	**Course Developer and Instructor**, Project Mercury	*Hyderabad, India*

Worked with a team of seven Stanford undergraduate students and two faculty members. Designed a professional development course for paramedic students and instructors. Developed and taught the curriculum at the GVK Emergency Research and Management Institute in Hyderabad, India.