

Stanford



Jesse Engreitz

Assistant Professor of Genetics

CONTACT INFORMATION

• Administrative Contact

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Bio

ACADEMIC APPOINTMENTS

- Assistant Professor, Genetics
- Member, Bio-X
- Member, Cardiovascular Institute
- Member, Maternal & Child Health Research Institute (MCHRI)

PROFESSIONAL EDUCATION

- PhD, MIT , Harvard-MIT Division of Health Sciences and Technology (2016)
- MS, Stanford University , Bioengineering (2010)
- BS, Stanford University , Biomedical Computation (2010)

LINKS

- My Lab Site: <https://www.engreitzlab.org>
- Basic Science and Engineering Initiative: <https://www.med.stanford.edu/base>

Teaching

STANFORD ADVISEES

Doctoral Dissertation Reader (AC)

Jason Cheng, Rosa Ma

Postdoctoral Faculty Sponsor

Dulguun Amgalan, Gabriella Martyn, Tri Nguyen

Doctoral Dissertation Advisor (AC)

Yannick Lee-Yow, Michael Montgomery, Ronghao Zhou

GRADUATE AND FELLOWSHIP PROGRAM AFFILIATIONS

- Genetics (Phd Program)

Publications

PUBLICATIONS

- **Genome-wide enhancer maps link risk variants to disease genes.** *Nature*
Nasser, J., Bergman, D. T., Fulco, C. P., Guckelberger, P., Doughty, B. R., Patwardhan, T. A., Jones, T. R., Nguyen, T. H., Ulirsch, J. C., Lekschas, F., Mualim, K., Natri, H. M., Weeks, et al
2021
- **HyPR-seq: Single-cell quantification of chosen RNAs via hybridization and sequencing of DNA probes.** *Proceedings of the National Academy of Sciences of the United States of America*
Marshall, J. L., Doughty, B. R., Subramanian, V., Guckelberger, P., Wang, Q., Chen, L. M., Rodrigues, S. G., Zhang, K., Fulco, C. P., Nasser, J., Grinkevich, E. J., Noel, T., Mangiameli, et al
2020; 117 (52): 33404–13
- **Activity-by-contact model of enhancer-promoter regulation from thousands of CRISPR perturbations** *NATURE GENETICS*
Fulco, C. P., Nasser, J., Jones, T. R., Munson, G., Bergman, D. T., Subramanian, V., Grossman, S. R., Anyoha, R., Doughty, B. R., Patwardhan, T. A., Nguyen, T. H., Kane, M., Perez, et al
2019; 51 (12): 1664–+
- **Local regulation of gene expression by lncRNA promoters, transcription and splicing** *NATURE*
Engreitz, J. M., Haines, J. E., Perez, E. M., Munson, G., Chen, J., Kane, M., McDonel, P. E., Guttman, M., Lander, E. S.
2016; 539 (7629): 452–55
- **Systematic mapping of functional enhancer-promoter connections with CRISPR interference** *SCIENCE*
Fulco, C. P., Munschauer, M., Anyoha, R., Munson, G., Grossman, S. R., Perez, E. M., Kane, M., Cleary, B., Lander, E. S., Engreitz, J. M.
2016; 354 (6313): 769–73
- **The Xist lncRNA Exploits Three-Dimensional Genome Architecture to Spread Across the X Chromosome** *SCIENCE*
Engreitz, J. M., Pandya-Jones, A., McDonel, P., Shishkin, A., Sirokman, K., Surka, C., Kadri, S., Xing, J., Goren, A., Lander, E. S., Plath, K., Guttman, M.
2013; 341 (6147): 767–+
- **Inherited causes of clonal haematopoiesis in 97,691 whole genomes (vol 586 , pg 763, 2020)** *NATURE*
Bick, A. G., Weinstock, J. S., Nandakumar, S. K., Fulco, C. P., Bao, E. L., Zekavat, S. M., Szeto, M. D., Liao, X., Leventhal, M. J., Nasser, J., Chang, K., Laurie, C., Burugula, et al
2021; 591 (7851): E27
- **Author Correction: Inherited causes of clonal haematopoiesis in 97,691 whole genomes.** *Nature*
Bick, A. G., Weinstock, J. S., Nandakumar, S. K., Fulco, C. P., Bao, E. L., Zekavat, S. M., Szeto, M. D., Liao, X., Leventhal, M. J., Nasser, J., Chang, K., Laurie, C., Burugula, et al
2021
- **Activity-dependent regulome of human GABAergic neurons reveals new patterns of gene regulation and neurological disease heritability.** *Nature neuroscience*
Boulting, G. L., Durrresi, E., Ataman, B., Sherman, M. A., Mei, K., Harmin, D. A., Carter, A. C., Hochbaum, D. R., Granger, A. J., Engreitz, J. M., Hrvatin, S., Blanchard, M. R., Yang, et al
2021
- **Inherited causes of clonal haematopoiesis in 97,691 whole genomes.** *Nature*
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2020
- **Publisher Correction: Deep coverage whole genome sequences and plasma lipoprotein(a) in individuals of European and African ancestries.** *Nature communications*
Zekavat, S. M., Ruotsalainen, S., Handsaker, R. E., Alver, M., Bloom, J., Poterba, T., Seed, C., Ernst, J., Chaffin, M., Engreitz, J., Peloso, G. M., Manichaikul, A., Yang, et al

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- **Prioritizing disease and trait causal variants at the TNFAIP3 locus using functional and genomic features** *NATURE COMMUNICATIONS*
Ray, J. P., de Boer, C. G., Fulco, C. P., Lareau, C. A., Kanai, M., Ulirsch, J. C., Tewhey, R., Ludwig, L. S., Reilly, S. K., Bergman, D. T., Engreitz, J. M., Issner, R., Finucane, et al
2020; 11 (1): 1237
- **Functional disease architectures reveal unique biological role of transposable elements** *NATURE COMMUNICATIONS*
Hormozdiari, F., van de Geijn, B., Nasser, J., Weissbrod, O., Gazal, S., Ju, C., O'Connor, L., Hujoel, M. A., Engreitz, J., Hormozdiari, F., Price, A. L.
2019; 10: 4054
- **CRISPR Tools for Systematic Studies of RNA Regulation** *COLD SPRING HARBOR PERSPECTIVES IN BIOLOGY*
Engreitz, J., Abudayyeh, O., Gootenberg, J., Zhang, F.
2019; 11 (8)
- **Discovering metabolic disease gene interactions by correlated effects on cellular morphology** *MOLECULAR METABOLISM*
Jiao, Y., Ahmed, U., Sim, M., Bejar, A., Zhang, X., Talukder, M., Rice, R., Flannick, J., Podgornaia, A., Reilly, D. F., Engreitz, J. M., Kost-Alimova, M., Hartland, et al
2019; 24: 108–19
- **Gene-centric functional dissection of human genetic variation uncovers regulators of hematopoiesis** *ELIFE*
Nandakumar, S. K., McFarland, S. K., Mateyka, L. M., Lareau, C. A., Ulirsch, J. C., Ludwig, L. S., Agarwal, G., Engreitz, J. M., Przychodzen, B., McConkey, M., Cowley, G. S., Doench, J. G., Maciejewski, et al
2019; 8
- **CRISPR-SURF: discovering regulatory elements by deconvolution of CRISPR tiling screen data** *NATURE METHODS*
Hsu, J. Y., Fulco, C. P., Cole, M. A., Canver, M. C., Pellin, D., Sher, F., Farouni, R., Clement, K., Guo, J. A., Biasco, L., Orkin, S. H., Engreitz, J. M., Lander, et al
2018; 15 (12): 992+
- **The NORAD lncRNA assembles a topoisomerase complex critical for genome stability (vol 561, pg 132, 2018)** *NATURE*
Munschauer, M., Nguyen, C. T., Sirokman, K., Hartigan, C. R., Hogstrom, L., Engreitz, J. M., Ulirsch, J. C., Fulco, C. P., Subramanian, V., Chen, J., Schenone, M., Guttman, M., Carr, et al
2018; 563 (7733): E32
- **The NORAD lncRNA assembles a topoisomerase complex critical for genome stability** *NATURE*
Munschauer, M., Nguyen, C. T., Sirokman, K., Hartigan, C. R., Hogstrom, L., Engreitz, J. M., Ulirsch, J. C., Fulco, C. P., Subramanian, V., Chen, J., Schenone, M., Guttman, M., Carr, et al
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- **Deep coverage whole genome sequences and plasma lipoprotein(a) in individuals of European and African ancestries (vol 9, 2606, 2018)** *NATURE COMMUNICATIONS*
Zekavat, S. M., Ruotsalainen, S., Handsaker, R. E., Alver, M., Bloom, J., Poterba, T., Seed, C., Ernst, J., Chaffin, M., Engreitz, J., Peloso, G. M., Manichaikul, A., Yang, et al
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- **Positional specificity of different transcription factor classes within enhancers** *PROCEEDINGS OF THE NATIONAL ACADEMY OF SCIENCES OF THE UNITED STATES OF AMERICA*
Grossman, S. R., Engreitz, J., Ray, J. P., Nguyen, T. H., Hacohen, N., Lander, E. S.
2018; 115 (30): E7222–E7230
- **Ribosome Levels Selectively Regulate Translation and Lineage Commitment in Human Hematopoiesis** *CELL*
Khajuria, R. K., Munschauer, M., Ulirsch, J. C., Fiorini, C., Ludwig, L. S., McFarland, S. K., Abdulhay, N. J., Specht, H., Keshishian, H., Mani, D. R., Jovanovic, M., Ellis, S. R., Fulco, et al
2018; 173 (1): 90+
- **Deep coverage whole genome sequences and plasma lipoprotein(a) in individuals of European and African ancestries.** *Nature communications*
Zekavat, S. M., Ruotsalainen, S. n., Handsaker, R. E., Alver, M. n., Bloom, J. n., Poterba, T. n., Seed, C. n., Ernst, J. n., Chaffin, M. n., Engreitz, J. n., Peloso, G. M., Manichaikul, A. n., Yang, et al
2018; 9 (1): 2606
- **Deep-coverage whole genome sequences and blood lipids among 16,324 individuals.** *Nature communications*

- Natarajan, P. n., Peloso, G. M., Zekavat, S. M., Montasser, M. n., Ganna, A. n., Chaffin, M. n., Khera, A. V., Zhou, W. n., Bloom, J. M., Engreitz, J. M., Ernst, J. n., O'Connell, J. R., Ruotsalainen, et al
2018; 9 (1): 3391
- **Genome-scale activation screen identifies a lncRNA locus regulating a gene neighbourhood** *NATURE*
Joung, J., Engreitz, J. M., Konermann, S., Abudayyeh, O. O., Verdine, V. K., Aguet, F., Gootenberg, J. S., Sanjana, N. E., Wright, J. B., Fulco, C. P., Tseng, Y., Yoon, C. H., Boehm, et al
2017; 548 (7667): 343-+
 - **A Genetic Variant Associated with Five Vascular Diseases Is a Distal Regulator of Endothelin-1 Gene Expression** *CELL*
Gupta, R. M., Hadaya, J., Trehan, A., Zekavat, S. M., Roselli, C., Klarin, D., Emdin, C. A., Hilvering, C. E., Bianchi, V., Mueller, C., Khera, A. V., Ryan, R. H., Engreitz, et al
2017; 170 (3): 522-+
 - **Recurrent and functional regulatory mutations in breast cancer** *NATURE*
Rheinbay, E., Parasuraman, P., Grimsby, J., Tiao, G., Engreitz, J. M., Kim, J., Lawrence, M. S., Taylor-Weiner, A., Rodriguez-Cuevas, S., Rosenberg, M., Hess, J., Stewart, C., Maruvka, et al
2017; 547 (7661): 55-+
 - **Systematic dissection of genomic features determining transcription factor binding and enhancer function** *PROCEEDINGS OF THE NATIONAL ACADEMY OF SCIENCES OF THE UNITED STATES OF AMERICA*
Grossman, S. R., Zhang, X., Wang, L., Engreitz, J., Melnikov, A., Rogov, P., Tewhey, R., Isakova, A., Deplancke, B., Bernstein, B. E., Mikkelsen, T. S., Lander, E. S.
2017; 114 (7): E1291–E1300
 - **Cohesin Loss Eliminates All Loop Domains.** *Cell*
Rao, S. S., Huang, S. C., Glenn St Hilaire, B. n., Engreitz, J. M., Perez, E. M., Kieffer-Kwon, K. R., Sanborn, A. L., Johnstone, S. E., Bascom, G. D., Bochkov, I. D., Huang, X. n., Shamim, M. S., Shin, et al
2017; 171 (2): 305–20.e24
 - **Long non-coding RNAs: spatial amplifiers that control nuclear structure and gene expression** *NATURE REVIEWS MOLECULAR CELL BIOLOGY*
Engreitz, J. M., Ollikainen, N., Guttman, M.
2016; 17 (12): 756–70
 - **Principles of Systems Biology-No. 10** *CELL SYSTEMS*
Sanjana, N., Zhang, F., Fulco, C., Lander, E., Engreitz, J., Costanzo, M., Myers, C. L., Andrews, B., Boone, C., Kwiecien, N., Coon, J., Stefely, J., Pagliarini, et al
2016; 3 (4): 318–20
 - **Eradication of large established tumors in mice by combination immunotherapy that engages innate and adaptive immune responses.** *Nature medicine*
Moynihan, K. D., Opel, C. F., Szeto, G. L., Tzeng, A., Zhu, E. F., Engreitz, J. M., Williams, R. T., Rakhra, K., Zhang, M. H., Rothschilds, A. M., Kumari, S., Kelly, R. L., Kwan, et al
2016
 - **RNA Antisense Purification (RAP) for Mapping RNA Interactions with Chromatin** *NUCLEAR BODIES AND NONCODING RNAs: METHODS AND PROTOCOLS*
Engreitz, J., Lander, E. S., Guttman, M., Nakagawa, S., Hirose, T.
2015; 1262: 183–97
 - **RNA-RNA Interactions Enable Specific Targeting of Noncoding RNAs to Nascent Pre-mRNAs and Chromatin Sites** *CELL*
Engreitz, J. M., Sirokman, K., McDonel, P., Shishkin, A. A., Surka, C., Russell, P., Grossman, S. R., Chow, A. Y., Guttman, M., Lander, E. S.
2014; 159 (1): 188–99
 - **Transcriptome-wide Mapping Reveals Widespread Dynamic-Regulated Pseudouridylation of ncRNA and mRNA** *CELL*
Schwartz, S., Bernstein, D. A., Mumbach, M. R., Jovanovic, M., Herbst, R. H., Leon-Ricardo, B. X., Engreitz, J. M., Guttman, M., Satija, R., Lander, E. S., Fink, G., Regev, A.
2014; 159 (1): 148–62
 - **Topological organization of multichromosomal regions by the long intergenic noncoding RNA Firre** *NATURE STRUCTURAL & MOLECULAR BIOLOGY*
Hacisuleyman, E., Goff, L. A., Trapnell, C., Williams, A., Henaio-Mejia, J., Sun, L., McClanahan, P., Hendrickson, D. G., Sauvageau, M., Kelley, D. R., Morse, M., Engreitz, J., Lander, et al
2014; 21 (2): 198-+

- **Neuregulin Autocrine Signaling Promotes Self-Renewal of Breast Tumor-Initiating Cells by Triggering HER2/HER3 Activation** *CANCER RESEARCH*
Lee, C. Y., Lin, Y., Bratman, S. V., Feng, W., Kuo, A. H., Scheeren, F. A., Engreitz, J. M., Varma, S., West, R. B., Diehn, M.
2014; 74 (1): 341-352
- **Three-Dimensional Genome Architecture Influences Partner Selection for Chromosomal Translocations in Human Disease** *PLOS ONE*
Engreitz, J. M., Agarwala, V., Mirny, L. A.
2012; 7 (9): e44196
- **ProfileChaser: searching microarray repositories based on genome-wide patterns of differential expression** *BIOINFORMATICS*
Engreitz, J. M., Chen, R., Morgan, A. A., Dudley, J. T., Mallelwar, R., Butte, A. J.
2011; 27 (23): 3317-3318
- **The Lin28/let-7 Axis Regulates Glucose Metabolism** *CELL*
Zhu, H., Shyh-Chang, N., Segre, A. V., Shinoda, G., Shah, S. P., Einhorn, W. S., Takeuchi, A., Engreitz, J. M., Hagan, J. P., Kharas, M. G., Urbach, A., Thornton, J. E., Triboulet, et al
2011; 147 (1): 81-94
- **Content-based microarray search using differential expression profiles** *BMC BIOINFORMATICS*
Engreitz, J. M., Morgan, A. A., Dudley, J. T., Chen, R., Thathoo, R., Altman, R. B., Butte, A. J.
2010; 11
- **Independent component analysis: Mining microarray data for fundamental human gene expression modules** *JOURNAL OF BIOMEDICAL INFORMATICS*
Engreitz, J. M., Daigle, B. J., Marshall, J. J., Altman, R. B.
2010; 43 (6): 932-944