Stanford

Jesse Engreitz

Assistant Professor of Genetics

CONTACT INFORMATION

- **Administrative Contact**

  Hadley Bickford - Administrative Associate

  Email hadleyb@stanford.edu

  Tel 650-497-2440

Bio

BIO

Jesse is currently an Assistant Professor at Stanford University in the Department of Genetics and the Children's Heart Center Basic Sciences and Engineering (BASE) Initiative, and is a recipient of the NHGRI Genomic Innovator Award. He co-leads a Functional Characterization Center at Stanford for the Impact of Genomic Variation on Function (IGVF) Consortium, and is an Associate Director of the Novo Nordisk Foundation Center for Genomic Mechanisms of Disease at the Broad Institute.

Previously, Jesse was a Junior Fellow at the Harvard Society of Fellows and led a research group at the Broad Institute of MIT and Harvard. During his postdoctoral fellowship at the Broad Institute, Jesse developed large-scale CRISPR tools to map enhancer-gene regulation with Eric Lander and Nir Hacohen, and launched the Variants-to-Function (V2F) Initiative to connect genetic disease variants to their molecular and cellular functions. Jesse previously attended Stanford University, where he developed computational algorithms for analyzing gene expression with Russ Altman, and completed his PhD in the Harvard-MIT Division of Health Sciences and Technology, where he studied genome regulation by long noncoding RNAs with Eric Lander and Mitch Guttman. His research has been supported by the National Human Genome Research Institute, National Heart, Lung, and Blood Institute, Additional Ventures, Foundations for the National Institutes of Health, Harvard Society of Fellows, Fannie and John Hertz Foundation, and Department of Defense. Outside the lab, Jesse enjoys playing jazz/rock/funk, testing Chinese recipes, and surfing.

ACADEMIC APPOINTMENTS

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

PROGRAM AFFILIATIONS

- Betty Irene Moore Children's Heart Center

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

Research & Scholarship

CURRENT RESEARCH AND SCHOLARLY INTERESTS

We are mapping the regulatory wiring of the genome to understand the genetic basis of heart diseases.

The human genome encodes 2 million enhancers, which act in combination to regulate nearby genes. Each of the thousands of cell types in the human body has its own precise wiring that is difficult to resolve. Enhancers contain tens of thousands of DNA variants that affect human diseases — and therefore hold the key to understanding molecular mechanisms that control genetic risk for disease. We aim to map enhancer-gene connections in every cell type in the human body to connect disease variants to the genes, cell types, and pathways they control.

Our approach:

• We invent new single-cell methods combining genomics, biochemistry, and molecular biology.

• We dissect molecular mechanisms of enhancer-gene communication.

• We build computational models to map genome regulation.

• We connect human genetic variants to biological mechanisms of disease by applying these tools in cellular and animal models.

Teaching

COURSES

2024-25

- Current Issues in Genetics: GENE 219 (Aut, Win, Spr, Sum)
- Genetics and Developmental Biology Training Camp: DBIO 200, GENE 200 (Aut)

2023-24

- Current Issues in Genetics: GENE 219 (Aut, Win, Spr, Sum)
- Genetics and Developmental Biology Training Camp: DBIO 200, GENE 200 (Aut)

2022-23

- Biology and Applications of CRISPR/Cas9: Genome Editing and Epigenome Modifications: BIOS 268, GENE 268 (Spr)
- Current Issues in Genetics: GENE 219 (Spr)

2021-22

- Biology and Applications of CRISPR/Cas9: Genome Editing and Epigenome Modifications: BIOS 268, GENE 268 (Spr)
- Current Issues in Genetics: GENE 219 (Spr)

STANFORD ADVISEES

Doctoral Dissertation Reader (AC)

Matthew Aguirre, Julia Bauman, Benjamin Doughty, Danilo Dubocanin, Simon Gaudin, Tami Gjorgjieva, Soumya Kundu, Julie Lake, Kate Lawrence, Vincent Liu, Anusri Pampari, Peter Suzuki

Postdoctoral Faculty Sponsor

Danila Bredikhin, Olga Pushkarev

Doctoral Dissertation Advisor (AC)

Yannick Lee-Yow, Michael Montgomery, Maya Sheth, Ronghao Zhou

Doctoral Dissertation Co-Advisor (AC)

Shawn Cai, Tony Zeng

Doctoral (Program)

Jason Tan

GRADUATE AND FELLOWSHIP PROGRAM AFFILIATIONS

- Genetics (Phd Program)

Publications

PUBLICATIONS

- **Compatibility rules of human enhancer and promoter sequences.** *Nature*
  Bergman, D. T., Jones, T. R., Liu, V., Ray, J., Jagoda, E., Siraj, L., Kang, H. Y., Nasser, J., Kane, M., Rios, A., Nguyen, T. H., Grossman, S. R., Fulco, et al
  2022

- **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., Rodriques, 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-+

- **Rewriting regulatory DNA to dissect and reprogram gene expression.** *Cell*

  Martyn, G. E., Montgomery, M. T., Jones, H., Guo, K., Doughty, B. R., Linder, J., Bisht, D., Xia, F., Cai, X. S., Chen, Z., Cochran, K., Lawrence, K. A., Munson, et al

  2025

- **Selective Enhancer Dependencies in MYC-Intact and MYC-Rearranged Germinal Center B-cell Diffuse Large B-cell Lymphoma.** *Blood cancer discovery*

  Iyer, A. R., Gurumurthy, A., Chu, S. A., Kodgule, R., Aguilar, A. R., Saari, T., Ramzan, A., Rosa, J., Gupta, J., Emmanuel, A., Hall, C. N., Runge, J. S., Owczarczyk, et al

  2025

- **Endothelial cell-related genetic variants identify LDL cholesterol-sensitive individuals who derive greater benefit from aggressive lipid lowering.** *Nature medicine*

  Marston, N. A., Kamanu, F. K., Melloni, G. E., Schnitzler, G., Hakim, A., Ma, R. X., Kang, H., Chasman, D. I., Giugliano, R. P., Ellinor, P. T., Ridker, P. M., Engreitz, J. M., Sabatine, et al

  2025

- **MorPhiC Consortium: towards functional characterization of all human genes.** *Nature*

  Adli, M., Przybyla, L., Burdett, T., Burridge, P. W., Cacheiro, P., Chang, H. Y., Engreitz, J. M., Gilbert, L. A., Greenleaf, W. J., Hsu, L., Huangfu, D., Hung, L. H., Kundaje, et al

  2025; 638 (8050): 351-359

- **High Shear Stress Reduces ERG Causing Endothelial-Mesenchymal Transition and Pulmonary Arterial Hypertension.** *Arteriosclerosis, thrombosis, and vascular biology*

  Shinohara, T., Moonen, J. R., Chun, Y. H., Lee-Yow, Y. C., Okamura, K., Szafron, J. M., Kaplan, J., Cao, A., Wang, L., Guntur, D., Taylor, S., Isobe, S., Dong, et al

  2024

- **An Expanded Registry of Candidate cis-Regulatory Elements for Studying Transcriptional Regulation.** *bioRxiv : the preprint server for biology*

  Moore, J. E., Pratt, H. E., Fan, K., Phalke, N., Fisher, J., Elhajjajy, S. I., Andrews, G., Gao, M., Shedd, N., Fu, Y., Lacadie, M. C., Meza, J., Ganna, et al

  2024

- **Molecular convergence of risk variants for congenital heart defects leveraging a regulatory map of the human fetal heart.** *medRxiv : the preprint server for health sciences*

  Ma, X. R., Conley, S. D., Kosicki, M., Bredikhin, D., Cui, R., Tran, S., Sheth, M. U., Qiu, W. L., Chen, S., Kundu, S., Kang, H. Y., Amgalan, D., Munger, et al

  2024

- **Single cell variant to enhancer to gene map for coronary artery disease.** *medRxiv : the preprint server for health sciences*

  Amrute, J. M., Lee, P. C., Eres, I., Lee, C. J., Bredemeyer, A., Sheth, M. U., Yamawaki, T., Gurung, R., Anene-Nzelu, C., Qiu, W. L., Kundu, S., Li, D. Y., Ramste, et al

  2024

- **Selective Enhancer Gain of Function Deregulates MYC Expression in Multiple Myeloma.** *Cancer research*

  Rahmat, M., Clement, K., Alberge, J. B., Sklavenitis-Pistofidis, R., Kodgule, R., Fulco, C. P., Heilpern-Mallory, D., Nilsson, K., Dorfman, D., Engreitz, J. M., Getz, G., Pinello, L., Ryan, et al

  2024

- **Deciphering the impact of genomic variation on function.** *Nature*

  2024; 633 (8028): 47-57

- **Genetic and functional analysis of Raynaud's syndrome implicates loci in vasculature and immunity.** *Cell genomics*

  Tervi, A., Ramste, M., Abner, E., Cheng, P., Lane, J. M., Maher, M., Valliere, J., Lammi, V., Strausz, S., Riikonen, J., Nguyen, T., Martyn, G. E., Sheth, et al

  2024: 100630

- **CRISPRi-Perturb-seq in endothelial cells links genetic variation in endothelin-1 to risk of coronary artery disease and hypertension** *CLINICAL SCIENCE*

  Gupta, R., Schnitzler, G., Lee-Kim, V., Fang, S., Kang, H., Ma, R., Finucane, H., Engreitz, J.

2024; 138

- **CRISPRi-Perturb-seq in endothelial cells links genetic variation in endothelin-1 to risk of coronary artery disease and hypertension**
  Gupta, R., Schnitzler, G., Lee-Kim, V., Fang, S., Kang, H., Ma, R., Finucane, H., Engreitz, J.
  PORTLAND PRESS LTD.2024: A55-A56

- **Multicenter integrated analysis of noncoding CRISPRi screens.** *Nature methods*
  Yao, D., Tycko, J., Oh, J. W., Bounds, L. R., Gosai, S. J., Lataniotis, L., Mackay-Smith, A., Doughty, B. R., Gabdank, I., Schmidt, H., Guerrero-Altamirano, T., Siklenka, K., Guo, et al
  2024

- **Convergence of coronary artery disease genes onto endothelial cell programs.** *Nature*
  Schnitzler, G. R., Kang, H., Fang, S., Angom, R. S., Lee-Kim, V. S., Ma, X. R., Zhou, R., Zeng, T., Guo, K., Taylor, M. S., Vellarikkal, S. K., Barry, A. E., Sias-Garcia, et al
  2024

- **Rewriting regulatory DNA to dissect and reprogram gene expression.** *bioRxiv : the preprint server for biology*
  Martyn, G. E., Montgomery, M. T., Jones, H., Guo, K., Doughty, B. R., Linder, J., Chen, Z., Cochran, K., Lawrence, K. A., Munson, G., Pampari, A., Fulco, C. P., Kelley, et al
  2023

- **Reduced FOXF1 links unrepaired DNA damage to pulmonary arterial hypertension.** *Nature communications*
  Isobe, S., Nair, R. V., Kang, H. Y., Wang, L., Moonen, J. R., Shinohara, T., Cao, A., Taylor, S., Otsuki, S., Marciano, D. P., Harper, R. L., Adil, M. S., Zhang, et al
  2023; 14 (1): 7578

- **An encyclopedia of enhancer-gene regulatory interactions in the human genome.** *bioRxiv : the preprint server for biology*
  Gschwind, A. R., Mualim, K. S., Karbalayghareh, A., Sheth, M. U., Dey, K. K., Jagoda, E., Nurtdinov, R. N., Xi, W., Tan, A. S., Jones, H., Ma, X. R., Yao, D., Nasser, et al
  2023

- **Leveraging polygenic enrichments of gene features to predict genes underlying complex traits and diseases.** *Nature genetics*
  Weeks, E. M., Ulirsch, J. C., Cheng, N. Y., Trippe, B. L., Fine, R. S., Miao, J., Patwardhan, T. A., Kanai, M., Nasser, J., Fulco, C. P., Tashman, K. C., Aguet, F., Li, et al
  2023

- **An Atlas of Variant Effects to understand the genome at nucleotide resolution.** *Genome biology*
  Fowler, D. M., Adams, D. J., Gloyn, A. L., Hahn, W. C., Marks, D. S., Muffley, L. A., Neal, J. T., Roth, F. P., Rubin, A. F., Starita, L. M., Hurles, M. E.
  2023; 24 (1): 147

- **Oligogenic Architecture of Rare Noncoding Variants Distinguishes 4 Congenital Heart Disease Phenotypes.** *Circulation. Genomic and precision medicine*
  Yu, M., Aguirre, M., Jia, M., Gjoni, K., Cordova-Palomera, A., Munger, C., Amgalan, D., Rosa Ma, X., Pereira, A., Tcheandjieu, C., Seidman, C., Seidman, J., Tristani-Firouzi, et al
  2023: e003968

- **Genetic Determinants of the Interventricular Septum Are Linked to Ventricular Septal Defects and Hypertrophic Cardiomyopathy.** *Circulation. Genomic and precision medicine*
  Yu, M., Harper, A. R., Aguirre, M., Pittman, M., Tcheandjieu, C., Amgalan, D., Grace, C., Goel, A., Farrall, M., Xiao, K., Engreitz, J., Pollard, K. S., Watkins, et al
  2023: e003708

- **The Type 2 Diabetes Knowledge Portal: An open access genetic resource dedicated to type 2 diabetes and related traits.** *Cell metabolism*
  Costanzo, M. C., von Grotthuss, M., Massung, J., Jang, D., Caulkins, L., Koesterer, R., Gilbert, C., Welch, R. P., Kudtarkar, P., Hoang, Q., Boughton, A. P., Singh, P., Sun, et al
  2023

- **Integrative single-cell analysis of cardiogenesis identifies developmental trajectories and non-coding mutations in congenital heart disease.** *Cell*
  Ameen, M., Sundaram, L., Shen, M., Banerjee, A., Kundu, S., Nair, S., Shcherbina, A., Gu, M., Wilson, K. D., Varadarajan, A., Vadgama, N., Balsubramani, A., Wu, et al
  2022; 185 (26): 4937

- **Identifying disease-critical cell types and cellular processes by integrating single-cell RNA-sequencing and human genetics.** *Nature genetics*
  Jagadeesh, K. A., Dey, K. K., Montoro, D. T., Mohan, R., Gazal, S., Engreitz, J. M., Xavier, R. J., Price, A. L., Regev, A.
  2022
- **KLF4 recruits SWI/SNF to increase chromatin accessibility and reprogram the endothelial enhancer landscape under laminar shear stress.** *Nature communications*
  Moonen, J. R., Chappell, J., Shi, M., Shinohara, T., Li, D., Mumbach, M. R., Zhang, F., Nair, R. V., Nasser, J., Mai, D. H., Taylor, S., Wang, L., Metzger, et al
  2022; 13 (1): 4941
- **SNP-to-gene linking strategies reveal contributions of enhancer-related and candidate master-regulator genes to autoimmune disease.** *Cell genomics*
  Dey, K. K., Gazal, S., van de Geijn, B., Kim, S. S., Nasser, J., Engreitz, J. M., Price, A. L.
  2022; 2 (7)
- **Combining SNP-to-gene linking strategies to identify disease genes and assess disease omnigenicity.** *Nature genetics*
  Gazal, S., Weissbrod, O., Hormozdiari, F., Dey, K. K., Nasser, J., Jagadeesh, K. A., Weiner, D. J., Shi, H., Fulco, C. P., O'Connor, L. J., Pasaniuc, B., Engreitz, J. M., Price, et al
  2022
- **Computational estimates of annular diameter reveal genetic determinants of mitral valve function and disease.** *JCI insight*
  Yu, M., Tcheandjieu, C., Georges, A., Xiao, K., Tejeda, H., Dina, C., Le Tourneau, T., Fiterau, M., Judy, R., Tsao, N. L., Amgalan, D., Munger, C. J., Engreitz, et al
  2022; 7 (3)
- **Systematic identification of genomic elements that regulate FCGR2A expression and harbor variants linked with autoimmune disease.** *Human molecular genetics*
  Dahlqvist, J., Fulco, C. P., Ray, J. P., Liechti, T., de Boer, C. G., Lieb, D. J., Eisenhaure, T. M., Engreitz, J. M., Roederer, M., Hacohen, N.
  1800
- **COVID-19 tissue atlases reveal SARS-CoV-2 pathology and cellular targets.** *Nature*
  Delorey, T. M., Ziegler, C. G., Heimberg, G., Normand, R., Yang, Y., Segerstolpe, A., Abbondanza, D., Fleming, S. J., Subramanian, A., Montoro, D. T., Jagadeesh, K. A., Dey, K. K., Sen, et al
  2021
- **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
- **A single-cell and spatial atlas of autopsy tissues reveals pathology and cellular targets of SARS-CoV-2.** *bioRxiv : the preprint server for biology*
  Delorey, T. M., Ziegler, C. G., Heimberg, G., Normand, R., Yang, Y., Segerstolpe, A., Abbondanza, D., Fleming, S. J., Subramanian, A., Montoro, D. T., Jagadeesh, K. A., Dey, K. K., Sen, 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., Durresi, 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*
  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

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
  2020; 11 (1): 1715

- **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
  2018; 561 (7721): 132-+

- **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
  2018; 9: 3493

- **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

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