Stanford



William Greenleaf

Professor of Genetics

Curriculum Vitae available Online

CONTACT INFORMATION

- **Administrative Assistant**

  Maxim Litvinov - Administrative Assistant

  Email mlitv@stanford.edu

Bio

BIO

William Greenleaf is a Professor in the Genetics Department at Stanford University School of Medicine, with a courtesy appointment in the Applied Physics Department. He is a member of Bio-X, the Biophysics Program, the Biomedical Informatics Program, and the Cancer Center. He received an A.B. in physics from Harvard University in 2002, and received a Gates Fellowship to study computer science for one year in Trinity College, Cambridge, UK. He returned to Stanford to carry out his Ph.D. in Applied Physics in the laboratory of Steven Block, where he investigated, at the single molecule level, the chemo-mechanics of RNA polymerase and the folding of RNA transcripts. He conducted postdoctoral work in the laboratory of X. Sunney Xie in the Chemistry and Chemical Biology Department at Harvard University, where he was awarded a Damon Runyon Cancer Research Foundation Fellowship, and developed new fluorescence-based high-throughput sequencing methodologies. He moved to Stanford as an Assistant Professor in November 2011. Since beginning his lab, he has been named a Rita Allen Foundation Young Scholar, an Ellison Foundation Young Scholar in Aging (declined), a Baxter Foundation Scholar, a Chan-Zuckerberg Investigator, and Arc Institute Innovation Investigator, and received the NIH Director's Pioneer Award. Will is the Director of the RNA Medicine Program at Stanford. His highly interdisciplinary research links molecular biology, computer science, bioengineering, and genomics a to understand how the physical state of the human genome controls gene regulation and biological state. Efforts in his lab are split between building new tools to leverage the power of high-throughput sequencing and cutting-edge microscopies, and bringing these new technologies to bear against basic biological questions of genomic and epigenomic regulation. His long-term goal is to unlock an understanding of the physical “regulome” — i.e. the factors that control how the genetic information is read into biological instructions — to develop a quantitative understanding of how cells maintain, or fail to maintain, their state in health and disease.

ACADEMIC APPOINTMENTS

- Professor, Genetics
- Member, Bio-X
- Member, Wu Tsai Human Performance Alliance
- Member, Maternal & Child Health Research Institute (MCHRI)
- Member, Stanford Cancer Institute
- Member, Wu Tsai Neurosciences Institute

HONORS AND AWARDS

- Arc Institute Innovation Investigator, Arc Institute (2023-)
- Pioneer Award, NIH (2023-)
- Chan-Zuckerberg Fellow, Chan-Zuckerberg Foundation (2017-2022)
- Baxter Foundation Faculty Fellow, Baxter Foundation (2014)
- Rita Allen Scholar, Rita Allen Foundation (2011)
- Damon Runyon Cancer Research Fellowship, Damon Runyon Foundation (2009-2011)
- ARCS Fellowship, ARCS (2006)
- Graduate Fellowship, National Science Foundation (2003-2005)
- Gates Cambridge Trust Scholar, Gates Foundation (2002-2003)

PROFESSIONAL EDUCATION

- Postdoctoral Fellow, Harvard University , Chemistry and Chemical Biology
- PhD, Stanford University , Applied Physics (2008)
- Dip Comp Sci, Trinity College, Cambridge University, UK , Computer Science (2003)
- AB, Harvard University , Physics (2002)

LINKS

- Greenleaf Lab Website: http://greenleaf.stanford.edu

Research & Scholarship

CURRENT RESEARCH AND SCHOLARLY INTERESTS

Our lab focuses on developing methods to probe both the structure and function of molecules encoded by the genome, as well as the physical configuration of the nucleoprotein components of the genome and epigenome. Our efforts are split between building new tools to leverage the power of high-throughput sequencing technologies, and bringing these technologies to bear against basic biological questions by linking DNA sequence, structure, and function.

Teaching

COURSES

2026-27

- Genetics and Developmental Biology Training Camp: DBIO 200, GENE 200 (Aut)

2025-26

- Advanced Imaging Lab in Biophysics: APPPHYS 232, BIO 132, BIO 232, BIOE 232, BIOPHYS 232, GENE 232 (Spr)
- Genetics and Developmental Biology Training Camp: DBIO 200, GENE 200 (Aut)

2024-25

- Advanced Imaging Lab in Biophysics: APPPHYS 232, BIO 132, BIO 232, BIOE 232, BIOPHYS 232, GENE 232 (Spr)
- Genetics and Developmental Biology Training Camp: DBIO 200, GENE 200 (Aut)

2023-24

- Advanced Imaging Lab in Biophysics: APPPHYS 232, BIO 132, BIO 232, BIOE 232, BIOPHYS 232, GENE 232 (Spr)

STANFORD ADVISEES

Doctoral Dissertation Reader (AC)

Olivia Crocker, Connor Duffy, Katie Fang, Drew Galls, Simon Gaudin, Kate Lawrence, Oliver Takacsi-Nagy, Xariana Vales Torres, Valeh Valiollah Pour Amiri, Sidney Vermeulen, Christine Zhou

Postdoctoral Faculty Sponsor

Jacob Blum, Vinson Fan, Sayeh Gorjifard, Guanhua He, Matt Kukurugya, Roman Reggiardo

Doctoral Dissertation Advisor (AC)

Benjamin Doughty, Logan Dunkenberger, Owen Dunkley, James Occean, Georgia Tully

Orals Evaluator

John Shin

Doctoral Dissertation Co-Advisor (AC)

Jason Tan

Postdoctoral Research Mentor

Yuxi Ke

GRADUATE AND FELLOWSHIP PROGRAM AFFILIATIONS

- Bioengineering (PhD Program)
- Biomedical Data Science (PhD Program)
- Biophysics (PhD Program)
- Cancer Biology (PhD Program)
- Genetics (PhD Program)

Publications

PUBLICATIONS

- **Expansion of functional human long-term HSCs through restraining excessive cell cycle activation.** *Blood*
  Mao, X., Zhang, N., He, X., Dong, R., Yang, Z., Epp, M., Hembree, M., Zhang, L., Meng, Y., Scott, A., Hall, K., Perera, A., Javier, et al
  2026; 148 (19): 2338-2353

- **Author Correction: Multiomic analysis of familial adenomatous polyposis reveals molecular pathways associated with early tumorigenesis.** *Nature cancer*
  Esplin, E. D., Hanson, C., Wu, S., Horning, A. M., Bararpour, N., Nevins, S. A., Jiang, L., Contrepois, K., Lee, H., Guha, T. K., Hu, Z., Laquindanum, R., Mills, et al
  2026

- **A practical guide to studying genome function using single-molecule genomics.** *Nature reviews. Molecular cell biology*
  Krebs, A. R., Altemose, N., Churchman, L. S., Greenleaf, W. J., Ramani, V., Stadler, M. B., Stergachis, A. B.
  2026

- **RNA delivery to the corneal endothelium using charge-altering releasable transporters.** *Science advances*
  Wang, S. K., Li, Z., Shah, S. H., Edwards, Q. A., Bouffard, R., Hines, E. S., Imventarza, J. A., Korte, S., Lawrence, M. S., Song, E., Helmy, E., Amaya, L., Kang, et al
  2026; 12 (34): eady8161

- **Memory encoding reprograms neuronal transcriptional responses via durable chromatin remodeling.** *bioRxiv : the preprint server for biology*
  Ke, Y., Sun, X., Greenleaf, W. J., Schnitzer, M. J.
  2026

- **Single-cell chromatin state transitions during epigenetic memory formation.** *Science advances*
  Fujimori, T., Thurm, A. R., Gaudin, S., Rios-Martinez, C., Doughty, B. R., Hinks, M. M., Sinha, J., Le, D., Hafner, A., Greenleaf, W. J., Boettiger, A. N., Bintu, L.
  2026; 12 (30): eaeb0060

- **An encyclopedia of human enhancer-gene regulatory interactions.** *Nature*
  Gschwind, A. R., Mualim, K. S., Karbalayghareh, A., Sheth, M. U., Dey, K. K., Jagoda, E., Nurtdinov, R. N., Xi, W., Tan, A. S., Galante, J., Jones, H., Ma, X. R., Yao, et al
  2026

- **Epigenetic landscape, key transcriptional regulators, and in vivo identification of human Tr1 cells.** *Science advances*
  Cepika, A. M., Amaya, L., Waichler, C., Narula, M., Mantilla, M., Thomas, B. C., Chen, P. P., Freeborn, R. A., Pavel-Dinu, M., Nideffer, J., Porteus, M., Bacchetta, R., Müller, et al
  2026; 12 (28): eaec6358

- **A Simple, Cost-Effective, High-Throughput Method for Measuring Chromatin Accessibility and Gene Expression in Single Nuclei.** *bioRxiv : the preprint server for biology*
  Luo, Z., Greenleaf, W. J.
  2026

- **Intrinsic promoter responsiveness dictates sensitivity to transcriptional activation by enhancers.** *bioRxiv : the preprint server for biology*
  Tan, Y., Ray, J., Sheth, M. U., Doughty, B. R., Greenleaf, W. J., Engreitz, J. M.
  2026

- **An emergent disease-associated motor neuron state precedes cell death in ALS.** *Cell*
  Gautier, O., Blum, J. A., Nguyen, T. P., Cao, S., Klemm, S., Yamakawa, M., Huh, D., Hurt, J. A., Sinnott-Armstrong, N., Zeng, Y., Davis, C. O., Bombosch, J., Liu, et al
  2026

- **RNA delivery to the corneal endothelium using charge-altering releasable transporters**
  Wang, S. K., Li, Z., Shah, S., Edwards, Q. A., Bouffard, R., Hines, E. S., Imventarza, J., Korte, S., Lawrence, M., Song, E., Helmy, E., Amaya, L., Kang, et al
  ASSOC RESEARCH VISION OPHTHALMOLOGY INC.2026

- **Prediction and functional interpretation of inter-chromosomal genome architecture from DNA sequence with TwinC.** *Nature communications*
  Jha, A., Hristov, B., Wang, X., Wang, S., Greenleaf, W. J., Kundaje, A., Aiden, E. L., Bertero, A., Noble, W. S.
  2026

- **Multiomics and deep learning dissect regulatory syntax in human development.** *Nature*
  Liu, B. B., Jessa, S., Kim, S. H., Ng, Y. T., Higashino, S. I., Marinov, G. K., Chen, D. C., Parks, B. E., Li, L., Nguyen, T. C., Wang, A. T., Wang, S. K., Tan, et al
  2026

- **Genetics and environment distinctively shape the human immune cell epigenome.** *Nature genetics*
  Wang, W., Hariharan, M., Ding, W., Bartlett, A., Barragan, C., Castanon, R., Wang, R., Rothenberg, V., Song, H., Nery, J. R., Aldridge, A., Altshul, J., Kenworthy, et al
  2026

- **Thermodynamic principles link in vitro transcription factor affinities to single-molecule chromatin states in cells.** *Cell*
  Schaepe, J. M., Fries, T., Doughty, B. R., Ramalingam, V., Liu, B. B., Crocker, O. J., Marinov, G. K., Hinks, M. M., Marklund, E., Greenleaf, W. J.
  2025

- **Polyclonal origins of human premalignant colorectal lesions.** *Nature*
  Van Egeren, D., Schenck, R. O., Khan, A., Horning, A. M., Mo, S., Weiß, C. L., Esplin, E. D., Becker, W. R., Wu, S., Hanson, C., Barapour, N., Jiang, L., Contrepois, et al
  2025

- **Compact RNA sensors for increasingly complex functions of multiple inputs.** *Nature chemistry*
  Choe, C. A., Andreasson, J. O., Melaine, F., Kladwang, W., Wu, M. J., Portela, F., Wellington-Oguri, R., Nicol, J. J., Wayment-Steele, H. K., Gotrik, M., Khatri, P., Greenleaf, W. J., Das, et al
  2025

- **Polyclonal origins of human premalignant colorectal lesions.** *bioRxiv : the preprint server for biology*
  Van Egeren, D., Schenck, R. O., Khan, A., Horning, A. M., Mo, S., Weiß, C. L., Esplin, E. D., Becker, W. R., Wu, S., Hanson, C., Barapour, N., Jiang, L., Contrepois, et al
  2025
- **Age-related microbiome metabolites alter RNA splicing and chromatin accessibility in the brain.** *bioRxiv : the preprint server for biology*
  Chakraborty, M., Shi, S. M., Porter, I. E., Richard, D. J., Marinov, G. K., Moore, A. A., Blum, J. L., Natarajan, A., Jahng, J. W., Wu, J. C., Lu, S. X., Davidson, S. M., Greenleaf, et al
  2025
- **GREGoR: accelerating genomics for rare diseases.** *Nature*
  Dawood, M., Heavner, B., Wheeler, M. M., Ungar, R. A., LoTempio, J., Wiel, L., Berger, S., Bernstein, J. A., Chong, J. X., Délot, E. C., Eichler, E. E., Lupski, J. R., Shojaie, et al
  2025; 647 (8089): 331-342
- **Deep learning the dynamic regulatory sequence code of cardiac organoid differentiation.** *bioRxiv : the preprint server for biology*
  Metzl-Raz, E., Zhao, R., Deshpande, S., Powell, J., Porter, E. G., Zouaghi, Y., Liu, B. B., Kim, S. H., Abdi, I., Evergreen, I., Agarwal, M., Sheth, M. U., Rico, et al
  2025
- **Functional mapping of epigenomic regulators uncovers coordinated tumor suppression by the HBO1 and MLL1 complexes.** *Cancer discovery*
  Tang, Y. J., Xu, H., Hughes, N. W., Ruiz, P., Kim, S. H., Shuldiner, E. G., Lopez, S. S., Hebert, J. D., Karmakar, S., Andrejka, L., Dolcen, D. N., Boross, G., Chu, et al
  2025
- **Sensitive, direct detection of non-coding off-target base editor unwinding and editing in primary cells.** *bioRxiv : the preprint server for biology*
  Wang, T., Jessa, S., Marinov, G. K., Klemm, S., Kundaje, A., Greenleaf, W. J.
  2025
- **Innate immune molecular landscape following controlled human influenza virus infection.** *Cell reports*
  Thistlethwaite, W., Vangeti, S., Cheng, W. S., Agarwal, P., Cappuccio, A., Wang, W., Wei, B., Myers, R., Rubenstein, A. B., Chawla, D., Hariharan, M., McClain, M. T., Burke, et al
  2025; 44 (10): 116312
- **An emergent disease-associated motor neuron state precedes cell death in a mouse model of ALS.** *bioRxiv : the preprint server for biology*
  Gautier, O., Blum, J. A., Nguyen, T. P., Klemm, S., Yamakawa, M., Sinnott-Armstrong, N., Zeng, Y., Davis, C. O., Bombosch, J., Nakayama, L., Guttenplan, K. A., Chen, D., Kathira, et al
  2025
- **Thymic epithelial cells amplify epigenetic noise to promote immune tolerance.** *Nature*
  Gamble, N., Caldwell, J. A., McKeever, J., Kaiser, C., Bradu, A., Dooley, P. J., Klemm, S., Greenleaf, W. J., Hibino, N., Dinner, A. R., Koh, A. S.
  2025
- **Cell type-specific purifying selection of synonymous mitochondrial DNA variation.** *Proceedings of the National Academy of Sciences of the United States of America*
  Lareau, C. A., Maschmeyer, P., Yin, Y., Gutierrez, J. C., Dhindsa, R. S., Gribling-Burrer, A. S., Zielinski, S., Hsieh, Y. H., Nitsch, L., Dimitrova, V., Nalbant, B., Buquicchio, F. A., Abay, et al
  2025; 122 (30): e2505704122
- **An automated ATAC-seq method reveals sequence determinants of transcription factor dose response in the open chromatin.** *bioRxiv : the preprint server for biology*
  Liu, B. B., Shimasawa, M., Vermeulen, S., Kim, S. H., Iremadze, N., Lipson, D., Shipony, Z., Greenleaf, W. J.
  2025
- **High-throughput DNA melt measurements enable improved models of DNA folding thermodynamics.** *Nature communications*
  Ke, Y., Sharma, E., Wayment-Steele, H. K., Becker, W. R., Ho, A., Marklund, E., Greenleaf, W. J.
  2025; 16 (1): 5572
- **Three-dimensional genome landscape of primary human cancers.** *Nature genetics*

Yost, K. E., Zhao, Y., Hung, K. L., Zhu, K., Xu, D., Corces, M. R., Shams, S., Louie, B. H., Sarmashghi, S., Sundaram, L., Luebeck, J., Clarke, S., Doane, et al
2025

- **Mapping the Simultaneously Accessible and ssDNA-Containing Genome With KAS-ATAC Sequencing** *BIO-PROTOCOL*
  Marinov, G. K., Greenleaf, W. J.
  2025; 15 (9): e5306

- **An updated compendium and reevaluation of the evidence for nuclear transcription factor occupancy over the mitochondrial genome.** *PloS one*
  Marinov, G. K., Ramalingam, V., Greenleaf, W. J., Kundaje, A.
  2025; 20 (3): e0318796

- **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

- **Thermodynamic principles link in vitro transcription factor affinities to single-molecule chromatin states in cells.** *bioRxiv : the preprint server for biology*
  Schaepe, J. M., Fries, T., Doughty, B. R., Crocker, O. J., Hinks, M. M., Marklund, E., Greenleaf, W. J.
  2025

- **Author Correction: Global loss of promoter-enhancer connectivity and rebalancing of gene expression during early colorectal cancer carcinogenesis.** *Nature cancer*
  Zhu, Y., Lee, H., White, S., Weimer, A. K., Monte, E., Horning, A., Nevins, S. A., Esplin, E. D., Paul, K., Krieger, G., Shipony, Z., Chiu, R., Laquindanum, et al
  2025

- **ChromBPNet: bias factorized, base-resolution deep learning models of chromatin accessibility reveal cis-regulatory sequence syntax, transcription factor footprints and regulatory variants.** *bioRxiv : the preprint server for biology*
  Pampari, A., Shcherbina, A., Kvon, E. Z., Kosicki, M., Nair, S., Kundu, S., Kathiria, A. S., Risca, V. I., Kuningas, K., Alasoo, K., Greenleaf, W. J., Pennacchio, L. A., Kundaje, et al
  2025

- **The chromatin landscape of the histone-possessing Bacteriovorax bacteria.** *Genome research*
  Marinov, G. K., Doughty, B., Kundaje, A., Greenleaf, W. J.
  2024

- **Single-cell spatial mapping reveals alteration of cell type composition and tissue microenvironment during early colorectal cancer formation.** *bioRxiv : the preprint server for biology*
  Guha, T. K., Esplin, E. D., Horning, A. M., Chiu, R., Paul, K., Weimer, A. K., Becker, W. R., Laquindanum, R., Mills, M. A., Glen Esplin, D., Shen, J., Monte, E., White, et al
  2024

- **KAS-ATAC reveals the genome-wide single-stranded accessible chromatin landscape of the human genome.** *Genome research*
  Kim, S. H., Marinov, G. K., Greenleaf, W.
  2024

- **Single-molecule states link transcription factor binding to gene expression.** *Nature*
  Doughty, B. R., Hinks, M. M., Schaepe, J. M., Marinov, G. K., Thurm, A. R., Rios-Martinez, C., Parks, B. E., Tan, Y., Marklund, E., Dubocanin, D., Bintu, L., Greenleaf, W. J.
  2024

- **Enhancing transcription-replication conflict targets ecDNA-positive cancers.** *Nature*
  Tang, J., Weiser, N. E., Wang, G., Chowdhry, S., Curtis, E. J., Zhao, Y., Wong, I. T., Marinov, G. K., Li, R., Hanoian, P., Tse, E., Mojica, S. G., Hansen, et al
  2024; 635 (8037): 210-218

- **Multiomic analysis of familial adenomatous polyposis reveals molecular pathways associated with early tumorigenesis.** *Nature cancer*
  Esplin, E. D., Hanson, C., Wu, S., Horning, A. M., Barapour, N., Nevins, S. A., Jiang, L., Contrepois, K., Lee, H., Guha, T. K., Hu, Z., Laquindanum, R., Mills, et al

2024

- **Global loss of promoter-enhancer connectivity and rebalancing of gene expression during early colorectal cancer carcinogenesis.** *Nature cancer*
  Zhu, Y., Lee, H., White, S., Weimer, A. K., Monte, E., Horning, A., Nevins, S. A., Esplin, E. D., Paul, K., Krieger, G., Shipony, Z., Chiu, R., Laquindanum, et al
  2024
- **Exploring the energetic and conformational properties of the sequence space connecting naturally occurring RNA tetraloop receptor motifs.** *RNA (New York, N.Y.)*
  Shin, J. H., Cuevas, L. M., Roy, R., Bonilla, S. L., Al-Hashimi, H., Greenleaf, W. J., Herschlag, D.
  2024
- **Prediction and functional interpretation of inter-chromosomal genome architecture from DNA sequence with TwinC.** *bioRxiv : the preprint server for biology*
  Jha, A., Hristov, B., Wang, X., Wang, S., Greenleaf, W. J., Kundaje, A., Aiden, E. L., Bertero, A., Noble, W. S.
  2024
- **Single-cell chromatin accessibility reveals malignant regulatory programs in primary human cancers.** *Science (New York, N.Y.)*
  Sundaram, L., Kumar, A., Zatzman, M., Salcedo, A., Ravindra, N., Shams, S., Louie, B. H., Bagdatli, S. T., Myers, M. A., Sarmashghi, S., Choi, H. Y., Choi, W. Y., Yost, et al
  2024; 385 (6713): eadk9217
- **Deciphering the impact of genomic variation on function.** *Nature*
  2024; 633 (8028): 47-57
- **Terminal deoxynucleotidyl transferase and CD84 identify human multi-potent lymphoid progenitors.** *Nature communications*
  Kim, Y., Calderon, A. A., Favaro, P., Glass, D. R., Tsai, A. G., Ho, D., Borges, L., Greenleaf, W. J., Bendall, S. C.
  2024; 15 (1): 5910
- **An updated compendium and reevaluation of the evidence for nuclear transcription factor occupancy over the mitochondrial genome.** *bioRxiv : the preprint server for biology*
  Marinov, G. K., Ramalingam, V., Greenleaf, W. J., Kundaje, A.
  2024
- **Publisher Correction: PU.1 and BCL11B sequentially cooperate with RUNX1 to anchor mSWI/SNF to poise the T cell effector landscape.** *Nature immunology*
  Gamble, N., Bradu, A., Caldwell, J. A., McKeever, J., Bolonduro, O., Ermis, E., Kaiser, C., Kim, Y., Parks, B., Klemm, S., Greenleaf, W. J., Crabtree, G. R., Koh, et al
  2024
- **The killifish germline regulates longevity and somatic repair in a sex-specific manner.** *Nature aging*
  Moses, E., Atlan, T., Sun, X., Franěk, R., Siddiqui, A., Marinov, G. K., Shifman, S., Zucker, D. M., Oron-Gottesman, A., Greenleaf, W. J., Cohen, E., Ram, O., Harel, et al
  2024
- **Genome-wide distribution of 5-hydroxymethyluracil and chromatin accessibility in the Breviolum minutum genome.** *Genome biology*
  Marinov, G. K., Chen, X., Swaffer, M. P., Xiang, T., Grossman, A. R., Greenleaf, W. J.
  2024; 25 (1): 115
- **PU.1 and BCL11B sequentially cooperate with RUNX1 to anchor mSWI/SNF to poise the T cell effector landscape.** *Nature immunology*
  Gamble, N., Bradu, A., Caldwell, J. A., McKeever, J., Bolonduro, O., Ermis, E., Kaiser, C., Kim, Y., Parks, B., Klemm, S., Greenleaf, W. J., Crabtree, G. R., Koh, et al
  2024
- **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
- **Protocol for mapping the three-dimensional organization of dinoflagellate genomes.** *STAR protocols*
  Marinov, G. K., Kundaje, A., Greenleaf, W. J., Grossman, A. R.

2024; 5 (2): 102941

- **Author Correction: Advances and prospects for the Human BioMolecular Atlas Program (HuBMAP).** *Nature cell biology*
  Jain, S., Pei, L., Spraggins, J. M., Angelo, M., Carson, J. P., Gehlenborg, N., Ginty, F., Goncalves, J. P., Hagood, J. S., Hickey, J. W., Kelleher, N. L., Laurent, L. C., Lin, et al
  2024

- **Single-molecule chromatin configurations link transcription factor binding to expression in human cells.** *bioRxiv : the preprint server for biology*
  Doughty, B. R., Hinks, M. M., Schaepe, J. M., Marinov, G. K., Thurm, A. R., Rios-Martinez, C., Parks, B. E., Tan, Y., Marklund, E., Dubocanin, D., Bintu, L., Greenleaf, W. J.
  2024

- **Compact RNA sensors for increasingly complex functions of multiple inputs.** *bioRxiv : the preprint server for biology*
  Choe, C., Andreasson, J. O., Melaine, F., Kladwang, W., Wu, M. J., Portela, F., Wellington-Oguri, R., Nicol, J. J., Wayment-Steele, H. K., Gotrik, M., Participants, E., Khatri, P., Greenleaf, et al
  2024

- **Detection and analysis of complex structural variation in human genomes across populations and in brains of donors with psychiatric disorders** *Cell*
  Zhou, B., Arthur, J. G., Guo, H., et al
  2024; Published online September 30, 2024

- **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

- **The chromatin landscape of the euryarchaeon Haloferax volcanii.** *Genome biology*
  Marinov, G. K., Bagdatli, S. T., Wu, T., He, C., Kundaje, A., Greenleaf, W. J.
  2023; 24 (1): 253

- **The landscape of the histone-organized chromatin of Bdellovibrionota bacteria.** *bioRxiv : the preprint server for biology*
  Marinov, G. K., Doughty, B., Kundaje, A., Greenleaf, W. J.
  2023

- **RNA polymerase II dynamics and mRNA stability feedback scale mRNA amounts with cell size.** *Cell*
  Swaffer, M. P., Marinov, G. K., Zheng, H., Fuentes Valenzuela, L., Tsui, C. Y., Jones, A. W., Greenwood, J., Kundaje, A., Greenleaf, W. J., Reyes-Lamothe, R., Skotheim, J. M.
  2023

- **Single-cell chromatin state transitions during epigenetic memory formation.** *bioRxiv : the preprint server for biology*
  Fujimori, T., Rios-Martinez, C., Thurm, A. R., Hinks, M. M., Doughty, B. R., Sinha, J., Le, D., Hafner, A., Greenleaf, W. J., Boettiger, A. N., Bintu, L.
  2023

- **Global mapping of RNA-chromatin contacts reveals a proximity-dominated connectivity model for ncRNA-gene interactions.** *Nature communications*
  Limouse, C., Smith, O. K., Jukam, D., Fryer, K. A., Greenleaf, W. J., Straight, A. F.
  2023; 14 (1): 6073

- **Short tandem repeats bind transcription factors to tune eukaryotic gene expression.** *Science (New York, N.Y.)*
  Horton, C. A., Alexandari, A. M., Hayes, M. G., Marklund, E., Schaepe, J. M., Aditham, A. K., Shah, N., Suzuki, P. H., Shrikumar, A., Afek, A., Greenleaf, W. J., Gordân, R., Zeitlinger, et al
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