Stanford

William Greenleaf

Professor of Genetics

Curriculum Vitae available Online

CONTACT INFORMATION

- **Administrative Assistant**

  Soon Il Higashino - Administrative Assistant

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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. 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 compaction and folding of the genome itself. Our efforts are split between building new tools to leverage the power of high-throughput sequencing technologies and cutting-edge optical microscopies, and bringing these technologies to bear against basic biological questions by linking DNA sequence, structure, and function.

Teaching

COURSES

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)

2022-23

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

STANFORD ADVISEES

Doctoral Dissertation Reader (AC)

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

Postdoctoral Faculty Sponsor

Vinson Fan, Sayeh Gorjifard, Guanhua He, Selin Jessa, Matvei Khoroshkin, Matt Kukurugya, Roman Reggiardo, Kseniia Vlasova

Doctoral Dissertation Advisor (AC)

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

Doctoral Dissertation Co-Advisor (AC)

Samuel Kim, Jason Tan

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

- **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

- **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
  2023; 381 (6664): eadd1250
- **Genome-wide distribution of 5-hydroxymethyluracil and chromatin accessibility in the Breviolum minutum genome.** *bioRxiv : the preprint server for biology*
  Marinov, G. K., Chen, X., Swaffer, M. P., Xiang, T., Grossman, A. R., Greenleaf, W. J.
  2023
- **Integration of spatial and single-cell data across modalities with weakly linked features.** *Nature biotechnology*
  Chen, S., Zhu, B., Huang, S., Hickey, J. W., Lin, K. Z., Snyder, M., Greenleaf, W. J., Nolan, G. P., Zhang, N. R., Ma, Z.
  2023
- **Systematic benchmarking of single-cell ATAC-sequencing protocols.** *Nature biotechnology*
  De Rop, F. V., Hulselmans, G., Flerin, C., Soler-Vila, P., Rafels, A., Christiaens, V., González-Blas, C. B., Marchese, D., Caratù, G., Poovathingal, S., Rozenblatt-Rosen, O., Slyper, M., Luo, et al
  2023
- **Integrated single-cell chromatin and transcriptomic analyses of human scalp identify gene-regulatory programs and critical cell types for hair and skin diseases.** *Nature genetics*
  Ober-Reynolds, B., Wang, C., Ko, J. M., Rios, E. J., Aasi, S. Z., Davis, M. M., Oro, A. E., Greenleaf, W. J.
  2023
- **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., Gonçalves, J. P., Hagood, J. S., Hickey, J. W., Kelleher, N. L., Laurent, L. C., Lin, et al
  2023
- **Organization of the human intestine at single-cell resolution.** *Nature*
  Hickey, J. W., Becker, W. R., Nevins, S. A., Horning, A., Perez, A. E., Zhu, C., Zhu, B., Wei, B., Chiu, R., Chen, D. C., Cotter, D. L., Esplin, E. D., Weimer, et al
  2023; 619 (7970): 572-584
- **Human Immune Cell Epigenomic Signatures in Response to Infectious Diseases and Chemical Exposures.** *bioRxiv : the preprint server for biology*
  Wang, W., Hariharan, M., Bartlett, A., Barragan, C., Castanon, R., Rothenberg, V., Song, H., Nery, J., Aldridge, A., Altshul, J., Kenworthy, M., Ding, W., Liu, et al
  2023

- **Discovery of Key Transcriptional Regulators of Alloantigen-Inducible Tregs Used for Cell Therapy**
  Cepika, A., Amaya, L., Waichler, C., Narula, M., Thomas, B. C., Chen, P. P., Mantilla, M. M., Pavel-Dinu, M., Freeborn, R., Porteus, M. H., Bacchetta, R., Mueller, F., Greenleaf, et al
  CELL PRESS.2023: 370-371

- **Single-cell transcriptomic landscape of the developing human spinal cord.** *Nature neuroscience*
  Andersen, J., Thom, N., Shadrach, J. L., Chen, X., Onesto, M. M., Amin, N. D., Yoon, S. J., Li, L., Greenleaf, W. J., Müller, F., Pașca, A. M., Kaltschmidt, J. A., Pașca, et al
  2023

- **CasKAS: direct profiling of genome-wide dCas9 and Cas9 specificity using ssDNA mapping.** *Genome biology*
  Marinov, G. K., Kim, S. H., Bagdatli, S. T., Higashino, S. I., Trevino, A. E., Tycko, J., Wu, T., Bintu, L., Bassik, M. C., He, C., Kundaje, A., Greenleaf, W. J.
  2023; 24 (1): 85

- **Systems biology approaches to unravel lymphocyte subsets and function.** *Current opinion in immunology*
  Kim, Y., Greenleaf, W. J., Bendall, S. C.
  2023; 82: 102323

- **Multifaceted role for p53 in pancreatic cancer suppression.** *Proceedings of the National Academy of Sciences of the United States of America*
  Mello, S. S., Flowers, B. M., Mazur, P. K., Lee, J. J., Müller, F., Denny, S. K., Ferreira, S., Hanson, K., Kim, S. K., Greenleaf, W. J., Wood, L. D., Attardi, L. D.
  2023; 120 (10): e2211937120

- **Building a quantitative and predictive model of 5 ' SS selection by human U1 snRNP using RNA-map**
  White, D. S., Carrocci, T. J., Shin, J., Lin, C., Black, D. L., Greenleaf, W., Herschlag, D., Hoskins, A. A.
  CELL PRESS.2023: 219A

- **Building a quantitative and predictive model of 5'SS selection by human U1 snRNP using RNA-map.** *Biophysical journal*
  White, D. S., Carrocci, T. J., Shin, J., Lin, C., Black, D. L., Greenleaf, W., Herschlag, D., Hoskins, A. A.
  2023; 122 (3S1): 219a

- **Malaria-driven expansion of adaptive-like functional CD56-negative NK cells correlates with clinical immunity to malaria.** *Science translational medicine*
  Ty, M., Sun, S., Callaway, P. C., Rek, J., Press, K. D., van der Ploeg, K., Nideffer, J., Hu, Z., Klemm, S., Greenleaf, W., Donato, M., Tukwasibwe, S., Arinaitwe, et al
  2023; 15 (680): eadd9012

- **High-throughput biochemistry in RNA sequence space: predicting structure and function.** *Nature reviews. Genetics*
  Marklund, E., Ke, Y., Greenleaf, W. J.
  2023

- **Statins improve endothelial function via suppression of epigenetic-driven EndMT** *Nature Cardiovascular Research*
  Liu, C., Shen, M., Tan, W. L., Chen, I. Y., Liu, Y., Yu, X., Zhang, A., Liu, Y., Zhao, M., Ameen, M., Zhang, M., Gross, E. R., Lei, et al
  2023

- **Current and future perspectives of single-cell multi-omics technologies in cardiovascular research.** *Nature cardiovascular research*
  Tan, W. L., Seow, W. Q., Zhang, A., Rhee, S., Wong, W. H., Greenleaf, W. J., Wu, J. C.
  2023; 2 (1): 20-34

- **Simultaneous Single-Cell Profiling of the Transcriptome and Accessible Chromatin Using SHARE-seq.** *Methods in molecular biology (Clifton, N.J.)*
  Kim, S. H., Marinov, G. K., Bagdatli, S. T., Higashino, S. I., Shipony, Z., Kundaje, A., Greenleaf, W. J.
  2023; 2611: 187-230

- **Genome-Wide Mapping of Active Regulatory Elements Using ATAC-seq.** *Methods in molecular biology (Clifton, N.J.)*
  Marinov, G. K., Shipony, Z., Kundaje, A., Greenleaf, W. J.
  2023; 2611: 3-19

- **Single-Molecule Mapping of Chromatin Accessibility Using NOMe-seq/dSMF.** *Methods in molecular biology (Clifton, N.J.)*
  Hinks, M., Marinov, G. K., Kundaje, A., Bintu, L., Greenleaf, W. J.

2023; 2611: 101-119

- **Chromatin Accessibility Methods and Protocols Preface** *CHROMATIN ACCESSIBILITY*
  Marinov, G. K., Greenleaf, W. J.
  edited by Marinov, G. K., Greenleaf, W. J.
  2023; 2611: V

- **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

- **Aging-associated HELIOS deficiency in naive CD4+ T cells alters chromatin remodeling and promotes effector cell responses.** *Nature immunology*
  Zhang, H., Jadhav, R. R., Cao, W., Goronzy, I. N., Zhao, T. V., Jin, J., Ohtsuki, S., Hu, Z., Morales, J., Greenleaf, W. J., Weyand, C. M., Goronzy, J. J.
  2022

- **Engineered cell entry links receptor biology with single-cell genomics.** *Cell*
  Yu, B., Shi, Q., Belk, J. A., Yost, K. E., Parker, K. R., Li, R., Liu, B. B., Huang, H., Lingwood, D., Greenleaf, W. J., Davis, M. M., Satpathy, A. T., Chang, et al
  2022

- **Targeted profiling of human extrachromosomal DNA by CRISPR-CATCH.** *Nature genetics*
  Hung, K. L., Luebeck, J., Dehkordi, S. R., Colon, C. I., Li, R., Wong, I. T., Coruh, C., Dharanipragada, P., Lomeli, S. H., Weiser, N. E., Moriceau, G., Zhang, X., Bailey, et al
  2022

- **PD-1 combination therapy with IL-2 modifies CD8+ T cell exhaustion program.** *Nature*
  Hashimoto, M., Araki, K., Cardenas, M. A., Li, P., Jadhav, R. R., Kissick, H. T., Hudson, W. H., McGuire, D. J., Obeng, R. C., Wieland, A., Lee, J., McManus, D. T., Ross, et al
  2022

- **A comprehensive thermodynamic model for RNA binding by the Saccharomyces cerevisiae Pumilio protein PUF4.** *Nature communications*
  Sadee, C., Hagler, L. D., Becker, W. R., Jarmoskaite, I., Vaidyanathan, P. P., Denny, S. K., Greenleaf, W. J., Herschlag, D.
  2022; 13 (1): 4522

- **Systematic discovery and perturbation of regulatory genes in human T cells reveals the architecture of immune networks.** *Nature genetics*
  Freimer, J. W., Shaked, O., Naqvi, S., Sinnott-Armstrong, N., Kathiria, A., Garrido, C. M., Chen, A. F., Cortez, J. T., Greenleaf, W. J., Pritchard, J. K., Marson, A.
  2022

- **Single-cell analyses define a continuum of cell state and composition changes in the malignant transformation of polyps to colorectal cancer.** *Nature genetics*
  Becker, W. R., Nevins, S. A., Chen, D. C., Chiu, R., Horning, A. M., Guha, T. K., Laquindanum, R., Mills, M., Chaib, H., Ladabaum, U., Longacre, T., Shen, J., Esplin, et al
  2022

- **Crowdsourced RNA design discovers diverse, reversible, efficient, self-contained molecular switches.** *Proceedings of the National Academy of Sciences of the United States of America*
  Andreasson, J. O., Gotrik, M. R., Wu, M. J., Wayment-Steele, H. K., Kladwang, W., Portela, F., Wellington-Oguri, R., Eterna Participants, Das, R., Greenleaf, W. J.
  2022; 119 (18): e2112979119

- **NEAT-seq: simultaneous profiling of intra-nuclear proteins, chromatin accessibility and gene expression in single cells.** *Nature methods*
  Chen, A. F., Parks, B., Kathiria, A. S., Ober-Reynolds, B., Goronzy, J. J., Greenleaf, W. J.
  2022

- **Integrating transcription-factor abundance with chromatin accessibility in human erythroid lineage commitment.** *Cell reports methods*
  Baskar, R., Chen, A. F., Favaro, P., Reynolds, W., Mueller, F., Borges, L., Jiang, S., Park, H. S., Kool, E. T., Greenleaf, W. J., Bendall, S. C.
  2022; 2 (3)

- **Generation of a dual edited human induced pluripotent stem cell Myl7-GFP reporter line with inducible CRISPRi/dCas9.** *Stem cell research*
  Metzl-Raz, E., Bharucha, N., Arthur Ataam, J., Gavidia, A. A., Greenleaf, W. J., Karakikes, I.
  2022; 61: 102754

- **High-throughput biochemical profiling reveals functional adaptation of a bacterial Argonaute.** *Molecular cell*
  Ober-Reynolds, B., Becker, W. R., Jouravleva, K., Jolly, S. M., Zamore, P. D., Greenleaf, W. J.
  2022

- **MITI minimum information guidelines for highly multiplexed tissue images.** *Nature methods*
  Schapiro, D., Yapp, C., Sokolov, A., Reynolds, S. M., Chen, Y., Sudar, D., Xie, Y., Muhlich, J., Arias-Camison, R., Arena, S., Taylor, A. J., Nikolov, M., Tyler, et al
  2022; 19 (3): 262-267

- **The chromatin organization of a chlorarachniophyte nucleomorph genome.** *Genome biology*
  Marinov, G. K., Chen, X., Wu, T., He, C., Grossman, A. R., Kundaje, A., Greenleaf, W. J.
  2022; 23 (1): 65

- **Short tandem repeats recruit transcription factors to tune eukaryotic gene expression**
  Horton, C. A., Alexandari, A. M., Hayes, M. G., Schaepe, J. M., Marklund, E., Shah, N., Aditham, A. K., Shrikumar, A., Afek, A., Greenleaf, W. J., Gordan, R., Zeitlinger, J., Kundaje, et al
  CELL PRESS.2022: 287A-288A

- **Reduced chromatin accessibility to CD4 T cell super-enhancers encompassing susceptibility loci of rheumatoid arthritis.** *EBioMedicine*
  Jadhav, R. R., Hu, B., Ye, Z., Sheth, K., Li, X., Greenleaf, W. J., Weyand, C. M., Goronzy, J. J.
  1800; 76: 103825

- **Single-Molecule Multikilobase-Scale Profiling of Chromatin Accessibility Using m6A-SMAC-Seq and m6A-CpG-GpC-SMAC-Seq.** *Methods in molecular biology (Clifton, N.J.)*
  Marinov, G. K., Shipony, Z., Kundaje, A., Greenleaf, W. J.
  2022; 2458: 269-298

- **An optimized ATAC-seq protocol for genome-wide mapping of active regulatory elements in primary mouse cortical neurons.** *STAR protocols*
  Maor-Nof, M., Shipony, Z., Marinov, G. K., Greenleaf, W. J., Gitler, A. D.
  2021; 2 (4): 100854

- **DIMINISHED V delta 2+delta gamma T CELL CYTOKINE PRODUCTION AND DEGRANULATION FOLLOWING IN VITRO MALARIA EXPOSURE**
  Dantzler, K., Klemm, S., Rek, J., Nankya, F., Ssewanyana, I., Kamya, M., Greenhouse, B., Dorsey, G., Feeney, M., Greenleaf, W., Jagannathan, P.
  AMER SOC TROP MED & HYGIENE.2021: 16

- **Transcriptional and chromatin-based partitioning mechanisms uncouple protein scaling from cell size.** *Molecular cell*
  Swaffer, M. P., Kim, J., Chandler-Brown, D., Langhinrichs, M., Marinov, G. K., Greenleaf, W. J., Kundaje, A., Schmoller, K. M., Skotheim, J. M.
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