



William Greenleaf

Associate Professor of Genetics and, by courtesy, of Applied Physics

 Curriculum Vitae available Online

CONTACT INFORMATION

- **Alternate Contact**

Alex Orantes - Administrative Assistant

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Bio

BIO

William Greenleaf is an Associate 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 (summa cum laude) in 2002, and received a Gates Fellowship to study computer science for one year in Trinity College, Cambridge, UK (with distinction). After this experience abroad, 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, and a Chan-Zuckerberg Investigator. His highly interdisciplinary research links molecular biology, computer science, bioengineering, and genomics 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 variation. 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 — profoundly impacting our understanding of how cells maintain, or fail to maintain, their state in health and disease.

ACADEMIC APPOINTMENTS

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

HONORS AND AWARDS

- Chan-Zuckerberg Fellow, Chan-Zuckerberg Foundation (2017-)
- 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

2020-21

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

2019-20

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

2018-19

- 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)

2017-18

- Advanced Imaging Lab in Biophysics: APPPHYS 232, BIO 132, BIO 232, BIOPHYS 232, GENE 232 (Spr)
- Next Generation Sequencing and Applications: BIOS 201 (Win)

STANFORD ADVISEES

Doctoral Dissertation Reader (AC)

Kevin Aris, Abhimanyu Banerjee, Reema Baskar, Jacob Blum, Olivia Gautier, Suhas Rao, Charles Starr, Josh Tycko, David Yao, Katie Yost

Postdoctoral Faculty Sponsor

Amy Chen, Sandy Klemm, Georgi Marinov, Eyal Metzl Raz, Fabian Müller, Eesha Sharma, Zohar Shipony, Bei Wei

Doctoral Dissertation Advisor (AC)

Winston Becker, Jeffrey Granja, Anthony Ho, Ben Ober-Reynolds, Alexandro Trevino

Doctoral Dissertation Co-Advisor (AC)

Michaela Hinks, Samuel Kim, YeEun Kim, Sarah Pierce, laksshman sundaram

Postdoctoral Research Mentor

Jordi Fernandez Albert

Doctoral (Program)

Ben Parks

GRADUATE AND FELLOWSHIP PROGRAM AFFILIATIONS

- Biomedical Informatics (Phd Program)
- Biophysics (Phd Program)
- Genetics (Phd Program)

Publications

PUBLICATIONS

- **Epigenetic signature of PD-1+ TCF1+ CD8 T cells that act as resource cells during chronic viral infection and respond to PD-1 blockade.** *Proceedings of the National Academy of Sciences of the United States of America*
Jadhav, R. R., Im, S. J., Hu, B., Hashimoto, M., Li, P., Lin, J., Leonard, W. J., Greenleaf, W. J., Ahmed, R., Goronzy, J. J.
2019
- **Demonstration of protein cooperativity mediated by RNA structure using the human protein PUM2 RNA**
Becker, W. R., Jarmoskaite, I., Vaidyanathan, P. P., Greenleaf, W. J., Herschlag, D.
2019; 25 (6): 702–12
- **Cell cycle dynamics of human pluripotent stem cells primed for differentiation.** *Stem cells (Dayton, Ohio)*
Shcherbina, A., Li, J., Narayanan, C., Greenleaf, W., Kundaje, A., Chetty, S.
2019
- **HiChIRP reveals RNA-associated chromosome conformation.** *Nature methods*
Mumbach, M. R., Granja, J. M., Flynn, R. A., Roake, C. M., Satpathy, A. T., Rubin, A. J., Qi, Y., Jiang, Z., Shams, S., Louie, B. H., Guo, J. K., Gennert, D. G., Corces, et al
2019
- **Blind tests of RNA-protein binding affinity prediction.** *Proceedings of the National Academy of Sciences of the United States of America*
Kappel, K., Jarmoskaite, I., Vaidyanathan, P. P., Greenleaf, W. J., Herschlag, D., Das, R.
2019
- **Demonstration of Protein Cooperativity Mediated by RNA Structure Using the Human Protein PUM2.** *RNA (New York, N.Y.)*
Becker, W. R., Jarmoskaite, I., Vaidyanathan, P. P., Greenleaf, W. J., Herschlag, D.
2019
- **Large-Scale, Quantitative Protein Assays on a High-Throughput DNA Sequencing Chip.** *Molecular cell*
Layton, C. J., McMahon, P. L., Greenleaf, W. J.
2019; 73 (5): 1075
- **Chromatin accessibility and the regulatory epigenome.** *Nature reviews. Genetics*
Klemm, S. L., Shipony, Z., Greenleaf, W. J.
2019
- **A Quantitative and Predictive Model for RNA Binding by Human Pumilio Proteins.** *Molecular cell*
Jarmoskaite, I., Denny, S. K., Vaidyanathan, P. P., Becker, W. R., Andreasson, J. O., Layton, C. J., Kappel, K., Shivashankar, V., Sreenivasan, R., Das, R., Greenleaf, W. J., Herschlag, D.
2019

- **OPEN CHROMATIN PROFILING IDENTIFIES FUNCTIONAL NONCODING RISK VARIANTS IN HUMAN IPSC MODEL OF PSYCHIATRIC DISORDERS**
Duan, J., Forrest, M., Zhang, H., Moy, W., McGowan, H., Leites, C., Shi, J., Sanders, A., Greenleaf, W., Cowan, C., Pang, Z., Gejman, P., Penzes, et al
ELSEVIER SCIENCE BV.2019: S765
- **High-Throughput Analysis Reveals Rules for Target RNA Binding and Cleavage by AGO2.** *Molecular cell*
Becker, W. R., Ober-Reynolds, B., Jouravleva, K., Jolly, S. M., Zamore, P. D., Greenleaf, W. J.
2019
- **Satb1 integrates DNA binding site geometry and torsional stress to differentially target nucleosome-dense regions.** *Nature communications*
Ghosh, R. P., Shi, Q., Yang, L., Reddick, M. P., Nikitina, T., Zhurkin, V. B., Fordyce, P., Stasevich, T. J., Chang, H. Y., Greenleaf, W. J., Liphardt, J. T.
2019; 10 (1): 3221
- **High-resolution mapping of cancer cell networks using co-functional interactions.** *Molecular systems biology*
Boyle, E. A., Pritchard, J. K., Greenleaf, W. J.
2018; 14 (12): e8594
- **Coupled Single-Cell CRISPR Screening and Epigenomic Profiling Reveals Causal Gene Regulatory Networks.** *Cell*
Rubin, A. J., Parker, K. R., Satpathy, A. T., Qi, Y., Wu, B., Ong, A. J., Mumbach, M. R., Ji, A. L., Kim, D. S., Cho, S. W., Zarnegar, B. J., Greenleaf, W. J., Chang, et al
2018
- **Deterministic Somatic Cell Reprogramming Involves Continuous Transcriptional Changes Governed by Myc and Epigenetic-Driven Modules.** *Cell stem cell*
Zviran, A., Mor, N., Rais, Y., Gingold, H., Peles, S., Chomsky, E., Viukov, S., Buenrostro, J. D., Scognamiglio, R., Weinberger, L., Manor, Y. S., Krupalnik, V., Zerbib, et al
2018
- **Identification of phagocytosis regulators using magnetic genome-wide CRISPR screens.** *Nature genetics*
Haney, M. S., Bohlen, C. J., Morgens, D. W., Ousey, J. A., Barkal, A. A., Tsui, C. K., Ego, B. K., Levin, R., Kamber, R. A., Collins, H., Tucker, A., Li, A., Vorselen, et al
2018
- **Joint single-cell DNA accessibility and protein epitope profiling reveals environmental regulation of epigenomic heterogeneity.** *Nature communications*
Chen, X., Litzenburger, U. M., Wei, Y., Schep, A. N., LaGory, E. L., Choudhry, H., Giaccia, A. J., Greenleaf, W. J., Chang, H. Y.
2018; 9 (1): 4590
- **Linking RNA Sequence, Structure, and Function on Massively Parallel High-Throughput Sequencers.** *Cold Spring Harbor perspectives in biology*
Denny, S. K., Greenleaf, W. J.
2018
- **Intertumoral Heterogeneity in SCLC Is Influenced by the Cell Type of Origin.** *Cancer discovery*
Yang, D., Denny, S. K., Greenside, P. G., Chaikovskiy, A. C., Brady, J. J., Ouadah, Y., Granja, J. M., Jahchan, N. S., Lim, J. S., Kwok, S., Kong, C. S., Berghoff, A. S., Schmitt, et al
2018
- **High-throughput chromatin accessibility profiling at single-cell resolution.** *Nature communications*
Mezger, A., Klemm, S., Mann, I., Brower, K., Mir, A., Bostick, M., Farmer, A., Fordyce, P., Linnarsson, S., Greenleaf, W.
2018; 9 (1): 3647
- **Neutralizing Gatad2a-Chd4-Mbd3/NuRD Complex Facilitates Deterministic Induction of Naive Pluripotency** *CELL STEM CELL*
Mor, N., Rais, Y., Sheban, D., Peles, S., Aguilera-Castrejon, A., Zviran, A., Elinger, D., Viukov, S., Geula, S., Krupalnik, V., Zerbib, M., Chomsky, E., Lasman, et al
2018; 23 (3): 412-+
- **A Chromatin Basis for Cell Lineage and Disease Risk in the Human Pancreas.** *Cell systems*
Arda, H. E., Tsai, J., Rosli, Y. R., Giresi, P., Bottino, R., Greenleaf, W. J., Chang, H. Y., Kim, S. K.
2018
- **Discovery of stimulation-responsive immune enhancers with CRISPR activation (vol 549, pg 111, 2017) NATURE**

- Simeonov, D. R., Gowen, B. G., Boontanrart, M., Roth, T. L., Gagnon, J. D., Mumbach, M. R., Satpathy, A. T., Lee, Y., Bray, N. L., Chan, A. Y., Lituiev, D. S., Nguyen, M. L., Gate, et al
2018; 559 (7715): E13
- **High-Throughput Investigation of Diverse Junction Elements in RNA Tertiary Folding.** *Cell*
Denny, S. K., Bisaria, N., Yesselman, J. D., Das, R., Herschlag, D., Greenleaf, W. J.
2018
 - **Unsupervised clustering and epigenetic classification of single cells** *NATURE COMMUNICATIONS*
Zamanighomi, M., Lin, Z., Daley, T., Chen, X., Duren, Z., Schep, A., Greenleaf, W. J., Wong, W.
2018; 9: 2410
 - **Integrated Single-Cell Analysis Maps the Continuous Regulatory Landscape of Human Hematopoietic Differentiation** *CELL*
Buenrostro, J. D., Corces, M., Lareau, C. A., Wu, B., Schep, A. N., Aryee, M. J., Majeti, R., Chang, H. Y., Greenleaf, W. J.
2018; 173 (6): 1535+
 - **Diff-seq: A high throughput sequencing-based mismatch detection assay for DNA variant enrichment and discovery** *NUCLEIC ACIDS RESEARCH*
Aggeli, D., Karas, V. O., Sinnott-Armstrong, N. A., Varghese, V., Shafer, R. W., Greenleaf, W. J., Sherlock, G.
2018; 46 (7)
 - **Chromatin-associated RNA sequencing (ChAR-seq) maps genome-wide RNA-to-DNA contacts** *ELIFE*
Bell, J. C., Jukam, D., Teran, N. A., Risca, V. I., Smith, O. K., Johnson, W. L., Skotheim, J. M., Greenleaf, W., Straight, A. F.
2018; 7
 - **Rapid chromatin repression by Aire provides precise control of immune tolerance** *NATURE IMMUNOLOGY*
Koh, A. S., Miller, E. L., Buenrostro, J. D., Moskowitz, D. M., Wang, J., Greenleaf, W. J., Chang, H. Y., Crabtree, G. R.
2018; 19 (2): 162+
 - **INO80 Chromatin Remodeling Coordinates Metabolic Homeostasis with Cell Division** *CELL REPORTS*
Gowans, G. J., Schep, A. N., Wong, K., King, D. A., Greenleaf, W. J., Morrison, A. J.
2018; 22 (3): 611–23
 - **Transcript-indexed ATAC-seq for precision immune profiling.** *Nature medicine*
Satpathy, A. T., Saligrama, N., Buenrostro, J. D., Wei, Y., Wu, B., Rubin, A. J., Granja, J. M., Lareau, C. A., Li, R., Qi, Y., Parker, K. R., Mumbach, M. R., Serrattelli, et al
2018
 - **The chromatin accessibility landscape of primary human cancers.** *Science (New York, N.Y.)*
Corces, M. R., Granja, J. M., Shams, S., Louie, B. H., Seoane, J. A., Zhou, W., Silva, T. C., Groeneveld, C., Wong, C. K., Cho, S. W., Satpathy, A. T., Mumbach, M. R., Hoadley, et al
2018; 362 (6413)
 - **Origin and differentiation of human memory CD8 T cells after vaccination** *NATURE*
Akondy, R. S., Fitch, M., Edupuganti, S., Yang, S., Kissick, H. T., Li, K. W., Youngblood, B. A., Abdelsamed, H. A., McGuire, D. J., Cohen, K. W., Alexe, G., Nagar, S., McCausland, et al
2017; 552 (7685): 362+
 - **Challenges and recommendations for epigenomics in precision health** *NATURE BIOTECHNOLOGY*
Carter, A. C., Chang, H. Y., Church, G., Dombkowski, A., Ecker, J. R., Gil, E., Giresi, P. G., Greely, H., Greenleaf, W. J., Hacohen, N., He, C., Hill, D., Ko, et al
2017; 35 (12): 1128–32
 - **Chromatin accessibility dynamics reveal novel functional enhancers in C. elegans** *GENOME RESEARCH*
Daugherty, A. C., Yeo, R. W., Buenrostro, J. D., Greenleaf, W. J., Kundaje, A., Brunet, A.
2017; 27 (12): 2096–2107
 - **Genome-scale measurement of off-target activity using Cas9 toxicity in high-throughput screens** *NATURE COMMUNICATIONS*
Morgens, D. W., Wainberg, M., Boyle, E. A., Ursu, O., Araya, C. L., Tsui, C. K., Haney, M. S., Hess, G. T., Han, K., Jeng, E. E., Li, A., Snyder, M. P., Greenleaf, et al
2017; 8

- **Comprehensive and quantitative mapping of RNA-protein interactions across a transcribed eukaryotic genome** *PROCEEDINGS OF THE NATIONAL ACADEMY OF SCIENCES OF THE UNITED STATES OF AMERICA*
She, R., Chakravarty, A. K., Layton, C. J., Chircus, L. M., Andreasson, J. O., Damaraju, N., McMahon, P. L., Buenrostro, J. D., Jarosz, D. F., Greenleaf, W. J.
2017; 114 (14): 3619-3624
- **Landscape of monoallelic DNA accessibility in mouse embryonic stem cells and neural progenitor cells.** *Nature genetics*
Xu, J., Carter, A. C., Gendrel, A., Attia, M., Loftus, J., Greenleaf, W. J., Tibshirani, R., Heard, E., Chang, H. Y.
2017; 49 (3): 377-386
- **TOP2 synergizes with BAF chromatin remodeling for both resolution and formation of facultative heterochromatin.** *Nature structural & molecular biology*
Miller, E. L., Hargreaves, D. C., Kadoch, C., Chang, C., Calarco, J. P., Hodges, C., Buenrostro, J. D., Cui, K., Greenleaf, W. J., Zhao, K., Crabtree, G. R.
2017
- **Epigenomics of human CD8 T cell differentiation and aging.** *Science immunology*
Moskowitz, D. M., Zhang, D. W., Hu, B., Le Saux, S., Yanes, R. E., Ye, Z., Buenrostro, J. D., Weyand, C. M., Greenleaf, W. J., Goronzy, J. J.
2017; 2 (8)
- **Single-cell epigenomic variability reveals functional cancer heterogeneity.** *Genome biology*
Litzenburger, U. M., Buenrostro, J. D., Wu, B., Shen, Y., Sheffield, N. C., Kathiria, A., Greenleaf, W. J., Chang, H. Y.
2017; 18 (1): 15-?
- **Multiparameter Particle Display (MPPD): A Quantitative Screening Method for the Discovery of Highly Specific Aptamers.** *Angewandte Chemie (International ed. in English)*
Wang, J., Yu, J., Yang, Q., McDermott, J., Scott, A., Vukovich, M., Lagrois, R., Gong, Q., Greenleaf, W., Eisenstein, M., Ferguson, B. S., Soh, H. T.
2017; 56 (3): 744-747
- **Variable chromatin structure revealed by in situ spatially correlated DNA cleavage mapping.** *Nature*
Risca, V. I., Denny, S. K., Straight, A. F., Greenleaf, W. J.
2017; 541 (7636): 237-241
- **Enhancer connectome in primary human cells identifies target genes of disease-associated DNA elements.** *Nature genetics*
Mumbach, M. R., Satpathy, A. T., Boyle, E. A., Dai, C., Gowen, B. G., Cho, S. W., Nguyen, M. L., Rubin, A. J., Granja, J. M., Kazane, K. R., Wei, Y., Nguyen, T., Greenside, et al
2017
- **Chromatin Accessibility Landscape of Cutaneous T Cell Lymphoma and Dynamic Response to HDAC Inhibitors.** *Cancer cell*
Qu, K., Zaba, L. C., Satpathy, A. T., Giresi, P. G., Li, R., Jin, Y., Armstrong, R., Jin, C., Schmitt, N., Rahbar, Z., Ueno, H., Greenleaf, W. J., Kim, et al
2017
- **chromVAR: inferring transcription-factor-associated accessibility from single-cell epigenomic data.** *Nature methods*
Schep, A. N., Wu, B., Buenrostro, J. D., Greenleaf, W. J.
2017; 14 (10): 975-78
- **An improved ATAC-seq protocol reduces background and enables interrogation of frozen tissues.** *Nature methods*
Corces, M. R., Trevino, A. E., Hamilton, E. G., Greenside, P. G., Sinnott-Armstrong, N. A., Vesuna, S., Satpathy, A. T., Rubin, A. J., Montine, K. S., Wu, B., Kathiria, A., Cho, S. W., Mumbach, et al
2017
- **Discovery of stimulation-responsive immune enhancers with CRISPR activation.** *Nature*
Simeonov, D. R., Gowen, B. G., Boontanart, M., Roth, T. L., Gagnon, J. D., Mumbach, M. R., Satpathy, A. T., Lee, Y., Bray, N. L., Chan, A. Y., Lituiev, D. S., Nguyen, M. L., Gate, et al
2017
- **Open Chromatin Profiling in hiPSC-Derived Neurons Prioritizes Functional Noncoding Psychiatric Risk Variants and Highlights Neurodevelopmental Loci.** *Cell stem cell*
Forrest, M. P., Zhang, H., Moy, W., McGowan, H., Leites, C., Dionisio, L. E., Xu, Z., Shi, J., Sanders, A. R., Greenleaf, W. J., Cowan, C. A., Pang, Z. P., Gejman, et al
2017; 21 (3): 305-18.e8
- **Lineage-specific dynamic and pre-established enhancer-promoter contacts cooperate in terminal differentiation.** *Nature genetics*

- Rubin, A. J., Barajas, B. C., Furlan-Magaril, M., Lopez-Pajares, V., Mumbach, M. R., Howard, I., Kim, D. S., Boxer, L. D., Cairns, J., Spivakov, M., Wingett, S. W., Shi, M., Zhao, et al
2017; 49 (10): 1522–28
- **HiChIP: efficient and sensitive analysis of protein-directed genome architecture.** *Nature methods*
Mumbach, M. R., Rubin, A. J., Flynn, R. A., Dai, C., Khavari, P. A., Greenleaf, W. J., Chang, H. Y.
2016; 13 (11): 919-922
 - **ATAC-seq reveals the accessible genome by transposase-mediated imaging and sequencing.** *Nature methods*
Chen, X., Shen, Y., Draper, W., Buenrostro, J. D., Litzenburger, U., Cho, S. W., Satpathy, A. T., Carter, A. C., Ghosh, R. P., East-Seletsky, A., Doudna, J. A., Greenleaf, W. J., Liphardt, et al
2016
 - **Lineage-specific and single-cell chromatin accessibility charts human hematopoiesis and leukemia evolution.** *Nature genetics*
Corces, M. R., Buenrostro, J. D., Wu, B., Greenside, P. G., Chan, S. M., Koenig, J. L., Snyder, M. P., Pritchard, J. K., Kundaje, A., Greenleaf, W. J., Majeti, R., Chang, H. Y.
2016; 48 (10): 1193-1203
 - **Nf1b Promotes Metastasis through a Widespread Increase in Chromatin Accessibility** *CELL*
Denny, S. K., Yang, D., Chuang, C., Brady, J. J., Lim, J. S., Gruner, B. M., Chiou, S., Schep, A. N., Baral, J., Hamard, C., Antoine, M., Wislez, M., Kong, et al
2016; 166 (2): 328-342
 - **Identification of significantly mutated regions across cancer types highlights a rich landscape of functional molecular alterations.** *Nature genetics*
Araya, C. L., Cenik, C., Reuter, J. A., Kiss, G., Pande, V. S., Snyder, M. P., Greenleaf, W. J.
2016; 48 (2): 117-125
 - **Structured nucleosome fingerprints enable high-resolution mapping of chromatin architecture within regulatory regions** *GENOME RESEARCH*
Schep, A. N., Buenrostro, J. D., Denny, S. K., Schwartz, K., Sherlock, G., Greenleaf, W. J.
2015; 25 (11): 1757-1770
 - **Individuality and Variation of Personal Regulomes in Primary Human T Cells** *CELL SYSTEMS*
Qu, K., Zaba, L. C., Giresi, P. G., Li, R., Longmire, M., Kim, Y. H., Greenleaf, W. J., Chang, H. Y.
2015; 1 (1): 51-61
 - **Individuality and variation of personal regulomes in primary human T cells.** *Cell systems*
Qu, K., Zaba, L. C., Giresi, P. G., Li, R., Longmire, M., Kim, Y. H., Greenleaf, W. J., Chang, H. Y.
2015; 1 (1): 51-61
 - **Single-cell chromatin accessibility reveals principles of regulatory variation** *NATURE*
Buenrostro, J. D., Wu, B., Litzenburger, U. M., Ruff, D., Gonzales, M. L., Snyder, M. P., Chang, H. Y., Greenleaf, W. J.
2015; 523 (7561): 486-U264
 - **Unraveling the 3D genome: genomics tools for multiscale exploration.** *Trends in genetics*
Risca, V. I., Greenleaf, W. J.
2015; 31 (7): 357-372
 - **Transient acquisition of pluripotency during somatic cell transdifferentiation with iPSC reprogramming factors** *NATURE BIOTECHNOLOGY*
Maza, I., Caspi, I., Zviran, A., Chomsky, E., Rais, Y., Viukov, S., Geula, S., Buenrostro, J. D., Weinberger, L., Krupalnik, V., Hanna, S., Zerbib, M., Dutton, et al
2015; 33 (7): 769-774
 - **Assaying the epigenome in limited numbers of cells.** *Methods*
Greenleaf, W. J.
2015; 72: 51-56
 - **ATAC-seq: A Method for Assaying Chromatin Accessibility Genome-Wide.** *Current protocols in molecular biology / edited by Frederick M. Ausubel ... [et al.]*
Buenrostro, J. D., Wu, B., Chang, H. Y., Greenleaf, W. J.
2015; 109: 21 29 1-9
 - **Transient acquisition of pluripotency during somatic cell transdifferentiation with iPSC reprogramming factors.** *Nature biotechnology*
Maza, I., Caspi, I., Zviran, A., Chomsky, E., Rais, Y., Viukov, S., Geula, S., Buenrostro, J. D., Weinberger, L., Krupalnik, V., Hanna, S., Zerbib, M., Dutton, et al
2015; 33 (7): 769–74

- **Beyond the Linear Genome: Paired-End Sequencing as a Biophysical Tool.** *Trends in cell biology*
Risca, V. I., Greenleaf, W. J.
2015; 25 (12): 716–19
- **A Conditional System to Specifically Link Disruption of Protein-Coding Function with Reporter Expression in Mice** *CELL REPORTS*
Chiou, S., Kim-Kiselak, C., Risca, V. I., Heimann, M. K., Chuang, C., Burds, A. A., Greenleaf, W. J., Jacks, T. E., Feldser, D. M., Winslow, M. M.
2014; 7 (6): 2078-2086
- **A conditional system to specifically link disruption of protein-coding function with reporter expression in mice.** *Cell reports*
Chiou, S., Kim-Kiselak, C., Risca, V. I., Heimann, M. K., Chuang, C., Burds, A. A., Greenleaf, W. J., Jacks, T. E., Feldser, D. M., Winslow, M. M.
2014; 7 (6): 2078-2086
- **Quantitative analysis of RNA-protein interactions on a massively parallel array reveals biophysical and evolutionary landscapes.** *Nature biotechnology*
Buenrostro, J. D., Araya, C. L., Chircus, L. M., Layton, C. J., Chang, H. Y., Snyder, M. P., Greenleaf, W. J.
2014; 32 (6): 562-568
- **A pause sequence enriched at translation start sites drives transcription dynamics in vivo.** *Science*
Larson, M. H., Mooney, R. A., Peters, J. M., Windgassen, T., Nayak, D., Gross, C. A., Block, S. M., Greenleaf, W. J., Landick, R., Weissman, J. S.
2014; 344 (6187): 1042-1047
- **Exome sequencing identifies a DNAJB6 mutation in a family with dominantly-inherited limb-girdle muscular dystrophy.** *Neuromuscular disorders*
Couthouis, J., Raphael, A. R., Siskind, C., Findlay, A. R., Buenrostro, J. D., Greenleaf, W. J., Vogel, H., Day, J. W., Flanigan, K. M., Gitler, A. D.
2014; 24 (5): 431-435
- **Transposition of native chromatin for fast and sensitive epigenomic profiling of open chromatin, DNA-binding proteins and nucleosome position** *NATURE METHODS*
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