

CURRICULUM VITAE
WILLIAM JAMES GREENLEAF

Department of Genetics
Stanford University
279 Campus Drive West
Beckman Center, Room 257A
wjg@stanford.edu
greenleaf.stanford.edu

ACADEMIC HISTORY

- 4/01/17-present Associate Professor (with tenure), Department of Genetics and, by courtesy, Applied Physics, Stanford University, Stanford, CA
- 9/1/14 - 4/01/17 Assistant Professor, by courtesy, Department of Applied Physics, Stanford University, Stanford, CA
- 11/1/11 - 10/31/18 Assistant Professor, Department of Genetics, Stanford University, Stanford, CA
- Jan 2008 –Sept 2011 Postdoctoral Training, Department of Chemistry and Chemical Biology, Harvard University, Cambridge, MA. Advisor: X. Sunney Xie
- Sept 2003 - Jan 2008 Ph.D., Applied Physics, Stanford University, Stanford, CA. Advisor: Steven M. Block. Thesis Topic: High-resolution Single-Molecule Measurements of Transcription and RNA Folding
- Oct 2002 - June 2003 Diploma in Computer Science (with distinction); Trinity College, Cambridge University, UK. Dissertation Topic: A Generalized Method for High-dimensional Time Series Modeling Using Neural Networks and Genetic Algorithms
- Sept 1998 - June 2002 A.B. Physics (summa cum laude); Harvard University, Cambridge, MA
- Summers: 1998-2000 Undergraduate Research Assistant Mayo Clinic, Rochester, MN. Advisor: Julio Fernandez
- Summers: 1994-1998 Research Assistant Mayo Clinic, Rochester, MN. Advisor: Mark Bolander

SCHOLARSHIPS & HONORS

- 2017 Chan Zuckerberg Biohub Investigator
- 2016 Wilson Prize, Harvard University
- 2014 Baxter Foundation Scholar
- 2013 Profiled young investigator, GenomeWeb
- 2013 Ellison Foundation Young Scholar in Aging (declined)
- 2013 Rita Allen Foundation Young Scholar
- 2009-2011 Damon Runyon Cancer Research Fellowship
- 2006 ARCS Fellowship
- 2002-2005 National Science Foundation Graduate Fellowship
- 2002 National Defense Sci. and Engineering Graduate Fellowship (declined)
- 2002 Outstanding Computer Science Diploma Student

2002	Gates Cambridge Trust Scholar
2002	<i>Phi Beta Kappa</i> , Harvard University
1998-2002	John Harvard Scholar
1999	Detur Prize, Harvard University
1998	6 th Place, Westinghouse Science Talent Search

PREPRINTS (articles that were subsequently published are not included)

- 1) Pierce, SE, Granja JM, **Greenleaf WJ**. High-throughput single-cell chromatin accessibility CRISPR screens enable unbiased identification of regulatory networks in cancer. (2020) <https://www.biorxiv.org/content/10.1101/2020.11.02.364265v1.full>
- 2) Marinov GK, Trevino, AE, Xiang T, Kundaje A, Grossman AR, **Greenleaf WJ**. (2020) Transcription-dependent domain-scale 3D genome organization in dinoflagellates. <https://www.biorxiv.org/content/10.1101/2020.07.01.181685v1>
- 3) Granja JM*, Corces MR*, Pierce SE, Bagdatli ST, Chang HY§, **Greenleaf WJ§**. (2020) ArchR - An integrative and scalable software package for single-cell chromatin accessibility analysis. <https://doi.org/10.1101/2020.04.28.066498>
- 4) Boyle, EA, Becker WR, Bai HB, Chen JS, Doudna JA, **Greenleaf WJ**. Quantification of Cas9 binding and cleavage across diverse guide sequences maps landscapes of target engagement (2020). <https://doi.org/10.1101/2020.09.09.290668>
- 5) Corces MR, Shcherbina A, Kundu S, Gloudemans MJ, Frésard L, Granja JM, Louie BH, Shams S, Bagdatli ST, Mumbach MR, Liu B, Montine KS, **Greenleaf WJ**, Kundaje A, Montgomery SB, Chang HY, Montine TJ. (2020) <https://doi.org/10.1101/2020.01.06.896159>
- 6) Andreasson JOL, Gotrik MR, Wu MJ, Wayment-Steele HK, Kladwang W, Portela F, Wellington-Oguri R, Eterna Participants, Das R§, **Greenleaf WJ§**. (2019) Crowdsourced RNA design discovers diverse, reversible, efficient, self-contained molecular sensors. <https://www.biorxiv.org/content/10.1101/2019.12.16.877183v1>
- 7) Becker WR, Jarmoskaite I, Kappel K, Vaidyanathan PP, Denny SK, Das R, **Greenleaf WJ**, Herschlag D. (2019) Quantitative high-throughput tests of ubiquitous RNA secondary structure prediction algorithms via RNA/protein binding. <https://www.biorxiv.org/content/10.1101/571588v1>
- 8) Moskowitz DM, Greenleaf WJ. (2018) Nonparametric analysis of contributions to variance in genomics and epigenomics data. <https://www.biorxiv.org/content/10.1101/314112v1>

PEER REVIEWED PUBLICATIONS

- 1) Andreasson JOL, Savinov A, Block SM, **Greenleaf WJ**. (2020) *Nature Communications*. 11(1):1663
- 2) Shipony Z*, Marinov GK*, Swaffer MP, Sinnott-Armstrong NA, Skotheim JM, Kundaje A, **Greenleaf WJ**. (2020) Long-range single-molecule mapping of chromatin accessibility in eukaryotes. *Nature Methods*. 17(3):319-327
- 3) Trevino AE, Sinnott-Armstrong N, Andersen J, Yoon SJ, Huber N, Pritchard JK, Chang

- HY, **Greenleaf WJ**[§], Paşca SP[§]. (2020) Chromatin accessibility dynamics in a model of human forebrain development. *Science*. 367(6476)
- 4) Granja JM, Klemm S[§], McGinnis LM[§], Kathiria AS, Mezger A, Corces MR, Parks B, Gars E, Liedtke M, Zheng GXY, Chang HY, Majeti R, **Greenleaf WJ**[§]. (2019) Single-cell multiomic analysis identifies regulatory programs in mixed-phenotype acute leukemia. *Nature Biotechnology*. 37(12):1458-1465.
 - 5) Hilgendorf KI, Johnson CT, Mezger A, Rice SL, Norris AM, Demeter J, **Greenleaf WJ**, Reiter JF, Kopinke D, Jackson PK. (2019) Omega-3 Fatty Acids Activate Ciliary FFAR4 to Control Adipogenesis. *Cell*. 179(6):1289-1305
 - 6) Calderon D, Nguyen MLT, Mezger A, Kathiria A, Müller F, Nguyen V, Lescano N, Wu B, Trombetta J, Ribado JV, Knowles DA, Gao Z, Blaesche F, Parent AV, Burt TD, Anderson MS, Criswell LA[§], **Greenleaf WJ**[§], Marson A[§], Pritchard JK[§]. (2019) Landscape of stimulation-responsive chromatin across diverse human immune cells. *Nature Genetics*. 51(10):1494-1505.
 - 7) Mitigation of off-target toxicity in CRISPR-Cas9 screens for essential non-coding elements. (2019) Tycko J, Wainberg M, Marinov GK, Ursu O, Hess GT, Ego BK, Aradhana, Li A, Truong A, Trevino AE, Spees K, Yao D, Kaplow IM, Greenside PG, Morgens DW, Phanstiel DH, Snyder MP, Bintu L, **Greenleaf WJ**[§], Kundaje A[§], Bassik MC[§]. *Nature Communications*. 10(1):4063
 - 8) Satpathy AT, Granja JM, Yost KE, Qi Y, Meschi F, McDermott GP, Olsen BN, Mumbach MR, Pierce SE, Corces MR, Shah P, Bell JC, Jhutti D, Nemeč CM, Wang J, Wang L, Yin Y, Giresi PG, Chang ALS, Zheng GXY, **Greenleaf WJ**[§], Chang HY[§]. (2019) Massively parallel single-cell chromatin landscapes of human immune cell development and intratumoral T cell exhaustion. *Nature Biotechnology*. 37(8):925-936
 - 9) Yesselman JD, Denny SK, Bisaria N, Herschlag D[§], **Greenleaf WJ**[§], Das R[§]. (2019) Sequence-dependent RNA helix conformational preferences predictably impact tertiary structure formation. *PNAS*. 116(34):16847-16855.
 - 10) Ghosh RP, Shi Q, Yang L, Reddick MP, Nikitina T, Zhurkin VB, Fordyce P, Stasevich TJ, Chang HY, **Greenleaf WJ**, Liphardt JT. (2019) Satb1 integrates DNA binding site geometry and torsional stress to differentially target nucleosome-dense regions. *Nature Communications*. 10(1):3221
 - 11) Becker WR, Ober-Reynolds B, Jouravleva K, Jolly SM, Zamore PD[§], **Greenleaf WJ**[§]. (2019) High-Throughput Analysis Reveals Rules for Target RNA Binding and Cleavage by AGO2. *Molecular Cell*. 75(4):741-755
 - 12) Jadhav RR, Im SJ, Hu B, Hashimoto M, Li P, Lin JX, Leonard WJ, **Greenleaf WJ**, Ahmed R, Goronzy JJ. (2019) Epigenetic signature of PD-1+ TCF1+ CD8 T cells that act as resource cells during chronic viral infection and respond to PD-1 blockade. *PNAS*. 116(28):14113-14118
 - 13) Mumbach MR, Granja JM, Flynn RA, Roake CM, Satpathy AT, Rubin AJ, Qi Y, Jiang Z, Shams S, Louie BH, Guo JK, Gennert DG, Corces MR, Khavari PA, Atianand MK, Artandi SE, Fitzgerald KA, **Greenleaf WJ**[§], Chang HY[§]. HiChIRP reveals RNA-associated chromosome conformation. *Nature Methods*. (2019) 16(6):489-492.

- 14) Jarmoskaite I, Denny SK, Vaidyanathan PP, Becker WR, Andreasson JOL, Layton CJ, Kappel K, Shivashankar V, Sreenivasan R, Das R, **Greenleaf WJ**[§], Herschlag D[§]. (2019) A Quantitative and Predictive Model for RNA Binding by Human Pumilio Proteins. *Molecular Cell*. 74(5):966-981
- 15) Kappel K, Jarmoskaite I, Vaidyanathan PP, **Greenleaf WJ**, Herschlag D, Das R. (2019) Blind tests of RNA-protein binding affinity prediction. *PNAS*. 116(17):8336-8341.
- 16) Becker WR, Jarmoskaite I, Vaidyanathan PP, **Greenleaf WJ**[§], Herschlag D[§]. Demonstration of protein cooperativity mediated by RNA structure using the human protein PUM2. *RNA*. (2019) 25(6):702-712.
- 17) Layton CJ, McMahon PL, **Greenleaf WJ**. (2019) Large-Scale, Quantitative Protein Assays on a High-Throughput DNA Sequencing Chip. *Molecular Cell*. 73(5):1075-1082
- 18) Rubin AJ, Parker KR, Satpathy AT, Qi Y, Wu B, Ong AJ, Mumbach MR, Ji AL, Kim DS, Cho SW, Zarnegar BJ, **Greenleaf WJ**, Chang HY, Khavari PA. Coupled Single-Cell CRISPR Screening and Epigenomic Profiling Reveals Causal Gene Regulatory Networks. *Cell*. (2019) 176(1-2):361-376.
- 19) Boyle EA, Pritchard JK, **Greenleaf WJ**. (2018) High-resolution mapping of cancer cell networks using co-functional interactions. *Molecular Systems Biology*. 14(12)
- 20) Zviran A, Mor N, Rais Y, Gingold H, Peles S, Chomsky E, Viukov S, Buenrostro JD, Scognamiglio R, Weinberger L, Manor YS, Krupalnik V, Zerbib M, Hezroni H, Jaitin DA, Larastasio D, Gilad S, Benjamin S, Gafni O, Mousa A, Ayyash M, Sheban D, Bayerl J, Aguilera-Castrejon A, Massarwa R, Maza I, Hanna S, Stelzer Y, Ulitsky I, **Greenleaf WJ**, Tanay A, Trumpp A, Amit I, Pilpel Y, Novershtern N, Hanna JH. (2019) Deterministic Somatic Cell Reprogramming Involves Continuous Transcriptional Changes Governed by Myc and Epigenetic-Driven Modules. *Cell Stem Cell*. 24(2):328-341
- 21) Haney MS, Bohlen CJ, Morgens DW, Ousey JA, Barkal AA, Tsui CK, Ego BK, Levin R, Kamber RA, Collins H, Tucker A, Li A, Vorselen D, Labitigan L, Crane E, Boyle E, Jiang L, Chan J, Rincón E, **Greenleaf WJ**, Li B, Snyder MP, Weissman IL, Theriot JA, Collins SR, Barres BA, Bassik MC. (2018) Identification of phagocytosis regulators using magnetic genome-wide CRISPR screens. *Nature Genetics*. 50(12):1716-1727.
- 22) Chen X, Litzénburger UM, Wei Y, Schep AN, LaGory EL, Choudhry H, Giaccia AJ, **Greenleaf WJ**, Chang HY. (2018) Joint single-cell DNA accessibility and protein epitope profiling reveals environmental regulation of epigenomic heterogeneity. *Nature Communications*. 9(1):4590
- 23) Corces MR, Granja JM, Shams S, Louie BH, Seoane JA, Zhou W, Silva TC, Groeneveld C, Wong CK, Cho SW, Satpathy AT, Mumbach MR, Hoadley KA, Robertson AG, Sheffield NC, Felau I, Castro MAA, Berman BP, Staudt LM, Zenklusen JC, Laird PW, Curtis C; Cancer Genome Atlas Analysis Network, **Greenleaf WJ**[§], Chang HY[§]. (2018) The chromatin accessibility landscape of primary human cancers. *Science*. 362(6413).
- 24) Yang D, Denny SK, Greenside PG, Chaikovskiy AC, Brady JJ, Ouadah Y, Granja JM, Jahchan NS, Lim JS, Kwok S, Kong CS, Berghoff AS, Schmitt A, Reinhardt HC, Park KS, Preusser M, Kundaje A, **Greenleaf WJ**, Sage J, Winslow MM. (2018) Intertumoral Heterogeneity in SCLC Is Influenced by the Cell Type of Origin. *Cancer Discovery*.

8(10):1316-1331

- 25) Arda HE, Tsai J, Rosli YR, Giresi P, Bottino R, **Greenleaf WJ**, Chang HY, Kim SK. (2018) A Chromatin Basis for Cell Lineage and Disease Risk in the Human Pancreas. *Cell Systems*. 7(3):310-322
- 26) 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 L, Shani T, Bayerl J, Gafni O, Hanna S, Buenrostro JD, Hagai T, Masika H, Vainorius G, Bergman Y, **Greenleaf WJ**, Esteban MA, Elling U, Levin Y, Massarwa R, Merbl Y, Novershtern N, Hanna JH. (2018) Neutralizing Gatad2a-Chd4-Mbd3/NuRD Complex Facilitates Deterministic Induction of Naive Pluripotency. *Cell Stem Cell*. 23(3):412-425
- 27) Denny SK, Bisaria N, Yesselman JD, Das R, Herschlag D[§], **Greenleaf WJ**[§]. (2018) High-Throughput Investigation of Diverse Junction Elements in RNA Tertiary Folding. *Cell*. 174(2):377-390
- 28) Zamanighomi M, Lin Z, Daley T, Chen X, Duren Z, Schep A, **Greenleaf WJ**, Wong WH. Unsupervised clustering and epigenetic classification of single cells. *Nature Communications*. (2018) 9(1):2410
- 29) Buenrostro JD, Corces MR, Lareau CA, Wu B, Schep AN, Aryee MJ, Majeti R, Chang HY, **Greenleaf WJ**. (2018) Integrated Single-Cell Analysis Maps the Continuous Regulatory Landscape of Human Hematopoietic Differentiation. *Cell*. 173(6):1535-1548
- 30) Satpathy AT, Saligrama N, Buenrostro JD, Wei Y, Wu B, Rubin AJ, Granja JM, Lareau CA, Li R, Qi Y, Parker KR, Mumbach MR, Serratelli WS, Gennert DG, Schep AN, Corces MR, Khodadoust MS, Kim YH, Khavari PA, **Greenleaf WJ**, Davis MM, Chang HY. (2018) Transcript-indexed ATAC-seq for precision immune profiling. *Nature Medicine*. 24(5):580-590
- 31) Bell JC, Jukam D, Teran NA, Risca VI, Smith OK, Johnson WL, Skotheim JM, **Greenleaf WJ**, Straight AF. (2018) Chromatin-associated RNA sequencing (ChAR-seq) maps genome-wide RNA-to-DNA contacts. *Elife*. 7. pii
- 32) Aggeli D, Karas VO, Sinnott-Armstrong NA, Varghese V, Shafer RW, **Greenleaf WJ**, Sherlock G. (2018) Diff-seq: A high throughput sequencing-based mismatch detection assay for DNA variant enrichment and discovery. *Nucleic Acids Res*. 46(7):e42
- 33) Gowans GJ, Schep AN, Wong KM, King DA, **Greenleaf WJ**, Morrison AJ. (2018) INO80 Chromatin Remodeling Coordinates Metabolic Homeostasis with Cell Division. *Cell Reports*. 22(3):611-623.
- 34) Koh AS, Miller EL, Buenrostro JD, Moskowitz DM, Wang J, **Greenleaf WJ**, Chang HY, Crabtree GR. Rapid chromatin repression by Aire provides precise control of immune tolerance. (2018) *Nature Immunology*. 19(2):162-172.
- 35) Akondy RS, Fitch M, Edupuganti S, Yang S, Kissick HT, Li KW, Youngblood BA, Abdelsamed HA, McGuire DJ, Cohen KW, Alexe G, Nagar S, McCausland MM, Gupta S, Tata P, Haining WN, McElrath MJ, Zhang D, Hu B, **Greenleaf WJ**, Goronzy JJ, Mulligan MJ, Hellerstein M, Ahmed R. (2017) Origin and differentiation of human memory CD8 T cells after vaccination. *Nature*. 552(7685):362-367

- 36) Daugherty AC, Yeo RW, Buenrostro JD, **Greenleaf WJ**, Kundaje A, Brunet A. (2017) Chromatin accessibility dynamics reveal novel functional enhancers in *C. elegans*. *Genome Research*. 27(12):2096-2107.
- 37) Mumbach MR, Satpathy AT, Boyle EA, Dai C, Gowen BG, Cho SW, Nguyen ML, Rubin AJ, Granja JM, Kazane KR, Wei Y, Nguyen T, Greenside PG, Corces MR, Tycko J, Simeonov DR, Suliman N, Li R, Xu J, Flynn RA, Kundaje A, Khavari PA, Marson A, Corn JE, Quertermous T, **Greenleaf WJ**[§], Chang HY[§]. (2017) Enhancer connectome in primary human cells identifies target genes of disease-associated DNA elements. *Nature Genetics* 49(11):1602-1612
- 38) Simeonov DR, Gowen BG, Boontanart M, Roth TL, Gagnon JD, Mumbach MR, Satpathy AT, Lee Y, Bray NL, Chan AY, Lituiev DS, Nguyen ML, Gate RE, Subramaniam M, Li Z, Woo JM, Mitros T, Ray GJ, Curie GL, Naddaf N, Chu JS, Ma H, Boyer E, Van Gool F, Huang H, Liu R, Tobin VR, Schumann K, Daly MJ, Farh KK, Ansel KM, Ye CJ, **Greenleaf WJ**, Anderson MS, Bluestone JA, Chang HY, Corn JE, Marson A. (2017) Discovery of stimulation-responsive immune enhancers with CRISPR activation. *Nature*. 549(7670):111-115.
- 39) Corces MR, Trevino AE, Hamilton EG, Greenside PG, Sinnott-Armstrong NA, Vesuna S, Satpathy AT, Rubin AJ, Montine KS, Wu B, Kathiria A, Cho SW, Mumbach MR, Carter AC, Kasowski M, Orloff LA, Risca VI, Kundaje A, Khavari PA, Montine TJ, **Greenleaf WJ**[§], Chang HY[§]. (2017) An improved ATAC-seq protocol reduces background and enables interrogation of frozen tissues. *Nature Methods*. 14(10):959-962
- 40) Qu K, Zaba LC, Satpathy AT, Giresi PG, Li R, Jin Y, Armstrong R, Jin C, Schmitt N, Rahbar Z, Ueno H, **Greenleaf WJ**, Kim YH, Chang HY. (2017) Chromatin Accessibility Landscape of Cutaneous T Cell Lymphoma and Dynamic Response to HDAC Inhibitors. *Cancer Cell*. 2017 Jul 10;32(1):27-41
- 41) Schep AN, Wu B, Buenrostro JD[§], **Greenleaf WJ**[§]. (2017) chromVAR: Inferring transcription factor variation from single-cell epigenomic data. *Nature Methods*. 14(10):975-978.
- 42) Akondy RS, Fitch M, Edupuganti S, Yang S, Kissick HT, Li KW, Youngblood BA, Abdelsamed HA, Cohen KW, Alexe G, Nagar S, McCausland MM, Gupta S, Tata P, Haining WN, McElrath MJ, Zhang D, Hu B, **Greenleaf WJ**, Goronzy JJ, Mulligan MJ, Hellerstein M, Ahmed R. (2017) Tracking the origin and differentiation of human memory CD8 T cells after vaccination. *Nature*. 552(7685):362-367.
- 43) Boyle EA*, Andreasson JOL*, Chircus LM*, Sternberg SH, Wu MJ, Guegler CK, Doudna JA, **Greenleaf WJ**. (2017) "High-throughput biochemical profiling reveals Cas9 off-target binding and unbinding heterogeneity." *PNAS* 114(21):5461-5466.
- 44) Morgens DW, Wainberg M, Boyle EA, Ursu O, Araya CL, Tsui CK, Haney MS, Hess GT, Han K, Jeng EE, Li A, Snyder MP, **Greenleaf WJ**[§], Kundaje A[§], Bassik MC[§]. (2017) Genome-scale measurement of off-target activity using Cas9 toxicity in high-throughput screens. *Nature Communications*. May 5;8:15178.

Papers above this point were published after April 2017 (promotion to Associate Professor)

- 45) Moskowitz DM*, Zhang DW*, Le Saux S, Hu B, Buenrostro JD, Weyand CM, **Greenleaf**

- WJ**[§], Goronzy JJ[§]. (2017) “Epigenomics of human CD8 T cell differentiation and aging.” *Science Immunology*. 2(8) pii.
- 46) She R*, Chakravarty AK*, Layton CJ*, Chircus LM, Andreasson JOL, Damaraju N, McMahon PL, Buenrostro JD, Jarosz DF[§], **Greenleaf WJ**[§]. (2017) “Comprehensive and quantitative mapping of RNA-protein interactions across a transcribed eukaryotic genome.” *PNAS*. 114(14):3619-24
- 47) Miller EL, Hargreaves DC, Kadoch C, Chang CY, Calarco JP, Hodges C, Buenrostro JD, Cui K, **Greenleaf WJ**, Zhao K, Crabtree GR. (2017) TOP2 synergizes with BAF chromatin remodeling for both resolution and formation of facultative heterochromatin. *Nat Struct Mol Biol*. 24(4):344-352
- 48) Litzenburger UM, Buenrostro JD, Wu B, Shen Y, Sheffield N, Kathiria A, **Greenleaf WJ**[§], Chang HY[§]. (2017) Single cell epigenomic variability reveals functional cancer heterogeneity. *Genome Biology*. 24;18(1):15
- 49) Xu J, Carter AC, Grendel AV, Attia M, Loftus J, **Greenleaf WJ**, Tibshirani R, Heard E, Chang HY. (2017) Landscape of monoallelic DNA accessibility in mouse embryonic stem cells and neural progenitor cells. *Nat Genet*. 49(3):377-386.
- 50) Wang J, Yu J, Yang Q, McDermott J, Scott A, Vukovitch M, Lagrois R, Gong Q, **Greenleaf WJ**, Eisenstein M, Ferguson BS, Soh HT. (2017) Multiparameter Particle Display (MPPD): A Quantitative Screening Method for the Discovery of Highly Specific Aptamers. *Angew Chem Int Ed Engl*. 56(3):744-747
- 51) Risca VI, Denny SJK, Straight AF, **Greenleaf WJ**. (2017) Variable chromatin structure revealed by in situ spatially correlated DNA cleavage mapping. *Nature* 541, 237–241.
- 52) Chen X, Shen Y, Draper W, Buenrostro JD, Litzenburger U, Cho SW, Satpathy A, Ghosh AP, East-Seletsky A, Doudna JA, **Greenleaf WJ**, Liphardt JT, Chang HY. (2016) ATAC-se reveals the accessible genome by transposase-mediated imaging and sequencing. *Nature Methods*. 13, 1013-1020.
- 53) Mumbach MR, Rubin AJ, Flynn RA, Khavari PA, **Greenleaf WJ**, Chang HY. (2016) HiChIP: Efficient and sensitive analysis of protein-directed genome architecture. *Nature Methods*, 13, 919-922.
- 54) Corces RM, Buenrostro JD, Wu B, Greenside PG, Chan SM, Koenig JL, Snyder MP, Pritchard JK, Kundaje A, **Greenleaf WJ**, Majeti R, Chang HY. (2016) Lineage-specific and single cell chromatin accessibility charts human hematopoiesis and leukemia evolution. *Nature Genetics*. 48, 1193-1203
- 55) Denny SK, Yang D, Chuang C-H, Brady JJ, Lim JS, Grüner BM, Chiou S-H, Schep AN, Baral J, Hamard C, Antoine M., Wislez M, Kong CS, Connolly AJ, Park K-S, Sage J, **Greenleaf WJ**[§], Winslow MM[§]. (2016) Nfib promotes Metastasis through a Widespread Increase in Chromatin Accessibility. *Cell* 166:2, 328-342.
- 56) Araya CL[§], Cenik C, Reuter JA, Kiss G, Pande VS, Snyder MP[§], **Greenleaf WJ**[§]. (2016) “Systematic identification of significantly mutated regions reveals a rich landscape of functional molecular alterations across cancer genomes” *Nature Genetics*, 48, 117–125.
- 57) Schep AN, Buenrostro JD, Denny SK, Schwartz K, Sherlock G, and **Greenleaf WJ**. (2015)

- Structured nucleosome fingerprints enable high-resolution mapping of chromatin architecture within regulatory regions. *Genome Research*. 25(11):1757-70
- 58) Qu K, Zaba LC, Giresi PG, Longmire M, Kim YH, **Greenleaf WJ**, and Chang HY. (2015) "Individuality and variation of personal regulomes in primary human T cells. *Cell Systems* 1:51-61.
- 59) Buenrostro JD, Wu B, Litzenburger U, Snyder M, Ruff D, Gonzales M, Chang H[§], **Greenleaf, WJ.**[§] (2015) Single-cell chromatin accessibility reveals principles of regulatory variation. *Nature*. 523:486-490.
- 60) Maza I, Caspi I, Zviran A, Chmosky E, Rais Y, Viukov S, Geula S, Buenrostro JD, Weinberger L, Krupalnik V, Zerbib M, Dutton JR, **Greenleaf WJ**, Massarwa R, Novershtern N and Hanna JH. (2015) Transient Acquisition of Pluripotency During Somatic Cell Transdifferentiation with iPSC Reprogramming Factors. *Nature Biotechnology*. doi:10.1038/nbt.3270.
- 61) Buenrostro JD, Wu B, Chang HY, **Greenleaf WJ**. "ATAC-seq: A method for Assaying Chromatin Accessibility Genome-wide" *Current Protocols in Mol. Bio.* 109:21.1-21.29.9
- 62) Chiou S-H, Kim-Kiselak C, Risca VI, Heimann M, Chuang C-H, Burds AA, **Greenleaf WJ**, Jacks TE, Feldser DM, and Winslow MM. (2014) "A conditional system to specifically link disruption of protein coding function with reporter expression in mice." *Cell Reports* 7(6):2078-86.
- 63) Larson MH, Mooney RA, Peters JM, Windgassen T, Nayak D, Gross CA, Block SM, **Greenleaf WJ**[§], Landick R[§], Weissman JS[§]. (2014) "A Pause Sequence Enriched at Translation Start Sites Drives Transcription Dynamics in Vivo." *Science*. 344(6187):1042-7.
- 64) Buenrostro JD, Araya CL, Chircus LM, Layton CJ, Chang HY, Snyder MP, **Greenleaf WJ**. (2014) "Quantitative variant analysis of RNA-protein interactions on a massively parallel array for mapping biophysical and evolutionary landscapes." *Nature Biotechnology*. 32, 562–568.
- 65) Couthouis J, Raphael AR, Siskind C, Findlay AR, Buenrostro JD, **Greenleaf WJ**, Vogel H, Day JW, Flanigan KM, and Gitler AD. (2014) "Exome Sequencing Identifies a DNAJB6 Mutation in a Family with Dominantly-Inherited Limb-Girdle Muscular Dystrophy." *Neuromuscul Disord*, S0960-8966(14)00047-9.
- 66) Carpenter ML, Buenrostro JD, Valdiosera C, Schroeder H, Allentoft ME, Sikora M, Rasmussen M, Gravel S, Guille'n S, Nekhrizov G, Leshtakov K, Dimitrova D, Theodossiev N, Pettener D, Luiselli D, Sandoval K, Moreno-Estrada A, Li Y, Wang J, Gilbert MTP, Willerslev E*, **Greenleaf WJ**^{§*} and Bustamante CD^{§*} (2013) "Pulling out the 1%: Whole-Genome Capture for the Targeted Enrichment of Ancient DNA Sequencing Libraries." *The American Journal of Human Genetics*. 93:5, 852-864.
- 67) Buenrostro JD, Giresi PG, Zaba LC, Chang H[§], **Greenleaf WJ**[§]. (2013) "Transposition of native chromatin for fast and sensitive epigenomic profiling of open chromatin, DNA-binding proteins and nucleosome position" *Nature Methods*. 10:1213-1218.
- 68) Men Y, Fu Y, Chen Z, Sims PA, **Greenleaf WJ**, and Huang Y. (2012) "Digital Polymerase Chain Reaction in an Array of Femtoliter Polydimethylsiloxane Microreactors." *Analytical Chemistry*, 84 (10) 4262-4266.

- 69) Sims PA*, **Greenleaf WJ***, Duan H, and Xie XS (2011) “Fluorogenic DNA Sequencing in PDMS Microreactors.” *Nature Methods* 8:575-580
- 70) Gutierrez-Medina B, Andreasson JOL, **Greenleaf WJ**, La Porta A, and Block SM. (2010) “An optical apparatus for rotation and trapping.” *Meth. Enzymol.* 475:377-404
- 71) Larson MH*, **Greenleaf WJ***, Landick R, and Block SM. (2008) “**Applied force reveals mechanistic and energetic details of transcription termination.**” *Cell*, 132:971-982
- 72) **Greenleaf WJ***, Frieda KL, Foster, DAN, Woodside MT*, and Block SM. (2008) “Direct observation of hierarchical folding in single riboswitch aptamers.” *Science*, 319:630-633.
- 73) **Greenleaf WJ**, and Block SM. (2006) “Single-molecule, motion-based DNA sequencing using RNA polymerase.” *Science* 313:801.
- 74) Abbondanzieri EA*, **Greenleaf WJ***, Shaevitz JW, Landick R, Block, SM. (2005) “Direct observation of basepair stepping by RNA polymerase.” *Nature*. 438(7067):460-465.
- 75) **Greenleaf WJ***, Woodside MT*, Abbondanzieri EA, Block SM. (2005) “Passive all-optical force clamp for high resolution laser trapping.” *Phys. Rev. Lett.* 95:208102.
- 76) Marszalek PE, **Greenleaf WJ**, Li HB, Oberhauser AF, Fernandez JM. (2000) “Atomic force microscopy captures quantized plastic deformation in gold nanowires.” *Proc. Natl. Acad. Sci. USA.* 97 (12): 6282-6286.
- 77) **Greenleaf WJ**, Bolander ME, Sarkar G, Goldring MB, Greenleaf JF. (1998). “Artificial cavitation nuclei significantly enhance acoustically induced cell transfection.” *Ultrasound in Medicine and Biology.* 24 (4): 587-595.

(§co-corresponding authors; *co-first authors)

PEER REVIEWED/EDITED REVIEWS

- 1) Klemm SL, Shipony Z, **Greenleaf WJ**. (2019) Chromatin accessibility and the regulatory epigenome. *Nat Rev Genet.* 20(4):207-220
- 2) Denny SK, **Greenleaf WJ**. (2019) Linking RNA Sequence, Structure, and Function on Massively Parallel High-Throughput Sequencers. *Cold Spring Harbor Perspectives Biology*11(10).
- 3) Risca VI, **Greenleaf WJ**. (2015) Beyond the linear genome: Paired-end sequencing as a biophysical tool. *Trends in Cell Biology*, 25:12, 716–719.
- 4) Risca VI, **Greenleaf WJ**. (2015) Unraveling the 3D genome: genomics tools for multiscale exploration. *Trends in Genetics.* 31(7):357-72.
- 5) **Greenleaf, WJ**. (2015) Assaying the epigenome in limited numbers of cells. *Methods* 72 51–56
- 6) Herbert, KM, **Greenleaf WJ**, and Block SM. (2008) Single molecule measurements of RNA polymerase: motoring along. *Ann. Rev. Biochem.* 77: 149-176.
- 7) **Greenleaf WJ**, Woodside MT, and Block SM. (2007) High-resolution, single-molecule measurements of biomolecular motion. *Ann. Rev Biophys. Biomol. Struct.* 36:171-90.

OTHER PUBLICATIONS

- 1) Carter AC, Chang HY, Church G, Dombkowski A, Ecker JR, Gil E, Giresi PG, Greely H, **Greenleaf WJ**, Hacohen N, He C, Hill D, Ko J, Kohane I, Kundaje A, Palmer M, Snyder MP, Tung J, Urban A, Vidal M, Wong W. (2017) Challenges and recommendations for epigenomics in precision health. *Nature Biotechnology*. 35(12):1128-1132.
- 2) **Greenleaf WJ** & Sidow, A. (2014) “The future of sequencing: convergence of intelligent design and market Darwinism.” *Genome Biol.* 15:303-5. (Meeting report)
- 3) Block SM, Larson MH, **Greenleaf WJ**, Herbert KM, Guydosh NR, Anthony PC. (2007) “Molecule by molecule, the physics and chemistry of life: SMB 2007.” *Nat. Chem. Biol.* 3(4):193-197 (Meeting report).
- 4) **Greenleaf WJ**, Frieda KL, Abbondanzieri EA, Woodside MT, Block SM. (2007) “High-resolution, single-molecule optical trapping measurements of transcription with basepair accuracy: Instrumentation and methods.” *Proc. SPIE* 6644.

PATENTS/APPLICATIONS

- 1) “Motion Resolved Molecular Sequencing.” **Greenleaf WJ** and Block SM. Patent #7556922, Issued 7 July 2009.*
- 2) “Methods and compositions for continuous single-molecule nucleic acid sequencing by synthesis with fluorogenic nucleotides.” Xie XS, Sims PA, and **Greenleaf WJ**. Application number 12/407486, 12/718421 and PCT application WO/2010/017487A1
- 3) “Systems and methods for high throughput, high fidelity, single molecule nucleic acid sequencing using time multiplexed excitation.” Xie XS, Sims PA, and **Greenleaf WJ**. PCT application WO/2010/091046A2
- 4) “Methods and systems for single-molecule RNA expression profiling.” Xie, XS, Sims PA, **Greenleaf WJ**, Taniguchi Y, Shiroguchi K, Kim S. PCT application WO/2010/138960
- 5) “Nucleic acid amplification and sequencing by synthesis with fluorogenic nucleotides” Xie XS, Sims PA, **Greenleaf WJ**, Duan H. PCT application WO/2011/038241
- 6) “In situ production of an ultra high-throughput protein array on a next generation sequencing flow cell” Layton, C and **Greenleaf WJ**. PCT application PCT/US2014/38236
- 7) “Fast and efficient chromatin hypersensitivity mapping in small cell numbers using direct transposition” Giresi, P, Buenrostro JD, Chang HY, and **Greenleaf WJ**. PCT application PCT/US2014/38825*
- 8) Whole-genome capture method for the enrichment of DNA sequencing libraries containing small amounts of target DNA” Carpenter ML, Bustamante C, Buenrostro JD, and **Greenleaf WJ**. PCT application PCT/US2014/36670.*
- 9) A system for multi-scale, annotation-independent detection of functionally-diverse units of recurrent genomic alteration. Araya C, **Greenleaf WJ**, Reuter JA, Cenik C, Snyder M. PCT application PCT/US2016/024109*
- 10) ATAC-see: a method for integrated imaging and sequencing of the accessible genome. **Greenleaf WJ**, Chang HY, Buenrostro J, Chen X. Provisional number 62/306,504*

- 11) Mapping chromatin conformation by radiation-induced spatially correlated DNA cleavage. Risca VI, Denny S, **Greenleaf WJ**. Application number 62/433.633
- 12) Diff-seq: A High-throughput sequencing-based mismatch detection assay for DNA variants. Sherlock GJ, **Greenleaf WJ**, Angeli D, Karas VO. Application number 62/590,043
- 13) SuperFLAG, a high-avidity epitope for the mouse M2 anti-FLAG antibody. Layton CJ, **Greenleaf WJ**. Application PCT/US2020/015033
- 14) Sequence design principles for siRNA specificity and efficacy. Ober-Reynolds B, **Greenleaf WJ**, Becker W, Jolly S, Jouravleva K, Zamore PD. PCT/US2020/0036919

*Currently licensed or optioned

SELECTED PRESENTATIONS AND SEMINARS

- | | |
|------------|---|
| July 2020 | San Diego Chromatin club (virtual; invited talk) |
| Sept 2020 | Stanford Genetics Faculty retreat (virtual). |
| Feb 2020 | Talk, Stanford leadership retreat. |
| Jan 2020 | Talk, Keystone Symposium: Gene Regulation: From Mechanisms to Disease/Cancer Epigenetics, Keystone CO (invited talk) |
| Dec 2019 | Functional Variant KOL event, Illumina, Seattle (invited talk) |
| Nov 2019 | Talk, Future Science Awards, Beijing China (invited talk) |
| Oct 2019 | Seminar, Single Cell Omics, Beijing China (invited talk) |
| Sept 2019 | Keynote, H-Foundation Symposium, Chicago (invited talk) |
| June 2019 | Seminar, LabLinks, Chicago (invited talk) |
| May 2019 | Human Cell Atlas General Assembly Meeting, Tokyo, (invited talk) |
| May 2019 | Human Immune Monitoring Tech. Meeting, Stanford. "Integrative, Multiomic, Single-Cell Dissection of Mixed-Phenotype Acute Leukemia" |
| Jan 2019 | Seminar, Northwestern University, "Exploring the Physical Genome" (invited talk) |
| Nov 2018 | CEGS grantee meeting, Chicago, lightning talk |
| Nov 2018 | Seminar, Washington University, St. Louis, "Exploring the Physical Genome" (invited talk) |
| Nov 2018 | Seminar, University of Texas, San Antonio, "Exploring the Physical Genome" (invited talk) |
| Nov 2018 | QBioS Seminar, Georgia Tech, "Exploring the physical Genome" (invited talk) |
| Nov 2018 | Distinguished Seminar Series in Genome Biology, Cornell University "Exploring the physical genome" (invited talk). |
| Oct 2018 | International Human Epigenome Consortium meeting, Hong Kong, "Exploring the Physical Genome" (invited talk) |
| Oct 2018 | Seminar, UT Southwestern Medical Center. "Gene Regulation and Genomics Seminar Series." (invited talk) |
| Sept 2018 | Stanford Genetics Retreat "Exploring the physical genome" |
| Sept 2018 | Keystone Symposia, Whistler BC "ATAC-ing single cell regulatory variation" (invited talk) |
| March 2018 | Quantitative Biology Seminar, Caltech, "ATAC-ing single cell regulatory variation" Invited talk |
| Feb 2018 | DNA and interacting proteins as single molecules conference, Cancun "ATAC-ing single cell regulatory variation" (invited talk) |

- Feb 2018 Keystone Symposia on Cancer Epigenetics “ATAC-ing single cell regulatory variation” (invited talk)
- Feb 2018 Seminar, Johns Hopkins “ATAC-ing single cell regulatory variation” (invited talk)
- Jan 2018 EMBL conference, Heidelberg, “ATAC-ing single cell regulatory variation” (invited talk)
- Nov 2017 PGQ seminar, Boston, “ATAC-ing single cell regulatory variation” (invited talk)
- Nov 2017 Seminar at NIH, “ATAC-ing single cell regulatory variation” (invited talk)
- Oct 2017 Presentation to Bill Gates describing biological importance of chromatin
- Oct 2017 Seminar, Penn State, “ATAC-ing single cell regulatory variation” (invited seminar)
- Oct 2017 Conference, Shanghai “ATAC-ing single cell regulatory variation” (invited talk)
- Sept 2017 International Conference on Advanced Genomics, Tokyo, “ATAC-ing single cell regulatory variation” (invited talk)
- June 2017 FOCIS conference, Chicago, “ATAC-ing single cell regulatory variation” (invited talk)
- June 2017 Keystone Symposium, Stockholm, “ATAC-ing single cell regulatory variation” (co-organizer of the conference)
- May 2017 Broad Institute, Boston MA “ATAC-ing single cell regulatory variation”
- April 2017 Keynote talk, Bethesda MD, “ATAC-ing single cell regulatory variation” (keynote talk)
- March 2017 Human Cell Atlas Meeting, Stanford CA, “ATAC-ing regulatory variation in single cells” (invited talk)
- Feb. 2017 AGBT, Hollywood FL, “ATAC-ing regulatory variation in single cells” (invited talk)
- Feb. 2017 Biophysical Society Meeting, New Orleans, “Quantitative characterization of the building blocks of RNA tertiary structure” (invited talk)
- Feb. 2017 Illumina, SSF, “ATAC-ing regulatory variation in single cells” (invited talk)
- Jan. 2017 Center for RNA Systems Biology (CRSB) symposium, Berkeley CA, "Exploring the physical genome" (invited speaker)
- Oct. 2016 Cold Spring Harbor Asia, Systems Biology of Gene Regulation & Genome Editing, "Exploring the physical genome." (keynote speaker)
- Oct. 2016 E. Bright Wilson Award Lecture, Harvard University, Department of Chemistry and Chemical Biology. "Exploring the physical genome"
- Oct. 2016 Single Cell Genomics Conference, Cambridge, UK, “ATAC-ing single cell regulatory variation” (invited speaker)
- Sept. 2016 Keystone: Understanding the Function of Human Genome Variation, Uppsala Sweden, “ATAC-Seq - Chromatin Accessibility at the Single Cell Level” (invited speaker)
- June 2016 GRC: Chromatin structure and function, Switzerland, "Sequencing-Based Methods for Exploring the Physical Genome" (invited speaker)
- May 2016 Biology of Genomes, Cold Spring Harbor, “ATAC-ing regulatory variation” (invited speaker)
- May 2016 Genome Center of Wisconsin Seminar, University of Wisconsin Madison, “Off-label’ uses of high-throughput sequencing to explore the physical genome (invited talk)
- April 2016

- April 2016 Emerging Innovations in Stem Cell and Developmental Biology Symposium, University of Southern California, “Single-cell chromatin accessibility reveals principles of regulatory variation” (invited speaker)
- March 2016 LabLinks Gene Circuits, Broad Institute, “Single-cell open chromatin landscapes provide a window during differentiation” (keynote speaker)
- March 2016 Global regulation of gene expression, Cold Spring Harbor NY, “Single-cell chromatin accessibility reveals principles of regulatory variation” (invited speaker)
- March 2016 CRUK CI Symposium, Cambridge UK, Unanswered Questions: Tumours at Cellular Resolution, “ATAC-ing gene regulation heterogeneity at the single cell level” (invited speaker)
- Feb 2016 Nuclear Reprogramming and the Cancer Genome, La Jolla, “Widespread Chromatin Accessibility Changes Associated with Metastasis in Small Cell Lung Cancer” (invited speaker)
- Feb 2016 Genomics and Personalized Medicine, Banff, Canada, “Single Cell ATAC-Seq” (invited speaker)
- Feb 2016 Epigenomics 2016, Puerto Rico “Single-cell Chromatin Accessibility Reveals Principles of Regulatory Variation” (invited talk)
- Nov 2015 Cancer epigenetics, GTCbio, San Francisco, “Single-cell Chromatin Accessibility Reveals Principles of Regulatory Variation” (invited talk)
- Nov 2015 CEGS grantee meeting, Broad Institute, “Single-cell Chromatin Accessibility Reveals Principles of Regulatory Variation”
- Nov 2015 International RA genetics meeting, San Francisco, “Single-cell open chromatin maps across diverse cell types reveal a rich landscape of cis- and trans-variability” (invited talk)
- June 2015 CEGS Scientific Advisory Board Meeting, Stanford University
- May 2015 NHGRI Advanced DNA Sequencing Technology Development Grantee Meeting, San Diego, “Hijacking Sequencers for Quantitative, Deep Mutational Profiling to Map the Biophysical and Functional Evolutionary Landscapes of RNA-Protein Interactions
- April 2015 Computational Biology Center Research Symposium, Columbia Univ. “Off-label uses of high-throughput sequencing to explore the physical genome” (invited talk)
- April 2015 Memorial Sloan Kettering Research Center “Off-label uses of high-throughput sequencing to explore the physical genome” (invited talk)
- March 2015 NHGRI workshop on Future Opportunities for Genome Annotation, Bethesda MD (invited talk).
- Jan. 2015 International Symposium on Genome Science, Tokyo, Japan (invited talk)
- Jan. 2015 RIKEN, Tokyo, Japan “Off-label uses of high-throughput sequencing to explore the physical genome” (invited talk)
- Dec. 2014 NIH CCHI U19 meeting, Bethesda MD, “ATAC-ing single immune cells” (invited/required talk)
- Dec. 2014 Fluidigm, S. SF, “ATAC-ing single immune cells” (invited talk)
- Nov 2014 CEGS meeting, Broad Inst. “ATAC-ing single cells” (invited/required talk)
- Oct 2014 Grand Rounds presentation to USC Div. of Hematology. “Off-label uses of high-throughput sequencing to explore the physical genome” (invited talk)

- Sept. 2014 Berkeley Biophysics Retreat Keynote Speaker, Marconi Center, “Off-label uses of high-throughput sequencing to explore the physical genome” (invited talk)
- Aug. 2014 Mayo Clinic, Rochester MN, “Off-label uses of high-throughput sequencing to explore the physical genome” (invited seminar)
- July 2014 ENCODE meeting, Stanford, “ATAC-seq” (invited talk)
- June 2014 4th annual NGS conference, San Diego, “Off-label uses of high-throughput sequencing to explore the physical genome” (invited talk)
- June 2014 Joint Genome Institute, Walnut Creek. “Off-label uses of high-throughput sequencing to explore the physical genome” (invited talk).
- June 2014 Broad Institute, Boston, “Off-label uses of high-throughput sequencing to explore the physical genome” (invited talk)
- May 2014 Biology of Genomes, CSHL, “Off-label uses of high-throughput sequencing to explore the physical genome” (selected abstract)
- Mar 2014 Clontech, Palo Alto, "Off Label" Uses of High-Throughput Sequencers” (invited talk)
- Mar 2014 Univ. Washington Genome Sciences, Seattle WA, "Off Label" Uses of High-Throughput Sequencers” (invited talk)
- Feb 2014 Biophysical Society, San Francisco, Future of Biophysics Burroughs Wellcome Fund Symposium “Off-label uses of high-throughput sequencing to explore the physical genome” (Invited talk)
- Feb 2014 AGBT, Marco Island, Florida, Selected talk “Transposition of Native Chromatin for Multitmodal Regulatory Analysis and Personal Epigenomics”
- Jan 2014 Fluidigm, S. SF, "Off Label" Uses of High-Throughput Sequencers”
- Nov 2013 Epigenomics of Common Disease, Wellcome Trust, UK “Transposition of native chromatin for multitmodal regulatory analysis and personal epigenomics”
- Nov 2013 Illumina, Hixton UK, “"Off Label" Uses of High-Throughput Sequencers.” (invited talk)
- Oct 2013 Agilent, Santa Clara, "Off Label" Uses of High-Throughput Sequencers,” (invited talk)
- Sept 2013 Genetics departmental retreat
- Apr 2013 Emory University, Atlanta GA, student-invited biophysics colloquium single molecule and high throughput methods for unravelling RNA structure and function.” (invited talk)
- Apr 2012 Fluidigm, S. SF (invited talk)
- Feb 2012 Molecular profiling club, Stanford, "Profiling two ways: Massively parallel RNA arrays and single molecule diffusion in nanoreactors"
- Nov 2011 Cancer Biology Journal Club , Stanford
- Oct 2011 Biochemistry departmental retreat, Fallen Leaf Lake
- Sept 2011 Biophysics departmental retreat, Allied Arts MP.
- Sept 2011 Genetics departmental retreat, Monterey
- Sept 2011 Damon Runyon Cancer Research retreat, CA.
- Mar 2011 MIT, Department of Mechanical Engineering, “Observing transcription with high-resolution optical tweezers, and sequencing DNA with reversibly sealable microreactors” (seminar)
- Mar 2011 Biophysical Society Meeting, “Fluorogenic pyrosequencing in microreactors” platform talk (and session co-chair)

- Mar 2011 University of Chicago, Dept. of Biochemistry & Molecular Biology, “Making light work in biology: Observing transcription with high-resolution optical tweezers, and sequencing DNA with fluorogenic nucleotides” (seminar)
- Feb 2011 New York University, Skirball Institute, Department of Struct. Biol., “The power of the force: probing transcription & riboswitch folding with optical tweezers” (seminar)
- Feb 2011 University of California San Diego, Department of Bioengineering, “Making light work in biology: Observing transcription with high-resolution optical tweezers, and sequencing DNA with fluorogenic nucleotides” (seminar)
- Feb 2011 Stanford University, Department of Chemical and Systems Biology, “Making light work in biology: Observing transcription with high-resolution optical tweezers, and sequencing DNA with fluorogenic nucleotides” (seminar)
- Feb 2011 Columbia University, Departments of Biology and Physics, “Making light work in biology: Observing transcription & RNA folding with optical tweezers, and sequencing DNA with fluorogenic nucleotides” (seminar)
- Feb 2011 MIT, Department of Physics, “Observing transcription with high-resolution optical tweezers, and sequencing DNA with reversibly sealable microreactors” (seminar)
- Feb 2011 University of Pennsylvania, Department of Bioengineering “Making light work in biology: Observing transcription & RNA folding with optical tweezers, and sequencing DNA with fluorogenic nucleotides” (seminar)
- Feb 2011 University of Pennsylvania, Physics Department, “Observing transcription with high-resolution optical tweezers, and sequencing DNA with reversibly sealable microreactors” (seminar)
- Feb 2011 Harvard Medical School, BCMP Department, “Making light work in biology: probing transcription & RNA folding with optical traps, and Sequencing DNA with Fluorogenic Nucleotides” (seminar)
- Jan 2011 Caltech, Division of Biology, "The power of the force: probing transcription and riboswitch folding with high-resolution optical tweezers" (seminar)
- Jan 2011 Stanford University, Department of Genetics, “DNA sequencing two ways: single-molecular, position-based sequencing with RNA polymerase, and fluorogenic pyrosequencing in microreactors” (seminar)
- Jan 2011 University of Texas, Austin Department of Biomedical Engineering, “Making light work in biology: Observing transcription with high-resolution optical tweezers, and sequencing DNA with fluorogenic nucleotides” (seminar)
- Jan 2011 MIT Department of Chemistry, “Making light work in biology: observing transcription & RNA folding with optical tweezers, and sequencing DNA with fluorogenic nucleotides” (seminar)
- Jan 2011 University of Pennsylvania, Department of Biochemistry & Biophysics, “Making light work in biology: observing transcription & RNA folding with optical tweezers, and sequencing DNA with fluorogenic nucleotides” (seminar)
- Jan 2011 UNC at Chapel Hill, Dept. of Biochemistry & Biophysics, “Making Light Work In Biology: observing transcription & RNA folding with optical tweezers” (seminar)

- Nov 2009 MCB seminar, MIT, “RNA under tension: The mechanics of transcription termination and riboswitch folding investigated with optical tweezers” (invited talk)
- Oct 2009 Damon Runyon Cancer Research Fellow’s Retreat (poster presentation)
- Aug 2007 Proceedings of SPIE Symposium on Nanoscience + Engineering “High-resolution single-molecule optical trapping measurements of transcription with basepair accuracy” (talk for invited paper)
- Mar 2007 Next generation sequencing: applications and case studies, “Single-molecule, motion-based DNA sequencing using RNA polymerase” (invited talk)
- Mar 2007 Annual Meeting of the Biophysical Society (poster presentation)
- Feb 2007 Single Molecule Biophysics conference, Aspen Center for Physics (poster presentation)
- Feb 2006 Annual Meeting of the Biophysical Society (poster presentation)
- May 2006 Biomedical engineering seminar, Mayo Clinic, Rochester MN “One small step for an enzyme: high resolution measurements of RNAP”
- Dec 2006 Biophysics seminar, Stanford University
- Oct 2005 Biological Science Seminar Series, Stanford
- Jun 2005 FASEB: Prokaryotic Transcription (poster presentation)

SCIENTIFIC ADVISORY BOARD/ADVISOR:

- 2019 – present Protillion Biosciences, Burlingame, CA, USA
- 2012 – 2014 Eve Biomedical, Palo Alto, CA, USA
- 2014 – 2018 Epinomics, San Jose, CA, USA
- 2016 – present Centrillion, Palo Alto, CA, USA

STANFORD AFFILIATIONS:

Bio-X
 Biophysics Program
 Biomedical Informatics
 Cancer Center
 Applied Physics Dept. (Courtesy Appt.)
 Stem Cell Biology

TEACHING:

- 2011 GENE 203: Advanced Genetics (section co-leader)
- 2011 GENE 222: Methods and Logic in Experimental Genetics 222 (Lecturer)
- 2012 BIOS 200: The Nucleus (Guest lecture)
- 2012 – 2020 GENE/DBIO 200: Genetics Training Camp (Instructor)
- 2013 – 2019 BIOS 201 Minicourse (Instructor)
- 2013 – 2019 APPHYS/BIPHYS 232: Adv. Imaging Lab in Biophysics (Instructor)
- 2014 Genetics online certificate (Instructor)
- 2015 – 2016 STEMREM 202 (Guest lecture)
- 2016 CSB250: The Biology of Chromatin Templated Processes (Guest lecture)
- 2016 MI 215 "Biotechniques" (Guest lecture)

GRADUATE ADVISOR TO:

Lauren Chircus (Chemical and Systems Biology)
Jason Buenrostro (Genetics)
Sarah Denny (Biophysics)
Alicia Schep (Genetic)
David Moskowitz (BMI)
Anthony Ho (Ap. Physics)
Ben Ober-Renyolds (MD/PhD)
Winston Becker (MD/PhD)
Alex Trevino (BioE)
Maxwell Mumbach (Genetics)
Evan Boyle (Genetics)
Jeff Granja (Biophysics)
YeEun Kim (Immunology)
Sam Kim (MD/PhD)
Michaela Hinks (BioE)
Benjamin Parks (Computer Science)
Lakshman Sundaram (Computer Science)
Sarah Pierce (Cancer Biology)

POSTDOCTORAL ADVISOR TO:

Curtis Layton
Viviana Risca
Carlos Araya
David Zhang
Dimitra Angeli
Johan Andreasson
Sandy Klemm
Peter Frick
Anja Mezker
Zohar Shipony
Grace Anderson
Lisa McGinnis
Fabien Muller
Georgi Marinov
Eyal Raz
Amy Chen
Bei Wei
Eesha Sharma
Jordi Fernandez

PHD/QUAL COMMITTEES:

Mara Pavel-Dinu (Biology)
Charles Hancock Starr (Biophysics)
Laura Donohue (Genetics)
Sam Piekos (Stem Cell Bio Regenerative Medicine)

Chris Probert (Genetics)
Suhass Rao (Biophysics)
Michael Rosen (Applied Physics)
Ava Carter (Stem Cell Biology and Regenerative Medicine)
Deyra Nichole Rodriguez (Biochemistry)
Alicia Martin (Genetics)
Hyunjoo J. Lee (Electrical Engineering)
Paul Martin Lebel (Applied Physics)
Furqan Fazal (Applied Physics)
Kirsten Frieda (Biophysics)
Christian Perez (Physics)
Siqi Tan (Biochemistry)
Mark Kelly (Biochemistry)
Becky Fu (Genetics)
Quintin Stedman (Applied Physics)
Marta Andres Terre (Genetics)
Julia Garcia (Genetics)
Bosh Liu (Biology)
Bojan Milic (Biophysics)
Sara Prescott (Chemical and systems biology)
Julia Garcia (Genetics)
Diego Calderon (BMI)
Daniel Kim (BMI)
Nurlybek Mursaliyev (Biology)
Dimitry Pushkarev (Physics)
Brooke Barajas (Cancer biology)
Chuan Sheng Foo (Computer science)
Johnny Isreali (Biophysics)
Kevin Larsen (Biophysics)
Maurice Lee (Biophysics)
Michael Reddick (Bioengineering)
Nikki Teran (Genetics)
Alicia Schep (Genetics)
Reema Baskar (Cancer Biology)
Michelle Wu (Biomedical Informatics)
Jacob Blum (Genetics)
Charles De Bourcy (Applied Physics)
Kade Ploussard Pettie (Biology)
Bruno Beltran (Biophysics)
Josh Tycko (Genetics)
Andrew Savinov (Biophysics)
Kristen Wells (Genetics)
David Yao (Genetics)
Kevin Daniel Palacio Aris (Biophysics)
Chris Probert (Genetics)
Bruno Beltran (Biophysics)

Robin Meyers (Genetics)

Thesis Defense:

Adam Rubin (ISCBRM)

Alicia Schep (Genetics)

David Moskowitz (Biomedical Informatics)

Andrew Savinov (Biophysics)

Ava Carter (Stem Cell Biology and Regenerative Medicine)

Jay Sarkar (Stem Cell Biology and Regenerative Medicine)

Michelle Wu (Biomedical Informatics)

Evan Boyle (Genetics)

Kevin Larsen (Biophysics)

Johnny Israeli (Biophysics)

Sarah Pierce (Cancer Biology)

Diego Calderon(BMI)

William Gilpin (Applied Physics)

Maxwell Mumbach (Genetics)

Bojan Millic (Biophysics)

Andrew Savinov (Biophysics)

Ava Carter (Stem Cell)

Kristin Wells (Genetics)

Diego Calderon (BMI)

Michelle Wu (Biomedical Informatics)

Evan Boyle (Genetics)

Kevin Larsen (Biophysics)

UNDERGRADUATE STUDENT MENTOR TO:

Daniel McHugh (Stanford)

Nandita Damaraju (IIT)

Connor Jordan (Stanford)

Margaret Shen (Stanford)

HIGH SCHOOL STUDENT MENTOR TO:

Rajiv Movva

COMMITTEES ON CAMPUS:

2011 – 2012 Genetics Graduate Student Admissions Committee

2012 – 2014 Genetics Retreat Organizing Committee

2013 – 2016 Biophysics Graduate Student Admissions Committee

2012 – 2016 Genetics Curriculum Committee

2012 – present Genetics “Bootcamp” Planning Committee