

**CURRICULUM VITAE**  
**WILLIAM JAMES GREENLEAF**

Department of Genetics  
Stanford University  
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**ACADEMIC HISTORY**

- 9/1/14 - 10/31/18 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**

- 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 *Phi Beta Kappa*, Harvard University
- 1998-2002 John Harvard Scholar

1999 Detur Prize, Harvard University  
 1998 6<sup>th</sup> Place, Westinghouse Science Talent Search

#### PUBLICATIONS UNDER REVIEW/SUBMITTED (6)

- 1) Boyle EA\*, Andreasson JOL\*, Chircus LM\*, Sternberg SH, Wu MJ, Guegler CK, Doudna JA, **Greenleaf WJ**. “High-throughput biochemical profiling reveals Cas9 off-target binding and unbinding heterogeneity.” In review at *PNAS*. She R\*, Chakravarty AK\*, Layton CJ\*, Chircus LM, Andreasson JOL, Damaraju N, McMahon PL, Buenrostro JD, Jarosz DF<sup>§</sup>, **Greenleaf WJ**<sup>§</sup>. “Comprehensive and quantitative mapping of RNA-protein interactions across a transcribed eukaryotic genome.” In revision at *PNAS*.
- 2) Barajas B\*, Rubin AJ\*, Furlan-Magaril M, Howard I, Mumbach M, Kim DS, Boxer L, Lopez-Pajares V, **Greenleaf WJ**, Kundaje A, Snyder M, Chang YM, Fraser P, Khavari PA. “Lineage-specific factors regulate dynamic and constitutive enhancer-promoter contacts to induce terminal differentiation.” In revision at *Nature*.
- 3) Mumbach MR, Satpathy AT, Boyle EA, Dai C, Wei Y, Rubin AJ, Nguyen T, Corces MR, Suliman N, Li R, Xu J, Flynn RA, Khavari PA, Quertermous T, **Greenleaf WJ**<sup>§</sup>, and Chang HY<sup>§</sup>. “Enhancer connectome in primary human cells reveals target genes of disease-associated DNA elements” In review at *Science*.
- 4) Buenrostro JD, Wu B, Chang HY, **Greenleaf WJ**. Single cell ATAC-seq: A single-cell method for Assaying Chromatin Accessibility in an Integrated Fluidics Circuit. In revision at *Nature Protocols*.
- 5) 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. Tracking the origin and differentiation of human memory CD8 T cells after vaccination. In revision, *Nature*.

#### PEER REVIEWED PUBLICATIONS (36)

- 1) Moskowitz DM\*, Zhang DW\*, Le Saux S, Hu B, Buenrostro JD, Weyand CM, **Greenleaf WJ**<sup>§</sup>, Goronzy JJ<sup>§</sup>. “Epigenomics of human CD8 T cell differentiation and aging.” In press, *Science Immunology*
- 2) Litzenger UM, Buenrostro JD, Wu B, Shen Y, Sheffield N, Kathiria A, **Greenleaf WJ**<sup>§</sup>, Chang HY<sup>§</sup>. (2017) Single cell epigenomic variability reveals functional cancer heterogeneity. *Genome Biology*. 24;18(1):15
- 3) 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*. doi: 10.1038/ng.3769
- 4) Wang J, Yu J, Yang Q, McDermott J, Scott A, Vukovitch M, Lagrois R, Gong Q, **Greenleaf WJ**, Eisenstein M, Ferguson BS, Soh HT. Multiparameter Particle Display (MPPD): A Quantitative Screening Method for the Discovery of Highly Specific Aptamers. *Angew Chem Int Ed Engl*. 56(3):744-747
- 5) 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.

- 6) 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-seq reveals the accessible genome by transposase-mediated imaging and sequencing. *Nature Methods*. 13, 1013-1020.
- 7) HiChIP: Efficient and sensitive analysis of protein-directed genome architecture. Mumbach MR, Rubin AJ, Flynn RA, Khavari PA, **Greenleaf WJ**, Chang HY. (2016) *Nature Methods*, 13, 919-922.
- 8) 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
- 9) 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**<sup>§</sup>, Winslow MM<sup>§</sup>. (2016) “Nfib promotes Metastasis through a Widespread Increase in Chromatin Accessibility” *Cell* 166:2, 328-342.
- 10) Araya CL<sup>§</sup>, Cenik C, Reuter JA, Kiss G, Pande VS, Snyder MP<sup>§</sup>, **Greenleaf WJ**<sup>§</sup>. (2016) “Systematic identification of significantly mutated regions reveals a rich landscape of functional molecular alterations across cancer genomes” *Nature Genetics*, 48, 117–125.
- 11) Risca VI, **Greenleaf WJ**. (2015) “Beyond the linear genome: Paired-end sequencing as a biophysical tool.” *Trends in Cell Biology*, 25:12, 716–719.
- 12) 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*. Doi:10.1101/gr.192294.115
- 13) 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.
- 14) Buenrostro JD, Wu B, Litzenburger U, Snyder M, Ruff D, Gonzales M, Chang H<sup>§</sup>, **Greenleaf, WJ**.<sup>§</sup> (2015) “Single-cell chromatin accessibility reveals principles of regulatory variation.” *Nature*. 523:486-490.
- 15) 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.
- 16) Risca VI, **Greenleaf WJ**. Unraveling the 3D genome: genomics tools for multiscale exploration. (2015) *Trends in Genetics*. <http://dx.doi.org/10.1016/j.tig.2015.03.010>
- 17) 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
- 18) **Greenleaf, WJ**. “Assaying the epigenome in limited numbers of cells.” (2015) *Methods* 72 51–56
- 19) 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.
- 20) Larson MH, Mooney RA, Peters JM, Windgassen T, Nayak D, Gross CA, Block SM, **Greenleaf WJ**<sup>§</sup>, Landick R<sup>§</sup>, Weissman JS<sup>§</sup>. (2014) "A Pause Sequence Enriched at Translation Start Sites Drives Transcription Dynamics in Vivo." *Science*. 344(6187): 1042-7.
  - 21) 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.
  - 22) 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.
  - 23) 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**<sup>§\*</sup> and Bustamante CD<sup>§\*</sup> (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.
  - 24) Buenrostro JD, Giresi PG, Zaba LC, Chang H<sup>§</sup>, **Greenleaf WJ**<sup>§</sup>. (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.
  - 25) 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.
  - 26) Sims PA\*, **Greenleaf WJ**\*, Duan H, and Xie XS (2011) “Fluorogenic DNA Sequencing in PDMS Microreactors.” *Nature Methods* 8:575-580
  - 27) 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
  - 28) Larson MH\*, **Greenleaf WJ**\*, Landick R, and Block SM. (2008) “Applied force reveals mechanistic and energetic details of transcription termination.” *Cell*, 132:971-982
  - 29) **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.
  - 30) Herbert, KM, **Greenleaf WJ**, and Block SM. (2008) “Single molecule measurements of RNA polymerase: motoring along.” *Ann. Rev. Biochem*. 77: 149-176.
  - 31) **Greenleaf WJ**, Woodside MT, and Block SM. (2007) “High-resolution, single-molecule measurements of biomolecular motion.” *Ann. Rev Biophys. Biomol. Struct*. 36:171-90.
  - 32) **Greenleaf WJ**, and Block SM. (2006) “Single-molecule, motion-based DNA sequencing using RNA polymerase.” *Science* 313:801.
  - 33) Abbondanzieri EA\*, **Greenleaf WJ**\*, Shaevitz JW, Landick R, Block, SM (2005) “Direct observation of basepair stepping by RNA polymerase.” *Nature*. 438(7067):460-465.

- 34) **Greenleaf WJ\***, Woodside MT\*, Abbondanzieri EA, Block SM. (2005) “Passive all-optical force clamp for high resolution laser trapping.” *Phys. Rev. Lett.* 95:208102.
- 35) 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.
- 36) **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.

(\*These authors contributed equally)

(<sup>§</sup>co-corresponding authors)

#### OTHER PUBLICATIONS (5)

- 1) Boyle EA\*, Andreasson JOL\*, Chircus LM\*, Sternberg SH, Wu MJ, Guegler CK, Doudna JA, **Greenleaf WJ**. High-throughput biochemical profiling reveals Cas9 off-target binding and unbinding heterogeneity. BioArXiv doi: <http://biorxiv.org/content/early/2016/06/19/059782>
- 2) Araya CL, Cenik C, Reuter JA, Kiss G, Pande VS, Snyder MP<sup>§</sup>, **Greenleaf WJ**<sup>§</sup>. “Systematic identification of significantly mutated regions reveals a rich landscape of functional molecular alterations across cancer genomes” BioArXiv doi: <http://dx.doi.org/10.1101/020875>
- 3) **Greenleaf WJ** & Sidow, A. (2014) “The future of sequencing: convergence of intelligent design and market Darwinism.” *Genome Biol.* 15:303-5. (Meeting report)
- 4) 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).
- 5) **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 (11)

- 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

\*Currently licensed or optioned

#### SELECTED PRESENTATIONS AND SEMINARS

- |            |  |
|------------|--|
| Oct. 2016  | 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"  |
| Sept. 2016 | Single Cell Genomics Conference, Cambridge, UK, “ATAC-ing single cell regulatory variation” (invited speaker)  |
| June 2016  | Keystone: Understanding the Function of Human Genome Variation, Uppsala Sweden, “ATAC-Seq - Chromatin Accessibility at the Single Cell Level” (invited speaker)  |
| May 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)  |
| April 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 | 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 4<sup>th</sup> 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:**

- 2012 – present Eve Biomedical, Palo Alto, CA, USA  
 2014 – present 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 – 2015 GENE/DBIO 200: Genetics Training Camp (Instructor)  
 2013 – 2015 BIOS 201 Minicourse (Instructor)  
 2013 – 2016 APPHYS/BIOPHYS 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)

**POSTDOCTORAL ADVISOR TO:**

Curtis Layton  
Viviana Risca  
Carlos Araya  
David Zhang  
Dimitra Angeli  
Johan Andreasson  
Sandy Klemm  
Peter Frick  
Anja Mezker  
Zohar Shipony

**PHD/QUAL COMMITTEES:**

Mara Pavel-Dinu (Biology)  
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)

**UNDERGRADUATE STUDENT MENTOR TO:**



Vaccine Induced Immunity in the Young and Aged

This project aims to map chromatin changes and gene expression in individual T-cells

Role: Co-I

1R01GM11990-01

09/15/14 - 08/31/19

NIH/NIGMS

Quantitative high-throughput nucleic acid assays on a sequencing chip

This project aims to develop method for quantitating nucleic acid protein interactions using high-throughput sequencing instrument.

Role: PI

P50HG007735 Chang (PI)

09/01/14 - 06/30/19

NIH/NHGRI

Center for personalized regulomes

This project aims to develop methods for profiling the regulatory state of clinical samples.

Role: Co-I

SPO114114

03/01/15 – 2/28/18

NIH/NHGRI SPO 114114 / NIH (U01)

Genomics of gene regulation

This project will explore gene regulatory changes associated with skin differentiation

Role: Co-I

Young Investigator Grant

05/01/2015 – 04/30/2018

Human Frontier Science Program

Deciphering chromatin dynamics during programming and reprogramming of pluripotent cells

This project aims to understand the epigenetic state as a function of programming and reprogramming over time in multiple model systems.

Role: PI

NIH R01 (PI Pritchard)

07/01/16-06/31/19

Using functional information from human blood to interpret the genetic basis of complex traits

To develop statistical approaches for integrating functional information from genome-wide assays with data from GWAS studies for complex traits and propose novel approaches to

validation, based on measuring cellular phenotypes in sorted immune cells and performing genome editing of specific sites.

Role: Co-PI

1UM1HG009436-01 (Greenleaf, William James) 12/01/16-11/30/20 1.20 cal mons  
NIH

High-throughput systematic characterization of regulatory element function

This project will deliver an immense corpus of functional data linking regulatory elements to genes, as well as extensive molecular characterization of a subset of these regulatory elements. This will provide a scaffold for understanding classes of functional elements, validating computational predictions, and providing techniques that broadly extend to other cell types/tissues.

UM1 (PI: Snyder) 12/01/16-11/30/20 0.60 cal mons  
NIH (received notice from PO of intent to fund)

Production Center for Mapping Regulatory Regions of the Human Genome

This project aims to map regulatory regions in a large variety of tissues and cell types.

### **COMPLETED**

Subproject of 2U19AI057229-07 (PI: M. Davis; co sub-PI J. Goronzy) 5/01/12 - 4/31/13  
NIH

Chromatin signatures in antigen-specific T cell responses

The major goal of this project was to determine how histone modifications contribute to differences in the responsiveness and activity of different virus-specific T cells.

1R21HG007726-01 04/01/14 - 03/31/16  
NIH/NIGMS

Mapping chromatin secondary structure by sequencing correlated DNA strand breaks

This project aims to map the three-dimensional structure of chromatin using ionizing radiation.

Role: PI

Baxter Foundation Faculty Scholar 2014-2015  
Gift Funding

Role:PI