Nicolas Altemose, DPhil, PhD

altemose@stanford.edu | www.altemoselab.org | *he/him/his*

APPOINTMENT: **Assistant Professor, Dept. of Genetics, Stanford University**

RESEARCH INTERESTS

Long-read sequencing technology development, centromeres & heterochromatin, chromatin dynamics, protein-DNA interactions

EDUCATION

University of California, Berkeley and University of California, San Francisco **2015-2021**
- PhD in Bioengineering (joint degree from UCB/UCSF)

University of Oxford, United Kingdom **2011-2015**
- DPhil in Statistics (Statistical Genetics)

Duke University, Durham, North Carolina **2007-2011**
- BS in Biology, with a Concentration in Genomics and a Minor in Computational Biology and Bioinformatics

HONORS AND AWARDS

- **Chan Zuckerberg Biohub Investigator (Campus-Nominated)** **2023-present**
  - Includes an extramural research grant totaling $1M over 5 years
- **Howard Hughes Medical Institute Hanna H. Gray Fellowship** **2021-present**
  - Postdoc-to-faculty transition award totaling $1.4M over 6-8 years; awarded to 21 fellows in 2020
- **Bioengineering Service and Diversity, Equity, Inclusion, & Belonging Award**, UC Berkeley **2021**
  - "Recognition of students who go above and beyond to improve the climate in the program"
- **Siebel Scholarship** **2020-2021**
  - Funding for the final year of my PhD; awarded to ~100 students nationally each year
- **Howard Hughes Medical Institute Gilliam Fellowship** **2013-2019**
  - 5-year PhD fellowship; awarded to 9 fellows in 2011 (deferred 2 years)
- **Marshall Scholarship**, United Kingdom **2011-2013**
  - UK postgrad merit scholarship for US citizens; awarded to 33 of 999 university-endorsed applicants
- **Angier B. Duke Scholarship**, Duke University **2007-2011**
  - Flagship full-ride academic merit scholarship at Duke; offered to 20 out of 19,000 applicants
- **Edward C. Horn Memorial Prize for Excellence in Biology**, Duke University **2011**
  - "Given each year to a graduating biology major who has shown, in the opinion of the biology faculty, the highest level of academic achievement and promise"
- **Summa Cum Laude & Graduation with Distinction**, Duke University **2011**
- **Barry M. Goldwater Scholarship** **2010**

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RESEARCH TRAINING

Professor Gary Karpen, PhD, Dept. of Molecular and Cell Biology, UC Berkeley **2021-2023**

- As a postdoctoral scholar, I worked with the T2T Consortium to annotate and characterize centromeric and pericentromeric sequences in the first complete sequence of a human genome.

Associate Professor Aaron Streets, PhD, Dept. of Bioengineering, UC Berkeley **2016-2021**

- As a PhD Student, I developed microfluidic and molecular tools for mapping protein-DNA interactions in single human cells and on single DNA molecules using microscopy and DNA sequencing methods.

Professor Simon Myers, DPhil, Dept. of Statistics, University of Oxford **2011-2015**

- As a DPhil Student, I used experimental & computational methods to characterize PRDM9, a rapidly evolving meiotic recombination protein. This work illuminated the first molecular mechanism of speciation in any mammal and generated the highest-resolution map ever of mammalian non-crossover gene conversions.

Professor David Reich, DPhil, Dept. of Genetics, Harvard Medical School **Summer 2011**

- As a summer research student, I identified a set of tagging polymorphisms in/near the very complex centromere gap on chromosome 1, which were genotyped in thousands of samples to help an effort to fine-map a multiple sclerosis association signal.

Professor Huntington Willard, PhD, Dept. of Biology, Duke University **2007-2011**
under the direct supervision of Karen H. Miga, PhD

- As an undergraduate researcher, I developed a new computational approach for characterizing highly repetitive satellite DNA sequences that were almost entirely missing from the human genome reference.

SELECTED PUBLICATIONS, ANNOTATED

‡ indicates co-first authorship; annotations are in the spirit of the San Francisco Declaration On Research Assessment (SF DORA)
See also: Google Scholar Profile (https://scholar.google.com/citations?user=aamOod8AAAAJ&hl=en)

Altemose N (2022). [Review] **A classical revival: Human satellite DNAs enter the genomics era.** *Seminars in Cell and Developmental Biology*, 128, 2-14.
https://doi.org/10.1016/j.semcdb.2022.04.012 [open-access preprint available]

Altemose N‡, Maslan A‡, Smith OK‡, Sundararajan K‡, Brown RR, Meeshra R, Detweiler A, Neff N, Miga KH, Straight AF, Streets A (2022). **DiMeLo-seq: a long-read, single-molecule method for mapping protein-DNA interactions genome-wide**. *Nature Methods*, 19, 711–723.
https://doi.org/10.1038/s41592-022-01475-6
[open-access preprint available, transparent review]

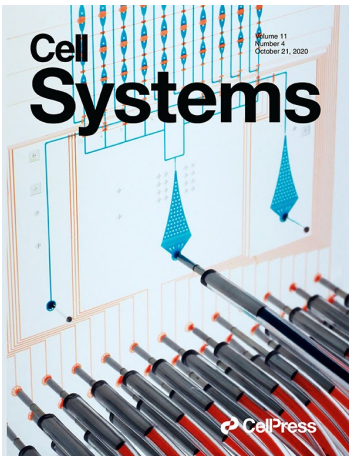
- Many open questions remain about the epigenetics and regulation of the newly assembled repetitive heterochromatic regions of the human genome. However, existing methods for mapping protein-DNA interactions use short DNA sequencing reads that cannot be reliably mapped to repetitive regions. To address this, **we developed a sequencing method for mapping protein-DNA interactions on long, single, native molecules of DNA that retain endogenous CpG methylation information. Then, we applied this method to produce the first high-resolution maps of histone variants and centromere proteins across human centromeres**. We joined forces with Aaron Straight's group at Stanford, who are experts in centromere biology and who were working on a similar method.

SELECTED PUBLICATIONS, ANNOTATED (continued)

Altemose N, *The Telomere-To-Telomere Consortium (56 authors)*, Alexandrov IA, Miga KH (2022). Complete genomic and epigenetic maps of human centromeres. *Science*, 376, eabl4178. https://doi.org/10.1126/science.abl4178 [free to read]

- As a side project during my PhD and postdoc, I joined the efforts of the Telomere-To-Telomere (T2T) Consortium to produce **the first complete sequence assembly of a human genome**, including repetitive heterochromatic regions. I helped lead our efforts to characterize some of the most challenging regions of the genome to assemble, which contain the peri/centromeric repetitive sequences in which I became an expert as an undergraduate. **I developed tailored computational tools for visualizing and quantifying the underlying repeat structure in these formerly missing regions of the genome**, discovered unexpected inversions and deletion polymorphisms, and wrote the manuscript along with the corresponding authors. This work was featured in the *New York Times*, for which I was interviewed: https://www.nytimes.com/2021/07/23/science/human-genome-complete.html.

Altemose N, Maslan A, Rios-Martinez C, Lai A, White JA, Streets A (2020). μDamID: a microfluidic approach for joint imaging and sequencing of protein-DNA interactions in single cells. *Cell Systems*, 11, 1-13. https://doi.org/10.1016/j.cels.2020.08.015 [open access, transparent review]



- Here, I describe the results from my first PhD project at UC Berkeley. Measuring protein-DNA interactions in single cells is critical for understanding key biological processes like embryonic development, stem cell differentiation, meiosis, and genome misregulation in disease. To enable the collection of joint imaging and protein-DNA mapping data from the same single cells, **I designed, built, and tested a microfluidic device that allows the user to isolate, image, sort, and amplify DNA from single cells to measure both the nuclear localization and sequence identity of specific protein-DNA interactions genome-wide.**

Li R‡, Bitoun E‡, **Altemose N‡**, Davies RW, Davies B, Myers SR (2019). A high-resolution map of non-crossover events reveals impacts of genetic diversity on mammalian meiotic recombination. *Nature Communications,* 10, 1-15. https://doi.org/10.1038/s41467-019-11675-y [open access, transparent review]

- **In this article, we present the highest-resolution map ever of mammalian non-crossover gene conversion events, which are difficult to detect and study despite their high frequency in each meiosis**. To accomplish this, we bred hybrid transgenic mice over 5 generations and deeply sequenced genomic DNA from over 100 offspring. Because these mice have high sequence diversity, we were able to detect short non-crossover gene conversions with unprecedented sensitivity and spatial resolution and discovered several new, fundamental properties of mammalian meiotic recombination. Most importantly, **we found strong evidence that the protein PRDM9 not only positions DNA double-strand breaks across the genome, but also guides their repair by binding to both homologous chromosomes**. This study represents one of my major research projects from Oxford, which I started in my final years. Reviewers called this work a "tour de force" and a "valuable resource for the community."

SELECTED PUBLICATIONS, ANNOTATED (continued)

Altemose N, Noor N, Bitoun E, Tumian A, Imbeault M, Chapman R, Aricescu AR, Myers SR (2017). **A map of human PRDM9 binding provides evidence for novel behaviors of PRDM9 and other zinc-finger proteins in meiosis.** *eLife*, 6, e28383.
https://doi.org/10.7554/eLife.28383 [open access, transparent review]

- This paper encompasses several additional branches of my thesis work from Oxford. **By building a high-resolution binding map of the meiotic recombination protein PRDM9 in a human cell line and comparing it to measurements of histone modifications, gene expression, and meiotic recombination rates, we discovered several novel properties of PRDM9 with consequences for fertility, genome evolution, and speciation**. We made the surprising discovery that PRDM9 frequently binds gene promoters and can even activate the expression of a small number of genes, expanding its known functions and evolutionary constraints. We also found that PRDM9 can bind different DNA motifs with different subsets and arrangements of its zinc fingers, and we showed that its zinc fingers are responsible for forming PRDM9 multimers. To perform these analyses, we developed a new ChIP-seq peak-calling algorithm as well as a new *ab initio* motif-finding algorithm that allows for joint discovery of multiple binding motifs with variable internal spacing. Our binding map, biological insights, and methods have proven useful for other groups.

Davies B[‡], Hatton E[‡], **Altemose N**, Hussin JG, Pratto F, Zhang G, Hinch AG, Moralli D, Biggs D, Diaz R, Preece C, Li R, Brick K, Green CM, Camerini-Otero RD, Myers SR, and Donnelly P (2016). **Re-engineering the zinc fingers of PRDM9 reverses hybrid sterility in mice.** *Nature*, 530, 171–176.
https://doi.org/10.1038/nature16931 [free to read on PubMed Central]

- **This study proposes the first molecular mechanism of speciation in any mammal**, resulting from a collaboration between four research groups (Ben Davies, R. Dan Camerini-Otero, Simon Myers, Peter Donnelly). Using maps of PRDM9 binding and double-strand break formation, we discovered that PRDM9-related hybrid infertility can be explained by PRDM9 binding unequally to each homologous chromosome at each binding site. My contribution stems from a chapter of my thesis work. **I helped design all experiments, led the breeding of hybrid mice, performed and analyzed the PRDM9 binding experiments, and generated the fourth and final main text figure.** My data and analyses proved essential for illuminating the proposed mechanism and reaching the main conclusion of the paper. Our results have inspired further investigations into this speciation mechanism by others. News & Views: https://www.nature.com/articles/nature16870

Altemose N, Miga KH, Maggioni M, Willard HF (2014). **Genomic characterization of large heterochromatic gaps in the human genome assembly.** *PLoS Computational Biology*, 10, e1003628.
https://doi.org/10.1371/journal.pcbi.1003628 [open access]

- **This study represents the first comprehensive genome-wide study of Human Satellites 2 and 3, which are poorly understood repetitive sequences that constitute 1-3% of the human genome and correspond to the largest gaps in the hg38 reference sequence.** As an undergraduate, I developed new computational methods to cluster and map these missing sequences genome-wide for the first time, and I provided resources, including a pseudo-reference, for their further study. By applying these resources, I discovered that a repetitive region of the Y chromosome can vary from 7 to 98 million base pairs among XY individuals, demonstrating that a large share of human genetic variation is still missing from the human reference assembly. The pseudo-reference that I published alongside this paper has been used by other groups to image and measure expression from these regions of the genome. Its conclusions and predictions have held up well in the T2T-CHM13 assembly.

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ADDITIONAL PUBLICATIONS

- Rhie A‡, Nurk S‡, Cechova M‡, Hoyt SJ‡, Taylor DJ‡, **Altemose N**, *The Telomere-To-Telomere Consortium (80 authors)*, Phillippy AM (2023). The complete sequence of a human Y chromosome. *Nature*, https://doi.org/10.1038/s41586-023-06457-y [open-access preprint]
- Nurk S‡, Koren S‡, Rhie A‡, Rautiainen M‡, Bzikadze AV, Mikheenko A, Vollger MR, **Altemose N**, Uralsky L, Gershman A, Aganezov S, Hoyt SJ, Diekhans M, Logsdon GA, *The Telomere-To-Telomere Consortium (74 authors)*, Surti U, McCoy RC, Dennis MY, Alexandrov IA, Gerton JL, O'Neill RJ, Timp W, Zook JM, Schatz MC, Eichler EE, Miga KH, Phillippy AM (2022). The complete sequence of a human genome. *Science,* 376, 44-53*,* https://doi.org/10.1126/science.abj6987 [free to read]
- Gershman A, Sauria MEG, Guitart X, Vollger MR, Hook PW, Hoyt SJ, Jain M,Shumate A, Razaghi R, Koren S, **Altemose N**, Caldas GV, Logsdon GA, Rhie A, Eichler EE, Schatz MC, O'Neill RJ, Phillippy AM, Miga KH, Timp W (2022). Epigenetic patterns in a complete human genome. *Science*, 375, eabj5089, https://doi.org/10.1126/science.abj5089 [free to read]
- Hoyt SJ, Storer JM, Hartley GA, Grady PGS, Gershman A, de Lima LG, Limouse C, Halabian R, Wojenski L, Rodriguez M, **Altemose N**, Rhie A, Core LJ, Gerton JL, Makalowski W, Olson D, Rosen J, Smit AFA, Straight AF, Vollger MR, Wheeler TJ, Schatz MC, Eichler EE, Phillippy AM, Timp W, Miga KH, O'Neill RJ (2022). From telomere to telomere: The transcriptional and epigenetic state of human repeat elements. *Science,* 375, eabk3112, https://doi.org/10.1126/science.abk3112 [free to read]
- Gupta A, Shamsi F, **Altemose N**, Dorlhiac GF, Cypess AM, White AP, Yosef N, Patti ME, Tseng Y-H, Streets A (2022). Characterization of transcript enrichment and detection bias in single-nuclei RNA-seq for mapping of distinct human adipocyte lineages. *Genome Research,* 32, 242-257, https://doi.org/10.1101/gr.275509.121 [open access preprint]
- Grist S, Geldert A, Gopal A, Su A, Balch H, Herr A, N95DECON Consortium (Rampazzi S, Smullin S, Starr N, Rempel D, Agarwal P, **Altemose N**, Chen T, Hu G, Tung M, Pillarisetti A, Robinowitz D, Shless J) (2021). Current understanding of ultraviolet-C decontamination of N95 filtering facepiece respirators. *Applied Biosafety*, 26, 90-102. https://doi.org/10.1089/apb.20.0051 [open access]
- Nakatsuka N, Patterson N, Patsopoulos N, De Jager P, **Altemose N**, Tandon A, Beecham AH, McCauley JL, Isobel N, Hauser S, Hafler DA, Oksenberg JR, Reich D (2020). Two genetic variants explain the association of European ancestry with multiple sclerosis risk in African-Americans. *Scientific Reports*, 10, 16902. https://doi.org/10.1038/s41598-020-74035-7 [open access]
- Lai A, **Altemose N**, White JA, Streets AM (2019). On-ratio PDMS bonding for multilayer microfluidic device fabrication. *Journal of Micromechanics and Microengineering*, 29, 107001. https://doi.org/10.1088/1361-6439/ab341e [open-access preprint]
- Williams AL, Genovese G, Dyer T, **Altemose N**, Truax K, Jun G, Patterson N, Myers SR, Curran JE, Duggirala R, Blangero J, Reich D, Przeworski M, on behalf of the T2D-GENES Consortium (2015). Non-crossover gene conversions show strong GC bias and unexpected clustering in humans. *eLife*, 4, e04637. https://doi.org/10.7554/eLife.04637 [open access]
- Hinch AG, **Altemose N**, Noor N, Donnelly P, Myers SR (2014). Recombination in the human pseudoautosomal region PAR1. *PLoS Genetics*, 10, e1004503. https://doi.org/10.1371/journal.pgen.1004503 [open access]
- Miga KH, Newton Y, Jain M, **Altemose N**, Willard HF, Kent WJ (2014). Centromere reference models for human chromosomes X and Y satellite arrays. *Genome Research*, 24, 697–707. https://doi.org/10.1101/gr.159624.113 [open access]
- Genovese G, Handsaker R, Li H, **Altemose N**, Lindgren AM, Chambert K, Pasaniuc B, Price AL, Reich D, Morton CC, Pollak MR, Wilson JG, McCarroll SA (2013). Using population admixture to help complete maps of the human genome. *Nature Genetics*, 45, 406-414. https://doi.org/10.1038/ng.2565 [free to read on PubMed Central]

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PRESENTATIONS

- **New Investigators in Chromatin & Epigenetics Conference**, Attendee and Speaker, Denver, CO **2023**
- **University of Colorado Anschutz Medical Campus**, Invited Dept. Seminar Speaker, Denver, CO **2023**
- **Institut Curie**, Invited Seminar Speaker, Paris, France **2023**
- **NHGRI Genome Technology Development Coordinating Center**, Invited Webinar Speaker **2023**
- **University of Oxford Dept. of Biochemistry**, Invited Dept. Seminar Speaker, Oxford, UK **2023**
- **EMBL Chromatin and Epigenetics Conference**, Selected Speaker, Heidelberg, Germany **2023**
- **UC Berkeley Dept. of Bioengineering**, Invited Dept. Seminar Speaker, Berkeley, CA **2023**
- **University of Chicago Dept. of Genetic Medicine**, Invited Seminar Speaker, Chicago, IL **2023**
- **SMBE Everywhere Virtual Symposium GS7: Beyond the SNP**, Organizer **2023**
- **American Society for Cell Biology Annual Meeting**, Invited Subgroup Speaker, Washington, D.C. **2022**
- **Stuck on Repeat Symposium, Stowers Institute**, Invited Speaker, Kansas City, MO **2022**
- **Stanford Structural Variants and DNA Repeats (SVAR) Conference**, Invited Speaker, Palo Alto, CA **2022**
- **Telomere-to-Telomere Consortium Face-to-Face Conference**, Speaker, Santa Cruz, CA **2022**
- **Gordon Research Conference: Centromere Biology**, Speaker, West Dover, VT **2022**
- **University of Washington Department of Genome Sciences**, Invited Seminar Speaker, Seattle, WA **2022**
- **Bay Area Chromatin Club**, Invited Speaker, Berkeley, CA **2022**
- **Broad Institute Next Generation in Biomedicine Symposium**, Invited Speaker, Cambridge, MA **2021**
- **American Society for Human Genetics Annual Meeting**, Invited Virtual Speaker **2021**
- **Stowers Institute for Medical Research**, Invited Seminar Speaker, Kansas City, MO **2021**
- **Stanford Department of Genetics**, Invited Seminar Speaker, Palo Alto, CA **2021**
- **Bay Area Population Genomics Meeting**, Selected Lightning Talk Speaker, Berkeley, CA **2019**
- **Gordon Research Conf.: The Physics and Chemistry of Microfluidics**, Poster Presenter, Hong Kong **2019**
- **Bioengineering Annual Retreat**, Selected Seminar Speaker, UCSF/UC Berkeley, CA **2019**
- **Center for Theoretical Evolutionary Genomics**, Invited Seminar Speaker, Berkeley, CA **2018**
- **HHMI Scientific Meetings**, Poster Presenter, HHMI Janelia Research Campus, VA **2017/18/21/22**
- **Quantitative Genomics Student Conference**, Seminar Speaker & Best Talk Winner, London, UK **2014**
- **The Biology of Genomes Conference**, Poster Presenter, Cold Spring Harbor Laboratory, NY **2013**
- **Keck Science Department**, Invited Seminar Speaker, Claremont, CA **2012**
- **HHMI Gilliam Fellowship Annual Meetings**, Seminar & Poster Presenter, Bethesda, MD **2011-2019**
- **Harvard Medical School Department of Genetics**, Invited Seminar Speaker by David Reich, MA **2010**

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RESEARCH MENTORING EXPERIENCE

Hugo Mendez, Stanford University, PhD Student **2023-Present**
J. Matthew Franklin, Stanford University, Postdoctoral Scholar **2023-Present**
Anthony Harris, Stanford University, Postdoctoral Scholar **2023-Present**
Danilo Dubocanin, Stanford University, PhD Student **2023-Present**
James "Cy" Chittenden, Stanford University, Research Technician **2023-Present**
Nathan Gamarra, Stanford University, Postdoctoral Scholar **2023-Present**
Emilia Volpe, Stanford University, Visiting PhD Student **2023**
Thomas O'Haren, Emory University, Visiting PhD Student **2023**
Sofia Lundqvist, UC Berkeley, Undergraduate **2022-2023**
Reet Meeshra, UC Berkeley, Undergraduate **2022-2023**
Denise Robles, UC Berkeley, Undergraduate **2021-2023**
Carolina Rios-Martinez, UC Berkeley, Undergraduate **2019-2021**
Romy Mastel, UC Berkeley, Undergraduate **2019-2020**
Andre Lai, UC Berkeley, Undergraduate **2017-2019**
Theresa Meyer, Duke University, High School Student **2010-2011**

TEACHING EXPERIENCE

Guest Lectures:

- Comp Bio Doctoral Seminar taught by Nilah Ioannidis, UC Berkeley, 9 Mar 2023
- Advanced Molecular Biology graduate class taught by Jim Pensavento, St. Mary's College, 1 Nov 2022

Graduate Student Instructor, Bioengineering Department, UC Berkeley **2018**

- I developed and ran discussion sections and office hours and generated/graded problem sets for a hybrid grad/undergrad class on **Biomedical MicroElectroMechanical Systems (BioMEMS) and Medical Devices**, taught by Professor Aaron Streets.
- Overall evaluation score by students: 4.59/5 (vs. dept. avg. 4.08/5); one student's anonymous feedback: "He's always willing to answer questions and is really approachable/accessible. Open to hearing about my ideas, I feel like I'm able to readily bounce ideas off of him, and he gives good feedback. Is very considerate of students' ideas and is engaging."

Graduate Instructor, Zoology Department, University of Oxford **2013-2014**

- I developed and ran discussions, assigned and graded essays, and taught a special lecture on statistical genetics for an undergraduate class on **Human Evolutionary Genetics**, taught by Professors Cristian Capelli and Rosalind Harding.

Undergraduate Teaching Assistant, Computer Science Department, Duke University **2010**

- I graded programming assignments and assisted undergraduate students enrolled in **Computational Genomics**, taught by Professor Alexander Hartemink.

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SERVICE ACTIVITIES

PhD Admissions Committee, Faculty Member, Stanford Genetics	**2023**
LatinX in BME, Member, assisted undergraduates with PhD admissions and fellowship applications, UCB	**2020-2022**
Diversity, Equity, and Inclusion Enhancement Committee, Founding Member, UCB/UCSF Bioengineering	**2017-2020**
PhD Admissions Committee, Full Voting Member, UCB/UCSF Bioengineering	**2018-2020**
Faculty Search DEI Evaluation Committee, Student Chair, UC Berkeley Department of Bioengineering	**2019-2020**
Science Advocacy, Communication, and Outreach Committee, Member, UCB/UCSF Bioengineering PhD	**2019-2020**
Científico Latino Mentorship Program, Mentored student applying to PhD programs, Científico Latino	**2019-2020**
LGBTQ+ STEM Mentorship Program, Mentored two graduate students, Out in STEM	**2019-2020**
Marshall/Rhodes/Mitchell Scholarship Internal Selection Committee, Full Voting Member, UC Berkeley	**2015-2020**
Latino Assoc. of Graduate Students in Engineering and Science, Fellowship App Mentor, UC Berkeley	**2018-2019**
Dean's Society Fundraising Event, Poster Presenter and Student Ambassador, UCB College of Engineering	**2018**
High School Student Visit Day, Lecturer and Tour Guide, Streets Lab, UC Berkeley	**2018**
Bioengineering Departmental Seminar Series, Student Host, UC Berkeley	**2017**
Marshall Scholar Service Project, Chair of Biology/Chemistry Outreach, London, UK	**2013**
Scientifica High School Research Mentorship Program, Co-founder, Duke University	**2008-2011**
LGBTQ Center Advisory Board, Member, Duke University	**2010**

EDITORIAL AND PEER REVIEW SERVICE

I am a Reviewing Editor for *eLife*. I have provided peer review services by request for the following journals:

2023: *Bioinformatics, PLoS Genetics, Science, Molecular Biology & Evolution*

2022: *Molecular Biology & Evolution, HardwareX, Genome Biology, Bioinformatics* (x2)*, BMC Biology*

Web of Science peer review record: https://www.webofscience.com/wos/author/record/EIR-2712-2022

PATENT APPLICATIONS

Altemose N, Maslan A, Streets A (Filed 2022-02-09). Imaging and sequencing protein-dna interactions in single cells using integrated microfluidics. PCT WO2021163059A1.

https://patents.google.com/patent/WO2021163059A1

Altemose N, Maslan A, Streets A, Smith OK, Sundararajan K, Straight AF (Filed 2022-06-02). Methods for measuring protein-dna interactions with long-read dna sequencing. PCT WO2022256469A1.

https://patents.google.com/patent/WO2022256469A1