Nicolas Altemose, DPhil, PhD

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CONTACT INFORMATION

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AFFILIATIONS

Assistant Professor, Dept. of Genetics, School of Medicine, Stanford University **2023-Present**
Investigator, Biohub – San Francisco **2023-Present**
Reviewing Editor, *eLife* **2023-Present**
Member, Bio-X, Stanford University **2023-Present**
Associate Member, Stanford Cancer Institute, Stanford University **2025-Present**
Member, Telomere-to-Telomere Consortium **2020-Present**

DISCIPLINARY FIELDS

Genomics, genetics, molecular & cell biology, computational biology, bioengineering, technology development, epigenetics & chromatin biology

EDUCATIONAL BACKGROUND

University of California, Berkeley & 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

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

HONORS & AWARDS

- **Pew Biomedical Scholar Award** **2024-2028**
- **Chan Zuckerberg Biohub Investigator Award** **2023-2026**
- **Howard Hughes Medical Institute Hanna H. Gray Faculty Fellowship** **2023-2027**
- **UC Berkeley Bioengineering Service Award** **2021**
- **Siebel Scholarship**, supporting PhD work **2020-2021**
- **Howard Hughes Medical Institute Gilliam Fellowship**, supporting PhD work **2013-2019**
- **Marshall Scholarship**, supporting postgraduate study in the United Kingdom **2011-2013**
- **Angier B. Duke Scholarship**, covering full costs of attending Duke University **2007-2011**
- **Edward C. Horn Memorial Prize for Excellence in Biology**, Duke University **2011**
- **Summa Cum Laude & Graduation with Distinction**, Duke University **2011**
- **Barry M. Goldwater Scholarship**, supporting undergraduate research **2010**

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PREVIOUS PROFESSIONAL POSITIONS HELD

Postdoctoral Fellow with Prof. Gary Karpen, PhD, Dept. of Mol. & Cell Biology, UC Berkeley **2021-2023**
- I worked with the T2T Consortium to annotate and characterize centromeric and pericentromeric sequences in the first complete sequence of a human genome.

PhD Student with Assoc. Prof. Aaron Streets, PhD, Dept. of Bioengineering, UC Berkeley **2016-2021**
- I developed microfluidic and genomic tools for mapping protein-DNA interactions in single cells and on single chromatin fibers.

DPhil Student with Prof. Simon Myers, DPhil, Dept. of Statistics, University of Oxford **2011-2015**
- I used experimental & computational methods to characterize PRDM9, a rapidly evolving meiotic recombination protein involved in speciation.

Summer Research Intern with Prof. David Reich, DPhil, Dept. of Genetics, Harvard Medical School **2011**
- I assisted with fine-mapping a multiple sclerosis association signal near the centromere on chromosome 1.

Undergraduate Researcher with Prof. Hunt Willard, PhD, Dept. of Biology, Duke University **2007-2011**
- With Karen H. Miga, PhD, I developed a new computational approach for characterizing satellite DNA.

CURRENT EXTERNAL RESEARCH SUPPORT

- Pew Biomedical Scholar Award | $300,000 for direct costs **2024-2028**
  Developing multi-modal, single-mol. methods for probing chromatin dynamics at human centromeres
- HHMI Hanna H. Gray Faculty Fellowship | $1,080,000 for direct costs **2023-2027**
- CZ Biohub Investigator Award | $1,000,000 for direct costs **2023-2026**
- Stanford Discovery Innovation Fund | $67,000 for direct costs **2026**
- Stanford Undiagnosed Diseases Network Seed Grant | $50,000 for direct costs **2025-2026**
  Combining machine learning with single-molecule sequencing to predict changes to 3D genome structure in mendelian disease patients
- Stanford ChEM-H Nucleus Seed Grant | $50,000 for direct costs **2025-2026**
  High-throughput imaging of repetitive DNA to screen small molecules in live cells
- Stanford c-ShaRP Equipment Grant | $160,000 for direct costs **2024**
  Purchase of an Agilent FemtoPulse system for use in the Protein and Nucleic Acids Core Facility
- Stanford c-ShaRP Core Facility Voucher | $10,000 for direct costs **2024**
  Human Satellite DNA arrays as a novel hub for Hippo transcription factors YAP and TEAD

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SENIOR AUTHOR PUBLICATIONS, ANNOTATED

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

Salinas-Luypaert C, Dubocanin D, Lee RJ, Ruiz LA, Gamba R, Grison M, Velikovsky L, Angrisani A, Scelfo A, Xu Y, Dumont M, Barra V, Wilhelm T, Velasco G, Losito M, Wardenaar R, Francastel C, Foijer F, Kops GJPL, Miga KH, **Altemose N‡**, Fachinetti D‡ (2025). **DNA methylation influences human centromere positioning and function.** *Nature Genetics*, 57, 2509-2521. https://doi.org/10.1038/s41588-025-02324-w [open-access, transparent review]

- One of the major discoveries from the T2T Consortium's assemblies across human centromeric repeat arrays was that centromere proteins only localize to a small region within each array, and this region tends to have low DNA methylation, while the rest of the array has very high DNA methylation. However, it has remained unknown whether this correlation between centromere protein localization and DNA hypomethylation is causal or important for centromere function. To address this, **we specifically perturbed the methylation state of centromeres by targeting them with DNA demethylases and DNA methyltransferases**, then we performed DiMeLo-seq to measure centromere protein localization. We found that hypomethylation of entire centromeric repeat arrays led to increased binding of centromere proteins, while hypermethylation of centromeres led to reduced centromere protein binding. Both perturbations increased chromosomal segregation errors and reduced cell proliferation rate. These results **confirm that DNA methylation causally influences human centromere positioning and function**, providing fundamental insights and raising new questions about the epigenetic maintenance of human centromere identity.

Gamarra N, Chittenden C, Sundararajan K, Schwartz JP, Lundqvist S, Robles D, Dixon-Luinenburg O, Marcus J, Maslan A, Franklin JM, Streets A, Straight AF, **Altemose N** (2025). [Preprint] **DiMeLo-cito: a one-tube protocol for mapping protein-DNA interactions reveals CTCF bookmarking in mitosis**. *bioRxiv*, 2025.03.11.642717. https://doi.org/10.1101/2025.03.11.642717

- Existing protocols for probing specific protein-DNA interactions genome-wide, such as CUT&RUN or DiMeLo-seq, involve lossy wash steps that can compromise sample quality and yield. To address this, **we invented an efficient one-pot protocol for performing DiMeLo-seq, by making key reagent optimizations and by replacing wash steps with affinity-based depletions**. This advance also eliminates the need for a nuclear envelope to contain chromatin during wash steps, enabling us to interrogate chromatin state in mitotic cells, in which the nuclear envelope is disassembled. In doing so, we resolved a disagreement in the field by uncovering **strong evidence that the 3D genome architecture protein CTCF remains bound to DNA in mitosis**.

Dubocanin D, Kalygina A, Franklin JM, Chittenden C, Vollger M, Neph S, Stergachis AB, **Altemose N** (2025). [Preprint] **Integrating single-molecule sequencing and deep learning to predict haplotype-specific 3D chromatin organization in a Mendelian condition.** *bioRxiv,* 2025.02.26.640261. https://doi.org/10.1101/2025.02.26.640261

- Each chromosome must fold up in 3D space to fit inside the cell, and the way it does this can affect how genes are turned on and off, sometimes in ways that lead to inborn diseases. Measuring this 3D organization across the genome with existing DNA sequencing technologies can be challenging and costly, making it difficult to study how changes in 3D organization contribute to disease. To address this, **we developed a machine learning model that can accurately predict 3D genome organization from a single long-read multi-omic sequencing experiment** called Fiber-seq, which is simpler and cheaper to perform on patient samples than the equivalent short-read sequencing experiments. **Our approach will make 3D genome analysis accessible for a wide range of basic research and clinical applications**, accelerating the discovery of genotype-phenotype relationships in human disease.

SENIOR AUTHOR PUBLICATIONS, ANNOTATED (continued)

Franklin JM, Dubocanin D, Chittenden C, Barillas A, Lee RJ, Ghosh RP, Gerton JL, Guan K-L‡, **Altemose N‡** (2024). [Preprint] **Human Satellite 3 DNA encodes megabase-scale transcription factor binding platforms**. *bioRxiv,* 2024.10.22.616524.

https://doi.org/10.1101/2024.10.22.616524

- Among the most mysterious regions of the human genome are highly repetitive satellite DNAs that do not participate in centromere function, including Human Satellite 3 (HSat3), which makes up roughly 2% of the genome and is made up of arrays as large as 30 Mb. To better understand the potential functions of these regions, we performed a systematic computational screen for novel HSat3-binding factors. Our work revealed that HSat3 arrays contain high densities of transcription factor (TF) motifs that are bound by factors related to multiple, highly conserved signaling pathways. By performing careful follow-up experiments on one of these factors, **we discovered a novel and unexpected regulatory axis connecting satellite DNA, the Hippo Pathway, and ribogenesis**. More broadly, this work demonstrates that **satellite DNA arrays can act as enormous transcription factor binding platforms for dozens of different pathways, opening up a new field for further discovery**.

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]

- The classical human satellite DNAs, which constitute roughly 3% of the genome, were among the first human DNA sequences to be isolated and characterized at the dawn of molecular biology, but they were among the last to be included in the human genome reference assembly. This review outlines the history and state of the field of human satellite DNA biology, with a view toward future studies unlocked by the potential of long-read sequencing technologies.

FIRST-AUTHOR PUBLICATIONS, ANNOTATED

‡ indicates co-first authorship

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, which remain challenging to study using short-read DNA sequencing methods. 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.

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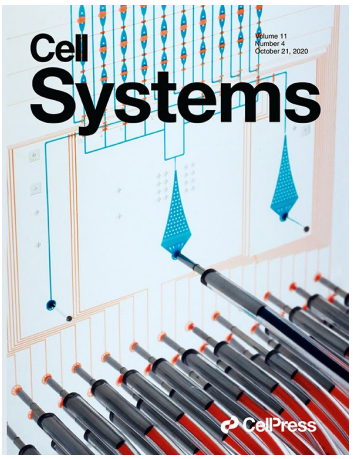
FIRST-AUTHOR PUBLICATIONS, ANNOTATED (continued)

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."

FIRST-AUTHOR 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.

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 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.

ADDITIONAL PUBLICATIONS

- Sohn MH*, Dubocanin D*, Vollger MR, Kwon Y, Minkina A, Munson KM, Hart SFM, Ranchalis JE, Parmalee NL, Sedeno-Cortes AE, Ou J, Au NYT, Bohaczuk S, Carroll B, Frazar CD, Harvey WT, Hoekzema K, Huang MF, Jacques CN, Jensen DM, Kolar JT, Lee R, Lin J, Loy K, Mack T, Mao Y, Pham MM, Ryke E, Smith JD, Sutherlin L, Swanson EG, Weiss JM, SMaHT Assembly Working Group, Carvalho C, Coorens THH, Harris K, Wei CL, Eichler EE, **Altemose N**, Bennett JT, Stergachis AB. [Preprint] A telomere-to-telomere map of somatic mutation burden and functional impact in cancer. *bioRxiv*, 2025.10.10.681725, https://doi.org/10.1101/2025.10.10.681725
- Hansen NF, Dwarshuis N, Ji HJ, Rhie A, Loucks H, Logsdon GA, Vollger MR, Storer JM, Kim J, Adam E, **Altemose N**, Antipov D, Asri M, Barreira S, Bohaczuk SC, Bzikadze AV, Carioscia SA, Carroll A, Chao KH, Chu Y, Das A, Ebert P, English A, Fleharty M, Fleming LE, Formenti G, Guarracino A, Hartley GA, Jenike K, Kalleberg J, Kang Y, King R, Lipovac J, Mastoras M, Mitchell MW, Negi S, Olson ND, Oshima KK, Paulin LF, Pickett BD, Porubsky D, Ranchalis J, Ranjan D, Rautiainen M, Riethman H, Schnabel RD, Sedlazeck FJ, Shafin K, Sikic M, Solar SJ, Sweeten AP, Timp W, Wagner J, Yoo D, Zhou Y, Garrison E, Eichler EE, Schatz MC, Stergachis AB, O'Neill RJ, Miga KH, Salzberg SL, Koren S, Zook JM, Phillippy AM (2025). [Preprint] A complete diploid human genome benchmark for personalized genomics. *bioRxiv*, 2025.09.21.677443. https://doi.org/10.1101/2025.09.21.677443

ADDITIONAL PUBLICATIONS (continued)

- Lu X, Keo V, Cheng I, Xie W, Gritsina G, Wang J, Lu L, Shiau C-K, He Y, Jin Q, Jin P, Yue F, Sanda MG, Corces VG, **Altemose N**, Gao R, Zhao JC, Yu J (2025). NKX2-1 drives neuroendocrine transdifferentiation of prostate cancer via epigenetic and 3D chromatin remodeling. *Nature Genetics*, 57, 1966-1980 https://doi.org/10.1038/s41588-025-02265-4
- Carty BL, Dubocanin D, Murillo-Pineda M, Dumont M, Volpe E, Mikulski P, Humes J, Whittingham O, Fachinetti D, Giunta S, **Altemose N**, Jansen LET (2025). Heterochromatin boundaries maintain centromere position, size and number. *Nature Structural & Molecular Biology*, 33, 220-234, https://doi.org/10.1038/s41594-025-01706-2
- Mahlke MA, Lumerman L, Nath P, Chittenden C, Hoyt S, Koeppel J, Xu Y, Raphael R, Zaffina K, Hook PW, Timp W, Miga KH, Campbell PJ, O'Neill R, **Altemose N**, Nechemia-Arbely Y (2025). [Preprint] Epigenetically dynamic human centromeres are maintained within a stable DNA methylation signature. *bioRxiv*, 2025.02.03.636285, https://doi.org/10.1101/2025.02.03.636285
- Tang J‡, Weiser NE‡, Wang G‡, Chowdhry S, Curtis EJ, Zhao Y, Wong I T-L, Marinov GK, Li R, Hanoian P, Tse E, Hansen R, Plum J, Steffy A, Mulutinovic S, Meyer T, Luebeck J, Wang Y, Zhang S, **Altemose N**, Curtis C, Greenleaf WJ, Bafna V, Benkovic SJ, Pinkerton AB, Kasibhatia S, Hassig CA, Mischel PS, Chang HY (2024). Enhancing transcription–replication conflict targets ecDNA-positive cancers. *Nature*, 635, 210–218, https://doi.org/10.1038/s41586-024-07802-5 [open-access preprint]
- Maslan A, **Altemose N**, Marcus J, Mishra R, Brennan LD, Sundararajan K, Karpen G, Straight AF, Streets A (2024). Mapping protein-DNA interactions with DiMeLo-seq. *Nature Protocols*, https://doi.org/10.1038/s41596-024-01032-9 [open-access preprint]
- 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]

ADDITIONAL PUBLICATIONS (continued)

- 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]
- 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]
- 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]

PATENT APPLICATIONS

Dubocanin D, **Altemose N**. PCT application filed.

Altemose N, Gamarra N, Sundararajan K, Straight AF (PCT filing date 2024-12-05). Dialysis-based method for affinity mapping of chromatin interactions. PCT App. Pub. No. WO2025122719A1. https://patents.google.com/patent/WO2025122719A1

Altemose N, Maslan A, Streets A, Smith OK, Sundararajan K, Straight AF (PCT filing date 2022-06-02). Methods for measuring protein-DNA interactions with long-read DNA sequencing. PCT App. Pub. No. WO2022256469A1. https://patents.google.com/patent/WO2022256469A1

Altemose N, Maslan A, Streets A (PCT filing date 2022-02-09). Imaging and sequencing protein-DNA interactions in single cells using integrated microfluidics. PCT App. Pub. No. WO2021163059A1. https://patents.google.com/patent/WO2021163059A1

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PRESENTATIONS

Invited Talks At Major Conferences:

- **Epicypher Conference on Epigenetics**, Invited Speaker, Cancún, Mexico **2025**
- **Gordon Research Conference: Epigenetics**, Invited Speaker, Barcelona, Spain **2025**
- **EMBL Conference: Gene Regulation One Molecule at a Time**, Invited Speaker, Heidelberg, Germany **2025**
- **Genetics Society of Japan Annual Meeting**, Invited Speaker for International Session, Kochi, Japan **2024**
- **Gordon Research Conference: Centromere Biology**, Invited Speaker, Portland, ME **2022/24**
- **American Society for Cell Biology Annual Meeting**, Invited Subgroup Speaker, Washington, D.C. **2022**
- **American Society for Human Genetics Annual Meeting**, Invited Virtual Speaker **2021**

Other Invited & Selected Talks:

- **UC Berkeley MCB Dept. Marian E. Koshland Seminar Series**, Invited Speaker, Berkeley, CA **2026**
- **Stanford School of Medicine Leadership Retreat**, Invited Faculty Speaker, Redwood City, CA **2026**
- **UC Davis Dept. of Microbiology & Molecular Genetics**, Invited Seminar Speaker, Davis, CA **2025**
- **Karlsruhe Institute of Technology**, Invited Seminar Speaker, Karlsruhe, Germany **2025**
- **Oxford Nanopore What You're Missing Matters Tour Bay Area**, Invited Speaker, San Carlos, CA **2025**
- **Stanford Biosciences PhD Admissions Interview Welcome Breakfast**, Faculty Speaker, Palo Alto, CA **2025**
- **Stanford Out in STEM Queer Perspectives Speaker Series**, Invited Speaker, Palo Alto, CA **2024**
- **New Investigators in Chromatin & Epigenetics Conference**, Attendee and Speaker **2023-25**
- **EMBL Conference: Chromatin & Epigenetics**, Selected Speaker, Heidelberg, Germany **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**
- **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**
- **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**
- **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**
- **Stowers Institute for Medical Research**, Invited Seminar Speaker, Kansas City, MO **2021**

PRESENTATIONS (continued)

Other Presentations:

- **Pew Biomedical Scholars Annual Meeting**, Flash Talk & Poster Presenter, Hamilton, Bermuda **2025**
- **Stanford BASE Seminar Series**, Speaker, Stanford, CA **2025**
- **SMBE Everywhere Virtual Symposium GS7: Beyond the SNP**, Organizer **2023**
- **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 **2017/18/21-25**
- **Quantitative Genomics Student Conference**, Seminar Speaker & Best Talk Winner, London, UK **2014**

RESEARCH MENTORING EXPERIENCE

Diego Pomales-Matos, Stanford University, Genetics PhD Student **2025-Present**
Maria Del Rio Pisula, Stanford University, Biology PhD Student **2025-Present**
Rosa Lee, Stanford University, Genetics PhD Student **2024-Present**
Ashlie Barillas, Stanford University, Genetics PhD Student (co-mentored) **2024-Present**
Robert Hall, Stanford University, Biology PhD Student (co-mentored) **2023-Present**
Anthony Harris, Stanford University, Postdoctoral Scholar **2023-Present**
Danilo Dubocanin, Stanford University, Genetics PhD Student **2023-Present**
Nathan Gamarra, Stanford University, Postdoctoral Scholar **2023-Present**
J. Matthew Franklin, Stanford University, Postdoctoral Scholar **2023-Present**
James "Cy" Chittenden, Stanford University, Research Technician **2023-Present**
Hugo Mendez, Stanford University, Chemistry PhD Student **2023-2025**
Krish Sharma, Stanford University, Undergraduate Student **2025**
Anna Kalygina, University of Oxford, Undergraduate Visiting Research Intern **2024**
Emilia Volpe, Sapienza Uni. Rome, 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**

Nicolas Altemose, DPhil, PhD

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TEACHING EXPERIENCE

Genomics Course Co-Director, Dept. of Genetics, Stanford University **2026-Present**

- Co-direct a core required course for Genetics PhD students and others (35 students)
- Develop course curriculum, deliver lectures, and lead discussion sections

Advanced Genetics Discussion Leader, Dept. of Genetics, Stanford University **2025**

- Led a discussion section for 15 PhD students enrolled in Advanced Genetics, directed by Prof. Doug Vollrath

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

BioMEMS 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.

Human Evolutionary Genetics Graduate Instructor, Zoology Dept., Univ. 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.

OTHER PROFESSIONAL DEVELOPMENT

HHMI Early Career Inclusive Lab Leadership Course **2024-2025**
HHMI Hanna Gray Retreat Workshops: Navigating Change & Uncertainty **2025**
HHMI Hanna Gray Retreat Workshops: Lab Administration **2025**
HHMI Hanna Gray Retreat Workshops: Grant Writing **2024**
HHMI Hanna Gray Retreat Workshops: Mentorship & Communication **2024**
Stanford Faculty Development Workshop: Promoting Agency **2025**
Stanford Faculty Development Workshop: Giving Feedback **2023**

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SERVICE ACTIVITIES

SF Bay Area NextGen Symposium, steering committee member	**2024-Present**
First-year PhD student advisor, Stanford Genetics	**2024-Present**
PhD Student Thesis Committees (7 students outside Altemose Lab), Stanford	**2024-Present**
Genetics Department Annual Retreat Committee, Co-Chair, Stanford Genetics	**2024-Present**
MSTP Admissions Committee, Faculty Member, Stanford School of Medicine	**2024-Present**
PhD Admissions Committee, Faculty Member, Stanford Genetics	**2023-Present**
Stanford Genomics Training Program, Faculty Mentor, Stanford Genetics	**2023-Present**
Stanford LGBTQ+ Postdocs & oSTEM Post-PhD Pathways Career Panel, Panelist	**2025**
HHMI Gilliam Fellowship Competition, application reviewer	**2025**
Stanford C-ShaRP Core Equipment Grant Competition, application reviewer	**2025**
Stanford Henzl-Gabor Postdoc Travel Fellowship, application reviewer	**2025**
PhD Student Defense Committees (6 students outside Altemose Lab), committee member or chair	**2024-2025**
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**

EDITORIAL & PEER REVIEW SERVICE

I am a **Reviewing Editor for *eLife***.

I have provided peer review services by request for the following journals:

> **2022-2025**: *Science*, *Nature (x3)*, *Nature Reviews Genetics*, *Bioinformatics* (x2), *Molecular Biology & Evolution* (x2), *Genome Biology & Evolution, Genome Biology (x2), Nature Communications (x3), HardwareX, BioEssays, BMC Biology, PLoS Genetics*

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