OMB No. 3145-0279 (Expiration Date 10/31/2026)

NIH Biographical Sketch Common Form

Name: Altemose, Nicolas

Persistent Identifier (PID) of the Senior/Key Person: https://orcid.org/0000-0002-7231-6026

Position Title: Assistant Professor

Organization and Location:Stanford University, Palo Alto, CA, United States

PROFESSIONAL PREPARATION

INSTITUTION AND LOCATION	DEGREE	Start Date	Completion Date	FIELD OF STUDY
University of California, Berkeley, Berkeley, California, United States	Postdoctoral Fellow	06/2021	07/2023	Molecular & Cell Biology
University of California, Berkeley and University of California, San Francisco, Berkeley, CA, United States	DOCTOR OF PHILOSOPHY	08/2015	05/2021	Bioengineering
University of Oxford, Oxford, Oxon, United Kingdom	DOCTOR OF PHILOSOPHY	10/2011	02/2016	Statistics
Duke University, Durham, NC, United States	BACHELOR OF SCIENCE	08/2007	05/2011	Biology

Appointments and Positions

2023 - present	Assistant Professor, Stanford University, Palo Alto, CA, United States
2023 - present	Biohub Investigator, Chan Zuckerberg Initiative, San Francisco, California, United States
2023 - present	Reviewing Editor, eLife, San Francisco, California, United States
2023 - present	Member, Stanford Bio-X, Palo Alto, California, United States
2019 - present	Member, Telomere-To-Telomere (T2T) Consortium, San Francisco, California, United States
2023 - 2024	Co-organizer, Society for Molecular Biology & Evolution Virtual Symposium GS7, San Francisco, California, United States
2023 - 2024	Member, Society for Molecular Biology & Evolution, San Francisco, California, United States
2022 - 2023	Member, American Society for Cell Biology, San Francisco, California, United States
2021 - 2023	Postdoctoral Fellow with Dr. Gary Karpen , UC Berkeley, Berkeley, California, United States
2021 - 2022	Member, American Society for Human Genetics, San Francisco, California, United States
2015 - 2021	PhD Student with Dr. Aaron Streets, UC Berkeley, Berkeley, California, United States
2011 - 2015	DPhil Student with Dr. Simon Myers , University of Oxford, Oxford, Not Applicable, N/A, United Kingdom
2011 - 2011	Summer Research Student with Dr. David Reich, Harvard Medical School, Boston, Massachusetts, United States
2007 - 2011	Undergraduate Research Student with Dr. Hunt Willard & Dr. Karen Miga, Duke University, Durham, North Carolina, United States

Products

Products Closely Related to the Proposed Project

1. Altemose N, Maslan A, Smith OK, Sundararajan K, Brown RR, Mishra R, Detweiler AM, Neff N, Miga KH, Straight AF, Streets A. DiMeLo-seq: a long-read, single-molecule method for mapping protein-DNA interactions genome wide. Nat Methods. 2022 Jun;19(6):711-723. PubMed Central PMCID: PMC9189060.
2. 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. DiMeLo-cito: a one-tube protocol for mapping protein-DNA interactions reveals CTCF bookmarking in mitosis. bioRxiv. 2025 Mar 14; PubMed Central PMCID: PMC11952428.
3. Salinas-Luypaert C, Dubocanin D, Lee RJ, Andrade Ruiz L, 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. DNA methylation influences human centromere positioning and function. Nat Genet. 2025 Oct;57(10):2509-2521. PubMed Central PMCID: PMC12513831.

4. Franklin JM, Dubocanin D, Chittenden C, Barillas A, Lee RJ, Ghosh RP, Gerton JL, Guan KL, Altemose N. Human Satellite 3 DNA encodes megabase-scale transcription factor binding platforms. bioRxiv. 2025 Mar 21; PubMed Central PMCID: PMC11526998.
5. Dubocanin D, Kalygina A, Franklin JM, Chittenden C, Vollger MR, Neph S, Stergachis AB, Altemose N. Integrating Single-Molecule Sequencing and Deep Learning to Predict Haplotype-Specific 3D Chromatin Organization in a Mendelian Condition. bioRxiv. 2025 Mar 20; PubMed Central PMCID: PMC11957061.

Other Significant Products Highlighting Contributions to Science

1. Altemose N, Logsdon GA, Bzikadze AV, Sidhwani P, Langley SA, Caldas GV, Hoyt SJ, Uralsky L, Ryabov FD, Shew CJ, Sauria MEG, Borchers M, Gershman A, Mikheenko A, Shepelev VA, Dvorkina T, Kunyavskaya O, Vollger MR, Rhie A, McCartney AM, Asri M, Lorig-Roach R, Shafin K, Lucas JK, Aganezov S, Olson D, de Lima LG, Potapova T, Hartley GA, Haukness M, Kerpedjiev P, Gusev F, Tigyi K, Brooks S, Young A, Nurk S, Koren S, Salama SR, Paten B, Rogaev EI, Streets A, Karpen GH, Dernburg AF, Sullivan BA, Straight AF, Wheeler TJ, Gerton JL, Eichler EE, Phillippy AM, Timp W, Dennis MY, O'Neill RJ, Zook JM, Schatz MC, Pevzner PA, Diekhans M, Langley CH, Alexandrov IA, Miga KH. Complete genomic and epigenetic maps of human centromeres. Science. 2022 Apr;376(6588):eabl4178. PubMed Central PMCID: PMC9233505.
2. Altemose N, Maslan A, Rios-Martinez C, Lai A, White JA, Streets A. µDamID: A Microfluidic Approach for Joint Imaging and Sequencing of Protein-DNA Interactions in Single Cells. Cell Syst. 2020 Oct 21;11(4):354-366.e9. PubMed Central PMCID: PMC7588622.
3. Li R, Bitoun E, Altemose N, Davies RW, Davies B, Myers SR. A high-resolution map of non-crossover events reveals impacts of genetic diversity on mammalian meiotic recombination. Nat Commun. 2019 Aug 29;10(1):3900. PubMed Central PMCID: PMC6715734.
4. Altemose N, Noor N, Bitoun E, Tumian A, Imbeault M, Chapman JR, Aricescu AR, Myers SR. A map of human PRDM9 binding provides evidence for novel behaviors of PRDM9 and other zinc-finger proteins in meiosis. Elife. 2017 Oct 26;6 PubMed Central PMCID: PMC5705219.
5. Altemose N, Miga KH, Maggioni M, Willard HF. Genomic characterization of large heterochromatic gaps in the human genome assembly. PLoS Comput Biol. 2014 May;10(5):e1003628. PubMed Central PMCID: PMC4022460.

Certification:

I certify that the information provided is current, accurate, and complete. This includes but is not limited to information related to domestic and foreign appointments and positions.

I also certify that, at the time of submission, I am not a party to a malign foreign talent recruitment program.

Misrepresentations and/or omissions may be subject to prosecution and liability pursuant to, but not limited to, 18 U.S.C. §§ 287, 1001, 1031 and 31 U.S.C. §§ 3729-3733 and 3802.

Certified by Altemose, Nicolas in SciENcv on 2026-02-11 21:18:25

NIH BIOGRAPHICAL SKETCH SUPPLEMENT

Name: Altemose, Nicolas

Persistent Identifier (PID) of the Senior/Key Person: https://orcid.org/0000-0002-7231-6026

Position Title: Assistant Professor

Organization and Location: Stanford University, Palo Alto, CA, United States

Personal Statement

I am an Assistant Professor at Stanford University in the Department of Genetics. My lab develops single- molecule genomic methods for studying chromatin organization and dynamics, including in highly challenging, repetitive regions of the genome such as pericentromeric satellite DNA repeats. During my training, as part of the Telomere-to-Telomere Consortium, I helped to validate and annotate the first truly complete human genome sequence, which revealed the detailed structure of all pericentromeric sequences in a human genome for the first time. To further extend our ability to study these regions, I co- invented DiMeLo-seq, a versatile long-read sequencing-based method for mapping single-molecule protein- DNA interactions genome-wide. My current research builds on my previous expertise and pushes the limits of single-molecule epigenomics, unlocking new ways of studying how proteins read, replicate, repair, regulate, and recombine DNA. During my training, I equipped myself with deep expertise in both computational and experimental biology, even going as far as completing two PhDs. This multidisciplinary expertise, along with my track record of creative and collaborative research and my numerous experiences mentoring others, makes me perfectly suited to lead an ambitious research program while providing excellent training to students and postdocs. Since I started my lab in 2023, we have released 4 manuscripts, describing how we: 1. Used DiMeLo-seq and genetic perturbations to reveal how DNA methylation influences human centromere function and localization [Salinas-Luypaert et al. Nature Genetics 2025, co-corresponding], 2. Discovered that a set of mysterious pericentromeric human satellite DNA repeats can recruit transcription factors that regulate the transcription of ribosomal RNA genes [Franklin et al. bioRxiv 2024, co-corresponding], 3. Engineered improved long-read epigenomic sequencing technologies that require 90% lower input [Gamarra et al. bioRxiv 2025, corresponding], and 4. Created a deep learning model that predicts 3D genome structure from long-read epigenomic data [Dubocanin et al. bioRxiv 2025, corresponding].

Honors

2024 - 2028	Pew Biomedical Scholar, Pew Scholars Program
2021 - 2027	HHMI Hanna H. Gray Faculty Fellow, Howard Hughes Medical Institute
2021 - 2021	UC Berkeley Bioengineering Service Award, UC Berkeley
2020 - 2021	Siebel Scholar, Siebel Scholars Foundation
2011 - 2019	HHMI Gilliam Fellowship, Howard Hughes Medical Institute
2011 - 2013	Marshall Scholarship, Marshall Aid Commemoration Committee
2011 - 2011	Summa Cum Laude, Duke University
2010 - 2010	Barry M. Goldwater Scholarship, Goldwater Scholarship Foundation
2007 - 2011	Angier B. Duke Scholarship, Duke University

Contributions to Science

1. Engineered single-cell and single-molecule technologies for mapping protein-DNA interactions: My work as a technology developer has produced new experimental methods for measuring protein-DNA interactions in single cells and along single DNA molecules. During my graduate work, I designed an integrated microfluidic platform (μDamID) that combines high-resolution imaging and sequencing information in the same single cells, allowing for the joint analysis of the nuclear localization, sequence identity, and variability of protein-DNA interactions in single cells (Altemose et al. Cell Systems 2020). Additionally, I co-invented a new method called DiMeLo-seq (Directed Methylation with Long-read sequencing), which uses cutting-edge DNA sequencing technologies to map protein-DNA interactions on long, single molecules of DNA, which retain endogenous DNA methylation marks and which can be mapped to highly repetitive regions of the genome (Altemose et al. Nature Methods 2022). Aaron Straight's lab at Stanford had been independently working on a similar technique, so we decided to join forces in a full collaboration to do the best possible science. In my lab at Stanford, we have recently released a fully re-engineered version of the DiMeLo-seq protocol that greatly increases the efficiency and flexibility of the method,

reducing the input material requirements by 90% (Gamarra et al. bioRxiv 2025, corresponding). Recently, my lab helped Howard Chang's and Paul Mischel's groups to apply one of our novel single-molecule epigenomic methods to study chromatin structure and heterogeneity on extrachromosomal circular DNAs in colorectal cancer cell lines (see full bibliography). My lab also assisted another group in studying the molecular origins of prostate cancer using our technology (see full bibliography). Together, these new methods expand the toolkit available to researchers to study the fundamental processes that regulate the genome.

2. Revealed the genomic organization of human centromeres and pericentromeres: My work has helped to improve our understanding of the genomic organization and variation of human centromeric and pericentromeric DNA sequences. As an undergraduate researcher, I carried out the first comprehensive genome-wide study of Human Satellites 2 and 3, which are poorly understood repetitive sequences that comprise roughly 1.4% of the human genome and correspond to the largest gaps in the hg38 reference sequence (Altemose et al. PLoS Computational Biology 2014). More recently, during my postdoc, I led the Telomere-to-Telomere (T2T) Consortium's computational efforts to characterize human centromeric and pericentromeric satellite sequences in the newly completed T2T genome assembly (Altemose et al. Science 2022). Using this assembly, we discovered large-scale patterns of centromere evolution and variation, we examined the relationship between centromeric sequences and centromere function, and we generated an encyclopedic resource for future studies of human centromeres (Altemose et al. Nature Methods 2022).
3. Probed the functional and epigenetic properties of highly repetitive DNA in the human genome: Recently, my lab at Stanford released its first preprint, in which we describe the discovery of a novel regulatory axis connecting satellite DNA, the Hippo pathway, and rDNA transcription, in collaboration with Hippo pathway expert Kun-Liang Guan (Franklin et al. bioRxiv 2024). We also had our first manuscript accepted, in which we describe the effects of perturbing DNA methylation on human centromere protein localization, in collaboration with centromere expert Daniele Fachinetti (Salinas-Luypaert et al. Nature Genetics 2025, co-corresponding). These studies shed important new light on these challenging regions of the human genome. My lab has also assisted others in exploring centromere biology using DiMeLo-seq (see full bibliography).
4. Developed a deep learning model to predict 3D genome structure from long-read epigenomic data: In my lab at Stanford, we have recently developed a deep learning method that enables accurate prediction of haplotype-specific 3D genome architecture from a single long-read epigenomic sequencing experiment, and we applied it to study how 3D genome architecture becomes altered around the breakpoint of a de novo genomic rearrangement (Dubocanin et al. bioRxiv 2025). This approach will make 3D genome analysis more accessible for a wide range of applications and help to uncover the effects of structural variation on 3D genome architecture.
5. Characterized protein-DNA interactions that underlie meiotic recombination and speciation: My contributions have also shed light on the molecular mechanisms underlying the initiation of mammalian meiotic recombination and its relationship to hybrid infertility. During my first PhD, I performed and analyzed chromatin immunoprecipitation experiments to build protein-DNA interaction maps for PRDM9, a protein that binds DNA to initiate the process of meiotic recombination in humans and mice. This body of work proposed the first molecular mechanism of speciation in any vertebrate (see full bibliography), produced the highest-resolution map of mammalian non-crossover recombination ever (Li et al. Nature Communications 2019, co-first author), and led to several fundamental discoveries about the behavior and function of PRDM9 in meiosis (Altemose et al. eLife 2017). During this work, I developed a new ChIP-seq peak-calling algorithm and a new ab initio motif-finding algorithm, both tailored to the specific datasets and questions we were targeting. Our high-resolution PRDM9 binding and recombination maps, biological insights, and analytical methods have proven useful for other groups.

Certification:

I certify that the information provided is current, accurate, and complete. This includes but is not limited to information related to domestic and foreign appointments and positions.

I also certify that, at the time of submission, I am not a party to a malign foreign talent recruitment program.

Misrepresentations and/or omissions may be subject to prosecution and liability pursuant to, but not limited to, 18 U.S.C. §§ 287, 1001, 1031 and 31 U.S.C. §§ 3729-3733 and 3802.

Certified by Altemose, Nicolas in SciENcv on 2026-02-1121:18:25