




Nicolas Altemose

Assistant Professor of Genetics

 NIH Biosketch available Online

 Curriculum Vitae available Online

CONTACT INFORMATION

• Administrative Contact

Chris Barone - Administrative Associate Level 3

Email cjbarone@stanford.edu

Bio

BIO

Nicolas Altemose is an Assistant Professor of Genetics and a Chan Zuckerberg Biohub Investigator. The Altemose Lab develops new experimental and analytical tools to study how chromatin proteins organize and regulate complex regions of the human genome. For more information see altemoselab.stanford.edu

ACADEMIC APPOINTMENTS

- Assistant Professor, Genetics
- Member, Bio-X

HONORS AND AWARDS

- Pew Biomedical Scholar Award, Pew Trusts (2024-2028)
- CZ Biohub Investigator Award, Chan Zuckerberg Biohub (2023-2028)
- HHMI Hanna H. Gray Fellowship, Howard Hughes Medical Institute (2020-2027)
- Siebel Scholarship, Siebel Scholars Foundation (2020)
- HHMI Gilliam Fellowship, Howard Hughes Medical Institute (2013-2018)
- Marshall Scholarship, UK Marshall Aid Commemoration Commission (2011-2013)
- Angier B. Duke Scholarship, Duke University (2007-2011)

PROFESSIONAL EDUCATION

- Postdoctoral Fellow, UC Berkeley , Molecular & Cell Biology
- PhD, UC Berkeley and UCSF , Bioengineering (2021)
- DPhil, University of Oxford , Statistics (2016)
- BS, Duke University , Biology (2011)

LINKS

- Altemose Lab Website: <https://altemoselab.stanford.edu>

Research & Scholarship

CURRENT RESEARCH AND SCHOLARLY INTERESTS

The Altemose Lab develops new experimental and analytical tools to study how chromatin proteins organize and regulate complex regions of the human genome.

Teaching

COURSES

2025-26

- Genomics: GENE 211 (Win)

STANFORD ADVISEES

Doctoral Dissertation Reader (AC)

Lynette Chan, Jane Cook, Ezekiel Delgado, Angela Hickey, Geo Janer Carattini, Carolina Rios-Martinez

Postdoctoral Faculty Sponsor

Nathan Gamarra, Anthony Harris

Doctoral Dissertation Advisor (AC)

Maria Del Rio Pisula, Danilo Dubocanin, Rosa Lee, Hugo Mendez, Diego Pomales-Matos

Doctoral Dissertation Co-Advisor (AC)

Ashlie Barillas, Robert Hall

GRADUATE AND FELLOWSHIP PROGRAM AFFILIATIONS

- Genetics (Phd Program)

Publications

PUBLICATIONS

- **DNA methylation influences human centromere positioning and function.** *Nature genetics*
Salinas-Luypaert, C., Dubocanin, D., Lee, R. J., Andrade Ruiz, L., Gamba, R., Grison, M., Velikovskiy, L., Angrisani, A., Scelfo, A., Xu, Y., Dumont, M., Barra, V., Wilhelm, et al
2025
- **Human Satellite 3 DNA encodes megabase-scale transcription factor binding platforms.** *bioRxiv : the preprint server for biology*
Franklin, J. M., Dubocanin, D., Chittenden, C., Barillas, A., Lee, R. J., Ghosh, R. P., Gerton, J. L., Guan, K. L., Altemose, N.
2025
- **Integrating Single-Molecule Sequencing and Deep Learning to Predict Haplotype-Specific 3D Chromatin Organization in a Mendelian Condition.** *bioRxiv : the preprint server for biology*
Dubocanin, D., Kalygina, A., Franklin, J. M., Chittenden, C., Vollger, M. R., Neph, S., Stergachis, A. B., Altemose, N.
2025
- **DiMeLo-cito: a one-tube protocol for mapping protein-DNA interactions reveals CTCF bookmarking in mitosis.** *bioRxiv : the preprint server for biology*
Gamarra, N., Chittenden, C., Sundararajan, K., Schwartz, J. P., Lundqvist, S., Robles, D., Dixon-Luinenburg, O., Marcus, J., Maslan, A., Franklin, J. M., Streets, A., Straight, A. F., Altemose, et al
2025
- **A classical revival: Human satellite DNAs enter the genomics era** *SEMINARS IN CELL & DEVELOPMENTAL BIOLOGY*

- Altemose, N.
2022; 128: 2-14
- **DiMeLo-seq: a long-read, single-molecule method for mapping protein-DNA interactions genome wide.** *Nature methods*
Altemose, N., Maslan, A., Smith, O. K., Sundararajan, K., Brown, R. R., Mishra, R., Detweiler, A. M., Neff, N., Miga, K. H., Straight, A. F., Streets, A.
2022
 - **Complete genomic and epigenetic maps of human centromeres.** *Science (New York, N.Y.)*
Altemose, N., Logsdon, G. A., Bzikadze, A. V., Sidhwani, P., Langley, S. A., Caldas, G. V., Hoyt, S. J., Uralsky, L., Ryabov, F. D., Shew, C. J., Sauria, M. E., Borchers, M., Gershman, et al
2022; 376 (6588): eabl4178
 - **Genomic Characterization of Large Heterochromatic Gaps in the Human Genome Assembly** *PLOS COMPUTATIONAL BIOLOGY*
Altemose, N., Miga, K. H., Maggioni, M., Willard, H. F.
2014; 10 (5): e1003628
 - **Heterochromatin boundaries maintain centromere position, size and number.** *Nature structural & molecular biology*
Carty, B. L., Dubocanin, D., Murillo-Pineda, M., Dumont, M., Volpe, E., Mikulski, P., Humes, J., Whittingham, O., Fachinetti, D., Giunta, S., Altemose, N., Jansen, L. E.
2025
 - **Integrated analysis of multimodal long-read epigenetic assays.** *bioRxiv : the preprint server for biology*
Marcus, J., Dixon-Luinenburg, O., Gamarra, N., Schwartz, J. P., Rozenwald, M., Maslan, A., Urnov, F. D., Straight, A. F., Altemose, N., Ioannidis, N. M., Streets, A.
2025
 - **A telomere-to-telomere map of somatic mutation burden and functional impact in cancer.** *bioRxiv : the preprint server for biology*
Sohn, M. H., Dubocanin, D., Vollger, M. R., Kwon, Y., Minkina, A., Munson, K. M., Hart, S. F., Ranchalis, J. E., Parmalee, N. L., Sedeño-Cortés, A. E., Ou, J., Au, N. Y., Bohaczuk, et al
2025
 - **A complete diploid human genome benchmark for personalized genomics.** *bioRxiv : the preprint server for biology*
Hansen, N. F., Dwarshuis, N., Ji, H. J., Rhie, A., Loucks, H., Logsdon, G. A., Vollger, M. R., Storer, J. M., Kim, J., Adam, E., Altemose, N., Antipov, D., Asri, et al
2025
 - **NKX2-1 drives neuroendocrine transdifferentiation of prostate cancer via epigenetic and 3D chromatin remodeling.** *Nature genetics*
Lu, X., Keo, V., Cheng, I., Xie, W., Gritsina, G., Wang, J., Lu, L., Shiau, C. K., He, Y., Jin, Q., Jin, P., Sanda, M. G., Corces, et al
2025
 - **Enhancing transcription-replication conflict targets ecDNA-positive cancers.** *Nature*
Tang, J., Weiser, N. E., Wang, G., Chowdhry, S., Curtis, E. J., Zhao, Y., Wong, I. T., Marinov, G. K., Li, R., Hanoian, P., Tse, E., Mojica, S. G., Hansen, et al
2024; 635 (8037): 210-218
 - **Mapping protein-DNA interactions with DiMeLo-seq.** *Nature protocols*
Maslan, A., Altemose, N., Marcus, J., Mishra, R., Brennan, L. D., Sundararajan, K., Karpen, G., Straight, A. F., Streets, A.
2024
 - **The complete sequence of a human Y chromosome** *NATURE*
Rhie, A., Nurk, S., Cechova, M., Hoyt, S. J., Taylor, D. J., Altemose, N., Hook, P. W., Koren, S., Rautiainen, M., Alexandrov, I. A., Allen, J., Asri, M., Bzikadze, et al
2023; 621 (7978): 344-354
 - **The complete sequence of a human genome** *SCIENCE*
Nurk, S., Koren, S., Rhie, A., Rautiainen, M., Bzikadze, A., Mikheenko, A., Vollger, M. R., Altemose, N., Uralsky, L., Gershman, A., Aganezov, S., Hoyt, S. J., Diekhans, et al
2022; 376 (6588): 44-+
 - **From telomere to telomere: The transcriptional and epigenetic state of human repeat elements.** *Science (New York, N.Y.)*

- Hoyt, S. J., Storer, J. M., Hartley, G. A., Grady, P. G., Gershman, A., de Lima, L. G., Limouse, C., Halabian, R., Wojenski, L., Rodriguez, M., Altemose, N., Rhie, A., Core, et al
2022; 376 (6588): eabk3112
- **Epigenetic patterns in a complete human genome** *SCIENCE*
Gershman, A., Sauria, M. E. G., Guitart, X., Vollger, M. R., Hook, P. W., Hoyt, S. J., Jain, M., Shumate, A., Razaghi, R., Koren, S., Altemose, N., Caldas, G., Logsdon, et al
2022; 376 (6588): 58-+
 - **Characterization of transcript enrichment and detection bias in single-nucleus RNA-seq for mapping of distinct human adipocyte lineages** *GENOME RESEARCH*
Gupta, A., Shamsi, F., Altemose, N., Dorlhiac, G. F., Cypess, A. M., White, A. P., Yosef, N., Patti, M., Tseng, Y., Streets, A.
2022; 32 (2): 242-257
 - **mu DamID: A Microfluidic Approach for Joint Imaging and Sequencing of Protein-DNA Interactions in Single Cells** *CELL SYSTEMS*
Altemose, N., Maslan, A., Rios-Martinez, C., Lai, A., White, J. A., Streets, A.
2020; 11 (4): 354-+
 - **Two genetic variants explain the association of European ancestry with multiple sclerosis risk in African-Americans** *SCIENTIFIC REPORTS*
Nakatsuka, N., Patterson, N., Patsopoulos, N. A., Altemose, N., Tandon, A., Beecham, A. H., McCauley, J. L., Isobe, N., Hauser, S., De Jager, P. L., Hafler, D. A., Oksenberg, J. R., Reich, et al
2020; 10 (1): 16902
 - **On-ratio PDMS bonding for multilayer microfluidic device fabrication** *JOURNAL OF MICROMECHANICS AND MICROENGINEERING*
Lai, A., Altemose, N., White, J. A., Streets, A. M.
2019; 29 (10)
 - **A high-resolution map of non-crossover events reveals impacts of genetic diversity on mammalian meiotic recombination** *NATURE COMMUNICATIONS*
Li, R., Bitoun, E., Altemose, N., Davies, R. W., Davies, B., Myers, S. R.
2019; 10: 3900
 - **A map of human PRDM9 binding provides evidence for novel behaviors of PRDM9 and other zinc-finger proteins in meiosis** *ELIFE*
Altemose, N., Noor, N., Bitoun, E., Tumian, A., Imbeault, M., Chapman, J., Aricescu, A., Myers, S. R.
2017; 6
 - **Re-engineering the zinc fingers of PRDM9 reverses hybrid sterility in mice** *NATURE*
Davies, B., Hatton, E., Altemose, N., Hussin, J. G., Pratto, F., Zhang, G., Hinch, A., Moralli, D., Biggs, D., Diaz, R., Preece, C., Li, R., Bitoun, et al
2016; 530 (7589): 171-+
 - **Non-crossover gene conversions show strong GC bias and unexpected clustering in humans** *ELIFE*
Williams, A. L., Genovese, G., Dyer, T., Altemose, N., Truax, K., Jun, G., Patterson, N., Myers, S. R., Curran, J. E., Duggirala, R., Blangero, J., Reich, D., Przeworski, et al
2015; 4
 - **Recombination in the Human Pseudoautosomal Region PAR1** *PLOS GENETICS*
Hinch, A. G., Altemose, N., Noor, N., Donnelly, P., Myers, S. R.
2014; 10 (7): e1004503
 - **Centromere reference models for human chromosomes X and Y satellite arrays** *GENOME RESEARCH*
Miga, K. H., Newton, Y., Jain, M., Altemose, N., Willard, H. F., Kent, W.
2014; 24 (4): 697-707
 - **Using population admixture to help complete maps of the human genome** *NATURE GENETICS*
Genovese, G., Handsaker, R. E., Li, H., Altemose, N., Lindgren, A. M., Chambert, K., Pasaniuc, B., Price, A. L., Reich, D., Morton, C. C., Pollak, M. R., Wilson, J. G., McCarroll, et al
2013; 45 (4): 406-414