Stanford

Nicolas Altemose

Assistant Professor of Genetics

Curriculum Vitae available Online

CONTACT INFORMATION

- **Administrative Contact**

  Chris Barone - Administrative Associate Level 3

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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

- 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

STANFORD ADVISEES

Doctoral Dissertation Reader (AC)

Rachel Ungar

Postdoctoral Faculty Sponsor

Matt Franklin, Nathan Gamarra, Anthony Harris

Doctoral Dissertation Advisor (AC)

Danilo Dubocanin

GRADUATE AND FELLOWSHIP PROGRAM AFFILIATIONS

- Genetics (Phd Program)

Publications

PUBLICATIONS

- **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
- **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-+
- **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
- **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
- **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. 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

- **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)

- **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