

# Nicolas Altemose

## List of Publications by Year in descending order

Source: <https://exaly.com/author-pdf/5856440/publications.pdf>

Version: 2024-02-01

18  
papers

2,902  
citations

516710

16  
h-index

839539

18  
g-index

37  
all docs

37  
docs citations

37  
times ranked

2527  
citing authors

| #  | ARTICLE  | IF   | CITATIONS |
|----|--|------|-----------|
| 1  | The complete sequence of a human genome. <i>Science</i> , 2022, 376, 44-53.  | 12.6 | 1,222     |
| 2  | Centromere reference models for human chromosomes X and Y satellite arrays. <i>Genome Research</i> , 2014, 24, 697-707.  | 5.5  | 210       |
| 3  | Complete genomic and epigenetic maps of human centromeres. <i>Science</i> , 2022, 376, eab14178.   | 12.6 | 204       |
| 4  | Re-engineering the zinc fingers of PRDM9 reverses hybrid sterility in mice. <i>Nature</i> , 2016, 530, 171-176.  | 27.8 | 194       |
| 5  | From telomere to telomere: The transcriptional and epigenetic state of human repeat elements. <i>Science</i> , 2022, 376, eabk3112.  | 12.6 | 146       |
| 6  | Epigenetic patterns in a complete human genome. <i>Science</i> , 2022, 376, eabj5089.  | 12.6 | 118       |
| 7  | Genomic Characterization of Large Heterochromatic Gaps in the Human Genome Assembly. <i>PLoS Computational Biology</i> , 2014, 10, e1003628.   | 3.2  | 99        |
| 8  | Non-crossover gene conversions show strong GC bias and unexpected clustering in humans. <i>ELife</i> , 2015, 4, .  | 6.0  | 95        |
| 9  | A map of human PRDM9 binding provides evidence for novel behaviors of PRDM9 and other zinc-finger proteins in meiosis. <i>ELife</i> , 2017, 6, .                                     | 6.0  | 80        |
| 10 | Recombination in the Human Pseudoautosomal Region PAR1. <i>PLoS Genetics</i> , 2014, 10, e1004503.   | 3.5  | 66        |
| 11 | A high-resolution map of non-crossover events reveals impacts of genetic diversity on mammalian meiotic recombination. <i>Nature Communications</i> , 2019, 10, 3900.                | 12.8 | 66        |
| 12 | Using population admixture to help complete maps of the human genome. <i>Nature Genetics</i> , 2013, 45, 406-414.  | 21.4 | 61        |
| 13 | DiMeLo-seq: a long-read, single-molecule method for mapping protein-DNA interactions genome wide. <i>Nature Methods</i> , 2022, 19, 711-723.   | 19.0 | 45        |
| 14 | Characterization of transcript enrichment and detection bias in single-nucleus RNA-seq for mapping of distinct human adipocyte lineages. <i>Genome Research</i> , 2022, 32, 242-257. | 5.5  | 39        |
| 15 | A classical revival: Human satellite DNAs enter the genomics era. <i>Seminars in Cell and Developmental Biology</i> , 2022, 128, 2-14.   | 5.0  | 23        |
| 16 | On-ratio PDMS bonding for multilayer microfluidic device fabrication. <i>Journal of Micromechanics and Microengineering</i> , 2019, 29, 107001.                                      | 2.6  | 21        |
| 17 | 1/4DamID: A Microfluidic Approach for Joint Imaging and Sequencing of Protein-DNA Interactions in Single Cells. <i>Cell Systems</i> , 2020, 11, 354-366.e9.                          | 6.2  | 15        |
| 18 | Two genetic variants explain the association of European ancestry with multiple sclerosis risk in African-Americans. <i>Scientific Reports</i> , 2020, 10, 16902.                    | 3.3  | 10        |