Nicolas Altemose

List of Publications by Year
in descending order

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	Characterization of transcript enrichment and detection bias in single-nucleus RNA-seq for mapping of distinct human adipocyte lineages. Genome Research, 2022, 32, 242-257.	5.5	39
2	Epigenetic patterns in a complete human genome. Science, 2022, 376, eabj5089.	12.6	118
3	Complete genomic and epigenetic maps of human centromeres. Science, 2022, 376, eabl4178.	12.6	204
4	From telomere to telomere: The transcriptional and epigenetic state of human repeat elements. Science, 2022, 376, eabk3112.	12.6	146
5	DiMeLo-seq: a long-read, single-molecule method for mapping protein–DNA interactions genome wide. Nature Methods, 2022, 19, 711-723.	19.0	45
6	The complete sequence of a human genome. Science, 2022, 376, 44-53.	12.6	1,222
7	A classical revival: Human satellite DNAs enter the genomics era. Seminars in Cell and Developmental Biology, 2022, 128, 2-14.	5.0	23
8	Two genetic variants explain the association of European ancestry with multiple sclerosis risk in African-Americans. Scientific Reports, 2020, 10, 16902.	3.3	10
9	μDamID: A Microfluidic Approach for Joint Imaging and Sequencing of Protein-DNA Interactions in Single Cells. Cell Systems, 2020, 11, 354-366.e9.	6.2	15
10	On-ratio PDMS bonding for multilayer microfluidic device fabrication. Journal of Micromechanics and Microengineering, 2019, 29, 107001.	2.6	21
11	A high-resolution map of non-crossover events reveals impacts of genetic diversity on mammalian meiotic recombination. Nature Communications, 2019, 10, 3900.	12.8	66
12	A map of human PRDM9 binding provides evidence for novel behaviors of PRDM9 and other zinc-finger proteins in meiosis. ELife, 2017, 6, .	6.0	80
13	Re-engineering the zinc fingers of PRDM9 reverses hybrid sterility in mice. Nature, 2016, 530, 171-176.	27.8	194
14	Non-crossover gene conversions show strong GC bias and unexpected clustering in humans. ELife, 2015, 4, .	6.0	95
15	Recombination in the Human Pseudoautosomal Region PAR1. PLoS Genetics, 2014, 10, e1004503.	3.5	66
16	Genomic Characterization of Large Heterochromatic Gaps in the Human Genome Assembly. PLoS Computational Biology, 2014, 10, e1003628.	3.2	99
17	Centromere reference models for human chromosomes X and Y satellite arrays. Genome Research, 2014, 24, 697-707.	5.5	210
18	Using population admixture to help complete maps of the human genome. Nature Genetics, 2013, 45, 406-414.	21.4	61