Michael C Zody

List of Publications by Year
in descending order

17	24,349	566801 15	887659 17
papers	citations	h-index	g-index

19	19	19	30053
all docs	docs citations	times ranked	citing authors

#	Article	IF	Citations
1	Initial sequencing and analysis of the human genome. Nature, 2001, 409, 860-921.	13.7	21,074
2	Sequencing of 53,831 diverse genomes from the NHLBI TOPMed Program. Nature, 2021, 590, 290-299.	13.7	1,069
3	Haplotype-resolved diverse human genomes and integrated analysis of structural variation. Science, 2021, 372, .	6.0	358
4	Genomic Patterns of De Novo Mutation in Simplex Autism. Cell, 2017, 171, 710-722.e12.	13.5	308
5	Genome Sequencing of Autism-Affected Families Reveals Disruption of Putative Noncoding Regulatory DNA. American Journal of Human Genetics, 2016, 98, 58-74.	2.6	248
6	Mapping and characterization of structural variation in 17,795 human genomes. Nature, 2020, 583, 83-89.	13.7	194
7	Evolutionary toggling of the MAPT 17q21.31 inversion region. Nature Genetics, 2008, 40, 1076-1083.	9.4	176
8	Functional equivalence of genome sequencing analysis pipelines enables harmonized variant calling across human genetics projects. Nature Communications, 2018, 9, 4038.	5.8	166
9	Distinct Classes of Complex Structural Variation Uncovered across Thousands of Cancer Genome Graphs. Cell, 2020, 183, 197-210.e32.	13.5	141
10	Type 2 and interferon inflammation regulate SARS-CoV-2 entry factor expression in the airway epithelium. Nature Communications, 2020, 11, 5139.	5.8	131
11	Pangenome-based genome inference allows efficient and accurate genotyping across a wide spectrum of variant classes. Nature Genetics, 2022, 54, 518-525.	9.4	92
12	Genome sequencing identifies multiple deleterious variants in autism patients with more severe phenotypes. Genetics in Medicine, 2019, 21, 1611-1620.	1.1	88
13	Recent ultra-rare inherited variants implicate new autism candidate risk genes. Nature Genetics, 2021, 53, 1125-1134.	9.4	68
14	Familial long-read sequencing increases yield of de novo mutations. American Journal of Human Genetics, 2022, 109, 631-646.	2.6	32
15	Nasal airway transcriptome-wide association study of asthma reveals genetically driven mucus pathobiology. Nature Communications, 2022, 13, 1632.	5.8	24
16	Whole-genome characterization of lung adenocarcinomas lacking alterations in the RTK/RAS/RAF pathway. Cell Reports, 2021, 34, 108707.	2.9	16
17	Optical genome mapping identifies rare structural variations as predisposition factors associated with severe COVID-19. IScience, 2022, 25, 103760.	1.9	15