

Michael C Zody

List of Publications by Year in descending order

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Version: 2024-02-01

17
papers

24,349
citations

567281
15
h-index

888059
17
g-index

19
all docs

19
docs citations

19
times ranked

30053
citing authors

#	ARTICLE	IF	CITATIONS
1	Optical genome mapping identifies rare structural variations as predisposition factors associated with severe COVID-19. IScience, 2022, 25, 103760.	4.1	15
2	Nasal airway transcriptome-wide association study of asthma reveals genetically driven mucus pathobiology. Nature Communications, 2022, 13, 1632.	12.8	24
3	Familial long-read sequencing increases yield of de novo mutations. American Journal of Human Genetics, 2022, 109, 631-646.	6.2	32
4	Pangenome-based genome inference allows efficient and accurate genotyping across a wide spectrum of variant classes. Nature Genetics, 2022, 54, 518-525.	21.4	92
5	Whole-genome characterization of lung adenocarcinomas lacking alterations in the RTK/RAS/RAF pathway. Cell Reports, 2021, 34, 108707.	6.4	16
6	Sequencing of 53,831 diverse genomes from the NHLBI TOPMed Program. Nature, 2021, 590, 290-299.	27.8	1,069
7	Haplotype-resolved diverse human genomes and integrated analysis of structural variation. Science, 2021, 372, .	12.6	358
8	Recent ultra-rare inherited variants implicate new autism candidate risk genes. Nature Genetics, 2021, 53, 1125-1134.	21.4	68
9	Distinct Classes of Complex Structural Variation Uncovered across Thousands of Cancer Genome Graphs. Cell, 2020, 183, 197-210.e32.	28.9	141
10	Type 2 and interferon inflammation regulate SARS-CoV-2 entry factor expression in the airway epithelium. Nature Communications, 2020, 11, 5139.	12.8	131
11	Mapping and characterization of structural variation in 17,795 human genomes. Nature, 2020, 583, 83-89.	27.8	194
12	Genome sequencing identifies multiple deleterious variants in autism patients with more severe phenotypes. Genetics in Medicine, 2019, 21, 1611-1620.	2.4	88
13	Functional equivalence of genome sequencing analysis pipelines enables harmonized variant calling across human genetics projects. Nature Communications, 2018, 9, 4038.	12.8	166
14	Genomic Patterns of De Novo Mutation in Simplex Autism. Cell, 2017, 171, 710-722.e12.	28.9	308
15	Genome Sequencing of Autism-Affected Families Reveals Disruption of Putative Noncoding Regulatory DNA. American Journal of Human Genetics, 2016, 98, 58-74.	6.2	248
16	Evolutionary toggling of the MAPT 17q21.31 inversion region. Nature Genetics, 2008, 40, 1076-1083.	21.4	176
17	Initial sequencing and analysis of the human genome. Nature, 2001, 409, 860-921.	27.8	21,074