

Michael C Zody

List of Publications by Year in descending order

Source: <https://exaly.com/author-pdf/763131/publications.pdf>

Version: 2024-02-01

17
papers

24,349
citations

566801

15
h-index

887659

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