

Zachary A Szpiech

List of Publications by Year in descending order

Source: <https://exaly.com/author-pdf/656827/publications.pdf>

Version: 2024-02-01

20
papers

4,359
citations

471509

17
h-index

713466

21
g-index

32
all docs

32
docs citations

32
times ranked

9992
citing authors

#	ARTICLE	IF	CITATIONS
1	Sequencing of 53,831 diverse genomes from the NHLBI TOPMed Program. <i>Nature</i> , 2021, 590, 290-299.	27.8	1,069
2	Genotype, haplotype and copy-number variation in worldwide human populations. <i>Nature</i> , 2008, 451, 998-1003.	27.8	780
3	selscan: An Efficient Multithreaded Program to Perform EHH-Based Scans for Positive Selection. <i>Molecular Biology and Evolution</i> , 2014, 31, 2824-2827.	8.9	555
4	Genome-wide association studies in diverse populations. <i>Nature Reviews Genetics</i> , 2010, 11, 356-366.	16.3	518
5	Genetic Ancestry and Natural Selection Drive Population Differences in Immune Responses to Pathogens. <i>Cell</i> , 2016, 167, 657-669.e21.	28.9	419
6	Long Runs of Homozygosity Are Enriched for Deleterious Variation. <i>American Journal of Human Genetics</i> , 2013, 93, 90-102.	6.2	227
7	Comparing Spatial Maps of Human Population-Genetic Variation Using Procrustes Analysis. <i>Statistical Applications in Genetics and Molecular Biology</i> , 2010, 9, Article 13.	0.6	103
8	Whole-Genome Sequencing of Pharmacogenetic Drug Response in Racially Diverse Children with Asthma. <i>American Journal of Respiratory and Critical Care Medicine</i> , 2018, 197, 1552-1564.	5.6	102
9	High-resolution network biology: connecting sequence with function. <i>Nature Reviews Genetics</i> , 2013, 14, 865-879.	16.3	92
10	Human demographic history has amplified the effects of background selection across the genome. <i>PLoS Genetics</i> , 2018, 14, e1007387.	3.5	71
11	Cancer-associated arginine-to-histidine mutations confer a gain in pH sensing to mutant proteins. <i>Science Signaling</i> , 2017, 10, .	3.6	54
12	On the size distribution of private microsatellite alleles. <i>Theoretical Population Biology</i> , 2011, 80, 100-113.	1.1	50
13	Ancestry-Dependent Enrichment of Deleterious Homozygotes in Runs of Homozygosity. <i>American Journal of Human Genetics</i> , 2019, 105, 747-762.	6.2	36
14	Application of a novel haplotype-based scan for local adaptation to study high-altitude adaptation in rhesus macaques. <i>Evolution Letters</i> , 2021, 5, 408-421.	3.3	35
15	Relationship between Deleterious Variation, Genomic Autozygosity, and Disease Risk: Insights from The 1000 Genomes Project. <i>American Journal of Human Genetics</i> , 2018, 102, 658-675.	6.2	29
16	Prominent features of the amino acid mutation landscape in cancer. <i>PLoS ONE</i> , 2017, 12, e0183273.	2.5	26
17	<i>GARLIC</i>: Genomic Autozygosity Regions Likelihood-based Inference and Classification. <i>Bioinformatics</i> , 2017, 33, 2059-2062.	4.1	22
18	A spatially aware likelihood test to detect sweeps from haplotype distributions. <i>PLoS Genetics</i> , 2022, 18, e1010134.	3.5	13

#	ARTICLE	IF	CITATIONS
19	Weighted likelihood inference of genomic autozygosity patterns in dense genotype data. BMC Genomics, 2017, 18, 928.	2.8	9
20	Evolution of genes involved in the unusual genitals of the bear macaque, <i>Macaca arctoides</i> . Ecology and Evolution, 2022, 12, .	1.9	2