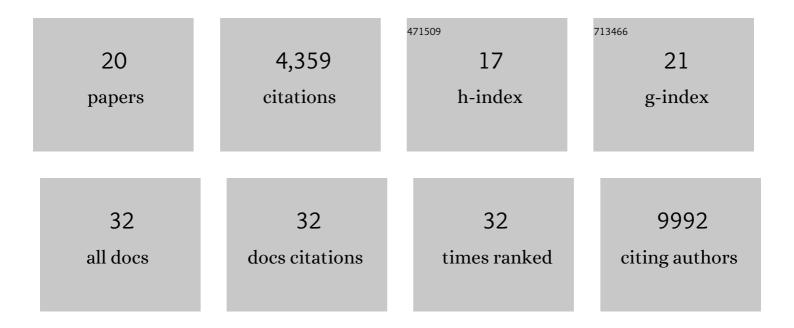
Zachary A Szpiech

List of Publications by Year in descending order

Source: https://exaly.com/author-pdf/656827/publications.pdf Version: 2024-02-01



ZACHADY A SZDIECH

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