

Joshua G Schraiber

List of Publications by Year in descending order

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Version: 2024-02-01

25
papers

5,995
citations

471509

17
h-index

580821

25
g-index

28
all docs

28
docs citations

28
times ranked

9518
citing authors

#	ARTICLE	IF	CITATIONS
1	Multiple episodes of interbreeding between Neanderthal and modern humans. <i>Nature Ecology and Evolution</i> , 2019, 3, 39-44.	7.8	148
2	Origins and genetic legacies of the Caribbean Taino. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2018, 115, 2341-2346.	7.1	64
3	Assessing the Relationship of Ancient and Modern Populations. <i>Genetics</i> , 2018, 208, 383-398.	2.9	18
4	Mitoâ€nuclear discordance across a recent contact zone for California voles. <i>Ecology and Evolution</i> , 2018, 8, 6226-6241.	1.9	6
5	A multispecies coalescent model for quantitative traits. <i>ELife</i> , 2018, 7, .	6.0	44
6	Pulsed evolution shaped modern vertebrate body sizes. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2017, 114, 13224-13229.	7.1	102
7	Bayesian Inference of Natural Selection from Allele Frequency Time Series. <i>Genetics</i> , 2016, 203, 493-511.	2.9	102
8	Emergence of a <i>Homo sapiens</i> -specific gene family and chromosome 16p11.2 CNV susceptibility. <i>Nature</i> , 2016, 536, 205-209.	27.8	102
9	Archaic Hominin Admixture Facilitated Adaptation to Out-of-Africa Environments. <i>Current Biology</i> , 2016, 26, 3375-3382.	3.9	156
10	Excavating Neanderthal and Denisovan DNA from the genomes of Melanesian individuals. <i>Science</i> , 2016, 352, 235-239.	12.6	391
11	Evolution of Tibetan wild boars. <i>Nature Genetics</i> , 2015, 47, 188-189.	21.4	10
12	Sensitivity of quantitative traits to mutational effects and number of loci. <i>Theoretical Population Biology</i> , 2015, 102, 85-93.	1.1	19
13	Evidence of long-term gene flow and selection during domestication from analyses of Eurasian wild and domestic pig genomes. <i>Nature Genetics</i> , 2015, 47, 1141-1148.	21.4	263
14	Methods and models for unravelling human evolutionary history. <i>Nature Reviews Genetics</i> , 2015, 16, 727-740.	16.3	166
15	Approximation to the Distribution of Fitness Effects across Functional Categories in Human Segregating Polymorphisms. <i>PLoS Genetics</i> , 2014, 10, e1004697.	3.5	59
16	Ancient human genomes suggest three ancestral populations for present-day Europeans. <i>Nature</i> , 2014, 513, 409-413.	27.8	1,179
17	A path integral formulation of the Wrightâ€™Fisher process with genic selection. <i>Theoretical Population Biology</i> , 2014, 92, 30-35.	1.1	10
18	Analysis and rejection sampling of Wrightâ€™Fisher diffusion bridges. <i>Theoretical Population Biology</i> , 2013, 89, 64-74.	1.1	16

#	ARTICLE	IF	CITATIONS
19	Inferring Evolutionary Histories of Pathway Regulation from Transcriptional Profiling Data. PLoS Computational Biology, 2013, 9, e1003255.	3.2	54
20	Phylogenetic Analysis Using Lévy Processes: Finding Jumps in the Evolution of Continuous Traits. Systematic Biology, 2013, 62, 193-204.	5.6	115
21	Evolution of a Membrane Protein Regulon in Saccharomyces. Molecular Biology and Evolution, 2012, 29, 1747-1756.	8.9	24
22	Analyses of pig genomes provide insight into porcine demography and evolution. Nature, 2012, 491, 393-398.	27.8	1,190
23	A High-Coverage Genome Sequence from an Archaic Denisovan Individual. Science, 2012, 338, 222-226.	12.6	1,695
24	Genomic Tests of Variation in Inbreeding Among Individuals and Among Chromosomes. Genetics, 2012, 192, 1477-1482.	2.9	5
25	Constraints on the use of lifespan-shortening Wolbachia to control dengue fever. Journal of Theoretical Biology, 2012, 297, 26-32.	1.7	52