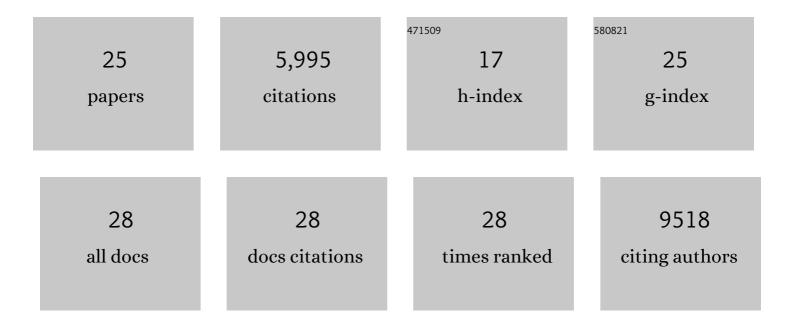
Joshua G Schraiber

List of Publications by Year in descending order

Source: https://exaly.com/author-pdf/6181918/publications.pdf Version: 2024-02-01



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

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#	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