

Simon Gravel

List of Publications by Year in descending order

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Version: 2024-02-01

43
papers

7,089
citations

279487

23
h-index

315357

38
g-index

61
all docs

61
docs citations

61
times ranked

13049
citing authors

#	ARTICLE	IF	CITATIONS
1	Evolution and Functional Impact of Rare Coding Variation from Deep Sequencing of Human Exomes. <i>Science</i> , 2012, 337, 64-69.	6.0	1,535
2	Human Demographic History Impacts Genetic Risk Prediction across Diverse Populations. <i>American Journal of Human Genetics</i> , 2017, 100, 635-649.	2.6	1,120
3	RFMix: A Discriminative Modeling Approach for Rapid and Robust Local-Ancestry Inference. <i>American Journal of Human Genetics</i> , 2013, 93, 278-288.	2.6	686
4	Demographic history and rare allele sharing among human populations. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2011, 108, 11983-11988.	3.3	589
5	Reconstructing the Population Genetic History of the Caribbean. <i>PLoS Genetics</i> , 2013, 9, e1003925.	1.5	296
6	Pulling out the 1%: Whole-Genome Capture for the Targeted Enrichment of Ancient DNA Sequencing Libraries. <i>American Journal of Human Genetics</i> , 2013, 93, 852-864.	2.6	284
7	Population Genetics Models of Local Ancestry. <i>Genetics</i> , 2012, 191, 607-619.	1.2	272
8	Estimating the mutation load in human genomes. <i>Nature Reviews Genetics</i> , 2015, 16, 333-343.	7.7	233
9	Genomic Insights into the Ancestry and Demographic History of South America. <i>PLoS Genetics</i> , 2015, 11, e1005602.	1.5	198
10	Reconstructing Native American Migrations from Whole-Genome and Whole-Exome Data. <i>PLoS Genetics</i> , 2013, 9, e1004023.	1.5	185
11	Inferring the Joint Demographic History of Multiple Populations: Beyond the Diffusion Approximation. <i>Genetics</i> , 2017, 206, 1549-1567.	1.2	176
12	The Great Migration and African-American Genomic Diversity. <i>PLoS Genetics</i> , 2016, 12, e1006059.	1.5	166
13	UMAP reveals cryptic population structure and phenotype heterogeneity in large genomic cohorts. <i>PLoS Genetics</i> , 2019, 15, e1008432.	1.5	166
14	Efficient ancestry and mutation simulation with msprime 1.0. <i>Genetics</i> , 2022, 220, .	1.2	133
15	Computationally Efficient Composite Likelihood Statistics for Demographic Inference. <i>Molecular Biology and Evolution</i> , 2016, 33, 591-593.	3.5	112
16	A community-maintained standard library of population genetic models. <i>ELife</i> , 2020, 9, .	2.8	112
17	The impact of agricultural emergence on the genetic history of African rainforest hunter-gatherers and agriculturalists. <i>Nature Communications</i> , 2014, 5, 3163.	5.8	96
18	Adaptive, convergent origins of the pygmy phenotype in African rainforest hunter-gatherers. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2014, 111, E3596-603.	3.3	91

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19	When Is Selection Effective?. <i>Genetics</i> , 2016, 203, 451-462.	1.2	73
20	A review of UMAP in population genetics. <i>Journal of Human Genetics</i> , 2021, 66, 85-91.	1.1	73
21	Spatially mapping the immune landscape of melanoma using imaging mass cytometry. <i>Science Immunology</i> , 2022, 7, eabi5072.	5.6	60
22	Models of archaic admixture and recent history from two-locus statistics. <i>PLoS Genetics</i> , 2019, 15, e1008204.	1.5	57
23	Dense Periodic Packings of Tetrahedra with Small Repeating Units. <i>Discrete and Computational Geometry</i> , 2010, 44, 245-252.	0.4	47
24	Accounting for long-range correlations in genome-wide simulations of large cohorts. <i>PLoS Genetics</i> , 2020, 16, e1008619.	1.5	43
25	Unbiased Estimation of Linkage Disequilibrium from Unphased Data. <i>Molecular Biology and Evolution</i> , 2020, 37, 923-932.	3.5	26
26	Genomic inference using diffusion models and the allele frequency spectrum. <i>Current Opinion in Genetics and Development</i> , 2018, 53, 140-147.	1.5	25
27	Legacy Data Confound Genomics Studies. <i>Molecular Biology and Evolution</i> , 2020, 37, 2-10.	3.5	23
28	Lessons Learned from Bugs in Models of Human History. <i>American Journal of Human Genetics</i> , 2020, 107, 583-588.	2.6	23
29	The existence and abundance of ghost ancestors in biparental populations. <i>Theoretical Population Biology</i> , 2015, 101, 47-53.	0.5	21
30	On the decidability of population size histories from finite allele frequency spectra. <i>Theoretical Population Biology</i> , 2018, 120, 42-51.	0.5	16
31	Intratumor Heterogeneity and Circulating Tumor Cell Clusters. <i>Molecular Biology and Evolution</i> , 2018, 35, 2135-2144.	3.5	16
32	Upper Bound on the Packing Density of Regular Tetrahedra and Octahedra. <i>Discrete and Computational Geometry</i> , 2011, 46, 799-818.	0.4	15
33	Recent shifts in the genomic ancestry of Mexican Americans may alter the genetic architecture of biomedical traits. <i>ELife</i> , 2020, 9, .	2.8	15
34	Predicting Discovery Rates of Genomic Features. <i>Genetics</i> , 2014, 197, 601-610.	1.2	14
35	Inferring Transmission Histories of Rare Alleles in Population-Scale Genealogies. <i>American Journal of Human Genetics</i> , 2018, 103, 893-906.	2.6	13
36	Assumptions about frequency-dependent architectures of complex traits bias measures of functional enrichment. <i>Genetic Epidemiology</i> , 2021, 45, 621-632.	0.6	5

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37	The Genetic and Molecular Analyses of RAD51C and RAD51D Identifies Rare Variants Implicated in Hereditary Ovarian Cancer from a Genetically Unique Population. <i>Cancers</i> , 2022, 14, 2251.	1.7	4
38	Accounting for long-range correlations in genome-wide simulations of large cohorts. , 2020, 16, e1008619.		0
39	Accounting for long-range correlations in genome-wide simulations of large cohorts. , 2020, 16, e1008619.		0
40	Accounting for long-range correlations in genome-wide simulations of large cohorts. , 2020, 16, e1008619.		0
41	Accounting for long-range correlations in genome-wide simulations of large cohorts. , 2020, 16, e1008619.		0
42	Accounting for long-range correlations in genome-wide simulations of large cohorts. , 2020, 16, e1008619.		0
43	Accounting for long-range correlations in genome-wide simulations of large cohorts. , 2020, 16, e1008619.		0