Simon Gravel

List of Publications by Year in descending order

43 papers	7,089 citations	318942 23 h-index	355658 38 g-index
61 all docs	61 docs citations	61 times ranked	14644 citing authors

#	Article	IF	Citations
1	Spatially mapping the immune landscape of melanoma using imaging mass cytometry. Science Immunology, 2022, 7, eabi5072.	5.6	60
2	Efficient ancestry and mutation simulation with msprime 1.0. Genetics, 2022, 220, .	1.2	133
3	The Genetic and Molecular Analyses of RAD51C and RAD51D Identifies Rare Variants Implicated in Hereditary Ovarian Cancer from a Genetically Unique Population. Cancers, 2022, 14, 2251.	1.7	4
4	A review of UMAP in population genetics. Journal of Human Genetics, 2021, 66, 85-91.	1.1	73
5	Assumptions about frequencyâ€dependent architectures of complex traits bias measures of functional enrichment. Genetic Epidemiology, 2021, 45, 621-632.	0.6	5
6	Legacy Data Confound Genomics Studies. Molecular Biology and Evolution, 2020, 37, 2-10.	3.5	23
7	Unbiased Estimation of Linkage Disequilibrium from Unphased Data. Molecular Biology and Evolution, 2020, 37, 923-932.	3.5	26
8	Lessons Learned from Bugs in Models of Human History. American Journal of Human Genetics, 2020, 107, 583-588.	2.6	23
9	Accounting for long-range correlations in genome-wide simulations of large cohorts. PLoS Genetics, 2020, 16, e1008619.	1.5	43
10	A community-maintained standard library of population genetic models. ELife, 2020, 9, .	2.8	112
11	Recent shifts in the genomic ancestry of Mexican Americans may alter the genetic architecture of biomedical traits. ELife, 2020, 9, .	2.8	15
12	Accounting for long-range correlations in genome-wide simulations of large cohorts. , 2020, 16, e1008619.		0
13	Accounting for long-range correlations in genome-wide simulations of large cohorts. , 2020, 16, e1008619.		0
14	Accounting for long-range correlations in genome-wide simulations of large cohorts. , 2020, 16, e1008619.		0
15	Accounting for long-range correlations in genome-wide simulations of large cohorts. , 2020, 16, e1008619.		0
16	Accounting for long-range correlations in genome-wide simulations of large cohorts. , 2020, 16, e1008619.		0
17	Accounting for long-range correlations in genome-wide simulations of large cohorts. , 2020, 16, e1008619.		0
18	UMAP reveals cryptic population structure and phenotype heterogeneity in large genomic cohorts. PLoS Genetics, 2019, 15, e1008432.	1.5	166

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19	Models of archaic admixture and recent history from two-locus statistics. PLoS Genetics, 2019, 15, e1008204.	1.5	57
20	On the decidability of population size histories from finite allele frequency spectra. Theoretical Population Biology, 2018, 120, 42-51.	0.5	16
21	Inferring Transmission Histories of Rare Alleles in Population-Scale Genealogies. American Journal of Human Genetics, 2018, 103, 893-906.	2.6	13
22	Genomic inference using diffusion models and the allele frequency spectrum. Current Opinion in Genetics and Development, 2018, 53, 140-147.	1.5	25
23	Intratumor Heterogeneity and Circulating Tumor Cell Clusters. Molecular Biology and Evolution, 2018, 35, 2135-2144.	3.5	16
24	Human Demographic History Impacts Genetic Risk Prediction across Diverse Populations. American Journal of Human Genetics, 2017, 100, 635-649.	2.6	1,120
25	Inferring the Joint Demographic History of Multiple Populations: Beyond the Diffusion Approximation. Genetics, 2017, 206, 1549-1567.	1.2	176
26	The Great Migration and African-American Genomic Diversity. PLoS Genetics, 2016, 12, e1006059.	1.5	166
27	When Is Selection Effective?. Genetics, 2016, 203, 451-462.	1.2	73
28	Computationally Efficient Composite Likelihood Statistics for Demographic Inference. Molecular Biology and Evolution, 2016, 33, 591-593.	3.5	112
29	Genomic Insights into the Ancestry and Demographic History of South America. PLoS Genetics, 2015, 11, e1005602.	1.5	198
30	The existence and abundance of ghost ancestors in biparental populations. Theoretical Population Biology, 2015, 101, 47-53.	0.5	21
31	Estimating the mutation load in human genomes. Nature Reviews Genetics, 2015, 16, 333-343.	7.7	233
32	Predicting Discovery Rates of Genomic Features. Genetics, 2014, 197, 601-610.	1.2	14
33	Adaptive, convergent origins of the pygmy phenotype in African rainforest hunter-gatherers. Proceedings of the National Academy of Sciences of the United States of America, 2014, 111, E3596-603.	3.3	91
34	The impact of agricultural emergence on the genetic history of African rainforest hunter-gatherers and agriculturalists. Nature Communications, 2014, 5, 3163.	5.8	96
35	RFMix: A Discriminative Modeling Approach for Rapid and Robust Local-Ancestry Inference. American Journal of Human Genetics, 2013, 93, 278-288.	2.6	686
36	Pulling out the 1%: Whole-Genome Capture for the Targeted Enrichment of Ancient DNA Sequencing Libraries. American Journal of Human Genetics, 2013, 93, 852-864.	2.6	284

#	Article	IF	Citations
37	Reconstructing Native American Migrations from Whole-Genome and Whole-Exome Data. PLoS Genetics, 2013, 9, e1004023.	1.5	185
38	Reconstructing the Population Genetic History of the Caribbean. PLoS Genetics, 2013, 9, e1003925.	1.5	296
39	Population Genetics Models of Local Ancestry. Genetics, 2012, 191, 607-619.	1.2	272
40	Evolution and Functional Impact of Rare Coding Variation from Deep Sequencing of Human Exomes. Science, 2012, 337, 64-69.	6.0	1,535
41	Upper Bound on the Packing Density of Regular Tetrahedra and Octahedra. Discrete and Computational Geometry, 2011, 46, 799-818.	0.4	15
42	Demographic history and rare allele sharing among human populations. Proceedings of the National Academy of Sciences of the United States of America, 2011, 108, 11983-11988.	3.3	589
43	Dense Periodic Packings of Tetrahedra with Small Repeating Units. Discrete and Computational Geometry, 2010, 44, 245-252.	0.4	47