

Graham Coop

List of Publications by Year in descending order

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Version: 2024-02-01

54
papers

9,266
citations

117453

34
h-index

189595

50
g-index

84
all docs

84
docs citations

84
times ranked

10221
citing authors

#	ARTICLE	IF	CITATIONS
1	Lottery, luck, or legacy. A review of "The Genetic Lottery: Why DNA matters for social equality" Evolution; International Journal of Organic Evolution, 2022, 76, 846-853.	1.1	23
2	Population differentiation of polygenic score predictions under stabilizing selection. Philosophical Transactions of the Royal Society B: Biological Sciences, 2022, 377, 20200416.	1.8	26
3	The timing of human adaptation from Neanderthal introgression. Genetics, 2021, 218, .	1.2	10
4	Selective sorting of ancestral introgression in maize and teosinte along an elevational cline. PLoS Genetics, 2021, 17, e1009810.	1.5	50
5	Donnelly (1983) and the limits of genetic genealogy. Theoretical Population Biology, 2020, 133, 23-24.	0.5	5
6	Attacks on genetic privacy via uploads to genealogical databases. ELife, 2020, 9, .	2.8	27
7	Estimating the genome-wide contribution of selection to temporal allele frequency change. Proceedings of the National Academy of Sciences of the United States of America, 2020, 117, 20672-20680.	3.3	75
8	Genetic Signatures of Evolutionary Rescue by a Selective Sweep. Genetics, 2020, 215, 813-829.	1.2	7
9	Selection and hybridization shaped the rapid spread of African honey bee ancestry in the Americas. PLoS Genetics, 2020, 16, e1009038.	1.5	42
10	Selection and hybridization shaped the rapid spread of African honey bee ancestry in the Americas. , 2020, 16, e1009038.		0
11	Selection and hybridization shaped the rapid spread of African honey bee ancestry in the Americas. , 2020, 16, e1009038.		0
12	Selection and hybridization shaped the rapid spread of African honey bee ancestry in the Americas. , 2020, 16, e1009038.		0
13	Selection and hybridization shaped the rapid spread of African honey bee ancestry in the Americas. , 2020, 16, e1009038.		0
14	The Linked Selection Signature of Rapid Adaptation in Temporal Genomic Data. Genetics, 2019, 213, 1007-1045.	1.2	58
15	Detecting Adaptive Differentiation in Structured Populations with Genomic Data and Common Gardens. Genetics, 2019, 211, 989-1004.	1.2	40
16	Population genomics perspectives on convergent adaptation. Philosophical Transactions of the Royal Society B: Biological Sciences, 2019, 374, 20180236.	1.8	56
17	Allele frequency dynamics in a pedigreed natural population. Proceedings of the National Academy of Sciences of the United States of America, 2019, 116, 2158-2164.	3.3	68
18	Reconstructing the History of Polygenic Scores Using Coalescent Trees. Genetics, 2019, 211, 235-262.	1.2	39

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19	Reduced signal for polygenic adaptation of height in UK Biobank. <i>ELife</i> , 2019, 8, .	2.8	283
20	Estimating Time to the Common Ancestor for a Beneficial Allele. <i>Molecular Biology and Evolution</i> , 2018, 35, 1003-1017.	3.5	53
21	Inferring Continuous and Discrete Population Genetic Structure Across Space. <i>Genetics</i> , 2018, 210, 33-52.	1.2	221
22	Inferring Recent Demography from Isolation by Distance of Long Shared Sequence Blocks. <i>Genetics</i> , 2017, 205, 1335-1351.	1.2	61
23	Population-genomic inference of the strength and timing of selection against gene flow. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2017, 114, 7061-7066.	3.3	114
24	Distinguishing Among Modes of Convergent Adaptation Using Population Genomic Data. <i>Genetics</i> , 2017, 207, 1591-1619.	1.2	112
25	Deconstructing isolation-by-distance: The genomic consequences of limited dispersal. <i>PLoS Genetics</i> , 2017, 13, e1006911.	1.5	91
26	A Genomic Map of the Effects of Linked Selection in <i>Drosophila</i> . <i>PLoS Genetics</i> , 2016, 12, e1006130.	1.5	145
27	A Genealogical Look at Shared Ancestry on the X Chromosome. <i>Genetics</i> , 2016, 204, 57-75.	1.2	10
28	The Strength of Selection against Neanderthal Introgression. <i>PLoS Genetics</i> , 2016, 12, e1006340.	1.5	257
29	Complex histories of repeated gene flow in Cameroon crater lake cichlids cast doubt on one of the clearest examples of sympatric speciation. <i>Evolution; International Journal of Organic Evolution</i> , 2015, 69, 1406-1422.	1.1	122
30	A Coalescent Model for a Sweep of a Unique Standing Variant. <i>Genetics</i> , 2015, 201, 707-725.	1.2	56
31	The Spatial Mixing of Genomes in Secondary Contact Zones. <i>Genetics</i> , 2015, 201, 243-261.	1.2	24
32	The Role of Standing Variation in Geographic Convergent Adaptation. <i>American Naturalist</i> , 2015, 186, S5-S23.	1.0	68
33	Convergent Evolution During Local Adaptation to Patchy Landscapes. <i>PLoS Genetics</i> , 2015, 11, e1005630.	1.5	44
34	Speciation and Introgression between <i>Mimulus nasutus</i> and <i>Mimulus guttatus</i> . <i>PLoS Genetics</i> , 2014, 10, e1004410.	1.5	252
35	A Population Genetic Signal of Polygenic Adaptation. <i>PLoS Genetics</i> , 2014, 10, e1004412.	1.5	447
36	Robust Identification of Local Adaptation from Allele Frequencies. <i>Genetics</i> , 2013, 195, 205-220.	1.2	518

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37	The Geography of Recent Genetic Ancestry across Europe. <i>PLoS Biology</i> , 2013, 11, e1001555.	2.6	316
38	Patterns of Neutral Diversity Under General Models of Selective Sweeps. <i>Genetics</i> , 2012, 192, 205-224.	1.2	81
39	Using Environmental Correlations to Identify Loci Underlying Local Adaptation. <i>Genetics</i> , 2010, 185, 1411-1423.	1.2	624
40	The Genetics of Human Adaptation: Hard Sweeps, Soft Sweeps, and Polygenic Adaptation. <i>Current Biology</i> , 2010, 20, R208-R215.	1.8	853
41	Parallel Adaptation: One or Many Waves of Advance of an Advantageous Allele?. <i>Genetics</i> , 2010, 186, 647-668.	1.2	163
42	The Role of Geography in Human Adaptation. <i>PLoS Genetics</i> , 2009, 5, e1000500.	1.5	358
43	High-Resolution Mapping of Crossovers Reveals Extensive Variation in Fine-Scale Recombination Patterns Among Humans. <i>Science</i> , 2008, 319, 1395-1398.	6.0	340
44	Adaptations to Climate in Candidate Genes for Common Metabolic Disorders. <i>PLoS Genetics</i> , 2008, 4, e32.	1.5	238
45	Live Hot, Die Young: Transmission Distortion in Recombination Hotspots. <i>PLoS Genetics</i> , 2007, 3, e35.	1.5	108
46	An evolutionary view of human recombination. <i>Nature Reviews Genetics</i> , 2007, 8, 23-34.	7.7	259
47	Sequencing and Analysis of Neanderthal Genomic DNA. <i>Science</i> , 2006, 314, 1113-1118.	6.0	547
48	A worldwide survey of haplotype variation and linkage disequilibrium in the human genome. <i>Nature Genetics</i> , 2006, 38, 1251-1260.	9.4	474
49	How reliable are empirical genomic scans for selective sweeps?. <i>Genome Research</i> , 2006, 16, 702-712.	2.4	352
50	THE SIGNATURE OF POSITIVE SELECTION ON STANDING GENETIC VARIATION. <i>Evolution; International Journal of Organic Evolution</i> , 2005, 59, 2312-2323.	1.1	267
51	THE SIGNATURE OF POSITIVE SELECTION ON STANDING GENETIC VARIATION. <i>Evolution; International Journal of Organic Evolution</i> , 2005, 59, 2312.	1.1	367
52	Can a genome change its (hot)spots?. <i>Trends in Ecology and Evolution</i> , 2005, 20, 643-645.	4.2	5
53	The signature of positive selection on standing genetic variation. <i>Evolution; International Journal of Organic Evolution</i> , 2005, 59, 2312-23.	1.1	224
54	Ancestral inference on gene trees under selection. <i>Theoretical Population Biology</i> , 2004, 66, 219-232.	0.5	88