

# Graham Coop

## List of Publications by Year in descending order

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Version: 2024-02-01

54  
papers

9,266  
citations

117625

34  
h-index

189892

50  
g-index

84  
all docs

84  
docs citations

84  
times ranked

10221  
citing authors

#	ARTICLE	IF	CITATIONS
1	The Genetics of Human Adaptation: Hard Sweeps, Soft Sweeps, and Polygenic Adaptation. <i>Current Biology</i> , 2010, 20, R208-R215.	3.9	853
2	Using Environmental Correlations to Identify Loci Underlying Local Adaptation. <i>Genetics</i> , 2010, 185, 1411-1423.	2.9	624
3	Sequencing and Analysis of Neanderthal Genomic DNA. <i>Science</i> , 2006, 314, 1113-1118.	12.6	547
4	Robust Identification of Local Adaptation from Allele Frequencies. <i>Genetics</i> , 2013, 195, 205-220.	2.9	518
5	A worldwide survey of haplotype variation and linkage disequilibrium in the human genome. <i>Nature Genetics</i> , 2006, 38, 1251-1260.	21.4	474
6	A Population Genetic Signal of Polygenic Adaptation. <i>PLoS Genetics</i> , 2014, 10, e1004412.	3.5	447
7	THE SIGNATURE OF POSITIVE SELECTION ON STANDING GENETIC VARIATION. <i>Evolution; International Journal of Organic Evolution</i> , 2005, 59, 2312.	2.3	367
8	The Role of Geography in Human Adaptation. <i>PLoS Genetics</i> , 2009, 5, e1000500.	3.5	358
9	How reliable are empirical genomic scans for selective sweeps?. <i>Genome Research</i> , 2006, 16, 702-712.	5.5	352
10	High-Resolution Mapping of Crossovers Reveals Extensive Variation in Fine-Scale Recombination Patterns Among Humans. <i>Science</i> , 2008, 319, 1395-1398.	12.6	340
11	The Geography of Recent Genetic Ancestry across Europe. <i>PLoS Biology</i> , 2013, 11, e1001555.	5.6	316
12	Reduced signal for polygenic adaptation of height in UK Biobank. <i>ELife</i> , 2019, 8, .	6.0	283
13	THE SIGNATURE OF POSITIVE SELECTION ON STANDING GENETIC VARIATION. <i>Evolution; International Journal of Organic Evolution</i> , 2005, 59, 2312-2323.	2.3	267
14	An evolutionary view of human recombination. <i>Nature Reviews Genetics</i> , 2007, 8, 23-34.	16.3	259
15	The Strength of Selection against Neanderthal Introgression. <i>PLoS Genetics</i> , 2016, 12, e1006340.	3.5	257
16	Speciation and Introgression between <i>Mimulus nasutus</i> and <i>Mimulus guttatus</i> . <i>PLoS Genetics</i> , 2014, 10, e1004410.	3.5	252
17	Adaptations to Climate in Candidate Genes for Common Metabolic Disorders. <i>PLoS Genetics</i> , 2008, 4, e32.	3.5	238
18	The signature of positive selection on standing genetic variation. <i>Evolution; International Journal of Organic Evolution</i> , 2005, 59, 2312-23.	2.3	224

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19	Inferring Continuous and Discrete Population Genetic Structure Across Space. <i>Genetics</i> , 2018, 210, 33-52.	2.9	221
20	Parallel Adaptation: One or Many Waves of Advance of an Advantageous Allele?. <i>Genetics</i> , 2010, 186, 647-668.	2.9	163
21	A Genomic Map of the Effects of Linked Selection in <i>Drosophila</i> . <i>PLoS Genetics</i> , 2016, 12, e1006130.	3.5	145
22	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.	2.3	122
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.	7.1	114
24	Distinguishing Among Modes of Convergent Adaptation Using Population Genomic Data. <i>Genetics</i> , 2017, 207, 1591-1619.	2.9	112
25	Live Hot, Die Young: Transmission Distortion in Recombination Hotspots. <i>PLoS Genetics</i> , 2007, 3, e35.	3.5	108
26	Deconstructing isolation-by-distance: The genomic consequences of limited dispersal. <i>PLoS Genetics</i> , 2017, 13, e1006911.	3.5	91
27	Ancestral inference on gene trees under selection. <i>Theoretical Population Biology</i> , 2004, 66, 219-232.	1.1	88
28	Patterns of Neutral Diversity Under General Models of Selective Sweeps. <i>Genetics</i> , 2012, 192, 205-224.	2.9	81
29	Estimating the genome-wide contribution of selection to temporal allele frequency change. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2020, 117, 20672-20680.	7.1	75
30	The Role of Standing Variation in Geographic Convergent Adaptation. <i>American Naturalist</i> , 2015, 186, S5-S23.	2.1	68
31	Allele frequency dynamics in a pedigreed natural population. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2019, 116, 2158-2164.	7.1	68
32	Inferring Recent Demography from Isolation by Distance of Long Shared Sequence Blocks. <i>Genetics</i> , 2017, 205, 1335-1351.	2.9	61
33	The Linked Selection Signature of Rapid Adaptation in Temporal Genomic Data. <i>Genetics</i> , 2019, 213, 1007-1045.	2.9	58
34	A Coalescent Model for a Sweep of a Unique Standing Variant. <i>Genetics</i> , 2015, 201, 707-725.	2.9	56
35	Population genomics perspectives on convergent adaptation. <i>Philosophical Transactions of the Royal Society B: Biological Sciences</i> , 2019, 374, 20180236.	4.0	56
36	Estimating Time to the Common Ancestor for a Beneficial Allele. <i>Molecular Biology and Evolution</i> , 2018, 35, 1003-1017.	8.9	53

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37	Selective sorting of ancestral introgression in maize and teosinte along an elevational cline. PLoS Genetics, 2021, 17, e1009810.	3.5	50
38	Convergent Evolution During Local Adaptation to Patchy Landscapes. PLoS Genetics, 2015, 11, e1005630.	3.5	44
39	Selection and hybridization shaped the rapid spread of African honey bee ancestry in the Americas. PLoS Genetics, 2020, 16, e1009038.	3.5	42
40	Detecting Adaptive Differentiation in Structured Populations with Genomic Data and Common Gardens. Genetics, 2019, 211, 989-1004.	2.9	40
41	Reconstructing the History of Polygenic Scores Using Coalescent Trees. Genetics, 2019, 211, 235-262.	2.9	39
42	Attacks on genetic privacy via uploads to genealogical databases. ELife, 2020, 9, .	6.0	27
43	Population differentiation of polygenic score predictions under stabilizing selection. Philosophical Transactions of the Royal Society B: Biological Sciences, 2022, 377, 20200416.	4.0	26
44	The Spatial Mixing of Genomes in Secondary Contact Zones. Genetics, 2015, 201, 243-261.	2.9	24
45	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.	2.3	23
46	A Genealogical Look at Shared Ancestry on the X Chromosome. Genetics, 2016, 204, 57-75.	2.9	10
47	The timing of human adaptation from Neanderthal introgression. Genetics, 2021, 218, .	2.9	10
48	Genetic Signatures of Evolutionary Rescue by a Selective Sweep. Genetics, 2020, 215, 813-829.	2.9	7
49	Can a genome change its (hot)spots?. Trends in Ecology and Evolution, 2005, 20, 643-645.	8.7	5
50	Donnelly (1983) and the limits of genetic genealogy. Theoretical Population Biology, 2020, 133, 23-24.	1.1	5
51	Selection and hybridization shaped the rapid spread of African honey bee ancestry in the Americas. , 2020, 16, e1009038.		0
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54	Selection and hybridization shaped the rapid spread of African honey bee ancestry in the Americas. , 2020, 16, e1009038.		0