

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 | The Genetics of Human Adaptation: Hard Sweeps, Soft Sweeps, and Polygenic Adaptation. <i>Current Biology</i> , 2010, 20, R208-R215. | 1.8 | 853 |
| 2 | Using Environmental Correlations to Identify Loci Underlying Local Adaptation. <i>Genetics</i> , 2010, 185, 1411-1423. | 1.2 | 624 |
| 3 | Sequencing and Analysis of Neanderthal Genomic DNA. <i>Science</i> , 2006, 314, 1113-1118. | 6.0 | 547 |
| 4 | Robust Identification of Local Adaptation from Allele Frequencies. <i>Genetics</i> , 2013, 195, 205-220. | 1.2 | 518 |
| 5 | A worldwide survey of haplotype variation and linkage disequilibrium in the human genome. <i>Nature Genetics</i> , 2006, 38, 1251-1260. | 9.4 | 474 |
| 6 | A Population Genetic Signal of Polygenic Adaptation. <i>PLoS Genetics</i> , 2014, 10, e1004412. | 1.5 | 447 |
| 7 | THE SIGNATURE OF POSITIVE SELECTION ON STANDING GENETIC VARIATION. <i>Evolution; International Journal of Organic Evolution</i> , 2005, 59, 2312. | 1.1 | 367 |
| 8 | The Role of Geography in Human Adaptation. <i>PLoS Genetics</i> , 2009, 5, e1000500. | 1.5 | 358 |
| 9 | How reliable are empirical genomic scans for selective sweeps?. <i>Genome Research</i> , 2006, 16, 702-712. | 2.4 | 352 |
| 10 | 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 |
| 11 | The Geography of Recent Genetic Ancestry across Europe. <i>PLoS Biology</i> , 2013, 11, e1001555. | 2.6 | 316 |
| 12 | Reduced signal for polygenic adaptation of height in UK Biobank. <i>ELife</i> , 2019, 8, . | 2.8 | 283 |
| 13 | THE SIGNATURE OF POSITIVE SELECTION ON STANDING GENETIC VARIATION. <i>Evolution; International Journal of Organic Evolution</i> , 2005, 59, 2312-2323. | 1.1 | 267 |
| 14 | An evolutionary view of human recombination. <i>Nature Reviews Genetics</i> , 2007, 8, 23-34. | 7.7 | 259 |
| 15 | The Strength of Selection against Neanderthal Introgression. <i>PLoS Genetics</i> , 2016, 12, e1006340. | 1.5 | 257 |
| 16 | Speciation and Introgression between <i>Mimulus nasutus</i> and <i>Mimulus guttatus</i> . <i>PLoS Genetics</i> , 2014, 10, e1004410. | 1.5 | 252 |
| 17 | Adaptations to Climate in Candidate Genes for Common Metabolic Disorders. <i>PLoS Genetics</i> , 2008, 4, e32. | 1.5 | 238 |
| 18 | The signature of positive selection on standing genetic variation. <i>Evolution; International Journal of Organic Evolution</i> , 2005, 59, 2312-23. | 1.1 | 224 |

| # | ARTICLE | IF | CITATIONS |
|----|--|-----|-----------|
| 19 | Inferring Continuous and Discrete Population Genetic Structure Across Space. <i>Genetics</i> , 2018, 210, 33-52. | 1.2 | 221 |
| 20 | Parallel Adaptation: One or Many Waves of Advance of an Advantageous Allele?. <i>Genetics</i> , 2010, 186, 647-668. | 1.2 | 163 |
| 21 | A Genomic Map of the Effects of Linked Selection in <i>Drosophila</i> . <i>PLoS Genetics</i> , 2016, 12, e1006130. | 1.5 | 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. | 1.1 | 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. | 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 | Live Hot, Die Young: Transmission Distortion in Recombination Hotspots. <i>PLoS Genetics</i> , 2007, 3, e35. | 1.5 | 108 |
| 26 | Deconstructing isolation-by-distance: The genomic consequences of limited dispersal. <i>PLoS Genetics</i> , 2017, 13, e1006911. | 1.5 | 91 |
| 27 | Ancestral inference on gene trees under selection. <i>Theoretical Population Biology</i> , 2004, 66, 219-232. | 0.5 | 88 |
| 28 | Patterns of Neutral Diversity Under General Models of Selective Sweeps. <i>Genetics</i> , 2012, 192, 205-224. | 1.2 | 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. | 3.3 | 75 |
| 30 | The Role of Standing Variation in Geographic Convergent Adaptation. <i>American Naturalist</i> , 2015, 186, S5-S23. | 1.0 | 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. | 3.3 | 68 |
| 32 | Inferring Recent Demography from Isolation by Distance of Long Shared Sequence Blocks. <i>Genetics</i> , 2017, 205, 1335-1351. | 1.2 | 61 |
| 33 | The Linked Selection Signature of Rapid Adaptation in Temporal Genomic Data. <i>Genetics</i> , 2019, 213, 1007-1045. | 1.2 | 58 |
| 34 | A Coalescent Model for a Sweep of a Unique Standing Variant. <i>Genetics</i> , 2015, 201, 707-725. | 1.2 | 56 |
| 35 | Population genomics perspectives on convergent adaptation. <i>Philosophical Transactions of the Royal Society B: Biological Sciences</i> , 2019, 374, 20180236. | 1.8 | 56 |
| 36 | Estimating Time to the Common Ancestor for a Beneficial Allele. <i>Molecular Biology and Evolution</i> , 2018, 35, 1003-1017. | 3.5 | 53 |

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|----|---|-----|-----------|
| 37 | Selective sorting of ancestral introgression in maize and teosinte along an elevational cline. PLoS Genetics, 2021, 17, e1009810. | 1.5 | 50 |
| 38 | Convergent Evolution During Local Adaptation to Patchy Landscapes. PLoS Genetics, 2015, 11, e1005630. | 1.5 | 44 |
| 39 | Selection and hybridization shaped the rapid spread of African honey bee ancestry in the Americas. PLoS Genetics, 2020, 16, e1009038. | 1.5 | 42 |
| 40 | Detecting Adaptive Differentiation in Structured Populations with Genomic Data and Common Gardens. Genetics, 2019, 211, 989-1004. | 1.2 | 40 |
| 41 | Reconstructing the History of Polygenic Scores Using Coalescent Trees. Genetics, 2019, 211, 235-262. | 1.2 | 39 |
| 42 | Attacks on genetic privacy via uploads to genealogical databases. ELife, 2020, 9, . | 2.8 | 27 |
| 43 | Population differentiation of polygenic score predictions under stabilizing selection. Philosophical Transactions of the Royal Society B: Biological Sciences, 2022, 377, 20200416. | 1.8 | 26 |
| 44 | The Spatial Mixing of Genomes in Secondary Contact Zones. Genetics, 2015, 201, 243-261. | 1.2 | 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. | 1.1 | 23 |
| 46 | A Genealogical Look at Shared Ancestry on the X Chromosome. Genetics, 2016, 204, 57-75. | 1.2 | 10 |
| 47 | The timing of human adaptation from Neanderthal introgression. Genetics, 2021, 218, . | 1.2 | 10 |
| 48 | Genetic Signatures of Evolutionary Rescue by a Selective Sweep. Genetics, 2020, 215, 813-829. | 1.2 | 7 |
| 49 | Can a genome change its (hot)spots?. Trends in Ecology and Evolution, 2005, 20, 643-645. | 4.2 | 5 |
| 50 | Donnelly (1983) and the limits of genetic genealogy. Theoretical Population Biology, 2020, 133, 23-24. | 0.5 | 5 |
| 51 | Selection and hybridization shaped the rapid spread of African honey bee ancestry in the Americas. , 2020, 16, e1009038. | | 0 |
| 52 | Selection and hybridization shaped the rapid spread of African honey bee ancestry in the Americas. , 2020, 16, e1009038. | | 0 |
| 53 | Selection and hybridization shaped the rapid spread of African honey bee ancestry in the Americas. , 2020, 16, e1009038. | | 0 |
| 54 | Selection and hybridization shaped the rapid spread of African honey bee ancestry in the Americas. , 2020, 16, e1009038. | | 0 |