

Daniel John Lawson

List of Publications by Year in descending order

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Version: 2024-02-01

49
papers

5,974
citations

236925

25
h-index

182427

51
g-index

65
all docs

65
docs citations

65
times ranked

12709
citing authors

| # | ARTICLE | IF | CITATIONS |
|----|--|------|-----------|
| 1 | The UK10K project identifies rare variants in health and disease. <i>Nature</i> , 2015, 526, 82-90. | 27.8 | 1,014 |
| 2 | Inference of Population Structure using Dense Haplotype Data. <i>PLoS Genetics</i> , 2012, 8, e1002453. | 3.5 | 983 |
| 3 | The fine-scale genetic structure of the British population. <i>Nature</i> , 2015, 519, 309-314. | 27.8 | 416 |
| 4 | Genomic analyses inform on migration events during the peopling of Eurasia. <i>Nature</i> , 2016, 538, 238-242. | 27.8 | 360 |
| 5 | A tutorial on how not to over-interpret STRUCTURE and ADMIXTURE bar plots. <i>Nature Communications</i> , 2018, 9, 3258. | 12.8 | 341 |
| 6 | Genetic architecture: the shape of the genetic contribution to human traits and disease. <i>Nature Reviews Genetics</i> , 2018, 19, 110-124. | 16.3 | 335 |
| 7 | RADpainter and fineRADstructure: Population Inference from RADseq Data. <i>Molecular Biology and Evolution</i> , 2018, 35, 1284-1290. | 8.9 | 265 |
| 8 | Apparent latent structure within the UK Biobank sample has implications for epidemiological analysis. <i>Nature Communications</i> , 2019, 10, 333. | 12.8 | 240 |
| 9 | Genomic and phenotypic insights from an atlas of genetic effects on DNA methylation. <i>Nature Genetics</i> , 2021, 53, 1311-1321. | 21.4 | 218 |
| 10 | Multiple Deeply Divergent Denisovan Ancestries in Papuans. <i>Cell</i> , 2019, 177, 1010-1021.e32. | 28.9 | 181 |
| 11 | Inference of Homologous Recombination in Bacteria Using Whole-Genome Sequences. <i>Genetics</i> , 2010, 186, 1435-1449. | 2.9 | 155 |
| 12 | Population genomics of the Viking world. <i>Nature</i> , 2020, 585, 390-396. | 27.8 | 143 |
| 13 | Genome-Wide Analysis of Cold Adaptation in Indigenous Siberian Populations. <i>PLoS ONE</i> , 2014, 9, e98076. | 2.5 | 128 |
| 14 | A Selective Sweep on a Deleterious Mutation in CPT1A in Arctic Populations. <i>American Journal of Human Genetics</i> , 2014, 95, 584-589. | 6.2 | 119 |
| 15 | Tracing Genetic Exchange and Biogeography of <i>Cryptococcus neoformans</i> var. <i>grubii</i> at the Global Population Level. <i>Genetics</i> , 2017, 207, 327-346. | 2.9 | 105 |
| 16 | Population Identification Using Genetic Data. <i>Annual Review of Genomics and Human Genetics</i> , 2012, 13, 337-361. | 6.2 | 76 |
| 17 | Likelihood-free estimation of model evidence. <i>Bayesian Analysis</i> , 2011, 6, . | 3.0 | 74 |
| 18 | Rapid evolution of distinct <i>Helicobacter pylori</i> subpopulations in the Americas. <i>PLoS Genetics</i> , 2017, 13, e1006546. | 3.5 | 73 |

| # | ARTICLE | IF | CITATIONS |
|----|---|------|-----------|
| 19 | Is population structure in the genetic biobank era irrelevant, a challenge, or an opportunity?. <i>Human Genetics</i> , 2020, 139, 23-41. | 3.8 | 72 |
| 20 | Complex Patterns of Admixture across the Indonesian Archipelago. <i>Molecular Biology and Evolution</i> , 2017, 34, 2439-2452. | 8.9 | 65 |
| 21 | Towards a decision support tool for intensive care discharge: machine learning algorithm development using electronic healthcare data from MIMIC-III and Bristol, UK. <i>BMJ Open</i> , 2019, 9, e025925. | 1.9 | 50 |
| 22 | Genetic evidence for assortative mating on alcohol consumption in the UK Biobank. <i>Nature Communications</i> , 2019, 10, 5039. | 12.8 | 48 |
| 23 | Disentangling Immediate Adaptive Introgression from Selection on Standing Introgressed Variation in Humans. <i>Molecular Biology and Evolution</i> , 2018, 35, 623-630. | 8.9 | 46 |
| 24 | Genomewide analysis of admixture and adaptation in the Africanized honeybee. <i>Molecular Ecology</i> , 2017, 26, 3603-3617. | 3.9 | 44 |
| 25 | Religious change preceded economic change in the 20th century. <i>Science Advances</i> , 2018, 4, eaar8680. | 10.3 | 30 |
| 26 | The Irish DNA Atlas: Revealing Fine-Scale Population Structure and History within Ireland. <i>Scientific Reports</i> , 2017, 7, 17199. | 3.3 | 29 |
| 27 | The species-area relationship and evolution. <i>Journal of Theoretical Biology</i> , 2006, 241, 590-600. | 1.7 | 27 |
| 28 | Estimating the COVID-19 epidemic trajectory and hospital capacity requirements in South West England: a mathematical modelling framework. <i>BMJ Open</i> , 2021, 11, e041536. | 1.9 | 24 |
| 29 | Differences in local population history at the finest level: the case of the Estonian population. <i>European Journal of Human Genetics</i> , 2020, 28, 1580-1591. | 2.8 | 23 |
| 30 | Investigating the origins of eastern Polynesians using genome-wide data from the Leeward Society Isles. <i>Scientific Reports</i> , 2018, 8, 1823. | 3.3 | 22 |
| 31 | SimMLST: simulation of multi-locus sequence typing data under a neutral model. <i>Bioinformatics</i> , 2009, 25, 1442-1444. | 4.1 | 21 |
| 32 | Performance comparison of renewable incentive schemes using optimal control. <i>Energy</i> , 2014, 64, 44-57. | 8.8 | 21 |
| 33 | On the use of genome-wide data to model and date the time of anthropogenic hybridisation: An example from the Scottish wildcat. <i>Molecular Ecology</i> , 2021, 30, 3688-3702. | 3.9 | 17 |
| 34 | Neutral Evolution in a Biological Population as Diffusion in Phenotype Space: Reproduction with Local Mutation but without Selection. <i>Physical Review Letters</i> , 2007, 98, 098102. | 7.8 | 15 |
| 35 | Cultural prerequisites of socioeconomic development. <i>Royal Society Open Science</i> , 2020, 7, 190725. | 2.4 | 13 |
| 36 | Population genetic considerations for using biobanks as international resources in the pandemic era and beyond. <i>BMC Genomics</i> , 2021, 22, 351. | 2.8 | 11 |

| # | ARTICLE | IF | CITATIONS |
|----|---|------|-----------|
| 37 | Past acidification and recovery of surface waters, soils and ecology in the United Kingdom: Prospects for the future under current deposition and land use protocols. <i>Ecological Indicators</i> , 2014, 37, 381-395. | 6.3 | 9 |
| 38 | Diversity as a product of inter-specific interactions. <i>Journal of Theoretical Biology</i> , 2006, 243, 299-307. | 1.7 | 8 |
| 39 | Meta-Analysis of Mid- <i>p</i> -Values: Some New Results based on the Convex Order. <i>Journal of the American Statistical Association</i> , 2019, 114, 1105-1112. | 3.1 | 8 |
| 40 | Is Dupuytren's disease really a "disease of the Vikings"? <i>Journal of Hand Surgery: European Volume</i> , 2020, 45, 273-279. | 1.0 | 8 |
| 41 | Genetic drift from the out-of-Africa bottleneck leads to biased estimation of genetic architecture and selection. <i>European Journal of Human Genetics</i> , 2021, 29, 1549-1556. | 2.8 | 8 |
| 42 | Anomaly detection for cyber security applications. <i>Security Science and Technology</i> , 2016, , 137-156. | 0.5 | 7 |
| 43 | Apparent Strength Conceals Instability in a Model for the Collapse of Historical States. <i>PLoS ONE</i> , 2014, 9, e96523. | 2.5 | 4 |
| 44 | Bayesian analysis of non-linear differential equation models with application to a gut microbial ecosystem. <i>Biometrical Journal</i> , 2011, 53, 543-556. | 1.0 | 3 |
| 45 | A Chromosome-Painting-Based Pipeline to Infer Local Ancestry under Limited Source Availability. <i>Genome Biology and Evolution</i> , 2021, 13, . | 2.5 | 3 |
| 46 | Understanding Clustering in Type Space Using Field Theoretic Techniques. <i>Bulletin of Mathematical Biology</i> , 2008, 70, 1065-1081. | 1.9 | 2 |
| 47 | The role of weak selection and high mutation rates in nearly neutral evolution. <i>Journal of Theoretical Biology</i> , 2009, 257, 696-703. | 1.7 | 1 |
| 48 | Heritable contributions versus genetic architecture. <i>Nature Reviews Genetics</i> , 2018, 19, 185-185. | 16.3 | 1 |
| 49 | CLARITY: comparing heterogeneous data using dissimilarity. <i>Royal Society Open Science</i> , 2021, 8, 202182. | 2.4 | 0 |