

# 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	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
2	A Chromosome-Painting-Based Pipeline to Infer Local Ancestry under Limited Source Availability. <i>Genome Biology and Evolution</i> , 2021, 13, .	2.5	3
3	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
4	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
5	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
6	Genomic and phenotypic insights from an atlas of genetic effects on DNA methylation. <i>Nature Genetics</i> , 2021, 53, 1311-1321.	21.4	218
7	CLARITY: comparing heterogeneous data using dissimilarity. <i>Royal Society Open Science</i> , 2021, 8, 202182.	2.4	0
8	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
9	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
10	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
11	Population genomics of the Viking world. <i>Nature</i> , 2020, 585, 390-396.	27.8	143
12	Cultural prerequisites of socioeconomic development. <i>Royal Society Open Science</i> , 2020, 7, 190725.	2.4	13
13	Apparent latent structure within the UK Biobank sample has implications for epidemiological analysis. <i>Nature Communications</i> , 2019, 10, 333.	12.8	240
14	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
15	Multiple Deeply Divergent Denisovan Ancestries in Papuans. <i>Cell</i> , 2019, 177, 1010-1021.e32.	28.9	181
16	Genetic evidence for assortative mating on alcohol consumption in the UK Biobank. <i>Nature Communications</i> , 2019, 10, 5039.	12.8	48
17	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
18	RADpainter and fineRADstructure: Population Inference from RADseq Data. <i>Molecular Biology and Evolution</i> , 2018, 35, 1284-1290.	8.9	265

#	ARTICLE	IF	CITATIONS
19	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
20	Heritable contributions versus genetic architecture. <i>Nature Reviews Genetics</i> , 2018, 19, 185-185.	16.3	1
21	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
22	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
23	Religious change preceded economic change in the 20th century. <i>Science Advances</i> , 2018, 4, eaar8680.	10.3	30
24	A tutorial on how not to over-interpret STRUCTURE and ADMIXTURE bar plots. <i>Nature Communications</i> , 2018, 9, 3258.	12.8	341
25	Genomewide analysis of admixture and adaptation in the Africanized honeybee. <i>Molecular Ecology</i> , 2017, 26, 3603-3617.	3.9	44
26	Complex Patterns of Admixture across the Indonesian Archipelago. <i>Molecular Biology and Evolution</i> , 2017, 34, 2439-2452.	8.9	65
27	The Irish DNA Atlas: Revealing Fine-Scale Population Structure and History within Ireland. <i>Scientific Reports</i> , 2017, 7, 17199.	3.3	29
28	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
29	Rapid evolution of distinct <i>Helicobacter pylori</i> subpopulations in the Americas. <i>PLoS Genetics</i> , 2017, 13, e1006546.	3.5	73
30	Genomic analyses inform on migration events during the peopling of Eurasia. <i>Nature</i> , 2016, 538, 238-242.	27.8	360
31	Anomaly detection for cyber security applications. <i>Security Science and Technology</i> , 2016, , 137-156.	0.5	7
32	The fine-scale genetic structure of the British population. <i>Nature</i> , 2015, 519, 309-314.	27.8	416
33	The UK10K project identifies rare variants in health and disease. <i>Nature</i> , 2015, 526, 82-90.	27.8	1,014
34	Apparent Strength Conceals Instability in a Model for the Collapse of Historical States. <i>PLoS ONE</i> , 2014, 9, e96523.	2.5	4
35	Genome-Wide Analysis of Cold Adaptation in Indigenous Siberian Populations. <i>PLoS ONE</i> , 2014, 9, e98076.	2.5	128
36	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

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37	Performance comparison of renewable incentive schemes using optimal control. <i>Energy</i> , 2014, 64, 44-57.	8.8	21
38	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
39	Inference of Population Structure using Dense Haplotype Data. <i>PLoS Genetics</i> , 2012, 8, e1002453.	3.5	983
40	Population Identification Using Genetic Data. <i>Annual Review of Genomics and Human Genetics</i> , 2012, 13, 337-361.	6.2	76
41	Likelihood-free estimation of model evidence. <i>Bayesian Analysis</i> , 2011, 6, .	3.0	74
42	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
43	Inference of Homologous Recombination in Bacteria Using Whole-Genome Sequences. <i>Genetics</i> , 2010, 186, 1435-1449.	2.9	155
44	SimMLST: simulation of multi-locus sequence typing data under a neutral model. <i>Bioinformatics</i> , 2009, 25, 1442-1444.	4.1	21
45	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
46	Understanding Clustering in Type Space Using Field Theoretic Techniques. <i>Bulletin of Mathematical Biology</i> , 2008, 70, 1065-1081.	1.9	2
47	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
48	Diversity as a product of inter-specific interactions. <i>Journal of Theoretical Biology</i> , 2006, 243, 299-307.	1.7	8
49	The species-area relationship and evolution. <i>Journal of Theoretical Biology</i> , 2006, 241, 590-600.	1.7	27