

# Daniel Wegmann

## List of Publications by Year in descending order

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Version: 2024-02-01

53  
papers

4,826  
citations

147726

31  
h-index

189801

50  
g-index

67  
all docs

67  
docs citations

67  
times ranked

9095  
citing authors

#	ARTICLE	IF	CITATIONS
1	The genomic origins of the world's first farmers. <i>Cell</i> , 2022, 185, 1842-1859.e18.	13.5	39
2	A sparse observation model to quantify species distributions and their overlap in space and time. <i>Ecography</i> , 2021, 44, 928-940.	2.1	7
3	Runes from Lány (Czech Republic) - The oldest inscription among Slavs. A new standard for multidisciplinary analysis of runic bones. <i>Journal of Archaeological Science</i> , 2021, 127, 105333.	1.2	5
4	Identifying loci under selection via explicit demographic models. <i>Molecular Ecology Resources</i> , 2021, 21, 2719-2737.	2.2	8
5	Selection on ancestral genetic variation fuels repeated ecotype formation in bottlenose dolphins. <i>Science Advances</i> , 2021, 7, eabg1245.	4.7	27
6	Trophic niche shifts and phenotypic trait evolution are largely decoupled in Australasian parrots. <i>Bmc Ecology and Evolution</i> , 2021, 21, 212.	0.7	0
7	Apex predators decline after an influx of pastoralists in former Central African Republic hunting zones. <i>Biological Conservation</i> , 2020, 241, 108326.	1.9	11
8	Low Prevalence of Lactase Persistence in Bronze Age Europe Indicates Ongoing Strong Selection over the Last 3,000 Years. <i>Current Biology</i> , 2020, 30, 4307-4315.e13.	1.8	54
9	Detecting Selection from Linked Sites Using an <i>i</i> -Model. <i>Genetics</i> , 2020, 216, 1205-1215.	1.2	6
10	Inference of natural selection from ancient DNA. <i>Evolution Letters</i> , 2020, 4, 94-108.	1.6	58
11	Estimating and accounting for genotyping errors in RAD-seq experiments. <i>Molecular Ecology Resources</i> , 2020, 20, 856-870.	2.2	34
12	Evolutionary transcriptomics reveals the origins of olives and the genomic changes associated with their domestication. <i>Plant Journal</i> , 2019, 100, 143-157.	2.8	64
13	Admixture mapping in interspecific <i>Populus</i> hybrids identifies classes of genomic architectures for phytochemical, morphological and growth traits. <i>New Phytologist</i> , 2019, 223, 2076-2089.	3.5	21
14	Population genomic analysis of elongated skulls reveals extensive female-biased immigration in Early Medieval Bavaria. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2018, 115, 3494-3499.	3.3	73
15	Ancient human parallel lineages within North America contributed to a coastal expansion. <i>Science</i> , 2018, 360, 1024-1027.	6.0	138
16	A Guide to General-Purpose ABC Software. , 2018, , 369-413.		7
17	Inference of Evolutionary Jumps in Large Phylogenies using <i>vy</i> Processes. <i>Systematic Biology</i> , 2017, 66, 950-963.	2.7	47
18	The Discovery of Wild Date Palms in Oman Reveals a Complex Domestication History Involving Centers in the Middle East and Africa. <i>Current Biology</i> , 2017, 27, 2211-2218.e8.	1.8	63

#	ARTICLE	IF	CITATIONS
19	First quantitative survey delineates the distribution of chimpanzees in the Eastern Central African Republic. <i>Biological Conservation</i> , 2017, 213, 84-94.	1.9	10
20	Inferring Heterozygosity from Ancient and Low Coverage Genomes. <i>Genetics</i> , 2017, 205, 317-332.	1.2	39
21	Normalisation against Circadian and Age-Related Disturbances Enables Robust Detection of Gene Expression Changes in Liver of Aged Mice. <i>PLoS ONE</i> , 2017, 12, e0169615.	1.1	6
22	Sino-Himalayan mountains act as cradles of diversity and immigration centres in the diversification of parrotbills (Paradoxornithidae). <i>Journal of Biogeography</i> , 2016, 43, 1488-1501.	1.4	40
23	An Approximate Markov Model for the Wright-Fisher Diffusion and Its Application to Time Series Data. <i>Genetics</i> , 2016, 203, 831-846.	1.2	70
24	Likelihood-Free Inference in High-Dimensional Models. <i>Genetics</i> , 2016, 203, 893-904.	1.2	29
25	Early Neolithic genomes from the eastern Fertile Crescent. <i>Science</i> , 2016, 353, 499-503.	6.0	230
26	Early farmers from across Europe directly descended from Neolithic Aegeans. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2016, 113, 6886-6891.	3.3	376
27	Selection against recombinant hybrids maintains reproductive isolation in hybridizing <i>Populus</i> species despite $F_1$ fertility and recurrent gene flow. <i>Molecular Ecology</i> , 2016, 25, 2482-2498.	2.0	95
28	Prospects and challenges for the conservation of farm animal genomic resources, 2015-2025. <i>Frontiers in Genetics</i> , 2015, 6, 314.	1.1	64
29	Influenza Virus Drug Resistance: A Time-Sampled Population Genetics Perspective. <i>PLoS Genetics</i> , 2014, 10, e1004185.	1.5	126
30	Recipient of the 2013 <i>Molecular Ecology</i> Prize: Laurent Excoffier. <i>Molecular Ecology</i> , 2014, 23, 16-19.	2.0	0
31	Demographic history of a recent invasion of house mice on the isolated island of Gough. <i>Molecular Ecology</i> , 2014, 23, 1923-1939.	2.0	50
32	Postglacial expansion and not human influence best explains the population structure in the endangered kea ( <i>Nestor notabilis</i> ). <i>Molecular Ecology</i> , 2014, 23, 2193-2209.	2.0	32
33	Analysis of rare variant population structure in Europeans explains differential stratification of gene-based tests. <i>European Journal of Human Genetics</i> , 2014, 22, 1137-1144.	1.4	21
34	<i>Drosophila suzukii</i> : The Genetic Footprint of a Recent, Worldwide Invasion. <i>Molecular Biology and Evolution</i> , 2014, 31, 3148-3163.	3.5	70
35	The influence of genomic context on mutation patterns in the human genome inferred from rare variants. <i>Genome Research</i> , 2013, 23, 1974-1984.	2.4	51
36	Inferring the Geographic Mode of Speciation by Contrasting Autosomal and Sex-Linked Genetic Diversity. <i>Molecular Biology and Evolution</i> , 2013, 30, 2519-2530.	3.5	19

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37	An Early Divergence of KhoeSan Ancestors from Those of Other Modern Humans Is Supported by an ABC-Based Analysis of Autosomal Resequencing Data. <i>Molecular Biology and Evolution</i> , 2012, 29, 617-630.	3.5	125
38	Bayesian inference analyses of the polygenic architecture of rheumatoid arthritis. <i>Nature Genetics</i> , 2012, 44, 483-489.	9.4	402
39	An Abundance of Rare Functional Variants in 202 Drug Target Genes Sequenced in 14,002 People. <i>Science</i> , 2012, 337, 100-104.	6.0	626
40	Deep sequencing of the <i>LRRK2</i> gene in 14,002 individuals reveals evidence of purifying selection and independent origin of the p.Arg1628Pro mutation in Europe. <i>Human Mutation</i> , 2012, 33, 1087-1098.	1.1	24
41	FITTING MODELS OF CONTINUOUS TRAIT EVOLUTION TO INCOMPLETELY SAMPLED COMPARATIVE DATA USING APPROXIMATE BAYESIAN COMPUTATION. <i>Evolution; International Journal of Organic Evolution</i> , 2012, 66, 752-762.	1.1	77
42	Recombination rates in admixed individuals identified by ancestry-based inference. <i>Nature Genetics</i> , 2011, 43, 847-853.	9.4	111
43	Genetic variation in the Sorbs of eastern Germany in the context of broader European genetic diversity. <i>European Journal of Human Genetics</i> , 2011, 19, 995-1001.	1.4	59
44	Historical sampling reveals dramatic demographic changes in western gorilla populations. <i>BMC Evolutionary Biology</i> , 2011, 11, 85.	3.2	45
45	ABCtoolbox: a versatile toolkit for approximate Bayesian computations. <i>BMC Bioinformatics</i> , 2010, 11, 116.	1.2	309
46	Distinguishing between population bottleneck and population subdivision by a Bayesian model choice procedure. <i>Molecular Ecology</i> , 2010, 19, 4648-4660.	2.0	110
47	Bayesian Computation and Model Selection Without Likelihoods. <i>Genetics</i> , 2010, 184, 243-252.	1.2	150
48	A Statistical Evaluation of Models for the Initial Settlement of the American Continent Emphasizes the Importance of Gene Flow with Asia. <i>Molecular Biology and Evolution</i> , 2010, 27, 337-345.	3.5	97
49	Bayesian Inference of the Demographic History of Chimpanzees. <i>Molecular Biology and Evolution</i> , 2010, 27, 1425-1435.	3.5	111
50	Efficient Approximate Bayesian Computation Coupled With Markov Chain Monte Carlo Without Likelihood. <i>Genetics</i> , 2009, 182, 1207-1218.	1.2	266
51	Large Allele Frequency Differences between Human Continental Groups are more Likely to have Occurred by Drift During range Expansions than by Selection. <i>Annals of Human Genetics</i> , 2009, 73, 95-108.	0.3	140
52	Width of Gene Expression Profile Drives Alternative Splicing. <i>PLoS ONE</i> , 2008, 3, e3587.	1.1	13
53	Molecular Diversity After a Range Expansion in Heterogeneous Environments. <i>Genetics</i> , 2006, 174, 2009-2020.	1.2	74