

Daniel Wegmann

List of Publications by Year in descending order

Source: <https://exaly.com/author-pdf/8553714/publications.pdf>

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 | 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 |
| 2 | Bayesian inference analyses of the polygenic architecture of rheumatoid arthritis. <i>Nature Genetics</i> , 2012, 44, 483-489. | 9.4 | 402 |
| 3 | 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 |
| 4 | ABCtoolbox: a versatile toolkit for approximate Bayesian computations. <i>BMC Bioinformatics</i> , 2010, 11, 116. | 1.2 | 309 |
| 5 | Efficient Approximate Bayesian Computation Coupled With Markov Chain Monte Carlo Without Likelihood. <i>Genetics</i> , 2009, 182, 1207-1218. | 1.2 | 266 |
| 6 | Early Neolithic genomes from the eastern Fertile Crescent. <i>Science</i> , 2016, 353, 499-503. | 6.0 | 230 |
| 7 | Bayesian Computation and Model Selection Without Likelihoods. <i>Genetics</i> , 2010, 184, 243-252. | 1.2 | 150 |
| 8 | 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 |
| 9 | Ancient human parallel lineages within North America contributed to a coastal expansion. <i>Science</i> , 2018, 360, 1024-1027. | 6.0 | 138 |
| 10 | Influenza Virus Drug Resistance: A Time-Sampled Population Genetics Perspective. <i>PLoS Genetics</i> , 2014, 10, e1004185. | 1.5 | 126 |
| 11 | 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 |
| 12 | Bayesian Inference of the Demographic History of Chimpanzees. <i>Molecular Biology and Evolution</i> , 2010, 27, 1425-1435. | 3.5 | 111 |
| 13 | Recombination rates in admixed individuals identified by ancestry-based inference. <i>Nature Genetics</i> , 2011, 43, 847-853. | 9.4 | 111 |
| 14 | Distinguishing between population bottleneck and population subdivision by a Bayesian model choice procedure. <i>Molecular Ecology</i> , 2010, 19, 4648-4660. | 2.0 | 110 |
| 15 | 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 |
| 16 | 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 |
| 17 | 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 |
| 18 | Molecular Diversity After a Range Expansion in Heterogeneous Environments. <i>Genetics</i> , 2006, 174, 2009-2020. | 1.2 | 74 |

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|----|---|------|-----------|
| 19 | 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 |
| 20 | <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 |
| 21 | An Approximate Markov Model for the Wright's Fisher Diffusion and Its Application to Time Series Data. <i>Genetics</i> , 2016, 203, 831-846. | 1.2 | 70 |
| 22 | Prospects and challenges for the conservation of farm animal genomic resources, 2015-2025. <i>Frontiers in Genetics</i> , 2015, 6, 314. | 1.1 | 64 |
| 23 | 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 |
| 24 | 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 |
| 25 | 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 |
| 26 | Inference of natural selection from ancient DNA. <i>Evolution Letters</i> , 2020, 4, 94-108. | 1.6 | 58 |
| 27 | 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 |
| 28 | 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 |
| 29 | 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 |
| 30 | Inference of Evolutionary Jumps in Large Phylogenies using Levy Processes. <i>Systematic Biology</i> , 2017, 66, 950-963. | 2.7 | 47 |
| 31 | Historical sampling reveals dramatic demographic changes in western gorilla populations. <i>BMC Evolutionary Biology</i> , 2011, 11, 85. | 3.2 | 45 |
| 32 | 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 |
| 33 | Inferring Heterozygosity from Ancient and Low Coverage Genomes. <i>Genetics</i> , 2017, 205, 317-332. | 1.2 | 39 |
| 34 | The genomic origins of the world's first farmers. <i>Cell</i> , 2022, 185, 1842-1859.e18. | 13.5 | 39 |
| 35 | Estimating and accounting for genotyping errors in RADseq experiments. <i>Molecular Ecology Resources</i> , 2020, 20, 856-870. | 2.2 | 34 |
| 36 | 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 |

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|----|--|-----|-----------|
| 37 | Likelihood-Free Inference in High-Dimensional Models. <i>Genetics</i> , 2016, 203, 893-904. | 1.2 | 29 |
| 38 | Selection on ancestral genetic variation fuels repeated ecotype formation in bottlenose dolphins. <i>Science Advances</i> , 2021, 7, eabg1245. | 4.7 | 27 |
| 39 | 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 |
| 40 | 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 |
| 41 | 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 |
| 42 | 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 |
| 43 | Width of Gene Expression Profile Drives Alternative Splicing. <i>PLoS ONE</i> , 2008, 3, e3587. | 1.1 | 13 |
| 44 | 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 |
| 45 | 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 |
| 46 | Identifying loci under selection via explicit demographic models. <i>Molecular Ecology Resources</i> , 2021, 21, 2719-2737. | 2.2 | 8 |
| 47 | 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 |
| 48 | A Guide to General-Purpose ABC Software. , 2018, , 369-413. | | 7 |
| 49 | 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 |
| 50 | Detecting Selection from Linked Sites Using an <i>F</i> -Model. <i>Genetics</i> , 2020, 216, 1205-1215. | 1.2 | 6 |
| 51 | Runes from L'Áiny (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 |
| 52 | Recipient of the 2013 <i>Molecular Ecology</i> Prize: Laurent Excoffier. <i>Molecular Ecology</i> , 2014, 23, 16-19. | 2.0 | 0 |
| 53 | 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 |