

# David Diez-del-Molino

## List of Publications by Year in descending order

Source: <https://exaly.com/author-pdf/7037831/publications.pdf>

Version: 2024-02-01

31  
papers

1,817  
citations

430754

18  
h-index

477173

29  
g-index

33  
all docs

33  
docs citations

33  
times ranked

3104  
citing authors

#	ARTICLE	IF	CITATIONS
1	Ancient and historical DNA in conservation policy. <i>Trends in Ecology and Evolution</i> , 2022, 37, 420-429.	4.2	31
2	GenErode: a bioinformatics pipeline to investigate genome erosion in endangered and extinct species. <i>BMC Bioinformatics</i> , 2022, 23, .	1.2	14
3	Million-year-old DNA sheds light on the genomic history of mammoths. <i>Nature</i> , 2021, 591, 265-269.	13.7	179
4	Genomic insights into the conservation status of the world's last remaining Sumatran rhinoceros populations. <i>Nature Communications</i> , 2021, 12, 2393.	5.8	39
5	Combining Bayesian age models and genetics to investigate population dynamics and extinction of the last mammoths in northern Siberia. <i>Quaternary Science Reviews</i> , 2021, 259, 106913.	1.4	14
6	<i>Mammuthus</i> sp. (Early and Middle Pleistocene Mammoths). <i>Trends in Genetics</i> , 2021, 37, 682-683.	2.9	0
7	Integrating multi-taxon palaeogenomes and sedimentary ancient DNA to study past ecosystem dynamics. <i>Proceedings of the Royal Society B: Biological Sciences</i> , 2021, 288, 20211252.	1.2	14
8	Population genomics of the critically endangered <i>Arctophila</i> . <i>Cell Genomics</i> , 2021, 1, 100002.	3.0	106
9	Pre-extinction Demographic Stability and Genomic Signatures of Adaptation in the Woolly Rhinoceros. <i>Current Biology</i> , 2020, 30, 3871-3879.e7.	1.8	41
10	Population genomics reveals lack of greater white-fronted introgression into the Swedish lesser white-fronted goose. <i>Scientific Reports</i> , 2020, 10, 18347.	1.6	9
11	Competitive mapping allows for the identification and exclusion of human DNA contamination in ancient faunal genomic datasets. <i>BMC Genomics</i> , 2020, 21, 844.	1.2	15
12	Moose genomes reveal past glacial demography and the origin of modern lineages. <i>BMC Genomics</i> , 2020, 21, 854.	1.2	23
13	Unroll Please: Deciphering the Genetic Code in Scrolls and Other Ancient Materials. <i>Cell</i> , 2020, 181, 1200-1201.	13.5	1
14	Inference of natural selection from ancient DNA. <i>Evolution Letters</i> , 2020, 4, 94-108.	1.6	58
15	The Arrival of Siberian Ancestry Connecting the Eastern Baltic to Uralic Speakers further East. <i>Current Biology</i> , 2019, 29, 1701-1711.e16.	1.8	80
16	A western route of prehistoric human migration from Africa into the Iberian Peninsula. <i>Proceedings of the Royal Society B: Biological Sciences</i> , 2019, 286, 20182288.	1.2	47
17	Consequences of past climate change and recent human persecution on mitogenomic diversity in the arctic fox. <i>Philosophical Transactions of the Royal Society B: Biological Sciences</i> , 2019, 374, 20190212.	1.8	12
18	Historical Genomes Reveal the Genomic Consequences of Recent Population Decline in Eastern Gorillas. <i>Current Biology</i> , 2019, 29, 165-170.e6.	1.8	126

#	ARTICLE	IF	CITATIONS
19	Quantifying Temporal Genomic Erosion in Endangered Species. Trends in Ecology and Evolution, 2018, 33, 176-185.	4.2	162
20	Effects of water pollution and river fragmentation on population genetic structure of invasive mosquitofish. Science of the Total Environment, 2018, 637-638, 1372-1382.	3.9	19
21	Genome-Based Sexing Provides Clues about Behavior and Social Structure in the Woolly Mammoth. Current Biology, 2017, 27, 3505-3510.e3.	1.8	53
22	Mitogenome evolution in the last surviving woolly mammoth population reveals neutral and functional consequences of small population size. Evolution Letters, 2017, 1, 292-303.	1.6	22
23	Multiple paternity and reproduction opportunities for invasive mosquitofish. Hydrobiologia, 2017, 795, 139-151.	1.0	8
24	Changes in variation at the MHC class II DQA locus during the final demise of the woolly mammoth. Scientific Reports, 2016, 6, 25274.	1.6	26
25	Early Neolithic genomes from the eastern Fertile Crescent. Science, 2016, 353, 499-503.	6.0	230
26	Early farmers from across Europe directly descended from Neolithic Aegeans. Proceedings of the National Academy of Sciences of the United States of America, 2016, 113, 6886-6891.	3.3	376
27	Genomic survey provides insights into the evolutionary changes that occurred during European expansion of the invasive mosquitofish ( <i>Gambusia holbrooki</i> ). Molecular Ecology, 2016, 25, 1089-1105.	2.0	38
28	Temporal genetic dynamics among mosquitofish ( <i>Gambusia holbrooki</i> ) populations in invaded watersheds. Biological Invasions, 2016, 18, 841-855.	1.2	7
29	Genetic characterization of the invasive mosquitofish ( <i>Gambusia</i> spp.) introduced to Europe: population structure and colonization routes. Biological Invasions, 2013, 15, 2333-2346.	1.2	24
30	Gene Flow and Maintenance of Genetic Diversity in Invasive Mosquitofish ( <i>Gambusia holbrooki</i> ). PLoS ONE, 2013, 8, e82501.	1.1	28
31	SNP diversity in introduced populations of the invasive <i>Gambusia holbrooki</i> . Ecology of Freshwater Fish, 2012, 21, 100-108.	0.7	11