

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 | 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 |
| 2 | Early Neolithic genomes from the eastern Fertile Crescent. <i>Science</i> , 2016, 353, 499-503. | 6.0 | 230 |
| 3 | Million-year-old DNA sheds light on the genomic history of mammoths. <i>Nature</i> , 2021, 591, 265-269. | 13.7 | 179 |
| 4 | Quantifying Temporal Genomic Erosion in Endangered Species. <i>Trends in Ecology and Evolution</i> , 2018, 33, 176-185. | 4.2 | 162 |
| 5 | 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 |
| 6 | Population genomics of the critically endangered kākāpō. <i>Cell Genomics</i> , 2021, 1, 100002. | 3.0 | 106 |
| 7 | 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 |
| 8 | Inference of natural selection from ancient DNA. <i>Evolution Letters</i> , 2020, 4, 94-108. | 1.6 | 58 |
| 9 | Genome-Based Sexing Provides Clues about Behavior and Social Structure in the Woolly Mammoth. <i>Current Biology</i> , 2017, 27, 3505-3510.e3. | 1.8 | 53 |
| 10 | 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 |
| 11 | 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 |
| 12 | 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 |
| 13 | Genomic survey provides insights into the evolutionary changes that occurred during European expansion of the invasive mosquitofish (<i>Gambusia holbrooki</i>). <i>Molecular Ecology</i> , 2016, 25, 1089-1105. | 2.0 | 38 |
| 14 | Ancient and historical DNA in conservation policy. <i>Trends in Ecology and Evolution</i> , 2022, 37, 420-429. | 4.2 | 31 |
| 15 | Gene Flow and Maintenance of Genetic Diversity in Invasive Mosquitofish (<i>Gambusia holbrooki</i>). <i>PLoS ONE</i> , 2013, 8, e82501. | 1.1 | 28 |
| 16 | Changes in variation at the MHC class II DQA locus during the final demise of the woolly mammoth. <i>Scientific Reports</i> , 2016, 6, 25274. | 1.6 | 26 |
| 17 | Genetic characterization of the invasive mosquitofish (<i>Gambusia</i> spp.) introduced to Europe: population structure and colonization routes. <i>Biological Invasions</i> , 2013, 15, 2333-2346. | 1.2 | 24 |
| 18 | Moose genomes reveal past glacial demography and the origin of modern lineages. <i>BMC Genomics</i> , 2020, 21, 854. | 1.2 | 23 |

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|----|---|------|-----------|
| 19 | Mitogenome evolution in the last surviving woolly mammoth population reveals neutral and functional consequences of small population size. <i>Evolution Letters</i> , 2017, 1, 292-303. | 1.6 | 22 |
| 20 | Effects of water pollution and river fragmentation on population genetic structure of invasive mosquitofish. <i>Science of the Total Environment</i> , 2018, 637-638, 1372-1382. | 3.9 | 19 |
| 21 | 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 |
| 22 | 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 |
| 23 | 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 |
| 24 | GenErode: a bioinformatics pipeline to investigate genome erosion in endangered and extinct species. <i>BMC Bioinformatics</i> , 2022, 23, . | 1.2 | 14 |
| 25 | 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 |
| 26 | SNP diversity in introduced populations of the invasive <i>Gambusia holbrooki</i> . <i>Ecology of Freshwater Fish</i> , 2012, 21, 100-108. | 0.7 | 11 |
| 27 | 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 |
| 28 | Multiple paternity and reproduction opportunities for invasive mosquitofish. <i>Hydrobiologia</i> , 2017, 795, 139-151. | 1.0 | 8 |
| 29 | Temporal genetic dynamics among mosquitofish (<i>Gambusia holbrooki</i>) populations in invaded watersheds. <i>Biological Invasions</i> , 2016, 18, 841-855. | 1.2 | 7 |
| 30 | Unroll Please: Deciphering the Genetic Code in Scrolls and Other Ancient Materials. <i>Cell</i> , 2020, 181, 1200-1201. | 13.5 | 1 |
| 31 | <i>Mammuthus</i> sp. (Early and Middle Pleistocene Mammoths). <i>Trends in Genetics</i> , 2021, 37, 682-683. | 2.9 | 0 |