

Eline D Lorenzen

List of Publications by Year in descending order

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Version: 2024-02-01

49
papers

4,014
citations

236925

25
h-index

214800

47
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56
all docs

56
docs citations

56
times ranked

6887
citing authors

#	ARTICLE	IF	CITATIONS
1	Ancient human genome sequence of an extinct Palaeo-Eskimo. <i>Nature</i> , 2010, 463, 757-762.	27.8	750
2	Species-specific responses of Late Quaternary megafauna to climate and humans. <i>Nature</i> , 2011, 479, 359-364.	27.8	586
3	Fifty thousand years of Arctic vegetation and megafaunal diet. <i>Nature</i> , 2014, 506, 47-51.	27.8	505
4	Population Genomics Reveal Recent Speciation and Rapid Evolutionary Adaptation in Polar Bears. <i>Cell</i> , 2014, 157, 785-794.	28.9	363
5	Ancient Hybridization and an Irish Origin for the Modern Polar Bear Matriline. <i>Current Biology</i> , 2011, 21, 1251-1258.	3.9	257
6	Population characteristics of a large whale shark aggregation inferred from seawater environmental DNA. <i>Nature Ecology and Evolution</i> , 2017, 1, 4.	7.8	223
7	Comparative phylogeography of African savannah ungulates ¹ . <i>Molecular Ecology</i> , 2012, 21, 3656-3670.	3.9	197
8	Extinct New Zealand megafauna were not in decline before human colonization. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2014, 111, 4922-4927.	7.1	109
9	Big data little help in megafauna mysteries. <i>Nature</i> , 2018, 558, 23-25.	27.8	69
10	Are There Really Twice as Many Bovid Species as We Thought?. <i>Systematic Biology</i> , 2013, 62, 490-493.	5.6	64
11	Pros and cons of methylation-based enrichment methods for ancient DNA. <i>Scientific Reports</i> , 2015, 5, 11826.	3.3	61
12	Inference of natural selection from ancient DNA. <i>Evolution Letters</i> , 2020, 4, 94-108.	3.3	58
13	Mid-Holocene decline in African buffalos inferred from Bayesian coalescent-based analyses of microsatellites and mitochondrial DNA. <i>Molecular Ecology</i> , 2008, 17, 4845-4858.	3.9	50
14	High variation and very low differentiation in wide ranging plains zebra (<i>Equus quagga</i>): insights from mtDNA and microsatellites. <i>Molecular Ecology</i> , 2008, 17, 2812-2824.	3.9	49
15	Narwhal Genome Reveals Long-Term Low Genetic Diversity despite Current Large Abundance Size. <i>IScience</i> , 2019, 15, 592-599.	4.1	49
16	Ancient and modern genomes unravel the evolutionary history of the rhinoceros family. <i>Cell</i> , 2021, 184, 4874-4885.e16.	28.9	49
17	A long-standing Pleistocene refugium in southern Africa and a mosaic of refugia in East Africa: insights from mtDNA and the common eland antelope. <i>Journal of Biogeography</i> , 2010, 37, 571-581.	3.0	45
18	Pre-extinction Demographic Stability and Genomic Signatures of Adaptation in the Woolly Rhinoceros. <i>Current Biology</i> , 2020, 30, 3871-3879.e7.	3.9	41

#	ARTICLE	IF	CITATIONS
19	Regional Genetic Structuring and Evolutionary History of the Impala <i>Aepyceros melampus</i> . <i>Journal of Heredity</i> , 2006, 97, 119-132.	2.4	40
20	Influence of past climate change on phylogeography and demographic history of narwhals, <i>Monodon monoceros</i> . <i>Proceedings of the Royal Society B: Biological Sciences</i> , 2020, 287, 20192964.	2.6	39
21	Hybridization between subspecies of waterbuck (<i>Kobus ellipsiprymnus</i>) in zones of overlap with limited introgression. <i>Molecular Ecology</i> , 2006, 15, 3787-3799.	3.9	34
22	Phylogenetic Estimation of Timescales Using Ancient DNA: The Effects of Temporal Sampling Scheme and Uncertainty in Sample Ages. <i>Molecular Biology and Evolution</i> , 2012, 30, 253-262.	8.9	34
23	Hybridization between two high Arctic cetaceans confirmed by genomic analysis. <i>Scientific Reports</i> , 2019, 9, 7729.	3.3	33
24	Phylogeography, hybridization and Pleistocene refugia of the kob antelope (<i>Kobus kob</i>). <i>Molecular Ecology</i> , 2007, 16, 3241-3252.	3.9	31
25	Evolutionary history and palaeoecology of brown bear in North-East Siberia re-examined using ancient DNA and stable isotopes from skeletal remains. <i>Scientific Reports</i> , 2019, 9, 4462.	3.3	29
26	Evaluating the role of reference genome phylogenetic distance on evolutionary inference. <i>Molecular Ecology Resources</i> , 2022, 22, 45-55.	4.8	28
27	No suggestion of hybridization between the vulnerable black-faced impala (<i>Aepyceros melampus</i>) Tj ETQq1 1 0.784314 rgBT /Overl 2004, 13, 3007-3019.	3.9	25
28	Population-specific sex and size variation in long-term foraging ecology of belugas and narwhals. <i>Royal Society Open Science</i> , 2021, 8, 202226.	2.4	21
29	Three reciprocally monophyletic mtDNA lineages elucidate the taxonomic status of Grant's gazelles. <i>Conservation Genetics</i> , 2008, 9, 593-601.	1.5	20
30	Is Diagnosability an Indicator of Speciation? Response to "Why One Century of Phenetics Is Enough". <i>Systematic Biology</i> , 2014, 63, 833-837.	5.6	19
31	Late Pleistocene paleoecology and phylogeography of woolly rhinoceroses. <i>Quaternary Science Reviews</i> , 2021, 263, 106993.	3.0	18
32	Persistent organic pollutants, skull size and bone density of polar bears (<i>Ursus maritimus</i>) from East Greenland 1892-2015 and Svalbard 1964-2004. <i>Environmental Research</i> , 2018, 162, 74-80.	7.5	17
33	Genomic analyses reveal an absence of contemporary introgressive admixture between fin whales and blue whales, despite known hybrids. <i>PLoS ONE</i> , 2019, 14, e0222004.	2.5	15
34	King Tutankhamun's Family and Demise. <i>JAMA - Journal of the American Medical Association</i> , 2010, 303, 2471.	7.4	13
35	Circumpolar phylogeography and demographic history of beluga whales reflect past climatic fluctuations. <i>Molecular Ecology</i> , 2021, 30, 2543-2559.	3.9	12
36	Micro Methods for Megafauna: Novel Approaches to Late Quaternary Extinctions and Their Contributions to Faunal Conservation in the Anthropocene. <i>BioScience</i> , 2019, 69, 877-887.	4.9	11

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37	Ocean-wide genomic variation in Gray's beaked whales, <i>Mesoplodon grayi</i> . Royal Society Open Science, 2021, 8, 201788.	2.4	11
38	A Genetic Perspective on Cetacean Evolution. Annual Review of Ecology, Evolution, and Systematics, 2021, 52, 131-151.	8.3	8
39	Population genetic structure of the intertidal kinorhynch <i>Echinoderes marthae</i> (Kinorhyncha). Tj ETQq1 1 0.784314 rgBT /Overl Society of Washington, 2018, 131, 36-46.	0.3	4
40	Analyses of key genes involved in Arctic adaptation in polar bears suggest selection on both standing variation and de novo mutations played an important role. BMC Genomics, 2020, 21, 543.	2.8	3
41	Diet and environment of <i>Myiodon darwinii</i> based on pollen of a Late-Glacial coprolite from the Myiodon Cave in southern Chile. Review of Palaeobotany and Palynology, 2022, 296, 104549.	1.5	3
42	A genomic exploration of the early evolution of extant cats and their sabre-toothed relatives. Open Research Europe, 2021, 1, 25.	2.0	2
43	High genomic diversity in the endangered East Greenland Svalbard Barents Sea stock of bowhead whales (<i>Balaena mysticetus</i>). Scientific Reports, 2022, 12, 6118.	3.3	2
44	Faster ocean warming threatens richest areas of marine biodiversity. Global Change Biology, 2022, 28, 5849-5858.	9.5	2
45	Mitochondrial genome divergence between beluga whales in Baffin Bay and the Sea of Okhotsk. Mitochondrial DNA Part B: Resources, 2017, 2, 257-258.	0.4	1
46	Thylacine tales. Nature Ecology and Evolution, 2018, 2, 7-8.	7.8	1
47	Unraveling elephant-shrews: Phylogenetic relationships and unexpected introgression among giant sengis. Molecular Phylogenetics and Evolution, 2021, 154, 107001.	2.7	1
48	Salty divides: geometric morphometrics reveal Danish straits as barriers to otter migration. Mammalian Biology, 0, , 1.	1.5	0
49	The Danish Polar Bear Skull Collection 1830–2016. Arctic, 2017, 70, 334.	0.4	0