Love Dalén

List of Publications by Year in descending order

Source: https://exaly.com/author-pdf/1567002/publications.pdf

Version: 2024-02-01

158 papers 8,495 citations

71102 41 h-index 81 g-index

172 all docs

172 docs citations

172 times ranked

10464 citing authors

#	Article	IF	CITATIONS
1	Refugia revisited: individualistic responses of species in space and time. Proceedings of the Royal Society B: Biological Sciences, 2010, 277, 661-671.	2.6	981
2	Genomics and the challenging translation into conservation practice. Trends in Ecology and Evolution, 2015, 30, 78-87.	8.7	469
3	Population Genomics Reveal Recent Speciation and Rapid Evolutionary Adaptation in Polar Bears. Cell, 2014, 157, 785-794.	28.9	363
4	Ancient Wolf Genome Reveals an Early Divergence of Domestic Dog Ancestors and Admixture into High-Latitude Breeds. Current Biology, 2015, 25, 1515-1519.	3.9	270
5	Complete Genomes Reveal Signatures of Demographic and Genetic Declines in the Woolly Mammoth. Current Biology, 2015, 25, 1395-1400.	3.9	263
6	Dense sampling of bird diversity increases power of comparative genomics. Nature, 2020, 587, 252-257.	27.8	251
7	Whole-Genome Shotgun Sequencing of Mitochondria from Ancient Hair Shafts. Science, 2007, 317, 1927-1930.	12.6	220
8	Million-year-old DNA sheds light on the genomic history of mammoths. Nature, 2021, 591, 265-269.	27.8	179
9	Quantifying Temporal Genomic Erosion in Endangered Species. Trends in Ecology and Evolution, 2018, 33, 176-185.	8.7	162
10	Origins and genetic legacy of prehistoric dogs. Science, 2020, 370, 557-564.	12.6	152
11	Intraspecific phylogenetic analysis of Siberian woolly mammoths using complete mitochondrial genomes. Proceedings of the National Academy of Sciences of the United States of America, 2008, 105, 8327-8332.	7.1	149
12	A comprehensive genomic history of extinct and living elephants. Proceedings of the National Academy of Sciences of the United States of America, 2018, 115, E2566-E2574.	7.1	142
13	Extensive Human DNA Contamination in Extracts from Ancient Dog Bones and Teeth. Molecular Biology and Evolution, 2005, 22, 2040-2047.	8.9	137
14	Ancient DNA reveals lack of postglacial habitat tracking in the arctic fox. Proceedings of the National Academy of Sciences of the United States of America, 2007, 104, 6726-6729.	7.1	137
15	Early Pleistocene enamel proteome from Dmanisi resolves Stephanorhinus phylogeny. Nature, 2019, 574, 103-107.	27.8	135
16	Partial genomic survival of cave bears in living brown bears. Nature Ecology and Evolution, 2018, 2, 1563-1570.	7.8	132
17	Population history and genetic structure of a circumpolar species: the arctic fox. Biological Journal of the Linnean Society, 2004, 84, 79-89.	1.6	130
18	Staying out in the cold: glacial refugia and mitochondrial DNA phylogeography in ancient European brown bears. Molecular Ecology, 2007, 16, 5140-5148.	3.9	130

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19	Historical Genomes Reveal the Genomic Consequences of Recent Population Decline in Eastern Gorillas. Current Biology, 2019, 29, 165-170.e6.	3.9	126
20	Population genomics of the critically endangered käkäpå. Cell Genomics, 2021, 1, 100002.	6.5	106
21	The mitochondrial genome sequence of the Tasmanian tiger (<i>Thylacinus cynocephalus</i>). Genome Research, 2009, 19, 213-220.	5.5	102
22	Carnivore conservation in practice: replicated management actions on a large spatial scale. Journal of Applied Ecology, 2013, 50, 59-67.	4.0	93
23	Partial Genetic Turnover in Neandertals: Continuity in the East and Population Replacement in the West. Molecular Biology and Evolution, 2012, 29, 1893-1897.	8.9	82
24	Index hopping on the Illumina HiseqX platform and its consequences for ancient DNA studies. Molecular Ecology Resources, 2020, 20, 1171-1181.	4.8	82
25	Genetic consequences of a demographic bottleneck in the Scandinavian arctic fox. Oikos, 2006, 114, 84-94.	2.7	81
26	Serial population extinctions in a small mammal indicate Late Pleistocene ecosystem instability. Proceedings of the National Academy of Sciences of the United States of America, 2012, 109, 20532-20536.	7.1	80
27	Identifying species from pieces of faeces. Conservation Genetics, 2004, 5, 109-111.	1.5	78
28	Sea ice occurrence predicts genetic isolation in the Arctic fox. Molecular Ecology, 2007, 16, 4241-4255.	3.9	77
29	Ancient genomes suggest the eastern Pontic-Caspian steppe as the source of western Iron Age nomads. Science Advances, 2018, 4, eaat4457.	10.3	76
30	The evolution and changing ecology of the African hominid oral microbiome. Proceedings of the National Academy of Sciences of the United States of America, 2021, 118, .	7.1	74
31	The wolf reference genome sequence (Canis lupus lupus) and its implications for Canis spp. population genomics. BMC Genomics, 2017, 18, 495.	2.8	73
32	Holarctic genetic structure and range dynamics in the woolly mammoth. Proceedings of the Royal Society B: Biological Sciences, 2013, 280, 20131910.	2.6	72
33	Extended and Continuous Decline in Effective Population Size Results in Low Genomic Diversity in the World's Rarest Hyena Species, the Brown Hyena. Molecular Biology and Evolution, 2018, 35, 1225-1237.	8.9	72
34	Arctic-adapted dogs emerged at the Pleistocene–Holocene transition. Science, 2020, 368, 1495-1499.	12.6	60
35	Inference of natural selection from ancient DNA. Evolution Letters, 2020, 4, 94-108.	3.3	58
36	Genetic turnovers and northern survival during the last glacial maximum in European brown bears. Ecology and Evolution, 2019, 9, 5891-5905.	1,9	56

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37	Puma genomes from North and South America provide insights into the genomic consequences of inbreeding. Nature Communications, 2019, 10, 4769.	12.8	55
38	Population genomics of grey wolves and wolf-like canids in North America. PLoS Genetics, 2018, 14, e1007745.	3.5	54
39	Genome-Based Sexing Provides Clues about Behavior and Social Structure in the Woolly Mammoth. Current Biology, 2017, 27, 3505-3510.e3.	3.9	53
40	Is the endangered Fennoscandian arctic fox (Alopex lagopus) population genetically isolated?. Biological Conservation, 2002, 105, 171-178.	4.1	50
41	Ancient and modern genomes unravel the evolutionary history of the rhinoceros family. Cell, 2021, 184, 4874-4885.e16.	28.9	49
42	Grey wolf genomic history reveals a dual ancestry of dogs. Nature, 2022, 607, 313-320.	27.8	48
43	Synchronous genetic turnovers across Western Eurasia in Late Pleistocene collared lemmings. Global Change Biology, 2016, 22, 1710-1721.	9.5	45
44	Population structure in a critically endangered arctic fox population: does genetics matter?. Molecular Ecology, 2006, 15, 2809-2819.	3.9	44
45	Population Demography and Genetic Diversity in the Pleistocene Cave Lion. Open Quaternary, 2015, 1, 4.	1.0	44
46	Interacting effects of change in climate, human population, land use, and water use on biodiversity and ecosystem services. Ecology and Society, 2015, 20, .	2.3	43
47	Pre-extinction Demographic Stability and Genomic Signatures of Adaptation in the Woolly Rhinoceros. Current Biology, 2020, 30, 3871-3879.e7.	3.9	41
48	Kin encounter rate and inbreeding avoidance in canids. Molecular Ecology, 2011, 20, 5348-5358.	3.9	40
49	Estimating population parameters in a threatened arctic fox population using molecular tracking and traditional field methods. Animal Conservation, 2008, 11 , 330-338.	2.9	39
50	The evolutionary and phylogeographic history of woolly mammoths: a comprehensive mitogenomic analysis. Scientific Reports, 2017, 7, 44585.	3.3	39
51	Genomic insights into the conservation status of the world's last remaining Sumatran rhinoceros populations. Nature Communications, 2021, 12, 2393.	12.8	39
52	Historical population declines prompted significant genomic erosion in the northern and southern white rhinoceros (<i>Ceratotherium simum</i>). Molecular Ecology, 2021, 30, 6355-6369.	3.9	39
53	Evolutionary History of the Nesophontidae, the Last Unplaced Recent Mammal Family. Molecular Biology and Evolution, 2016, 33, 3095-3103.	8.9	38
54	Specialized sledge dogs accompanied Inuit dispersal across the North American Arctic. Proceedings of the Royal Society B: Biological Sciences, 2019, 286, 20191929.	2.6	38

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55	Hyena paleogenomes reveal a complex evolutionary history of cross-continental gene flow between spotted and cave hyena. Science Advances, 2020, 6, eaay0456.	10.3	38
56	On the origin of the <scp>N</scp> orwegian lemming. Molecular Ecology, 2014, 23, 2060-2071.	3.9	37
57	Is the glacial refugium concept relevant for northern species? A comment on Pruett and Winker 2005. Climatic Change, 2008, 86, 19-22.	3.6	36
58	Microsatellite genotyping reveals endâ€Pleistocene decline in mammoth autosomal genetic variation. Molecular Ecology, 2012, 21, 3391-3402.	3.9	36
59	From the Past to the Present: Wolf Phylogeography and Demographic History Based on the Mitochondrial Control Region. Frontiers in Ecology and Evolution, 2016, 4, .	2.2	35
60	Convergent evolution, habitat shifts and variable diversification rates in the ovenbird-woodcreeper family (Furnariidae). BMC Evolutionary Biology, 2009, 9, 268.	3.2	34
61	Consequences of a demographic bottleneck on geneticÂstructure and variation in the Scandinavian brown bear. Molecular Ecology, 2015, 24, 3441-3454.	3.9	34
62	Inbreeding depression in a critically endangered carnivore. Molecular Ecology, 2016, 25, 3309-3318.	3.9	34
63	Genomic Adaptations and Evolutionary History of the Extinct Scimitar-Toothed Cat, Homotherium latidens. Current Biology, 2020, 30, 5018-5025.e5.	3.9	34
64	Spatial subsidies in spider diets vary with shoreline structure: Complementary evidence from molecular diet analysis and stable isotopes. Ecology and Evolution, 2016, 6, 8431-8439.	1.9	33
65	Whole mitochondrial genome capture from faecal samples and museumâ€preserved specimens. Molecular Ecology Resources, 2017, 17, e111-e121.	4.8	32
66	Human population dynamics and <i>Yersinia pestis</i> in ancient northeast Asia. Science Advances, 2021, 7, .	10.3	32
67	Detection of farm fox and hybrid genotypes among wild arctic foxes in Scandinavia. Conservation Genetics, 2006, 6, 885-894.	1.5	31
68	Resolution of the type material of the Asian elephant, <i>Elephas maximus </i> Linnaeus, 1758 (Proboscidea, Elephantidae). Zoological Journal of the Linnean Society, 2014, 170, 222-232.	2.3	31
69	50,000â€∫years of genetic uniformity in the critically endangered Iberian lynx. Molecular Ecology, 2011, 20, 3785-3795.	3.9	30
70	Ancient horse genomes reveal the timing and extent of dispersals across the Bering Land Bridge. Molecular Ecology, 2021, 30, 6144-6161.	3.9	30
71	DNA analysis on fox faeces and competition induced niche shifts. Molecular Ecology, 2004, 13, 2389-2392.	3.9	29
72	Unveiling the Ecological Applications of Ancient DNA From Mollusk Shells. Frontiers in Ecology and Evolution, 2020, 8, .	2.2	29

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73	Metagenomic Analysis from the Interior of a Speleothem in Tjuv-Ante's Cave, Northern Sweden. PLoS ONE, 2016, 11, e0151577.	2.5	29
74	Typing single polymorphic nucleotides in mitochondrial DNA as a way to access Middle Pleistocene DNA. Biology Letters, 2006, 2, 601-603.	2.3	28
75	Temporal genetic change in the last remaining population of woolly mammoth. Proceedings of the Royal Society B: Biological Sciences, 2010, 277, 2331-2337.	2.6	28
76	Arctic fox <i>Vulpes lagopus</i> population structure: circumpolar patterns and processes. Oikos, 2011, 120, 873-885.	2.7	28
77	Significant loss of mitochondrial diversity within the last century due to extinction of peripheral populations in eastern gorillas. Scientific Reports, 2018, 8, 6551.	3.3	28
78	Dental Calculus as a Tool to Study the Evolution of the Mammalian Oral Microbiome. Molecular Biology and Evolution, 2020, 37, 3003-3022.	8.9	28
79	THE MONOPHYLETIC ORIGIN OF DELAYED IMPLANTATION IN CARNIVORES AND ITS IMPLICATIONS. Evolution; International Journal of Organic Evolution, 2003, 57, 1952-1956.	2.3	27
80	Middle Pleistocene genome calibrates a revised evolutionary history of extinct cave bears. Current Biology, 2021, 31, 1771-1779.e7.	3.9	27
81	Recovery of DNA from Footprints in the Snow. Canadian Field-Naturalist, 2007, 121, 321.	0.1	26
82	Changes in variation at the MHC class II DQA locus during the final demise of the woolly mammoth. Scientific Reports, 2016, 6, 25274.	3.3	26
83	Range shifts or extinction? Ancient <scp>DNA</scp> and distribution modelling reveal past and future responses to climate warming in coldâ€adapted birds. Global Change Biology, 2017, 23, 1425-1435.	9.5	25
84	Altitude effects on spatial components of vascular plant diversity in a subarctic mountain tundra. Ecology and Evolution, 2019, 9, 4783-4795.	1.9	25
85	Population persistence in a landscape context: the case of endangered arctic fox populations in Fennoscandia. Ecography, 2010, 33, 932-941.	4.5	24
86	Reply to Garner et al Trends in Ecology and Evolution, 2016, 31, 83-84.	8.7	24
87	Full Mitogenomes in the Critically Endangered KÄkÄpÅ•Reveal Major Post-Glacial and Anthropogenic Effects on Neutral Genetic Diversity. Genes, 2018, 9, 220.	2.4	24
88	Evolutionary History, Genomic Adaptation to Toxic Diet, and Extinction of the Carolina Parakeet. Current Biology, 2020, 30, 108-114.e5.	3.9	24
89	Moose genomes reveal past glacial demography and the origin of modern lineages. BMC Genomics, 2020, 21, 854.	2.8	23

Resolution of the type material of the Asian elephant, Elephas maximus Linnaeus, 1758 (Proboscidea,) Tj ETQq0 0 0 grgBT /Overlock 10 T

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91	Mitogenome evolution in the last surviving woolly mammoth population reveals neutral and functional consequences of small population size. Evolution Letters, 2017, 1, 292-303.	3.3	22
92	Comparative analyses identify genomic features potentially involved in the evolution of birds-of-paradise. GigaScience, 2019, 8 , .	6.4	22
93	Unraveling the genetic history of the European wild goats. Quaternary Science Reviews, 2018, 185, 189-198.	3.0	21
94	Genomic and fitness consequences of inbreeding in an endangered carnivore. Molecular Ecology, 2021, 30, 2790-2799.	3.9	21
95	Interspecific Gene Flow and the Evolution of Specialization in Black and White Rhinoceros. Molecular Biology and Evolution, 2020, 37, 3105-3117.	8.9	20
96	Heterogeneous Hunter-Gatherer and Steppe-Related Ancestries in Late Neolithic and Bell Beaker Genomes from Present-Day France. Current Biology, 2021, 31, 1072-1083.e10.	3.9	20
97	African and Asian leopards are highly differentiated at the genomic level. Current Biology, 2021, 31, 1872-1882.e5.	3.9	20
98	The history of Crimean red deer population and Cervus phylogeography in Eurasia. Zoological Journal of the Linnean Society, 2018, 183, 208-225.	2.3	19
99	Modern Siberian dog ancestry was shaped by several thousand years of Eurasian-wide trade and human dispersal. Proceedings of the National Academy of Sciences of the United States of America, 2021, 118, .	7.1	19
100	Population structure in relation to host-plant ecology and Wolbachia infestation in the comma butterfly. Journal of Evolutionary Biology, 2011, 24, 2173-2185.	1.7	18
101	Complete genomes of two extinct New Zealand passerines show responses to climate fluctuations but no evidence for genomic erosion prior to extinction. Biology Letters, 2019, 15, 20190491.	2.3	18
102	Eradication genomicsâ€"lessons for parasite control. Science, 2018, 361, 130-131.	12.6	18
103	Nonreceding hare lines: genetic continuity since the Late Pleistocene in European mountain hares (Lepus timidus). Biological Journal of the Linnean Society, 2017, 120, 891-908.	1.6	17
104	From monogamy to complexity: social organization of arctic foxes (<i>Vulpes lagopus</i>) in contrasting ecosystems. Canadian Journal of Zoology, 2012, 90, 1102-1116.	1.0	16
105	Signature of post-glacial expansion and genetic structure at the northern range limit of the speckled wood butterfly. Biological Journal of the Linnean Society, 2014, 113, 136-148.	1.6	16
106	First de novo whole genome sequencing and assembly of the pink-footed goose. Genomics, 2018, 110, 75-79.	2.9	16
107	Effect of local prey availability on gyrfalcon diet: DNA analysis on ptarmigan remains at nest sites. Journal of Zoology, 2006, 269, 57-64.	1.7	15
108	Competitive mapping allows for the identification and exclusion of human DNA contamination in ancient faunal genomic datasets. BMC Genomics, 2020, 21, 844.	2.8	15

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109	Ecological Specialization and Evolutionary Reticulation in Extant Hyaenidae. Molecular Biology and Evolution, 2021, 38, 3884-3897.	8.9	15
110	Farmed arctic foxes on the Fennoscandian mountain tundra: implications for conservation. Animal Conservation, 2009, 12, 434-444.	2.9	14
111	Population structure and recent temporal changes in genetic variation in Eurasian otters from Sweden. Conservation Genetics, 2015, 16, 371-384.	1.5	14
112	Demographic inference from wholeâ€genome and RAD sequencing data suggests alternating human impacts on goose populations since the last ice age. Molecular Ecology, 2017, 26, 6270-6283.	3.9	14
113	Combining Bayesian age models and genetics to investigate population dynamics and extinction of the last mammoths in northern Siberia. Quaternary Science Reviews, 2021, 259, 106913.	3.0	14
114	Integrating multi-taxon palaeogenomes and sedimentary ancient DNA to study past ecosystem dynamics. Proceedings of the Royal Society B: Biological Sciences, 2021, 288, 20211252.	2.6	14
115	GenErode: a bioinformatics pipeline to investigate genome erosion in endangered and extinct species. BMC Bioinformatics, 2022, 23, .	2.6	14
116	No particular genomic features underpin the dramatic economic consequences of 17th century plague epidemics in Italy. IScience, 2021, 24, 102383.	4.1	13
117	The impact of past climate change on genetic variation and population connectivity in the Icelandic arctic fox. Proceedings of the Royal Society B: Biological Sciences, 2012, 279, 4568-4573.	2.6	12
118	Identifying Bird Remains Using Ancient DNA Barcoding. Genes, 2017, 8, 169.	2.4	12
119	Consequences of past climate change and recent human persecution on mitogenomic diversity in the arctic fox. Philosophical Transactions of the Royal Society B: Biological Sciences, 2019, 374, 20190212.	4.0	12
120	EarlyÂPleistocene origin and extensive intra-species diversity of the extinct cave lion. Scientific Reports, 2020, 10, 12621.	3.3	12
121	Circumpolar phylogeography and demographic history of beluga whales reflect past climatic fluctuations. Molecular Ecology, 2021, 30, 2543-2559.	3.9	12
122	Phylogenetic placement and population structure of Indoâ€Pacific bottlenose dolphins (<i>Tursiops) Tj ETQq0 0 C</i>) rgBT /Ov	erlock 10 Tf 11
123	Testosterone in ancient hair from an extinct species. Palaeontology, 2018, 61, 797-802.	2.2	11
124	$31 {\hat A}^\circ$ South: The physiology of adaptation to arid conditions in a passerine bird. Molecular Ecology, 2019, 28, 3709-3721.	3.9	11
125	Back to BaySICS: A User-Friendly Program for Bayesian Statistical Inference from Coalescent Simulations. PLoS ONE, 2014, 9, e98011.	2.5	11
126	Run to the hills: gene flow among mountain areas leads to low genetic differentiation in the Norwegian lemming. Biological Journal of the Linnean Society, 2017, 121, 1-14.	1.6	10

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127	Evolution, ecology and conservationâ€"revisiting three decades of Arctic fox population genetic research. Polar Research, 2017, 36, 4.	1.6	10
128	Complete mitochondrial genome of the Oriental Hornet, Vespa orientalis F. (Hymenoptera: Vespidae). Mitochondrial DNA Part B: Resources, 2017, 2, 139-140.	0.4	10
129	Postâ€glacial range revolutions in South European hares (<i>Lepus</i> Àspp.): Insights from ancient <scp>DNA</scp> and ecological niche modelling. Journal of Biogeography, 2018, 45, 2609-2618.	3.0	10
130	A polar bear paleogenome reveals extensive ancient gene flow from polar bears into brown bears. Nature Ecology and Evolution, 2022, 6, 936-944.	7.8	10
131	Genetic landscape with sharp discontinuities shaped by complex demographic history in moose (Alces) Tj ETQq1	1,0,78431 [,]	4 ₉ rgBT /Ove
132	Population genomics reveals lack of greater white-fronted introgression into the Swedish lesser white-fronted goose. Scientific Reports, 2020, 10, 18347.	3.3	9
133	The genome sequence of the grey wolf, Canis lupus Linnaeus 1758. Wellcome Open Research, 2021, 6, 310.	1.8	9
134	Genomic basis for skin phenotype and cold adaptation in the extinct Steller's sea cow. Science Advances, 2022, 8, eabl6496.	10.3	9
135	Ancient mitochondrial and modern whole genomes unravel massive genetic diversity loss during near extinction of Alpine ibex. Molecular Ecology, 2022, 31, 3548-3565.	3.9	9
136	Rapid size change associated with intra-island evolutionary radiation in extinct Caribbean "island-shrews― BMC Evolutionary Biology, 2020, 20, 106.	3.2	8
137	Museomics Dissects the Genetic Basis for Adaptive Seasonal Coloration in the Least Weasel. Molecular Biology and Evolution, 2021, 38, 4388-4402.	8.9	8
138	Population-level genotyping of coat colour polymorphism in woolly mammoth (Mammuthus) Tj ETQq0 0 0 rgBT /C)yerlock 1(0 ₇ Tf 50 302
139	Ancient microRNA profiles of 14,300-yr-old canid samples confirm taxonomic origin and provide glimpses into tissue-specific gene regulation from the Pleistocene. Rna, 2021, 27, 324-334.	3.5	7
140	Restoration of transborder connectivity for Fennoscandian brown bears (Ursus arctos). Biological Conservation, 2021, 253, 108936.	4.1	7
141	Evolutionary history of the extinct Sardinian dhole. Current Biology, 2021, 31, 5571-5579.e6.	3.9	7
142	Archives of human-dog relationships: Genetic and stable isotope analysis of Arctic fur clothing. Journal of Anthropological Archaeology, 2020, 59, 101200.	1.6	6
143	Middle Pleistocene Cave Bear Genome Calibrates the Evolutionary History of Palaearctic Bears. SSRN Electronic Journal, 0, , .	0.4	6
144	Who are you, Griselda? A replacement name for a new genus of the Asiatic short-tailed shrews (Mammalia, Eulipotyphla, Soricidae): molecular and morphological analyses with the discussion of tribal affinities. ZooKeys, 2019, 888, 133-158.	1.1	6

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145	Development and Optimization of a Silica Column-Based Extraction Protocol for Ancient DNA. Genes, 2022, 13, 687.	2.4	6
146	Spatial variation in Arctic hare (Lepus arcticus) populations around the Hall Basin. Polar Biology, 2017, 40, 2113-2118.	1.2	5
147	The Preliminary Analysis of Cave Lion Cubs Panthera spelaea (Goldfuss, 1810) from the Permafrost of Siberia. Quaternary, 2021, 4, 24.	2.0	5
148	Genomics of Extinction. Population Genomics, 2018, , 393-418.	0.5	4
149	Biomolecular analyses reveal the age, sex and species identity of a near-intact Pleistocene bird carcass. Communications Biology, 2020, 3, 84.	4.4	4
150	The Arctic fox (Vulpes lagopus L.) on the Kola Peninsula (Russia): silently disappearing in the mist of data deficiency?. Polar Biology, 2021, 44, 913-925.	1.2	3
151	Ancient genome provides insights into the history of Eurasian lynx in Iberia and Western Europe. Quaternary Science Reviews, 2022, 285, 107518.	3.0	3
152	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
153	Unroll Please: Deciphering the Genetic Code in Scrolls and Other Ancient Materials. Cell, 2020, 181, 1200-1201.	28.9	1
154	Historical Genomes Reveal the Genomic Consequences of Recent Population Decline in Eastern Gorillas. SSRN Electronic Journal, 0 , , .	0.4	1
155	THE MONOPHYLETIC ORIGIN OF DELAYED IMPLANTATION IN CARNIVORES AND ITS IMPLICATIONS. Evolution; International Journal of Organic Evolution, 2003, 57, 1952.	2.3	0
156	The history of Crimean red deer population and Cervus phylogeography in Eurasia. Zoological Journal of the Linnean Society, 2018, 182, 478-478.	2.3	0
157	Mammuthus sp. (Early and Middle Pleistocene Mammoths). Trends in Genetics, 2021, 37, 682-683.	6.7	0
158	The kÄkÄpÅ•(Strigops habroptilus). Trends in Genetics, 2022, , .	6.7	0