

# Love DalÃ©n

## List of Publications by Year in descending order

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Version: 2024-02-01

158  
papers

8,495  
citations

71102

41  
h-index

60623

81  
g-index

172  
all docs

172  
docs citations

172  
times ranked

10464  
citing authors

#	ARTICLE	IF	CITATIONS
1	Genomic basis for skin phenotype and cold adaptation in the extinct Steller's sea cow. <i>Science Advances</i> , 2022, 8, eabl6496.	10.3	9
2	The kÄkÄpÄ•(Strigops habroptilus). <i>Trends in Genetics</i> , 2022, , .	6.7	0
3	Development and Optimization of a Silica Column-Based Extraction Protocol for Ancient DNA. <i>Genes</i> , 2022, 13, 687.	2.4	6
4	Ancient mitochondrial and modern whole genomes unravel massive genetic diversity loss during near extinction of Alpine ibex. <i>Molecular Ecology</i> , 2022, 31, 3548-3565.	3.9	9
5	Ancient genome provides insights into the history of Eurasian lynx in Iberia and Western Europe. <i>Quaternary Science Reviews</i> , 2022, 285, 107518.	3.0	3
6	GenErode: a bioinformatics pipeline to investigate genome erosion in endangered and extinct species. <i>BMC Bioinformatics</i> , 2022, 23, .	2.6	14
7	A polar bear paleogenome reveals extensive ancient gene flow from polar bears into brown bears. <i>Nature Ecology and Evolution</i> , 2022, 6, 936-944.	7.8	10
8	Grey wolf genomic history reveals a dual ancestry of dogs. <i>Nature</i> , 2022, 607, 313-320.	27.8	48
9	Ancient microRNA profiles of 14,300-yr-old canid samples confirm taxonomic origin and provide glimpses into tissue-specific gene regulation from the Pleistocene. <i>Rna</i> , 2021, 27, 324-334.	3.5	7
10	Ecological Specialization and Evolutionary Reticulation in Extant Hyaenidae. <i>Molecular Biology and Evolution</i> , 2021, 38, 3884-3897.	8.9	15
11	Million-year-old DNA sheds light on the genomic history of mammoths. <i>Nature</i> , 2021, 591, 265-269.	27.8	179
12	Heterogeneous Hunter-Gatherer and Steppe-Related Ancestries in Late Neolithic and Bell Beaker Genomes from Present-Day France. <i>Current Biology</i> , 2021, 31, 1072-1083.e10.	3.9	20
13	Middle Pleistocene genome calibrates a revised evolutionary history of extinct cave bears. <i>Current Biology</i> , 2021, 31, 1771-1779.e7.	3.9	27
14	No particular genomic features underpin the dramatic economic consequences of 17th century plague epidemics in Italy. <i>IScience</i> , 2021, 24, 102383.	4.1	13
15	The Arctic fox ( <i>Vulpes lagopus</i> L.) on the Kola Peninsula (Russia): silently disappearing in the mist of data deficiency?. <i>Polar Biology</i> , 2021, 44, 913-925.	1.2	3
16	Genomic insights into the conservation status of the world's last remaining Sumatran rhinoceros populations. <i>Nature Communications</i> , 2021, 12, 2393.	12.8	39
17	Circumpolar phylogeography and demographic history of beluga whales reflect past climatic fluctuations. <i>Molecular Ecology</i> , 2021, 30, 2543-2559.	3.9	12
18	The evolution and changing ecology of the African hominid oral microbiome. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2021, 118, .	7.1	74

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19	African and Asian leopards are highly differentiated at the genomic level. <i>Current Biology</i> , 2021, 31, 1872-1882.e5.	3.9	20
20	Genomic and fitness consequences of inbreeding in an endangered carnivore. <i>Molecular Ecology</i> , 2021, 30, 2790-2799.	3.9	21
21	Ancient horse genomes reveal the timing and extent of dispersals across the Bering Land Bridge. <i>Molecular Ecology</i> , 2021, 30, 6144-6161.	3.9	30
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.	3.0	14
23	Museomics Dissects the Genetic Basis for Adaptive Seasonal Coloration in the Least Weasel. <i>Molecular Biology and Evolution</i> , 2021, 38, 4388-4402.	8.9	8
24	Historical population declines prompted significant genomic erosion in the northern and southern white rhinoceros ( <i>Ceratotherium simum</i> ). <i>Molecular Ecology</i> , 2021, 30, 6355-6369.	3.9	39
25	<i>Mammuthus</i> sp. (Early and Middle Pleistocene Mammoths). <i>Trends in Genetics</i> , 2021, 37, 682-683.	6.7	0
26	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.	2.6	14
27	The Preliminary Analysis of Cave Lion Cubs <i>Panthera spelaea</i> (Goldfuss, 1810) from the Permafrost of Siberia. <i>Quaternary</i> , 2021, 4, 24.	2.0	5
28	Population genomics of the critically endangered <i>Arctopithecus</i> . <i>Cell Genomics</i> , 2021, 1, 100002.	6.5	106
29	Modern Siberian dog ancestry was shaped by several thousand years of Eurasian-wide trade and human dispersal. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2021, 118, .	7.1	19
30	Ancient and modern genomes unravel the evolutionary history of the rhinoceros family. <i>Cell</i> , 2021, 184, 4874-4885.e16.	28.9	49
31	Restoration of transborder connectivity for Fennoscandian brown bears ( <i>Ursus arctos</i> ). <i>Biological Conservation</i> , 2021, 253, 108936.	4.1	7
32	Human population dynamics and <i>Yersinia pestis</i> in ancient northeast Asia. <i>Science Advances</i> , 2021, 7, .	10.3	32
33	Evolutionary history of the extinct Sardinian dhole. <i>Current Biology</i> , 2021, 31, 5571-5579.e6.	3.9	7
34	The genome sequence of the grey wolf, <i>Canis lupus</i> Linnaeus 1758. <i>Wellcome Open Research</i> , 2021, 6, 310.	1.8	9
35	Index hopping on the Illumina HiSeqX platform and its consequences for ancient DNA studies. <i>Molecular Ecology Resources</i> , 2020, 20, 1171-1181.	4.8	82
36	Evolutionary History, Genomic Adaptation to Toxic Diet, and Extinction of the Carolina Parakeet. <i>Current Biology</i> , 2020, 30, 108-114.e5.	3.9	24

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37	Genomic Adaptations and Evolutionary History of the Extinct Scimitar-Toothed Cat, <i>Homotherium latidens</i> . <i>Current Biology</i> , 2020, 30, 5018-5025.e5.	3.9	34
38	Dense sampling of bird diversity increases power of comparative genomics. <i>Nature</i> , 2020, 587, 252-257.	27.8	251
39	Archives of human-dog relationships: Genetic and stable isotope analysis of Arctic fur clothing. <i>Journal of Anthropological Archaeology</i> , 2020, 59, 101200.	1.6	6
40	Early Pleistocene origin and extensive intra-species diversity of the extinct cave lion. <i>Scientific Reports</i> , 2020, 10, 12621.	3.3	12
41	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
42	Origins and genetic legacy of prehistoric dogs. <i>Science</i> , 2020, 370, 557-564.	12.6	152
43	Population genomics reveals lack of greater white-fronted introgression into the Swedish lesser white-fronted goose. <i>Scientific Reports</i> , 2020, 10, 18347.	3.3	9
44	Rapid size change associated with intra-island evolutionary radiation in extinct Caribbean island-shrews. <i>BMC Evolutionary Biology</i> , 2020, 20, 106.	3.2	8
45	Competitive mapping allows for the identification and exclusion of human DNA contamination in ancient faunal genomic datasets. <i>BMC Genomics</i> , 2020, 21, 844.	2.8	15
46	Moose genomes reveal past glacial demography and the origin of modern lineages. <i>BMC Genomics</i> , 2020, 21, 854.	2.8	23
47	Unroll Please: Deciphering the Genetic Code in Scrolls and Other Ancient Materials. <i>Cell</i> , 2020, 181, 1200-1201.	28.9	1
48	Dental Calculus as a Tool to Study the Evolution of the Mammalian Oral Microbiome. <i>Molecular Biology and Evolution</i> , 2020, 37, 3003-3022.	8.9	28
49	Inference of natural selection from ancient DNA. <i>Evolution Letters</i> , 2020, 4, 94-108.	3.3	58
50	Hyena paleogenomes reveal a complex evolutionary history of cross-continental gene flow between spotted and cave hyena. <i>Science Advances</i> , 2020, 6, eaay0456.	10.3	38
51	Unveiling the Ecological Applications of Ancient DNA From Mollusk Shells. <i>Frontiers in Ecology and Evolution</i> , 2020, 8, .	2.2	29
52	Interspecific Gene Flow and the Evolution of Specialization in Black and White Rhinoceros. <i>Molecular Biology and Evolution</i> , 2020, 37, 3105-3117.	8.9	20
53	Arctic-adapted dogs emerged at the Pleistocene-Holocene transition. <i>Science</i> , 2020, 368, 1495-1499.	12.6	60
54	Biomolecular analyses reveal the age, sex and species identity of a near-intact Pleistocene bird carcass. <i>Communications Biology</i> , 2020, 3, 84.	4.4	4

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55	31° South: The physiology of adaptation to arid conditions in a passerine bird. <i>Molecular Ecology</i> , 2019, 28, 3709-3721.	3.9	11
56	Puma genomes from North and South America provide insights into the genomic consequences of inbreeding. <i>Nature Communications</i> , 2019, 10, 4769.	12.8	55
57	Complete genomes of two extinct New Zealand passerines show responses to climate fluctuations but no evidence for genomic erosion prior to extinction. <i>Biology Letters</i> , 2019, 15, 20190491.	2.3	18
58	Early Pleistocene enamel proteome from Dmanisi resolves <i>Stephanorhinus</i> phylogeny. <i>Nature</i> , 2019, 574, 103-107.	27.8	135
59	Comparative analyses identify genomic features potentially involved in the evolution of birds-of-paradise. <i>GigaScience</i> , 2019, 8, .	6.4	22
60	Genetic turnovers and northern survival during the last glacial maximum in European brown bears. <i>Ecology and Evolution</i> , 2019, 9, 5891-5905.	1.9	56
61	Altitude effects on spatial components of vascular plant diversity in a subarctic mountain tundra. <i>Ecology and Evolution</i> , 2019, 9, 4783-4795.	1.9	25
62	Specialized sledge dogs accompanied Inuit dispersal across the North American Arctic. <i>Proceedings of the Royal Society B: Biological Sciences</i> , 2019, 286, 20191929.	2.6	38
63	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.	4.0	12
64	Historical Genomes Reveal the Genomic Consequences of Recent Population Decline in Eastern Gorillas. <i>Current Biology</i> , 2019, 29, 165-170.e6.	3.9	126
65	Who are you, <i>Griselda</i> ? 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. <i>ZooKeys</i> , 2019, 888, 133-158.	1.1	6
66	Unraveling the genetic history of the European wild goats. <i>Quaternary Science Reviews</i> , 2018, 185, 189-198.	3.0	21
67	A comprehensive genomic history of extinct and living elephants. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2018, 115, E2566-E2574.	7.1	142
68	The history of Crimean red deer population and <i>Cervus</i> phylogeography in Eurasia. <i>Zoological Journal of the Linnean Society</i> , 2018, 183, 208-225.	2.3	19
69	Quantifying Temporal Genomic Erosion in Endangered Species. <i>Trends in Ecology and Evolution</i> , 2018, 33, 176-185.	8.7	162
70	The history of Crimean red deer population and <i>Cervus</i> phylogeography in Eurasia. <i>Zoological Journal of the Linnean Society</i> , 2018, 182, 478-478.	2.3	0
71	Significant loss of mitochondrial diversity within the last century due to extinction of peripheral populations in eastern gorillas. <i>Scientific Reports</i> , 2018, 8, 6551.	3.3	28
72	Extended and Continuous Decline in Effective Population Size Results in Low Genomic Diversity in the World's Rarest Hyena Species, the Brown Hyena. <i>Molecular Biology and Evolution</i> , 2018, 35, 1225-1237.	8.9	72

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73	First de novo whole genome sequencing and assembly of the pink-footed goose. <i>Genomics</i> , 2018, 110, 75-79.	2.9	16
74	Population genomics of grey wolves and wolf-like canids in North America. <i>PLoS Genetics</i> , 2018, 14, e1007745.	3.5	54
75	Genomics of Extinction. <i>Population Genomics</i> , 2018, , 393-418.	0.5	4
76	Ancient genomes suggest the eastern Pontic-Caspian steppe as the source of western Iron Age nomads. <i>Science Advances</i> , 2018, 4, eaat4457.	10.3	76
77	Post-glacial range revolutions in South European hares ( <i>Lepus</i> spp.): Insights from ancient DNA and ecological niche modelling. <i>Journal of Biogeography</i> , 2018, 45, 2609-2618.	3.0	10
78	Testosterone in ancient hair from an extinct species. <i>Palaeontology</i> , 2018, 61, 797-802.	2.2	11
79	Full Mitogenomes in the Critically Endangered <i>KÄkÄpÄ</i> Reveal Major Post-Glacial and Anthropogenic Effects on Neutral Genetic Diversity. <i>Genes</i> , 2018, 9, 220.	2.4	24
80	Partial genomic survival of cave bears in living brown bears. <i>Nature Ecology and Evolution</i> , 2018, 2, 1563-1570.	7.8	132
81	Eradication genomicsâ€”lessons for parasite control. <i>Science</i> , 2018, 361, 130-131.	12.6	18
82	Mitochondrial genome divergence between beluga whales in Baffin Bay and the Sea of Okhotsk. <i>Mitochondrial DNA Part B: Resources</i> , 2017, 2, 257-258.	0.4	1
83	Run to the hills: gene flow among mountain areas leads to low genetic differentiation in the Norwegian lemming. <i>Biological Journal of the Linnean Society</i> , 2017, 121, 1-14.	1.6	10
84	The evolutionary and phylogeographic history of woolly mammoths: a comprehensive mitogenomic analysis. <i>Scientific Reports</i> , 2017, 7, 44585.	3.3	39
85	Genome-Based Sexing Provides Clues about Behavior and Social Structure in the Woolly Mammoth. <i>Current Biology</i> , 2017, 27, 3505-3510.e3.	3.9	53
86	Demographic inference from whole-genome and RAD sequencing data suggests alternating human impacts on goose populations since the last ice age. <i>Molecular Ecology</i> , 2017, 26, 6270-6283.	3.9	14
87	Evolution, ecology and conservationâ€”revisiting three decades of Arctic fox population genetic research. <i>Polar Research</i> , 2017, 36, 4.	1.6	10
88	Whole mitochondrial genome capture from faecal samples and museum-preserved specimens. <i>Molecular Ecology Resources</i> , 2017, 17, e111-e121.	4.8	32
89	Complete mitochondrial genome of the Oriental Hornet, <i>Vespa orientalis</i> F. (Hymenoptera: Vespidae). <i>Mitochondrial DNA Part B: Resources</i> , 2017, 2, 139-140.	0.4	10
90	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.	3.3	22

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91	Spatial variation in Arctic hare ( <i>Lepus arcticus</i> ) populations around the Hall Basin. <i>Polar Biology</i> , 2017, 40, 2113-2118.	1.2	5
92	The wolf reference genome sequence ( <i>Canis lupus lupus</i> ) and its implications for <i>Canis</i> spp. population genomics. <i>BMC Genomics</i> , 2017, 18, 495.	2.8	73
93	Nonreceding hare lines: genetic continuity since the Late Pleistocene in European mountain hares ( <i>Lepus timidus</i> ). <i>Biological Journal of the Linnean Society</i> , 2017, 120, 891-908.	1.6	17
94	Range shifts or extinction? Ancient <i>mtDNA</i> and distribution modelling reveal past and future responses to climate warming in cold-adapted birds. <i>Global Change Biology</i> , 2017, 23, 1425-1435.	9.5	25
95	Identifying Bird Remains Using Ancient DNA Barcoding. <i>Genes</i> , 2017, 8, 169.	2.4	12
96	From the Past to the Present: Wolf Phylogeography and Demographic History Based on the Mitochondrial Control Region. <i>Frontiers in Ecology and Evolution</i> , 2016, 4, .	2.2	35
97	Synchronous genetic turnovers across Western Eurasia in Late Pleistocene collared lemmings. <i>Global Change Biology</i> , 2016, 22, 1710-1721.	9.5	45
98	Inbreeding depression in a critically endangered carnivore. <i>Molecular Ecology</i> , 2016, 25, 3309-3318.	3.9	34
99	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.	3.3	26
100	Evolutionary History of the Nesophontidae, the Last Unplaced Recent Mammal Family. <i>Molecular Biology and Evolution</i> , 2016, 33, 3095-3103.	8.9	38
101	Spatial subsidies in spider diets vary with shoreline structure: Complementary evidence from molecular diet analysis and stable isotopes. <i>Ecology and Evolution</i> , 2016, 6, 8431-8439.	1.9	33
102	Genetic landscape with sharp discontinuities shaped by complex demographic history in moose ( <i>Alces</i> ) in the Oyertlock 1000-year-old forest. <i>Ecology and Evolution</i> , 2016, 7, 1370-1380.	1.3	10
103	Reply to Garner et al.. <i>Trends in Ecology and Evolution</i> , 2016, 31, 83-84.	8.7	24
104	Metagenomic Analysis from the Interior of a Speleothem in Tjuv-Ante's Cave, Northern Sweden. <i>PLoS ONE</i> , 2016, 11, e0151577.	2.5	29
105	Consequences of a demographic bottleneck on genetic structure and variation in the Scandinavian brown bear. <i>Molecular Ecology</i> , 2015, 24, 3441-3454.	3.9	34
106	Ancient Wolf Genome Reveals an Early Divergence of Domestic Dog Ancestors and Admixture into High-Latitude Breeds. <i>Current Biology</i> , 2015, 25, 1515-1519.	3.9	270
107	Interacting effects of change in climate, human population, land use, and water use on biodiversity and ecosystem services. <i>Ecology and Society</i> , 2015, 20, .	2.3	43
108	Complete Genomes Reveal Signatures of Demographic and Genetic Declines in the Woolly Mammoth. <i>Current Biology</i> , 2015, 25, 1395-1400.	3.9	263

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109	Population Demography and Genetic Diversity in the Pleistocene Cave Lion. <i>Open Quaternary</i> , 2015, 1, 4.	1.0	44
110	Genomics and the challenging translation into conservation practice. <i>Trends in Ecology and Evolution</i> , 2015, 30, 78-87.	8.7	469
111	Population structure and recent temporal changes in genetic variation in Eurasian otters from Sweden. <i>Conservation Genetics</i> , 2015, 16, 371-384.	1.5	14
112	On the origin of the Norwegian lemming. <i>Molecular Ecology</i> , 2014, 23, 2060-2071.	3.9	37
113	Population Genomics Reveal Recent Speciation and Rapid Evolutionary Adaptation in Polar Bears. <i>Cell</i> , 2014, 157, 785-794.	28.9	363
114	Resolution of the type material of the Asian elephant, <i>Elephas maximus</i> Linnaeus, 1758 (Proboscidea, Elephantidae). <i>Zoological Journal of the Linnean Society</i> , 2014, 170, 222-232.	2.3	31
115	Signature of post-glacial expansion and genetic structure at the northern range limit of the speckled wood butterfly. <i>Biological Journal of the Linnean Society</i> , 2014, 113, 136-148.	1.6	16
116	Resolution of the type material of the Asian elephant, <i>Elephas maximus</i> Linnaeus, 1758 (Proboscidea). <i>Tj ETQq0 0 0 rgBT /Overlock 10 T</i>	2.3	22
117	Back to BaySICS: A User-Friendly Program for Bayesian Statistical Inference from Coalescent Simulations. <i>PLoS ONE</i> , 2014, 9, e98011.	2.5	11
118	Carnivore conservation in practice: replicated management actions on a large spatial scale. <i>Journal of Applied Ecology</i> , 2013, 50, 59-67.	4.0	93
119	Holarctic genetic structure and range dynamics in the woolly mammoth. <i>Proceedings of the Royal Society B: Biological Sciences</i> , 2013, 280, 20131910.	2.6	72
120	Partial Genetic Turnover in Neandertals: Continuity in the East and Population Replacement in the West. <i>Molecular Biology and Evolution</i> , 2012, 29, 1893-1897.	8.9	82
121	Serial population extinctions in a small mammal indicate Late Pleistocene ecosystem instability. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2012, 109, 20532-20536.	7.1	80
122	From monogamy to complexity: social organization of arctic foxes ( <i>Vulpes lagopus</i> ) in contrasting ecosystems. <i>Canadian Journal of Zoology</i> , 2012, 90, 1102-1116.	1.0	16
123	The impact of past climate change on genetic variation and population connectivity in the Icelandic arctic fox. <i>Proceedings of the Royal Society B: Biological Sciences</i> , 2012, 279, 4568-4573.	2.6	12
124	Microsatellite genotyping reveals end-Pleistocene decline in mammoth autosomal genetic variation. <i>Molecular Ecology</i> , 2012, 21, 3391-3402.	3.9	36
125	Population-level genotyping of coat colour polymorphism in woolly mammoth ( <i>Mammuthus</i> ). <i>Tj ETQq1 1 0.784314 rgBT /Overlock 10 T</i>	3.8	7
126	Population structure in relation to host-plant ecology and <i>Wolbachia</i> infestation in the comma butterfly. <i>Journal of Evolutionary Biology</i> , 2011, 24, 2173-2185.	1.7	18



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127	50,000 years of genetic uniformity in the critically endangered Iberian lynx. <i>Molecular Ecology</i> , 2011, 20, 3785-3795.	3.9	30
128	Kin encounter rate and inbreeding avoidance in canids. <i>Molecular Ecology</i> , 2011, 20, 5348-5358.	3.9	40
129	Phylogenetic placement and population structure of Indo-Pacific bottlenose dolphins ( <i>Tursiops</i> ). <i>Trends in Ecology and Evolution</i> , 2011, 26, 431-448.	1.8	11
130	Arctic fox <i>Vulpes lagopus</i> population structure: circumpolar patterns and processes. <i>Oikos</i> , 2011, 120, 873-885.	2.7	28
131	Population persistence in a landscape context: the case of endangered arctic fox populations in Fennoscandia. <i>Ecography</i> , 2010, 33, 932-941.	4.5	24
132	Refugia revisited: individualistic responses of species in space and time. <i>Proceedings of the Royal Society B: Biological Sciences</i> , 2010, 277, 661-671.	2.6	981
133	Temporal genetic change in the last remaining population of woolly mammoth. <i>Proceedings of the Royal Society B: Biological Sciences</i> , 2010, 277, 2331-2337.	2.6	28
134	The mitochondrial genome sequence of the Tasmanian tiger ( <i>Thylacinus cynocephalus</i> ). <i>Genome Research</i> , 2009, 19, 213-220.	5.5	102
135	Convergent evolution, habitat shifts and variable diversification rates in the ovenbird-woodcreeper family (Furnariidae). <i>BMC Evolutionary Biology</i> , 2009, 9, 268.	3.2	34
136	Farmed arctic foxes on the Fennoscandian mountain tundra: implications for conservation. <i>Animal Conservation</i> , 2009, 12, 434-444.	2.9	14
137	Is the glacial refugium concept relevant for northern species? A comment on Pruett and Winker 2005. <i>Climatic Change</i> , 2008, 86, 19-22.	3.6	36
138	Estimating population parameters in a threatened arctic fox population using molecular tracking and traditional field methods. <i>Animal Conservation</i> , 2008, 11, 330-338.	2.9	39
139	Intraspecific phylogenetic analysis of Siberian woolly mammoths using complete mitochondrial genomes. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2008, 105, 8327-8332.	7.1	149
140	Ancient DNA reveals lack of postglacial habitat tracking in the arctic fox. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2007, 104, 6726-6729.	7.1	137
141	Whole-Genome Shotgun Sequencing of Mitochondria from Ancient Hair Shafts. <i>Science</i> , 2007, 317, 1927-1930.	12.6	220
142	Recovery of DNA from Footprints in the Snow. <i>Canadian Field-Naturalist</i> , 2007, 121, 321.	0.1	26
143	Sea ice occurrence predicts genetic isolation in the Arctic fox. <i>Molecular Ecology</i> , 2007, 16, 4241-4255.	3.9	77
144	Staying out in the cold: glacial refugia and mitochondrial DNA phylogeography in ancient European brown bears. <i>Molecular Ecology</i> , 2007, 16, 5140-5148.	3.9	130

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145	Genetic consequences of a demographic bottleneck in the Scandinavian arctic fox. <i>Oikos</i> , 2006, 114, 84-94.	2.7	81
146	Typing single polymorphic nucleotides in mitochondrial DNA as a way to access Middle Pleistocene DNA. <i>Biology Letters</i> , 2006, 2, 601-603.	2.3	28
147	Effect of local prey availability on gyrfalcon diet: DNA analysis on ptarmigan remains at nest sites. <i>Journal of Zoology</i> , 2006, 269, 57-64.	1.7	15
148	Population structure in a critically endangered arctic fox population: does genetics matter?. <i>Molecular Ecology</i> , 2006, 15, 2809-2819.	3.9	44
149	Detection of farm fox and hybrid genotypes among wild arctic foxes in Scandinavia. <i>Conservation Genetics</i> , 2006, 6, 885-894.	1.5	31
150	Extensive Human DNA Contamination in Extracts from Ancient Dog Bones and Teeth. <i>Molecular Biology and Evolution</i> , 2005, 22, 2040-2047.	8.9	137
151	DNA analysis on fox faeces and competition induced niche shifts. <i>Molecular Ecology</i> , 2004, 13, 2389-2392.	3.9	29
152	Population history and genetic structure of a circumpolar species: the arctic fox. <i>Biological Journal of the Linnean Society</i> , 2004, 84, 79-89.	1.6	130
153	Identifying species from pieces of faeces. <i>Conservation Genetics</i> , 2004, 5, 109-111.	1.5	78
154	THE MONOPHYLETIC ORIGIN OF DELAYED IMPLANTATION IN CARNIVORES AND ITS IMPLICATIONS. <i>Evolution; International Journal of Organic Evolution</i> , 2003, 57, 1952-1956.	2.3	27
155	THE MONOPHYLETIC ORIGIN OF DELAYED IMPLANTATION IN CARNIVORES AND ITS IMPLICATIONS. <i>Evolution; International Journal of Organic Evolution</i> , 2003, 57, 1952.	2.3	0
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