Michael Hofreiter

List of Publications by Year in descending order

Source: https://exaly.com/author-pdf/7392007/publications.pdf

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244 papers

22,797 citations

7551 77 h-index 139 g-index

262 all docs 262 docs citations

times ranked

262

18338 citing authors

#	Article	IF	CITATIONS
1	Genetic Analyses from Ancient DNA. Annual Review of Genetics, 2004, 38, 645-679.	3.2	1,084
2	Ancient DNA. Nature Reviews Genetics, 2001, 2, 353-359.	7.7	774
3	Recalibrating Equus evolution using the genome sequence of an early Middle Pleistocene horse. Nature, 2013, 499, 74-78.	13.7	717
4	Species-specific responses of Late Quaternary megafauna to climate and humans. Nature, 2011, 479, 359-364.	13.7	586
5	DNA sequences from multiple amplifications reveal artifacts induced by cytosine deamination in ancient DNA. Nucleic Acids Research, 2001, 29, 4793-4799.	6.5	555
6	Genome flux and stasis in a five millennium transect of European prehistory. Nature Communications, 2014, 5, 5257.	5.8	542
7	Assessing ancient DNA studies. Trends in Ecology and Evolution, 2005, 20, 541-544.	4.2	525
8	Ancient DNA extraction from bones and teeth. Nature Protocols, 2007, 2, 1756-1762.	5.5	491
9	Multilocus Resolution of Phylogeny and Timescale in the Extant Adaptive Radiation of Hawaiian Honeycreepers. Current Biology, 2011, 21, 1838-1844.	1.8	431
10	Molecular Coproscopy: Dung and Diet of the Extinct Ground Sloth Nothrotheriops shastensis. , 1998, 281, 402-406.		401
11	Ancient Biomolecules from Deep Ice Cores Reveal a Forested Southern Greenland. Science, 2007, 317, 111-114.	6.0	393
12	Upper Palaeolithic genomes reveal deep roots of modern Eurasians. Nature Communications, 2015, 6, 8912.	5.8	334
13	Optimal Ancient DNA Yields from the Inner Ear Part of the Human Petrous Bone. PLoS ONE, 2015, 10, e0129102.	1.1	332
14	Comparison and optimization of ancient DNA extraction. BioTechniques, 2007, 42, 343-352.	0.8	331
15	No Evidence of Neandertal mtDNA Contribution to Early Modern Humans. PLoS Biology, 2004, 2, e57.	2.6	327
16	Fossil dogs and wolves from Palaeolithic sites in Belgium, the Ukraine and Russia: osteometry, ancient DNA and stable isotopes. Journal of Archaeological Science, 2009, 36, 473-490.	1.2	315
17	Parallel tagged sequencing on the 454 platform. Nature Protocols, 2008, 3, 267-278.	5.5	289
18	DNA from Pre-Clovis Human Coprolites in Oregon, North America. Science, 2008, 320, 786-789.	6.0	283

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19	Ancient Ethiopian genome reveals extensive Eurasian admixture in Eastern Africa. Science, 2015, 350, 820-822.	6.0	277
20	Ancient proteins resolve the evolutionary history of Darwin's South American ungulates. Nature, 2015, 522, 81-84.	13.7	273
21	A Melanocortin 1 Receptor Allele Suggests Varying Pigmentation Among Neanderthals. Science, 2007, 318, 1453-1455.	6.0	264
22	Mitochondrial genomes reveal an explosive radiation of extinct and extant bears near the Miocene-Pliocene boundary. BMC Evolutionary Biology, 2008, 8, 220.	3.2	261
23	Prehistoric genomes reveal the genetic foundation and cost of horse domestication. Proceedings of the National Academy of Sciences of the United States of America, 2014, 111, E5661-9.	3.3	260
24	Paternity and relatedness in wild chimpanzee communities. Proceedings of the National Academy of Sciences of the United States of America, 2001, 98, 12890-12895.	3.3	254
25	Coat Color Variation at the Beginning of Horse Domestication. Science, 2009, 324, 485-485.	6.0	244
26	Ancient genomes revisit the ancestry of domestic and Przewalski's horses. Science, 2018, 360, 111-114.	6.0	241
27	Genomic Sequencing of Pleistocene Cave Bears. Science, 2005, 309, 597-599.	6.0	221
28	Colours of domestication. Biological Reviews, 2011, 86, 885-899.	4.7	218
29	A Mitogenomic Phylogeny of Living Primates. PLoS ONE, 2013, 8, e69504.	1.1	217
30	Clovis Age Western Stemmed Projectile Points and Human Coprolites at the Paisley Caves. Science, 2012, 337, 223-228.	6.0	211
31	The future of ancient DNA: Technical advances and conceptual shifts. BioEssays, 2015, 37, 284-293.	1.2	209
32	Ecological Change, Range Fluctuations and Population Dynamics during the Pleistocene. Current Biology, 2009, 19, R584-R594.	1.8	208
33	Lack of phylogeography in European mammals before the last glaciation. Proceedings of the National Academy of Sciences of the United States of America, 2004, 101, 12963-12968.	3.3	201
34	A Paleogenomic Perspective on Evolution and Gene Function: New Insights from Ancient DNA. Science, 2014, 343, 1236573.	6.0	197
35	Tracking Five Millennia of Horse Management with Extensive Ancient Genome Time Series. Cell, 2019, 177, 1419-1435.e31.	13.5	195
36	Multiplex amplification of the mammoth mitochondrial genome and the evolution of Elephantidae. Nature, 2006, 439, 724-727.	13.7	194

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37	Molecular Phylogeny, Biogeography, and Habitat Preference Evolution of Marsupials. Molecular Biology and Evolution, 2014, 31, 2322-2330.	3.5	189
38	Ancient genomic changes associated with domestication of the horse. Science, 2017, 356, 442-445.	6.0	185
39	Early Holocene chicken domestication in northern China. Proceedings of the National Academy of Sciences of the United States of America, 2014, 111, 17564-17569.	3.3	181
40	Million-year-old DNA sheds light on the genomic history of mammoths. Nature, 2021, 591, 265-269.	13.7	179
41	Capturing protein-coding genes across highly divergent species. BioTechniques, 2013, 54, 321-326.	0.8	175
42	Targeted high-throughput sequencing of tagged nucleic acid samples. Nucleic Acids Research, 2007, 35, e97.	6.5	171
43	Patterns of nucleotide misincorporations during enzymatic amplification and direct large-scale sequencing of ancient DNA. Proceedings of the National Academy of Sciences of the United States of America, 2006, 103, 13578-13584.	3.3	164
44	A rapid columnâ€based ancient DNA extraction method for increased sample throughput. Molecular Ecology Resources, 2010, 10, 677-683.	2.2	164
45	Identification of the remains of King Richard III. Nature Communications, 2014, 5, 5631.	5.8	163
46	Genomic DNA Sequences from Mastodon and Woolly Mammoth Reveal Deep Speciation of Forest and Savanna Elephants. PLoS Biology, 2010, 8, e1000564.	2.6	162
47	Next Generation Sequencing of Ancient DNA: Requirements, Strategies and Perspectives. Genes, 2010, 1, 227-243.	1.0	157
48	Proboscidean Mitogenomics: Chronology and Mode of Elephant Evolution Using Mastodon as Outgroup. PLoS Biology, 2007, 5, e207.	2.6	150
49	A molecular analysis of ground sloth diet through the last glaciation. Molecular Ecology, 2000, 9, 1975-1984.	2.0	144
50	Animal DNA in PCR reagents plagues ancient DNA research. Journal of Archaeological Science, 2007, 34, 1361-1366.	1.2	142
51	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.	3.3	142
52	The origins and spread of domestic horses from the Western Eurasian steppes. Nature, 2021, 598, 634-640.	13.7	142
53	Ancient and modern DNA reveal dynamics of domestication and cross-continental dispersal of the dromedary. Proceedings of the National Academy of Sciences of the United States of America, 2016, 113, 6707-6712.	3.3	141
54	Nondestructive DNA extraction method for mitochondrial DNA analyses of museum specimens. BioTechniques, 2004, 36, 814-821.	0.8	136

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55	Nuclear Gene Indicates Coat-Color Polymorphism in Mammoths. Science, 2006, 313, 62-62.	6.0	135
56	Computational challenges in the analysis of ancient DNA. Genome Biology, 2010, 11, R47.	13.9	135
57	Partial genomic survival of cave bears in living brown bears. Nature Ecology and Evolution, 2018, 2, 1563-1570.	3.4	132
58	Origin and History of Mitochondrial DNA Lineages in Domestic Horses. PLoS ONE, 2010, 5, e15311.	1.1	129
59	The Population History of Extant and Extinct Hyenas. Molecular Biology and Evolution, 2005, 22, 2435-2443.	3.5	128
60	Withering Away-25,000 Years of Genetic Decline Preceded Cave Bear Extinction. Molecular Biology and Evolution, 2010, 27, 975-978.	3. 5	117
61	Molecular breeding of polymerases for amplification of ancient DNA. Nature Biotechnology, 2007, 25, 939-943.	9.4	115
62	Evidence for a Retroviral Insertion in TRPM1 as the Cause of Congenital Stationary Night Blindness and Leopard Complex Spotting in the Horse. PLoS ONE, 2013, 8, e78280.	1.1	115
63	Phylogenetic Distribution of Extant Richness Suggests Metamorphosis Is a Key Innovation Driving Diversification in Insects. PLoS ONE, 2014, 9, e109085.	1.1	115
64	True single-molecule DNA sequencing of a pleistocene horse bone. Genome Research, 2011, 21, 1705-1719.	2.4	114
65	Paleogenomic Evidence for Multi-generational Mixing between Neolithic Farmers and Mesolithic Hunter-Gatherers in the Lower Danube Basin. Current Biology, 2017, 27, 1801-1810.e10.	1.8	110
66	From micrograms to picograms: quantitative PCR reduces the material demands of high-throughput sequencing. Nucleic Acids Research, 2008, 36, e5-e5.	6.5	105
67	Molecular caving. Current Biology, 2003, 13, R693-R695.	1.8	102
68	Direct multiplex sequencing (DMPS)a novel method for targeted high-throughput sequencing of ancient and highly degraded DNA. Genome Research, 2009, 19, 1843-1848.	2.4	102
69	The genetic history of Europeans. Trends in Genetics, 2012, 28, 496-505.	2.9	102
70	Evidence for Reproductive Isolation between Cave Bear Populations. Current Biology, 2004, 14, 40-43.	1.8	100
71	Genome-wide data from two early Neolithic East Asian individuals dating to 7700 years ago. Science Advances, 2017, 3, e1601877.	4.7	100
72	Ancient DNA: the first three decades. Philosophical Transactions of the Royal Society B: Biological Sciences, 2015, 370, 20130371.	1.8	97

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73	Ancient DNA Analyses Reveal High Mitochondrial DNA Sequence Diversity and Parallel Morphological Evolution of Late Pleistocene Cave Bears. Molecular Biology and Evolution, 2002, 19, 1244-1250.	3.5	94
74	Isotopic evidence for omnivory among European cave bears: Late Pleistocene <i>Ursus spelaeus</i> from the PeÅŸtera cu Oase, Romania. Proceedings of the National Academy of Sciences of the United States of America, 2008, 105, 600-604.	3.3	94
75	The genetic and evolutionary basis of colour variation in vertebrates. Cellular and Molecular Life Sciences, 2010, 67, 2591-2603.	2.4	94
76	Whole mitochondrial genome sequencing of domestic horses reveals incorporation of extensive wild horse diversity during domestication. BMC Evolutionary Biology, 2011, 11, 328.	3.2	92
77	Mitochondrial Diversity and Distribution of African Green Monkeys (Chlorocebus Gray, 1870). American Journal of Primatology, 2013, 75, 350-360.	0.8	87
78	Surprising migration and population size dynamics in ancient Iberian brown bears (Ursus arctos). Proceedings of the National Academy of Sciences of the United States of America, 2008, 105, 5123-5128.	3.3	86
79	Substitutions in woolly mammoth hemoglobin confer biochemical properties adaptive for cold tolerance. Nature Genetics, 2010, 42, 536-540.	9.4	86
80	Genotypes of predomestic horses match phenotypes painted in Paleolithic works of cave art. Proceedings of the National Academy of Sciences of the United States of America, 2011, 108, 18626-18630.	3.3	85
81	Morphological and genetic evidence for early Holocene cattle management in northeastern China. Nature Communications, 2013, 4, 2755.	5.8	82
82	First DNA sequences from Asian cave bear fossils reveal deep divergences and complex phylogeographic patterns. Molecular Ecology, 2009, 18, 1225-1238.	2.0	80
83	Pleistocene bears in the Swabian Jura (Germany): Genetic replacement, ecological displacement, extinctions and survival. Quaternary International, 2011, 245, 225-237.	0.7	80
84	Multiplex amplification of ancient DNA. Nature Protocols, 2006, 1, 720-728.	5.5	78
85	Inactivation of thermogenic UCP1 as a historical contingency in multiple placental mammal clades. Science Advances, 2017, 3, e1602878.	4.7	78
86	Interordinal gene capture, the phylogenetic position of Steller's sea cow based on molecular and morphological data, and the macroevolutionary history of Sirenia. Molecular Phylogenetics and Evolution, 2015, 91, 178-193.	1.2	75
87	G Protein-Coupled Time Travel: Evolutionary Aspects of GPCR Research. Molecular Interventions: Pharmacological Perspectives From Biology, Chemistry and Genomics, 2007, 7, 17-25.	3.4	75
88	Tenrec Phylogeny and the Noninvasive Extraction of Nuclear DNA. Systematic Biology, 2006, 55, 181-194.	2.7	72
89	Discovery of lost diversity of paternal horse lineages using ancient DNA. Nature Communications, 2011, 2, 450.	5.8	72
90	Faunal histories from Holocene ancient DNA. Trends in Ecology and Evolution, 2011, 26, 405-413.	4.2	72

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91	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.	3.5	72
92	Sudden replacement of cave bear mitochondrial DNA in the late Pleistocene. Current Biology, 2007, 17, R122-R123.	1.8	71
93	Is amino acid racemization a useful tool for screening for ancient DNA in bone?. Proceedings of the Royal Society B: Biological Sciences, 2009, 276, 2971-2977.	1.2	71
94	A mitogenomic timetree for Darwin's enigmatic South American mammal Macrauchenia patachonica. Nature Communications, 2017, 8, 15951.	5.8	71
95	Niche partitioning between two sympatric genetically distinct cave bears (Ursus spelaeus and Ursus) Tj ETQq1 1 Quaternary International, 2011, 245, 238-248.	0.784314 0.7	rgBT /Overlo
96	Impact of enrichment conditions on crossâ€species capture of fresh and degraded <scp>DNA</scp> . Molecular Ecology Resources, 2016, 16, 42-55.	2.2	70
97	Kiwi genome provides insights into evolution of a nocturnal lifestyle. Genome Biology, 2015, 16, 147.	3.8	68
98	DNA capture reveals transoceanic gene flow in endangered river sharks. Proceedings of the National Academy of Sciences of the United States of America, 2015, 112, 13302-13307.	3.3	65
99	Phylogeny, diet, and habitat of an extinct ground sloth from Cuchillo CurÃ _i , Neuquén Province, southwest Argentina. Quaternary Research, 2003, 59, 364-378.	1.0	64
100	The genetics of an early Neolithic pastoralist from the Zagros, Iran. Scientific Reports, 2016, 6, 31326.	1.6	61
101	Mitochondrial DNA diversity and evolution of the Pleistocene cave bear complex. Quaternary International, 2014, 339-340, 224-231.	0.7	60
102	Ancient DNA sequences point to a large loss of mitochondrial genetic diversity in the saiga antelope (<i>Saiga tatarica</i>) since the Pleistocene. Molecular Ecology, 2010, 19, 4863-4875.	2.0	59
103	Molecular breeding of polymerases for resistance to environmental inhibitors. Nucleic Acids Research, 2011, 39, e51-e51.	6.5	58
104	Ancient DNA reveals differences in behaviour and sociality between brown bears and extinct cave bears. Molecular Ecology, 2016, 25, 4907-4918.	2.0	58
105	Mitogenomic analyses from ancient DNA. Molecular Phylogenetics and Evolution, 2013, 69, 404-416.	1.2	55
106	Tropical ancient DNA reveals relationships of the extinct Bahamian giant tortoise <i>Chelonoidis alburyorum</i> . Proceedings of the Royal Society B: Biological Sciences, 2017, 284, 20162235.	1.2	55
107	Paging through history: parchment as a reservoir of ancient DNA for next generation sequencing. Philosophical Transactions of the Royal Society B: Biological Sciences, 2015, 370, 20130379.	1.8	52
108	Learning from the past: evolution of GPCR functions. Trends in Pharmacological Sciences, 2007, 28, 117-121.	4.0	51

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109	Ancient biomolecules in Quaternary palaeoecology. Quaternary Science Reviews, 2012, 33, 1-13.	1.4	50
110	Palaeogenomes of Eurasian straight-tusked elephants challenge the current view of elephant evolution. ELife, 2017, 6, .	2.8	50
111	Influence of Climate Warming on Arctic Mammals? New Insights from Ancient DNA Studies of the Collared Lemming Dicrostonyx torquatus. PLoS ONE, 2010, 5, e10447.	1.1	48
112	Grey wolf genomic history reveals a dual ancestry of dogs. Nature, 2022, 607, 313-320.	13.7	48
113	Diversity lost: are all Holarctic large mammal species just relict populations?. BMC Biology, 2010, 8, 46.	1.7	47
114	Road blocks on paleogenomesâ€"polymerase extension profiling reveals the frequency of blocking lesions in ancient DNA. Nucleic Acids Research, 2010, 38, e161-e161.	6.5	47
115	A western route of prehistoric human migration from Africa into the Iberian Peninsula. Proceedings of the Royal Society B: Biological Sciences, 2019, 286, 20182288.	1.2	47
116	Nuclear insertions help and hinder inference of the evolutionary history of gorilla mtDNA. Molecular Ecology, 2004, 14, 179-188.	2.0	46
117	A rapid loss of stripes: the evolutionary history of the extinct quagga. Biology Letters, 2005, 1, 291-295.	1.0	46
118	Mitochondrial Genomes Reveal Slow Rates of Molecular Evolution and the Timing of Speciation in Beavers (Castor), One of the Largest Rodent Species. PLoS ONE, 2011, 6, e14622.	1.1	46
119	Losing ground: past history and future fate of <scp>A</scp> rctic small mammals in a changing climate. Global Change Biology, 2013, 19, 1854-1864.	4.2	46
120	Evolutionary History of Saber-Toothed Cats Based on Ancient Mitogenomics. Current Biology, 2017, 27, 3330-3336.e5.	1.8	45
121	Twenty-five thousand years of fluctuating selection on leopard complex spotting and congenital night blindness in horses. Philosophical Transactions of the Royal Society B: Biological Sciences, 2015, 370, 20130386.	1.8	43
122	The evolutionary and phylogeographic history of woolly mammoths: a comprehensive mitogenomic analysis. Scientific Reports, 2017, 7, 44585.	1.6	39
123	Palaeolithic dogs and Pleistocene wolves revisited: a reply to Morey (2014). Journal of Archaeological Science, 2015, 54, 210-216.	1.2	38
124	Climate impacts on transocean dispersal and habitat in gray whales from the Pleistocene to 2100. Molecular Ecology, 2015, 24, 1510-1522.	2.0	38
125	Hyena paleogenomes reveal a complex evolutionary history of cross-continental gene flow between spotted and cave hyena. Science Advances, 2020, 6, eaay0456.	4.7	38
126	Once lost, twice found: Combined analysis of ancient giant panda sequences characterises extinct clade. Journal of Biogeography, 2019, 46, 251-253.	1.4	37

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127	Novel Genes, Ancient Genes, and Gene Co-Option Contributed to the Genetic Basis of the Radula, a Molluscan Innovation. Molecular Biology and Evolution, 2018, 35, 1638-1652.	3.5	36
128	Successful application of ancient DNA extraction and library construction protocols to museum wet collection specimens. Molecular Ecology Resources, 2021, 21, 2299-2315.	2.2	36
129	Response to Comment by Poinar <i>et al</i> . on "DNA from Pre-Clovis Human Coprolites in Oregon, North Americaâ€. Science, 2009, 325, 148-148.	6.0	34
130	The last of its kind? Radiocarbon, ancient DNA and stable isotope evidence from a late cave bear (Ursus) Tj ETQq	0 0 0 rgB1	· /Overlock 10 34
131	Spatiotemporal Dynamics of Genetic Variation in the Iberian Lynx along Its Path to Extinction Reconstructed with Ancient DNA. Molecular Biology and Evolution, 2017, 34, 2893-2907.	3.5	33
132	Origin and dispersal of early domestic pigs in northern China. Scientific Reports, 2017, 7, 5602.	1.6	32
133	Palaeolithic dogs and the early domestication of the wolf: a reply to the comments of Crockford and Kuzmin (2012). Journal of Archaeological Science, 2013, 40, 786-792.	1.2	31
134	Spotted phenotypes in horses lost attractiveness in the Middle Ages. Scientific Reports, 2016, 6, 38548.	1.6	31
135	Optimized <scp>DNA</scp> sampling of ancient bones using Computed Tomography scans. Molecular Ecology Resources, 2018, 18, 1196-1208.	2.2	31
136	Progress in forensic bone DNA analysis: Lessons learned from ancient DNA. Forensic Science International: Genetics, 2021, 54, 102538.	1.6	31
137	Barcoding the largest animals on Earth: ongoing challenges and molecular solutions in the taxonomic identification of ancient cetaceans. Philosophical Transactions of the Royal Society B: Biological Sciences, 2016, 371, 20150332.	1.8	30
138	Complex Admixture Preceded and Followed the Extinction of Wisent in the Wild. Molecular Biology and Evolution, 2017, 34, msw254.	3.5	30
139	A phylogenetic estimate for golden moles (Mammalia, Afrotheria, Chrysochloridae). BMC Evolutionary Biology, 2010, 10, 69.	3.2	29
140	Ancient DNA from marine mammals: Studying long-lived species over ecological and evolutionary timescales. Annals of Anatomy, 2012, 194, 112-120.	1.0	29
141	Decline of genetic diversity in ancient domestic stallions in Europe. Science Advances, 2018, 4, eaap9691.	4.7	29
142	Middle Pleistocene genome calibrates a revised evolutionary history of extinct cave bears. Current Biology, 2021, 31, 1771-1779.e7.	1.8	27
143	Phenotypes from ancient <scp>DNA</scp> : Approaches, insights and prospects. BioEssays, 2013, 35, 690-695.	1.2	25
144	Combined hybridization capture and shotgun sequencing for ancient <scp>DNA</scp> analysis of extinct wild and domestic dromedary camel. Molecular Ecology Resources, 2017, 17, 300-313.	2.2	25

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145	Effects of late quaternary climate change on <scp>P</scp> alearctic shrews. Global Change Biology, 2013, 19, 1865-1874.	4.2	24
146	Ancient mitochondrial <scp>DNA</scp> and the genetic history of <scp>E</scp> urasian beaver (<i><scp>C</scp>astor fiber</i>) in <scp>E</scp> urope. Molecular Ecology, 2014, 23, 1717-1729.	2.0	24
147	Moose genomes reveal past glacial demography and the origin of modern lineages. BMC Genomics, 2020, 21, 854.	1.2	23
148	Reply to Peters et al.: Further discussions confirm early Holocene chicken domestication in northern China. Proceedings of the National Academy of Sciences of the United States of America, 2015, 112, E2416.	3.3	22
149	Paleogenome Reveals Genetic Contribution of Extinct Giant Panda to Extant Populations. Current Biology, 2019, 29, 1695-1700.e6.	1.8	22
150	Phylotranscriptomic evidence for pervasive ancient hybridization among Old World salamanders. Molecular Phylogenetics and Evolution, 2021, 155, 106967.	1.2	22
151	Vertebrate DNA in Fecal Samples from Bonobos and Gorillas: Evidence for Meat Consumption or Artefact?. PLoS ONE, 2010, 5, e9419.	1.1	21
152	Nondestructive DNA Extraction from Museum Specimens. Methods in Molecular Biology, 2012, 840, 93-100.	0.4	21
153	Phylogenetic analyses suggest that diversification and body size evolution are independent in insects. BMC Evolutionary Biology, 2016, 16, 8.	3.2	21
154	Burial condition is the most important factor for mtDNA PCR amplification success in Palaeolithic equid remains from the Alpine foreland. Archaeological and Anthropological Sciences, 2015, 7, 505-515.	0.7	20
155	High-throughput DNA sequencing of museum specimens sheds light on the long-missing species of the <i>Bokermannohyla claresignata </i> group (Anura: Hylidae: Cophomantini). Zoological Journal of the Linnean Society, 2020, 190, 1235-1255.	1.0	20
156	African and Asian leopards are highly differentiated at the genomic level. Current Biology, 2021, 31, 1872-1882.e5.	1.8	20
157	Mitochondrial DNA sequence from an enigmatic gorilla population (Gorilla gorilla uellensis). American Journal of Physical Anthropology, 2003, 121, 361-368.	2.1	19
158	Mutations Induced by Ancient DNA Extracts?. Molecular Biology and Evolution, 2004, 21, 1463-1467.	3.5	19
159	Analysis of ancient human genomes. BioEssays, 2010, 32, 388-391.	1.2	19
160	Re-inventing ancient human DNA. Investigative Genetics, 2015, 6, 4.	3.3	19
161	The origin of ambling horses. Current Biology, 2016, 26, R697-R699.	1.8	19
162	Improving draft genome contiguity with reference-derived in silico mate-pair libraries. GigaScience, 2018, 7, .	3.3	19

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163	Targeted resequencing of coding <scp>DNA</scp> sequences for <scp>SNP</scp> discovery in nonmodel species. Molecular Ecology Resources, 2018, 18, 1356-1373.	2.2	19
164	Heavy reliance on plants for Romanian cave bears evidenced by amino acid nitrogen isotope analysis. Scientific Reports, 2020, 10, 6612.	1.6	19
165	Pleistocene Extinctions: Haunting the Survivors. Current Biology, 2007, 17, R609-R611.	1.8	18
166	Long DNA sequences and large data sets: investigating the Quaternary via ancient DNA. Quaternary Science Reviews, 2008, 27, 2586-2592.	1.4	18
167	A genetically distinct lion (Panthera leo) population from Ethiopia. European Journal of Wildlife Research, 2013, 59, 215-225.	0.7	18
168	Drafting Human Ancestry: What Does the Neanderthal Genome Tell Us about Hominid Evolution? Commentary on Green et al. (2010). Human Biology, 2011, 83, 1-11.	0.4	17
169	Pleistocene Brown Bears in the Mid-Continent of North America. Science, 2004, 306, 1150-1150.	6.0	16
170	Historical biogeography of the leopard (Panthera pardus) and its extinct Eurasian populations. BMC Evolutionary Biology, 2018, 18, 156.	3.2	16
171	â€~Barcode fishing' for archival DNA from historical type material overcomes taxonomic hurdles, enabling the description of a new frog species. Scientific Reports, 2020, 10, 19109.	1.6	16
172	Target-enriched DNA sequencing from historical type material enables a partial revision of the Madagascar giant stream frogs (genus <i>Mantidactylus</i>). Journal of Natural History, 2020, 54, 87-118.	0.2	16
173	SHORT COMMUNICATION: A phantom extinction? New insights into extinction dynamics of the Donâ€hare <i>Lepus tanaiticus</i> . Journal of Evolutionary Biology, 2010, 23, 2022-2029.	0.8	15
174	Comparing mitogenomic timetrees for two African savannah primate genera (Chlorocebus and Papio). Zoological Journal of the Linnean Society, 2017, 181, 471-483.	1.0	15
175	Cryptic species in a well-known habitat: applying taxonomics to the amphipod genus Epimeria (Crustacea, Peracarida). Scientific Reports, 2018, 8, 6893.	1.6	15
176	Molecular identification of late and terminal Pleistocene Equus ovodovi from northeastern China. PLoS ONE, 2019, 14, e0216883.	1.1	15
177	Consensify: A Method for Generating Pseudohaploid Genome Sequences from Palaeogenomic Datasets with Reduced Error Rates. Genes, 2020, $11,50$.	1.0	15
178	Ecological Specialization and Evolutionary Reticulation in Extant Hyaenidae. Molecular Biology and Evolution, 2021, 38, 3884-3897.	3.5	15
179	Demographic reconstruction from ancient DNA supports rapid extinction of the great auk. ELife, 2019, 8, .	2.8	15
180	Ancient DNA from Giant Panda (Ailuropoda melanoleuca) of South-Western China Reveals Genetic Diversity Loss during the Holocene. Genes, 2018, 9, 198.	1.0	14

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