List of Publications by Year in descending order

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#	Article	IF	CITATIONS
1	A Study on Burrows-Wheeler Aligner's Performance Optimization for Ancient DNA Mapping. Lecture Notes in Networks and Systems, 2022, , 105-114.	0.7	1
2	The kÄkÄpÅ•(Strigops habroptilus). Trends in Genetics, 2022, , .	6.7	0
3	A multidisciplinary study of Iberian Chalcolithic dogs. Journal of Archaeological Science: Reports, 2022, 42, 103338.	0.5	0
4	Development and Optimization of a Silica Column-Based Extraction Protocol for Ancient DNA. Genes, 2022, 13, 687.	2.4	6
5	The genetic origin of Huns, Avars, and conquering Hungarians. Current Biology, 2022, 32, 2858-2870.e7.	3.9	18
6	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
7	Bioarchaeological evidence of one of the earliest Islamic burials in the Levant. Communications Biology, 2022, 5, .	4.4	3
8	Planned cull endangers Swedish wolf population. Science, 2022, 377, 162-162.	12.6	5
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. Rna, 2021, 27, 324-334.	3.5	7
10	Million-year-old DNA sheds light on the genomic history of mammoths. Nature, 2021, 591, 265-269.	27.8	179
11	Mobility patterns in inland southwestern Sweden during the Neolithic and Early Bronze Age. Archaeological and Anthropological Sciences, 2021, 13, 1.	1.8	11
12	African and Asian leopards are highly differentiated at the genomic level. Current Biology, 2021, 31, 1872-1882.e5.	3.9	20
13	Ancient horse genomes reveal the timing and extent of dispersals across the Bering Land Bridge. Molecular Ecology, 2021, 30, 6144-6161.	3.9	30
14	Variable kinship patterns in Neolithic Anatolia revealed by ancient genomes. Current Biology, 2021, 31, 2455-2468.e18.	3.9	47
15	Related in death? A curious case of a foetus hidden in bishop Peder Winstrup's coffin in Lund, Sweden. Journal of Archaeological Science: Reports, 2021, 37, 102939.	0.5	0
16	Maternal genetic origin of the late and final Neolithic human populations from presentâ€day Poland. American Journal of Physical Anthropology, 2021, 176, 223-236.	2.1	3
17	Mammuthus sp. (Early and Middle Pleistocene Mammoths). Trends in Genetics, 2021, 37, 682-683.	6.7	0
18	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

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19	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
20	Human inbreeding has decreased in time through the Holocene. Current Biology, 2021, 31, 3925-3934.e8.	3.9	20
21	Ancient and modern genomes unravel the evolutionary history of the rhinoceros family. Cell, 2021, 184, 4874-4885.e16.	28.9	49
22	Human population dynamics and <i>Yersinia pestis</i> in ancient northeast Asia. Science Advances, 2021, 7, .	10.3	32
23	Archaeogenetic analysis of Neolithic sheep from Anatolia suggests a complex demographic history since domestication. Communications Biology, 2021, 4, 1279.	4.4	16
24	Pre-extinction Demographic Stability and Genomic Signatures of Adaptation in the Woolly Rhinoceros. Current Biology, 2020, 30, 3871-3879.e7.	3.9	41
25	Origins and genetic legacy of prehistoric dogs. Science, 2020, 370, 557-564.	12.6	152
26	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
27	The Neolithic Pitted Ware culture foragers were culturally but not genetically influenced by the Battle Axe culture herders. American Journal of Physical Anthropology, 2020, 172, 638-649.	2.1	20
28	Corded Ware cultural complexity uncovered using genomic and isotopic analysis from south-eastern Poland. Scientific Reports, 2020, 10, 6885.	3.3	29
29	Ancient pigs reveal a near-complete genomic turnover following their introduction to Europe. Proceedings of the National Academy of Sciences of the United States of America, 2019, 116, 17231-17238.	7.1	101
30	The genomic ancestry of the Scandinavian Battle Axe Culture people and their relation to the broader Corded Ware horizon. Proceedings of the Royal Society B: Biological Sciences, 2019, 286, 20191528.	2.6	35
31	Early Pleistocene enamel proteome from Dmanisi resolves Stephanorhinus phylogeny. Nature, 2019, 574, 103-107.	27.8	135
32	Ancient DNA from mastics solidifies connection between material culture and genetics of mesolithic hunter–gatherers in Scandinavia. Communications Biology, 2019, 2, 185.	4.4	32
33	The curious case of the Mesolithic Iberian dogs: An archaeogenetic study. Journal of Archaeological Science, 2019, 105, 116-129.	2.4	18
34	Megalithic tombs in western and northern Neolithic Europe were linked to a kindred society. Proceedings of the National Academy of Sciences of the United States of America, 2019, 116, 9469-9474.	7.1	81
35	Viking warrior women? Reassessing Birka chamber grave Bj.581. Antiquity, 2019, 93, 181-198.	1.0	31
36	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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37	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
38	Elucidating recent history by tracing genetic affinity of three 16th century miners from Sweden. Journal of Archaeological Science: Reports, 2018, 19, 651-657.	0.5	0
39	Four millennia of Iberian biomolecular prehistory illustrate the impact of prehistoric migrations at the far end of Eurasia. Proceedings of the National Academy of Sciences of the United States of America, 2018, 115, 3428-3433.	7.1	96
40	New insights on cultural dualism and population structure in the Middle Neolithic Funnel Beaker culture on the island of Gotland. Journal of Archaeological Science: Reports, 2018, 17, 325-334.	0.5	10
41	Population genomics of grey wolves and wolf-like canids in North America. PLoS Genetics, 2018, 14, e1007745.	3.5	54
42	Ancient genomes suggest the eastern Pontic-Caspian steppe as the source of western Iron Age nomads. Science Advances, 2018, 4, eaat4457.	10.3	76
43	The stone cist conundrum: A multidisciplinary approach to investigate Late Neolithic/Early Bronze Age population demography on the island of Gotland. Journal of Archaeological Science: Reports, 2018, 20, 324-337.	0.5	4
44	Genomic and Strontium Isotope Variation Reveal Immigration Patterns in a Viking Age Town. Current Biology, 2018, 28, 2730-2738.e10.	3.9	44
45	Partial genomic survival of cave bears in living brown bears. Nature Ecology and Evolution, 2018, 2, 1563-1570.	7.8	132
46	Investigating Holocene human population history in North Asia using ancient mitogenomes. Scientific Reports, 2018, 8, 8969.	3.3	15
47	Population genomics of Mesolithic Scandinavia: Investigating early postglacial migration routes and high-latitude adaptation. PLoS Biology, 2018, 16, e2003703.	5.6	174
48	Diverse origin of mitochondrial lineages in Iron Age Black Sea Scythians. Scientific Reports, 2017, 7, 43950.	3.3	24
49	The evolutionary and phylogeographic history of woolly mammoths: a comprehensive mitogenomic analysis. Scientific Reports, 2017, 7, 44585.	3.3	39
50	Genomic Analyses of Pre-European Conquest Human Remains from the Canary Islands Reveal Close Affinity to Modern North Africans. Current Biology, 2017, 27, 3396-3402.e5.	3.9	62
51	Genome-Based Sexing Provides Clues about Behavior and Social Structure in the Woolly Mammoth. Current Biology, 2017, 27, 3505-3510.e3.	3.9	53
52	A female Viking warrior confirmed by genomics. American Journal of Physical Anthropology, 2017, 164, 853-860.	2.1	69
53	Evolution, ecology and conservation—revisiting three decades of Arctic fox population genetic research. Polar Research, 2017, 36, 4.	1.6	10
54	Archaeogenomic analysis of the first steps of Neolithization in Anatolia and the Aegean. Proceedings of the Royal Society B: Biological Sciences, 2017, 284, 20172064.	2.6	26

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55	Spatial variation in Arctic hare (Lepus arcticus) populations around the Hall Basin. Polar Biology, 2017, 40, 2113-2118.	1.2	5
56	Inbreeding depression in a critically endangered carnivore. Molecular Ecology, 2016, 25, 3309-3318.	3.9	34
57	The Demographic Development of the First Farmers in Anatolia. Current Biology, 2016, 26, 2659-2666.	3.9	163
58	Genomic Evidence Establishes Anatolia as the Source of the European Neolithic Gene Pool. Current Biology, 2016, 26, 270-275.	3.9	111
59	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
60	Complete Genomes Reveal Signatures of Demographic and Genetic Declines in the Woolly Mammoth. Current Biology, 2015, 25, 1395-1400.	3.9	263
61	Population Demography and Genetic Diversity in the Pleistocene Cave Lion. Open Quaternary, 2015, 1, 4.	1.0	44
62	Ancient genomes link early farmers from Atapuerca in Spain to modern-day Basques. Proceedings of the United States of America, 2015, 112, 11917-11922.	7.1	255
63	Mitochondrial DNA variation in the Viking age population of Norway. Philosophical Transactions of the Royal Society B: Biological Sciences, 2015, 370, 20130384.	4.0	25
64	Ancient mitochondrial DNA from the northern fringe of the Neolithic farming expansion in Europe sheds light on the dispersion process. Philosophical Transactions of the Royal Society B: Biological Sciences, 2015, 370, 20130373.	4.0	65
65	Worldwide Patterns of Ancestry, Divergence, and Admixture in Domesticated Cattle. PLoS Genetics, 2014, 10, e1004254.	3.5	391
66	Slaves as burial gifts in Viking Age Norway? Evidence from stable isotope and ancient DNA analyses. Journal of Archaeological Science, 2014, 41, 533-540.	2.4	51
67	Genomic Diversity and Admixture Differs for Stone-Age Scandinavian Foragers and Farmers. Science, 2014, 344, 747-750.	12.6	315
68	Direct Estimates of Natural Selection in Iberia Indicate Calcium Absorption Was Not the Only Driver of Lactase Persistence in Europe. Molecular Biology and Evolution, 2014, 31, 975-983.	8.9	52
69	The genetic prehistory of the New World Arctic. Science, 2014, 345, 1255832.	12.6	264
70	Accurate sex identification of ancient human remains using DNA shotgun sequencing. Journal of Archaeological Science, 2013, 40, 4477-4482.	2.4	337
71	Carnivore conservation in practice: replicated management actions on a large spatial scale. Journal of Applied Ecology, 2013, 50, 59-67.	4.0	93
72	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

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73	Neolithic Hedgehogs (Erinaceus europaeus) from the Island of Gotland show early contacts with the Swedish mainland. Journal of Archaeological Science, 2012, 39, 229-233.	2.4	7
74	Molecular and osteometric sexing of cattle metacarpals: a case study from 15th century AD Beja, Portugal. Journal of Archaeological Science, 2012, 39, 1445-1454.	2.4	32
75	Origins and Genetic Legacy of Neolithic Farmers and Hunter-Gatherers in Europe. Science, 2012, 336, 466-469.	12.6	507
76	Finding the founder of Stockholm $\hat{a} \in$ A kinship study based on Y-chromosomal, autosomal and mitochondrial DNA. Annals of Anatomy, 2012, 194, 138-145.	1.9	12
77	Coat colour and sex identification in horses from Iron Age Sweden. Annals of Anatomy, 2012, 194, 82-87.	1.9	8
78	Further developments in molecular sex assignment: a blind test of 18th and 19th century human skeletons. Journal of Archaeological Science, 2011, 38, 1326-1330.	2.4	15
79	Population-level genotyping of coat colour polymorphism in woolly mammoth (Mammuthus) Tj ETQq1 1 0.78431	4_rgBT /O\ 3.0	verlock 10 T
80	50,000 years of genetic uniformity in the critically endangered Iberian lynx. Molecular Ecology, 2011, 20, 3785-3795.	3.9	30
81	Phylogenetic placement and population structure of Indoâ€Pacific bottlenose dolphins (<i>Tursiops) Tj ETQq1 1 0 431-448.</i>).784314 ı 1.8	rgBT /Overlo 11
82	Arctic fox <i>Vulpes lagopus</i> population structure: circumpolar patterns and processes. Oikos, 2011, 120, 873-885.	2.7	28
83	Estimation of Population Divergence Times from Non-Overlapping Genomic Sequences: Examples from Dogs and Wolves. Molecular Biology and Evolution, 2011, 28, 1505-1517.	8.9	61
84	Typing Late Prehistoric Cows and Bulls—Osteology and Genetics of Cattle at the Eketorp Ringfort on the Ā−land Island in Sweden. PLoS ONE, 2011, 6, e20748.	2.5	14
85	High frequency of lactose intolerance in a prehistoric hunter-gatherer population in northern Europe. BMC Evolutionary Biology, 2010, 10, 89.	3.2	73
86	Ancient DNA reveals traces of Iberian Neolithic and Bronze Age lineages in modern Iberian horses. Molecular Ecology, 2010, 19, 64-78.	3.9	56
87	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.	3.9	59
88	The mitochondrial genome sequence of the Tasmanian tiger (<i>Thylacinus cynocephalus</i>). Genome Research, 2009, 19, 213-220.	5.5	102
89	Response to Comment by Poinar <i>et al</i> . on "DNA from Pre-Clovis Human Coprolites in Oregon, North America― Science, 2009, 325, 148-148.	12.6	34
90	Ancient DNA Reveals Lack of Continuity between Neolithic Hunter-Gatherers and Contemporary Scandinavians. Current Biology, 2009, 19, 1758-1762.	3.9	217

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91	Paleo-Eskimo mtDNA Genome Reveals Matrilineal Discontinuity in Greenland. Science, 2008, 320, 1787-1789.	12.6	184
92	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.	7.1	86
93	Barking up the wrong tree: Modern northern European dogs fail to explain their origin. BMC Evolutionary Biology, 2008, 8, 71.	3.2	22
94	Temporal fluctuations of Y-chromosomal variation in Bos taurus. Biology Letters, 2008, 4, 752-754.	2.3	30
95	A DNA test for sex identification in cattle confirms osteometric results. Journal of Archaeological Science, 2008, 35, 942-946.	2.4	34
96	Comparing the survival of osteocalcin and mtDNA in archaeological bone from four European sites. Journal of Archaeological Science, 2008, 35, 1756-1764.	2.4	73
97	Fishing for ancient DNA. Forensic Science International: Genetics, 2008, 2, 104-107.	3.1	39
98	DNA from Pre-Clovis Human Coprolites in Oregon, North America. Science, 2008, 320, 786-789.	12.6	283
99	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
100	Cryptic Contamination and Phylogenetic Nonsense. PLoS ONE, 2008, 3, e2316.	2.5	7
101	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
102	Whole-Genome Shotgun Sequencing of Mitochondria from Ancient Hair Shafts. Science, 2007, 317, 1927-1930.	12.6	220
103	Recovery of DNA from Footprints in the Snow. Canadian Field-Naturalist, 2007, 121, 321.	0.1	26
104	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
105	More on Contamination: The Use of Asymmetric Molecular Behavior to Identify Authentic Ancient Human DNA. Molecular Biology and Evolution, 2007, 24, 998-1004.	8.9	114
106	Typing single polymorphic nucleotides in mitochondrial DNA as a way to access Middle Pleistocene DNA. Biology Letters, 2006, 2, 601-603.	2.3	28
107	Medieval remains from Lithuania indicate loss of a mitochondrial haplotype in Bison bonasus. Molecular Ecology, 2006, 15, 3083-3083.	3.9	9
108	Y-chromosome diversity in Sweden – A long-time perspective. European Journal of Human Genetics, 2006, 14, 963-970.	2.8	65

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109	Detection of farm fox and hybrid genotypes among wild arctic foxes in Scandinavia. Conservation Genetics, 2006, 6, 885-894.	1.5	31
110	Extensive Human DNA Contamination in Extracts from Ancient Dog Bones and Teeth. Molecular Biology and Evolution, 2005, 22, 2040-2047.	8.9	137
111	Cattle domestication in the Near East was followed by hybridization with aurochs bulls in Europe. Proceedings of the Royal Society B: Biological Sciences, 2005, 272, 2345-2351.	2.6	151
112	Prehistoric contacts over the Straits of Gibraltar indicated by genetic analysis of Iberian Bronze Age cattle. Proceedings of the National Academy of Sciences of the United States of America, 2005, 102, 8431-8435.	7.1	109
113	"The wet and the wild followed by the dry and the tame―– or did they occur at the same time? Diet in Mesolithic – Neolithic southern Sweden. Antiquity, 2004, 78, 23-33.	1.0	90
114	DNA analysis on fox faeces and competition induced niche shifts. Molecular Ecology, 2004, 13, 2389-2392.	3.9	29
115	Identifying species from pieces of faeces. Conservation Genetics, 2004, 5, 109-111.	1.5	78
116	Molecular phylogeny of the extinct cave lion Panthera leo spelaea. Molecular Phylogenetics and Evolution, 2004, 30, 841-849.	2.7	131
117	Is the endangered Fennoscandian arctic fox (Alopex lagopus) population genetically isolated?. Biological Conservation, 2002, 105, 171-178.	4.1	50
118	The Jettbole Middle Neolithic Site on the Aland Islands Human Remains, Ancient dna and Pottery. European Journal of Archaeology, 2002, 5, 42-68.	0.5	2
119	Not just old but old and cold?. Nature, 2001, 410, 772-772.	27.8	17
120	Molecular analysis of Neanderthal DNA from the northern Caucasus. Nature, 2000, 404, 490-493.	27.8	508