Eske Willerslev

List of Publications by Year
in descending order

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321	53,082	910 119	2108 210
papers	citations	h-index	g-index

350	350	350	44638
all docs	docs citations	times ranked	citing authors

#	Article	IF	Citations
1	Chiquihuite Cave and Americaâ€™s Hidden Limestone Industries: A Reply to Chatters et al.. PaleoAmerica, 2022, 8, 17-28.	0.4	3
2	Late Pleistocene palaeoenvironments and a possible glacial refugium on northern Vancouver Island, Canada: Evidence for the viability of early human settlement on the northwest coast of North America. Quaternary Science Reviews, 2022, 279, 107388.	1.4	14
3	A Middle Pleistocene Denisovan molar from the Annamite Chain of northern Laos. Nature Communications, 2022, 13, 2557.	5.8	20
4	Grey wolf genomic history reveals a dual ancestry of dogs. Nature, 2022, 607, 313-320.	13.7	48
5	Genomes of Pleistocene Siberian Wolves Uncover Multiple Extinct Wolf Lineages. Current Biology, 2021, 31, 198-206.e8.	1.8	26
6	Genomic Steppe ancestry in skeletons from the Neolithic Single Grave Culture in Denmark. PLoS ONE, 2021, 16, e0244872.	1.1	11
7	Lake Sedimentary DNA Research on Past Terrestrial and Aquatic Biodiversity: Overview and Recommendations. Quaternary, 2021, 4, 6.	1.0	121
8	Ancient DNA analysis. Nature Reviews Methods Primers, 2021, 1, .	11.8	133
9	Peopling of the Americas as inferred from ancient genomics. Nature, 2021, 594, 356-364.	13.7	63
10	Environmental genomics of Late Pleistocene black bears and giant short-faced bears. Current Biology, 2021, 31, 2728-2736.e8.	1.8	42
11	Late Pleistocene paleoecology and phylogeography of woolly rhinoceroses. Quaternary Science Reviews, 2021, 263, 106993.	1.4	18
12	Ancient DNA reveals multiple origins and migration waves of extinct Japanese brown bear lineages. Royal Society Open Science, 2021, 8, 210518.	1.1	8
13	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, .	3.3	19
14	Late Quaternary dynamics of Arctic biota from ancient environmental genomics. Nature, 2021, 600, 86-92.	13.7	81
15	Identifying a living great-grandson of the Lakota Sioux leader Tatanka Iyotake (Sitting Bull). Science Advances, 2021, 7, eabh2013.	4.7	5
16	AMS dating and ancient DNA analysis of bone relics associated with St John the Baptist from Sveti Ivan (Sozopol, Bulgaria). Journal of Archaeological Science: Reports, 2020, 29, 102082.	0.2	0
17	Ancient DNA suggests modern wolves trace their origin to a Late Pleistocene expansion from Beringia. Molecular Ecology, 2020, 29, 1596-1610.	2.0	70
18	Evidence of human occupation in Mexico around the Last Glacial Maximum. Nature, 2020, 584, 87-92.	13.7	115

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19	Diverse variola virus (smallpox) strains were widespread in northern Europe in the Viking Age. Science, 2020, 369, .	6.0	108
20	Insights Into Aboriginal Australian Mortuary Practices: Perspectives From Ancient DNA. Frontiers in Ecology and Evolution, 2020, 8, .	1.1	4
21	Pre-extinction Demographic Stability and Genomic Signatures of Adaptation in the Woolly Rhinoceros. Current Biology, 2020, 30, 3871-3879.e7.	1.8	41
22	Ancient Jomon genome sequence analysis sheds light on migration patterns of early East Asian populations. Communications Biology, 2020, 3, 437.	2.0	44
23	Population genomics of the Viking world. Nature, 2020, 585, 390-396.	13.7	143
24	Multi-proxy analyses of a mid-15th century Middle Iron Age Bantu-speaker palaeo-faecal specimen elucidates the configuration of the â€˜ancestralâ€™ sub-Saharan African intestinal microbiome. Microbiome, 2020, 8, 62.	4.9	14
25	The dental proteome of Homo antecessor. Nature, 2020, 580, 235-238.	13.7	100
26	Arctic-adapted dogs emerged at the Pleistoceneâ€“Holocene transition. Science, 2020, 368, 1495-1499.	6.0	60
27	Re-theorising mobility and the formation of culture and language among the Corded Ware Culture in Europeâ€”CORRIGENDUM. Antiquity, 2020, 94, 839-839.	0.5	0
28	An Ancient Baboon Genome Demonstrates Long-Term Population Continuity in Southern Africa. Genome Biology and Evolution, 2020, 12, 407-412.	1.1	13
29	Influence of past climate change on phylogeography and demographic history of narwhals, Monodon monoceros. Proceedings of the Royal Society B: Biological Sciences, 2020, 287, 20192964.	1.2	39
30	High-Throughput Sequencing-Based Investigation of Viruses in Human Cancers by Multienrichment Approach. Journal of Infectious Diseases, 2019, 220, 1312-1324.	1.9	13
31	Early Pleistocene enamel proteome from Dmanisi resolves Stephanorhinus phylogeny. Nature, 2019, 574, 103-107.	13.7	135
32	Contaminating viral sequences in high-throughput sequencing viromics: a linkage study of 700 sequencing libraries. Clinical Microbiology and Infection, 2019, 25, 1277-1285.	2.8	109
33	The population history of northeastern Siberia since the Pleistocene. Nature, 2019, 570, 182-188.	13.7	259
34	Unraveling ancestry, kinship, and violence in a Late Neolithic mass grave. Proceedings of the National Academy of Sciences of the United States of America, 2019, 116, 10705-10710.	3.3	119
35	Joint Estimates of Heterozygosity and Runs of Homozygosity for Modern and Ancient Samples. Genetics, 2019, 212, 587-614.	1.2	61
36	DNA metabarcodingâ€”Need for robust experimental designs to draw sound ecological conclusions. Molecular Ecology, 2019, 28, 1857-1862.	2.0	300

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37	Tracking Five Millennia of Horse Management with Extensive Ancient Genome Time Series. Cell, 2019, 177, 1419-1435.e31.	13.5	195
38	Human Disease Variation in the Light of Population Genomics. Cell, 2019, 177, 115-131.	13.5	75
39	Environmental DNA for improved detection and environmental surveillance of schistosomiasis. Proceedings of the National Academy of Sciences of the United States of America, 2019, 116, 8931-8940.	3.3	94
40	Mitogenomic diversity in Sacred Ibis Mummies sheds light on early Egyptian practices. PLoS ONE, 2019, 14, e0223964.	1.1	14
41	Emergence and Spread of Basal Lineages of YersiniaÂpestis during the Neolithic Decline. Cell, 2019, 176, 295-305.e10.	13.5	168
42	Origins and genetic legacies of the Caribbean Taino. Proceedings of the National Academy of Sciences of the United States of America, 2018, 115, 2341-2346.	3.3	64
43	Ancient genomes revisit the ancestry of domestic and Przewalskiâ€™s horses. Science, 2018, 360, 111-114.	6.0	241
44	Ancient pathogen <scp>DNA</scp> in human teeth and petrous bones. Ecology and Evolution, 2018, 8, 3534-3542.	0.8	38
45	Physiological and Genetic Adaptations to Diving in Sea Nomads. Cell, 2018, 173, 569-580.e15.	13.5	129
46	Genomic insights into the origin and diversification of late maritime hunter-gatherers from the Chilean Patagonia. Proceedings of the National Academy of Sciences of the United States of America, 2018, 115, E4006-E4012.	3.3	50
47	Disentangling Immediate Adaptive Introgression from Selection on Standing Introgressed Variation in Humans. Molecular Biology and Evolution, 2018, 35, 623-630.	3.5	46
48	Ancient environmental DNA reveals shifts in dominant mutualisms during the lateÂQuaternary. Nature Communications, 2018, 9, 139.	5.8	24
49	Terminal Pleistocene Alaskan genome reveals first founding population of Native Americans. Nature, 2018, 553, 203-207.	13.7	304
50	Demographic analysis of cyanobacteria based on the mutation rates estimated from an ancient ice core. Heredity, 2018, 120, 562-573.	1.2	19
51	Ancient Biomolecules and Evolutionary Inference. Annual Review of Biochemistry, 2018, 87, 1029-1060.	5.0	76
52	Discussion: Are the Origins of Indo-European Languages Explained by the Migration of the Yamnaya Culture to the West?. European Journal of Archaeology, 2018, 21, 3-17.	0.3	17
53	Early human dispersals within the Americas. Science, 2018, 362, .	6.0	230
54	Quantitative metaproteomics of medieval dental calculus reveals individual oral health status. Nature Communications, 2018, 9, 4744.	5.8	63

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55	A large impact crater beneath Hiawatha Glacier in northwest Greenland. Science Advances, 2018, 4, eaar8173.	4.7	97
56	Ancient nuclear genomes enable repatriation of Indigenous human remains. Science Advances, 2018, 4, eaau5064.	4.7	41
57	The evolutionary history of dogs in the Americas. Science, 2018, 361, 81-85.	6.0	140
58	The prehistoric peopling of Southeast Asia. Science, 2018, 361, 88-92.	6.0	291
59	Ancient human parvovirus B19 in Eurasia reveals its long-term association with humans. Proceedings of the National Academy of Sciences of the United States of America, 2018, 115, 7557-7562.	3.3	64
60	Parasitic infections and resource economy of Danish Iron Age settlement through ancient DNA sequencing. PLoS ONE, 2018, 13, e0197399.	1.1	8
61	Ancient DNA from latrines in Northern Europe and the Middle East (500 BCâ€“1700 AD) reveals past parasites and diet. PLoS ONE, 2018, 13, e0195481.	1.1	63
62	137 ancient human genomes from across the Eurasian steppes. Nature, 2018, 557, 369-374.	13.7	325
63	Ancient hepatitis B viruses from the Bronze Age to the Medieval period. Nature, 2018, 557, 418-423.	13.7	155
64	The first horse herders and the impact of early Bronze Age steppe expansions into Asia. Science, 2018, 360, .	6.0	262
65	Evolutionary Patterns and Processes: Lessons from Ancient DNA. Systematic Biology, 2017, 66, syw059.	2.7	73
66	gargammel: a sequence simulator for ancient DNA. Bioinformatics, 2017, 33, 577-579.	1.8	85
67	Tracing the peopling of the world through genomics. Nature, 2017, 541, 302-310.	13.7	562
68	Selection in Europeans on Fatty Acid Desaturases Associated with Dietary Changes. Molecular Biology and Evolution, 2017, 34, 1307-1318.	3.5	90
69	Ancient genomic changes associated with domestication of the horse. Science, 2017, 356, 442-445.	6.0	185
70	Ancient individuals from the North American Northwest Coast reveal 10,000 years of regional genetic continuity. Proceedings of the National Academy of Sciences of the United States of America, 2017, 114, 4093-4098.	3.3	100
71	Re-theorising mobility and the formation of culture and language among the Corded Ware Culture in Europe. Antiquity, 2017, 91, 334-347.	0.5	157
72	The evolutionary and phylogeographic history of woolly mammoths: a comprehensive mitogenomic analysis. Scientific Reports, 2017, 7, 44585.	1.6	39

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73	Human evolution: a tale from ancient genomes. Philosophical Transactions of the Royal Society B: Biological Sciences, 2017, 372, 20150484.	1.8	51
74	Phylogenomics and Morphology of Extinct Paleognaths Reveal the Origin and Evolution of the Ratites. Current Biology, 2017, 27, 68-77.	1.8	123
75	A communal catalogue reveals Earthâ€™s multiscale microbial diversity. Nature, 2017, 551, 457-463.	13.7	1,942
76	Ancient genomes show social and reproductive behavior of early Upper Paleolithic foragers. Science, 2017, 358, 659-662.	6.0	263
77	Extensive Farming in Estonia Started through a Sex-Biased Migration from the Steppe. Current Biology, 2017, 27, 2185-2193.e6.	1.8	111
78	High Yâ€chromosomal Differentiation Among Ethnic Groups of Dir and Swat Districts, Pakistan. Annals of Human Genetics, 2017, 81, 234-248.	0.3	9
79	Data sharing: do scientists know best?. Nature, 2017, 548, 281-281.	13.7	2
80	Evaluating the impact of domestication and captivity on the horse gut microbiome. Scientific Reports, 2017, 7, 15497.	1.6	112
81	Early Modern Humans from Tam PÃ Ling, Laos. Current Anthropology, 2017, 58, S527-S538.	0.8	32
82	Eight Millennia of Matrilineal Genetic Continuity in the South Caucasus. Current Biology, 2017, 27, 2023-2028.e7.	1.8	37
83	Experimental conditions improving inâ€solution target enrichment for ancient <scp>DNA</scp>. Molecular Ecology Resources, 2017, 17, 508-522.	2.2	67
84	Population characteristics of a large whale shark aggregation inferred from seawater environmental DNA. Nature Ecology and Evolution, 2017, 1, 4.	3.4	223
85	A matter of months: High precision migration chronology of a Bronze Age female. PLoS ONE, 2017, 12, e0178834.	1.1	60
86	Cutavirus in Cutaneous Malignant Melanoma. Emerging Infectious Diseases, 2017, 23, 363-365.	2.0	22
87	Comparing Ancient DNA Preservation in Petrous Bone and Tooth Cementum. PLoS ONE, 2017, 12, e0170940.	1.1	136
88	Identification of Known and Novel Recurrent Viral Sequences in Data from Multiple Patients and Multiple Cancers. Viruses, 2016, 8, 53.	1.5	11
89	Nextâ€generation monitoring of aquatic biodiversity using environmental <scp>DNA</scp> metabarcoding. Molecular Ecology, 2016, 25, 929-942.	2.0	873
90	Substitutions of short heterologous DNA segments of intragenomic or extragenomic origins produce clustered genomic polymorphisms. Proceedings of the National Academy of Sciences of the United States of America, 2016, 113, 15066-15071.	3.3	8

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91	Postglacial viability and colonization in North Americaâ€™s ice-free corridor. Nature, 2016, 537, 45-49.	13.7	363
92	High diversity of picornaviruses in rats from different continents revealed by deep sequencing. Emerging Microbes and Infections, 2016, 5, 1-8.	3.0	14
93	Vancomycin gene selection in the microbiome of urbanRattus norvegicusfrom hospital environment. Evolution, Medicine and Public Health, 2016, 2016, 219-226.	1.1	9
94	A time transect of exomes from a Native American population before and after European contact. Nature Communications, 2016, 7, 13175.	5.8	134
95	Fast, Accurate and Automatic Ancient Nucleosome and Methylation Maps with epiPALEOMIX. Molecular Biology and Evolution, 2016, 33, 3284-3298.	3.5	53
96	A genomic history of Aboriginal Australia. Nature, 2016, 538, 207-214.	13.7	439
97	Genomic analyses inform on migration events during the peopling of Eurasia. Nature, 2016, 538, 238-242.	13.7	360
98	DNA evidence of bowhead whale exploitation by Greenlandic Paleo-Inuit 4,000 years ago. Nature Communications, 2016, 7, 13389.	5.8	63
99	Ancient mtDNA sequences from the First Australians revisited. Proceedings of the National Academy of Sciences of the United States of America, 2016, 113, 6892-6897.	3.3	26
100	Environmental DNA from Seawater Samples Correlate with Trawl Catches of Subarctic, Deepwater Fishes. PLoS ONE, 2016, 11, e0165252.	1.1	296
101	The origin and evolution of maize in the Southwestern United States. Nature Plants, 2015, 1, 14003.	4.7	138
102	Pros and cons of methylation-based enrichment methods for ancient DNA. Scientific Reports, 2015, 5, 11826.	1.6	61
103	Characterizing novel endogenous retroviruses from genetic variation inferred from short sequence reads. Scientific Reports, 2015, 5, 15644.	1.6	2
104	Investigation of Human Cancers for Retrovirus by Low-Stringency Target Enrichment and High-Throughput Sequencing. Scientific Reports, 2015, 5, 13201.	1.6	34
105	New Type of Papillomavirus and Novel Circular Single Stranded DNA Virus Discovered in Urban Rattus norvegicus Using Circular DNA Enrichment and Metagenomics. PLoS ONE, 2015, 10, e0141952.	1.1	14
106	Tracing the dynamic life story of a Bronze Age Female. Scientific Reports, 2015, 5, 10431.	1.6	112
107	Population genomics of Bronze Age Eurasia. Nature, 2015, 522, 167-172.	13.7	1,166
108	Reconstructing ancient genomes and epigenomes. Nature Reviews Genetics, 2015, 16, 395-408.	7.7	197

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109	Interordinal gene capture, the phylogenetic position of Stellerâ€™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
110	Genome-wide ancestry of 17th-century enslaved Africans from the Caribbean. Proceedings of the National Academy of Sciences of the United States of America, 2015, 112, 3669-3673.	3.3	110
111	Amplification of TruSeq ancient DNA libraries with AccuPrime Pfx: consequences on nucleotide misincorporation and methylation patterns. Science and Technology of Archaeological Research, 2015, 1, 1-9.	2.4	12
112	Spatial and temporal distribution of mass loss from the Greenland Ice Sheet since AD 1900. Nature, 2015, 528, 396-400.	13.7	210
113	Radiocarbon dating of Sacred Ibis mummies from ancient Egypt. Journal of Archaeological Science: Reports, 2015, 4, 355-361.	0.2	9
114	Ancient genomics. Philosophical Transactions of the Royal Society B: Biological Sciences, 2015, 370, 20130387.	1.8	142
115	Traces of ATCV-1 associated with laboratory component contamination. Proceedings of the National Academy of Sciences of the United States of America, 2015, 112, E925-6.	3.3	24
116	Genomic evidence for the Pleistocene and recent population history of Native Americans. Science, 2015, 349, aab3884.	6.0	449
117	The ancestry and affiliations of Kennewick Man. Nature, 2015, 523, 455-458.	13.7	241
118	Improving access to endogenous DNA in ancient bones and teeth. Scientific Reports, 2015, 5, 11184.	1.6	182
119	Lake sediment multi-taxon DNA from North Greenland records early post-glacial appearance of vascular plants and accurately tracks environmental changes. Quaternary Science Reviews, 2015, 117, 152-163.	1.4	88
120	Ancient proteins resolve the evolutionary history of Darwinâ€™s South American ungulates. Nature, 2015, 522, 81-84.	13.7	273
121	Mitochondrial genomes reveal the extinct Hippidion as an outgroup to all living equids. Biology Letters, 2015, 11, 20141058.	1.0	36
122	A recent bottleneck of Y chromosome diversity coincides with a global change in culture. Genome Research, 2015, 25, 459-466.	2.4	348
123	Early Divergent Strains of Yersinia pestis in Eurasia 5,000 Years Ago. Cell, 2015, 163, 571-582.	13.5	425
124	Evolutionary Genomics and Conservation of the Endangered Przewalskiâ€™s Horse. Current Biology, 2015, 25, 2577-2583.	1.8	161
125	Tracking the origins of Yakutian horses and the genetic basis for their fast adaptation to subarctic environments. Proceedings of the National Academy of Sciences of the United States of America, 2015, 112, E6889-97.	3.3	139
126	Major transitions in human evolution revisited: A tribute to ancientÂDNA. Journal of Human Evolution, 2015, 79, 4-20.	1.3	37

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127	Environmental DNA â€“ An emerging tool in conservation for monitoring past and present biodiversity. Biological Conservation, 2015, 183, 4-18.	1.9	1,421
128	Ancient and modern environmental DNA. Philosophical Transactions of the Royal Society B: Biological Sciences, 2015, 370, 20130383.	1.8	292
129	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.	1.8	65
130	Target-Dependent Enrichment of Virions Determines the Reduction of High-Throughput Sequencing in Virus Discovery. PLoS ONE, 2015, 10, e0122636.	1.1	28
131	Genome-Wide Analysis of Cold Adaptation in Indigenous Siberian Populations. PLoS ONE, 2014, 9, e98076.	1.1	128
132	Ancient DNA Reveals Matrilineal Continuity in Present-Day Poland over the Last Two Millennia. PLoS ONE, 2014, 9, e110839.	1.1	27
133	Transposable elements in cancer as a by-product of stress-induced evolvability. Frontiers in Genetics, 2014, 5, 156.	1.1	26
134	Genome-wide nucleosome map and cytosine methylation levels of an ancient human genome. Genome Research, 2014, 24, 454-466.	2.4	161
135	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
136	Speciation with gene flow in equids despite extensive chromosomal plasticity. Proceedings of the National Academy of Sciences of the United States of America, 2014, 111, 18655-18660.	3.3	183
137	Whole-genome analyses resolve early branches in the tree of life of modern birds. Science, 2014, 346, 1320-1331.	6.0	1,583
138	Comparative genomics reveals insights into avian genome evolution and adaptation. Science, 2014, 346, 1311-1320.	6.0	895
139	bammds: a tool for assessing the ancestry of low-depth whole-genome data using multidimensional scaling (MDS). Bioinformatics, 2014, 30, 2962-2964.	1.8	40
140	Pathogens and host immunity in the ancient human oral cavity. Nature Genetics, 2014, 46, 336-344.	9.4	482
141	The genome of a Late Pleistocene human from a Clovis burial site in western Montana. Nature, 2014, 506, 225-229.	13.7	500
142	Genomic Diversity and Admixture Differs for Stone-Age Scandinavian Foragers and Farmers. Science, 2014, 344, 747-750.	6.0	315
143	Characterization of ancient and modern genomes by SNP detection and phylogenomic and metagenomic analysis using PALEOMIX. Nature Protocols, 2014, 9, 1056-1082.	5.5	403
144	Population Genomics Reveal Recent Speciation and Rapid Evolutionary Adaptation in Polar Bears. Cell, 2014, 157, 785-794.	13.5	363

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145	Derived immune and ancestral pigmentation alleles in a 7,000-year-old Mesolithic European. Nature, 2014, 507, 225-228.	13.7	328
146	Fifty thousand years of Arctic vegetation and megafaunal diet. Nature, 2014, 506, 47-51.	13.7	505
147	Upper Palaeolithic Siberian genome reveals dual ancestry of Native Americans. Nature, 2014, 505, 87-91.	13.7	821
148	Genomic structure in Europeans dating back at least 36,200 years. Science, 2014, 346, 1113-1118.	6.0	287
149	Horizontal transfer of short and degraded DNA has evolutionary implications for microbes and eukaryotic sexual reproduction. BioEssays, 2014, 36, 1005-1010.	1.2	22
150	Genome-wide Ancestry Patterns in Rapanui Suggest Pre-European Admixture with Native Americans. Current Biology, 2014, 24, 2518-2525.	1.8	50
151	Two ancient human genomes reveal Polynesian ancestry among the indigenous Botocudos of Brazil. Current Biology, 2014, 24, R1035-R1037.	1.8	73
152	A Selective Sweep on a Deleterious Mutation in CPT1A in Arctic Populations. American Journal of Human Genetics, 2014, 95, 584-589.	2.6	119
153	An epigenetic window into the past?. Science, 2014, 345, 511-512.	6.0	41
154	Early Americans: Respecting ancestors. Science, 2014, 345, 390-390.	6.0	0
155	Rodents of the Caribbean: origin and diversification of hutias unravelled by next-generation museomics. Biology Letters, 2014, 10, 20140266.	1.0	87
156	The genetic prehistory of the New World Arctic. Science, 2014, 345, 1255832.	6.0	264
157	A comparative study of ancient environmental DNA to pollen and macrofossils from lake sediments reveals taxonomic overlap and additional plant taxa. Quaternary Science Reviews, 2013, 75, 161-168.	1.4	99
158	Molecularâ€•and pollenâ€based vegetation analysis in lake sediments from central <scp>S</scp>candinavia. Molecular Ecology, 2013, 22, 3511-3524.	2.0	84
159	Pulling out the 1%: Whole-Genome Capture for the Targeted Enrichment of Ancient DNA Sequencing Libraries. American Journal of Human Genetics, 2013, 93, 852-864.	2.6	284
160	Identification of Polynesian mtDNA haplogroups in remains of Botocudo Amerindians from Brazil. Proceedings of the National Academy of Sciences of the United States of America, 2013, 110, 6465-6469.	3.3	42
161	Bacterial natural transformation by highly fragmented and damaged DNA. Proceedings of the National Academy of Sciences of the United States of America, 2013, 110, 19860-19865.	3.3	170
162	Genomic Diversity and Evolution of the Head Crest in the Rock Pigeon. Science, 2013, 339, 1063-1067.	6.0	230

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163	Fungal palaeodiversity revealed using highâ€throughput metabarcoding of ancient <scp>DNA</scp> from arctic permafrost. Environmental Microbiology, 2013, 15, 1176-1189.	1.8	115
164	Ancient DNA reveals that bowhead whale lineages survived Late Pleistocene climate change and habitat shifts. Nature Communications, 2013, 4, 1677.	5.8	66
165	Recalibrating Equus evolution using the genome sequence of an early Middle Pleistocene horse. Nature, 2013, 499, 74-78.	13.7	717
166	Reconstructing genome evolution in historic samples of the Irish potato famine pathogen. Nature Communications, 2013, 4, 2172.	5.8	103
167	One Hundred Twenty Years of Koala Retrovirus Evolution Determined from Museum Skins. Molecular Biology and Evolution, 2013, 30, 1237-1237.	3.5	0
168	One Hundred Twenty Years of Koala Retrovirus Evolution Determined from Museum Skins. Molecular Biology and Evolution, 2013, 30, 299-304.	3.5	85
169	Living at the margin of the retreating Fennoscandian Ice Sheet: The early Mesolithic sites at Aareavaara, northernmost Sweden. Holocene, 2013, 23, 104-116.	0.9	10
170	Deep Sequencing of RNA from Ancient Maize Kernels. PLoS ONE, 2013, 8, e50961.	1.1	38
171	Ligation Bias in Illumina Next-Generation DNA Libraries: Implications for Sequencing Ancient Genomes. PLoS ONE, 2013, 8, e78575.	1.1	68
172	Partial Genetic Turnover in Neandertals: Continuity in the East and Population Replacement in the West. Molecular Biology and Evolution, 2012, 29, 1893-1897.	3.5	82
173	Clovis Age Western Stemmed Projectile Points and Human Coprolites at the Paisley Caves. Science, 2012, 337, 223-228.	6.0	211
174	Aerial Photographs Reveal Lateâ€“20th-Century Dynamic Ice Loss in Northwestern Greenland. Science, 2012, 337, 569-573.	6.0	81
175	Response to Comment on â€œGlacial Survival of Boreal Trees in Northern Scandinaviaâ€. Science, 2012, 338, 742-742.	6.0	23
176	Next-generation sequencing offers new insights into DNA degradation. Trends in Biotechnology, 2012, 30, 364-368.	4.9	39
177	Plasmodium falciparum erythrocyte membrane protein 1 domain cassettes 8 and 13 are associated with severe malaria in children. Proceedings of the National Academy of Sciences of the United States of America, 2012, 109, E1791-800.	3.3	232
178	The half-life of DNA in bone: measuring decay kinetics in 158 dated fossils. Proceedings of the Royal Society B: Biological Sciences, 2012, 279, 4724-4733.	1.2	478
179	Statistical Guidelines for Detecting Past Population Shifts Using Ancient DNA. Molecular Biology and Evolution, 2012, 29, 2241-2251.	3.5	40
180	Fellow travellers: a concordance of colonization patterns between mice and men in the North Atlantic region. BMC Evolutionary Biology, 2012, 12, 35.	3.2	49

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181	Improving the performance of true single molecule sequencing for ancient DNA. BMC Genomics, 2012, 13, 177.	1.2	35
182	Improving ancient DNA read mapping against modern reference genomes. BMC Genomics, 2012, 13, 178.	1.2	247
183	Glacial Survival of Boreal Trees in Northern Scandinavia. Science, 2012, 335, 1083-1086.	6.0	287
184	Screening mammal biodiversity using DNA from leeches. Current Biology, 2012, 22, 1980.	1.8	17
185	Variola Virus in a 300-Year-Old Siberian Mummy. New England Journal of Medicine, 2012, 367, 2057-2059.	13.9	97
186	Detection of a Diverse Marine Fish Fauna Using Environmental DNA from Seawater Samples. PLoS ONE, 2012, 7, e41732.	1.1	747
187	Origins and Genetic Legacy of Neolithic Farmers and Hunter-Gatherers in Europe. Science, 2012, 336, 466-469.	6.0	507
188	Proteomic Analysis of a Pleistocene Mammoth Femur Reveals More than One Hundred Ancient Bone Proteins. Journal of Proteome Research, 2012, 11, 917-926.	1.8	196
189	DNA from keratinous tissue. Annals of Anatomy, 2012, 194, 31-35.	1.0	8
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