

# Eske Willerslev

## List of Publications by Year in descending order

Source: <https://exaly.com/author-pdf/5784890/publications.pdf>

Version: 2024-02-01

321  
papers

53,082  
citations

767

119  
h-index

1825

210  
g-index

350  
all docs

350  
docs citations

350  
times ranked

40198  
citing authors

#	ARTICLE	IF	CITATIONS
1	A communal catalogue reveals Earth's multiscale microbial diversity. <i>Nature</i> , 2017, 551, 457-463.	27.8	1,942
2	Whole-genome analyses resolve early branches in the tree of life of modern birds. <i>Science</i> , 2014, 346, 1320-1331.	12.6	1,583
3	Environmental DNA – An emerging tool in conservation for monitoring past and present biodiversity. <i>Biological Conservation</i> , 2015, 183, 4-18.	4.1	1,421
4	Towards next-generation biodiversity assessment using DNA metabarcoding. <i>Molecular Ecology</i> , 2012, 21, 2045-2050.	3.9	1,253
5	Population genomics of Bronze Age Eurasia. <i>Nature</i> , 2015, 522, 167-172.	27.8	1,166
6	Comparative genomics reveals insights into avian genome evolution and adaptation. <i>Science</i> , 2014, 346, 1311-1320.	12.6	895
7	Monitoring endangered freshwater biodiversity using environmental DNA. <i>Molecular Ecology</i> , 2012, 21, 2565-2573.	3.9	882
8	Next-generation monitoring of aquatic biodiversity using environmental <scp>DNA</scp> metabarcoding. <i>Molecular Ecology</i> , 2016, 25, 929-942.	3.9	873
9	Power and limitations of the chloroplast trnL (UAA) intron for plant DNA barcoding. <i>Nucleic Acids Research</i> , 2007, 35, e14-e14.	14.5	842
10	Upper Palaeolithic Siberian genome reveals dual ancestry of Native Americans. <i>Nature</i> , 2014, 505, 87-91.	27.8	821
11	Ancient human genome sequence of an extinct Palaeo-Eskimo. <i>Nature</i> , 2010, 463, 757-762.	27.8	750
12	Detection of a Diverse Marine Fish Fauna Using Environmental DNA from Seawater Samples. <i>PLoS ONE</i> , 2012, 7, e41732.	2.5	747
13	Worldwide Phylogeography of Wild Boar Reveals Multiple Centers of Pig Domestication. <i>Science</i> , 2005, 307, 1618-1621.	12.6	729
14	Recalibrating Equus evolution using the genome sequence of an early Middle Pleistocene horse. <i>Nature</i> , 2013, 499, 74-78.	27.8	717
15	An Aboriginal Australian Genome Reveals Separate Human Dispersals into Asia. <i>Science</i> , 2011, 334, 94-98.	12.6	675
16	Review Paper. Ancient DNA. <i>Proceedings of the Royal Society B: Biological Sciences</i> , 2005, 272, 3-16.	2.6	610
17	Rise and Fall of the Beringian Steppe Bison. <i>Science</i> , 2004, 306, 1561-1565.	12.6	601
18	Species-specific responses of Late Quaternary megafauna to climate and humans. <i>Nature</i> , 2011, 479, 359-364.	27.8	586

#	ARTICLE	IF	CITATIONS
19	Diverse Plant and Animal Genetic Records from Holocene and Pleistocene Sediments. <i>Science</i> , 2003, 300, 791-795.	12.6	571
20	Tracing the peopling of the world through genomics. <i>Nature</i> , 2017, 541, 302-310.	27.8	562
21	Origins and Genetic Legacy of Neolithic Farmers and Hunter-Gatherers in Europe. <i>Science</i> , 2012, 336, 466-469.	12.6	507
22	Fifty thousand years of Arctic vegetation and megafaunal diet. <i>Nature</i> , 2014, 506, 47-51.	27.8	505
23	The genome of a Late Pleistocene human from a Clovis burial site in western Montana. <i>Nature</i> , 2014, 506, 225-229.	27.8	500
24	Pathogens and host immunity in the ancient human oral cavity. <i>Nature Genetics</i> , 2014, 46, 336-344.	21.4	482
25	The half-life of DNA in bone: measuring decay kinetics in 158 dated fossils. <i>Proceedings of the Royal Society B: Biological Sciences</i> , 2012, 279, 4724-4733.	2.6	478
26	The Use of Coded PCR Primers Enables High-Throughput Sequencing of Multiple Homolog Amplification Products by 454 Parallel Sequencing. <i>PLoS ONE</i> , 2007, 2, e197.	2.5	453
27	Genomic evidence for the Pleistocene and recent population history of Native Americans. <i>Science</i> , 2015, 349, aab3884.	12.6	449
28	A genomic history of Aboriginal Australia. <i>Nature</i> , 2016, 538, 207-214.	27.8	439
29	Early Divergent Strains of <i>Yersinia pestis</i> in Eurasia 5,000 Years Ago. <i>Cell</i> , 2015, 163, 571-582.	28.9	425
30	Characterization of ancient and modern genomes by SNP detection and phylogenomic and metagenomic analysis using PALEOMIX. <i>Nature Protocols</i> , 2014, 9, 1056-1082.	12.0	403
31	Ancient Biomolecules from Deep Ice Cores Reveal a Forested Southern Greenland. <i>Science</i> , 2007, 317, 111-114.	12.6	393
32	Population Genomics Reveal Recent Speciation and Rapid Evolutionary Adaptation in Polar Bears. <i>Cell</i> , 2014, 157, 785-794.	28.9	363
33	Postglacial viability and colonization in North America's ice-free corridor. <i>Nature</i> , 2016, 537, 45-49.	27.8	363
34	Genomic analyses inform on migration events during the peopling of Eurasia. <i>Nature</i> , 2016, 538, 238-242.	27.8	360
35	A recent bottleneck of Y chromosome diversity coincides with a global change in culture. <i>Genome Research</i> , 2015, 25, 459-466.	5.5	348
36	Complete mitochondrial genome phylogeographic analysis of killer whales ( <i>Orcinus orca</i> ) indicates multiple species. <i>Genome Research</i> , 2010, 20, 908-916.	5.5	330

#	ARTICLE	IF	CITATIONS
37	Derived immune and ancestral pigmentation alleles in a 7,000-year-old Mesolithic European. <i>Nature</i> , 2014, 507, 225-228.	27.8	328
38	137 ancient human genomes from across the Eurasian steppes. <i>Nature</i> , 2018, 557, 369-374.	27.8	325
39	Radiation of Extant Cetaceans Driven by Restructuring of the Oceans. <i>Systematic Biology</i> , 2009, 58, 573-585.	5.6	315
40	Genomic Diversity and Admixture Differs for Stone-Age Scandinavian Foragers and Farmers. <i>Science</i> , 2014, 344, 747-750.	12.6	315
41	Terminal Pleistocene Alaskan genome reveals first founding population of Native Americans. <i>Nature</i> , 2018, 553, 203-207.	27.8	304
42	DNA metabarcoding—Need for robust experimental designs to draw sound ecological conclusions. <i>Molecular Ecology</i> , 2019, 28, 1857-1862.	3.9	300
43	Environmental DNA from Seawater Samples Correlate with Trawl Catches of Subarctic, Deepwater Fishes. <i>PLoS ONE</i> , 2016, 11, e0165252.	2.5	296
44	Ancient and modern environmental DNA. <i>Philosophical Transactions of the Royal Society B: Biological Sciences</i> , 2015, 370, 20130383.	4.0	292
45	The prehistoric peopling of Southeast Asia. <i>Science</i> , 2018, 361, 88-92.	12.6	291
46	mapDamage: testing for damage patterns in ancient DNA sequences. <i>Bioinformatics</i> , 2011, 27, 2153-2155.	4.1	287
47	Glacial Survival of Boreal Trees in Northern Scandinavia. <i>Science</i> , 2012, 335, 1083-1086.	12.6	287
48	Genomic structure in Europeans dating back at least 36,200 years. <i>Science</i> , 2014, 346, 1113-1118.	12.6	287
49	Pulling out the 1%: Whole-Genome Capture for the Targeted Enrichment of Ancient DNA Sequencing Libraries. <i>American Journal of Human Genetics</i> , 2013, 93, 852-864.	6.2	284
50	DNA from Pre-Clovis Human Coprolites in Oregon, North America. <i>Science</i> , 2008, 320, 786-789.	12.6	283
51	Meta-barcoding of environmental DNA from soil reflects vertebrate biodiversity. <i>Molecular Ecology</i> , 2012, 21, 1966-1979.	3.9	276
52	Ancient proteins resolve the evolutionary history of Darwin's South American ungulates. <i>Nature</i> , 2015, 522, 81-84.	27.8	273
53	The genetic prehistory of the New World Arctic. <i>Science</i> , 2014, 345, 1255-1258.	12.6	264
54	Ancient genomes show social and reproductive behavior of early Upper Paleolithic foragers. <i>Science</i> , 2017, 358, 659-662.	12.6	263

#	ARTICLE	IF	CITATIONS
55	DNA from soil mirrors plant taxonomic and growth form diversity. <i>Molecular Ecology</i> , 2012, 21, 3647-3655.	3.9	262
56	The first horse herders and the impact of early Bronze Age steppe expansions into Asia. <i>Science</i> , 2018, 360, .	12.6	262
57	Prehistoric genomes reveal the genetic foundation and cost of horse domestication. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2014, 111, E5661-9.	7.1	260
58	New environmental metabarcodes for analysing soil DNA: potential for studying past and present ecosystems. <i>Molecular Ecology</i> , 2012, 21, 1821-1833.	3.9	259
59	The population history of northeastern Siberia since the Pleistocene. <i>Nature</i> , 2019, 570, 182-188.	27.8	259
60	Ancient Hybridization and an Irish Origin for the Modern Polar Bear Matriline. <i>Current Biology</i> , 2011, 21, 1251-1258.	3.9	257
61	Ancient DNA reveals late survival of mammoth and horse in interior Alaska. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2009, 106, 22352-22357.	7.1	255
62	Ancient bacteria show evidence of DNA repair. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2007, 104, 14401-14405.	7.1	249
63	Improving ancient DNA read mapping against modern reference genomes. <i>BMC Genomics</i> , 2012, 13, 178.	2.8	247
64	The ancestry and affiliations of Kennewick Man. <i>Nature</i> , 2015, 523, 455-458.	27.8	241
65	Ancient genomes revisit the ancestry of domestic and Przewalski's horses. <i>Science</i> , 2018, 360, 111-114.	12.6	241
66	<i>Plasmodium falciparum</i> erythrocyte membrane protein 1 domain cassettes 8 and 13 are associated with severe malaria in children. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2012, 109, E1791-800.	7.1	232
67	Isolation of nucleic acids and cultures from fossil ice and permafrost. <i>Trends in Ecology and Evolution</i> , 2004, 19, 141-147.	8.7	231
68	Genomic Diversity and Evolution of the Head Crest in the Rock Pigeon. <i>Science</i> , 2013, 339, 1063-1067.	12.6	230
69	Early human dispersals within the Americas. <i>Science</i> , 2018, 362, .	12.6	230
70	Population characteristics of a large whale shark aggregation inferred from seawater environmental DNA. <i>Nature Ecology and Evolution</i> , 2017, 1, 4.	7.8	223
71	Whole-Genome Shotgun Sequencing of Mitochondria from Ancient Hair Shafts. <i>Science</i> , 2007, 317, 1927-1930.	12.6	220
72	Characterization of Genetic Miscoding Lesions Caused by Postmortem Damage. <i>American Journal of Human Genetics</i> , 2003, 72, 48-61.	6.2	217

#	ARTICLE	IF	CITATIONS
73	Ancient DNA Reveals Lack of Continuity between Neolithic Hunter-Gatherers and Contemporary Scandinavians. <i>Current Biology</i> , 2009, 19, 1758-1762.	3.9	217
74	Clovis Age Western Stemmed Projectile Points and Human Coprolites at the Paisley Caves. <i>Science</i> , 2012, 337, 223-228.	12.6	211
75	Distribution Patterns of Postmortem Damage in Human Mitochondrial DNA. <i>American Journal of Human Genetics</i> , 2003, 72, 32-47.	6.2	210
76	Spatial and temporal distribution of mass loss from the Greenland Ice Sheet since AD 1900. <i>Nature</i> , 2015, 528, 396-400.	27.8	210
77	Ancient DNA analyses exclude humans as the driving force behind late Pleistocene musk ox ( <i>Ovibos</i> ) in the States of America, 2010, 107, 5675-5680.	10.784314 7.1	208
78	Ancient DNA Chronology within Sediment Deposits: Are Paleobiological Reconstructions Possible and Is DNA Leaching a Factor?. <i>Molecular Biology and Evolution</i> , 2007, 24, 982-989.	8.9	202
79	Reconstructing ancient genomes and epigenomes. <i>Nature Reviews Genetics</i> , 2015, 16, 395-408.	16.3	197
80	Using next-generation sequencing for molecular reconstruction of past Arctic vegetation and climate. <i>Molecular Ecology Resources</i> , 2010, 10, 1009-1018.	4.8	196
81	Proteomic Analysis of a Pleistocene Mammoth Femur Reveals More than One Hundred Ancient Bone Proteins. <i>Journal of Proteome Research</i> , 2012, 11, 917-926.	3.7	196
82	Tracking Five Millennia of Horse Management with Extensive Ancient Genome Time Series. <i>Cell</i> , 2019, 177, 1419-1435.e31.	28.9	195
83	Long-term persistence of bacterial DNA. <i>Current Biology</i> , 2004, 14, R9-R10.	3.9	189
84	Ancient genomic changes associated with domestication of the horse. <i>Science</i> , 2017, 356, 442-445.	12.6	185
85	Paleo-Eskimo mtDNA Genome Reveals Matrilineal Discontinuity in Greenland. <i>Science</i> , 2008, 320, 1787-1789.	12.6	184
86	Speciation with gene flow in equids despite extensive chromosomal plasticity. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2014, 111, 18655-18660.	7.1	183
87	Improving access to endogenous DNA in ancient bones and teeth. <i>Scientific Reports</i> , 2015, 5, 11184.	3.3	182
88	The Human Genome Project Reveals a Continuous Transfer of Large Mitochondrial Fragments to the Nucleus. <i>Molecular Biology and Evolution</i> , 2001, 18, 1833-1837.	8.9	175
89	Molecular Diet Analysis of Two African Free-Tailed Bats ( <i>Molossidae</i> ) Using High Throughput Sequencing. <i>PLoS ONE</i> , 2011, 6, e21441.	2.5	175
90	Statistical Assignment of DNA Sequences Using Bayesian Phylogenetics. <i>Systematic Biology</i> , 2008, 57, 750-757.	5.6	170

#	ARTICLE	IF	CITATIONS
91	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.	7.1	170
92	Emergence and Spread of Basal Lineages of <i>Yersinia</i> †pestis during the Neolithic Decline. Cell, 2019, 176, 295-305.e10.	28.9	168
93	Recharacterization of ancient DNA miscoding lesions: insights in the era of sequencing-by-synthesis. Nucleic Acids Research, 2006, 35, 1-10.	14.5	166
94	Genetic evidence for patrilocality mating behavior among Neandertal groups. Proceedings of the National Academy of Sciences of the United States of America, 2011, 108, 250-253.	7.1	165
95	A 10,000-Year Record of Arctic Ocean Sea-Ice Variability†View from the Beach. Science, 2011, 333, 747-750.	12.6	162
96	Genome-wide nucleosome map and cytosine methylation levels of an ancient human genome. Genome Research, 2014, 24, 454-466.	5.5	161
97	Evolutionary Genomics and Conservation of the Endangered Przewalski†™s Horse. Current Biology, 2015, 25, 2577-2583.	3.9	161
98	Re-theorising mobility and the formation of culture and language among the Corded Ware Culture in Europe. Antiquity, 2017, 91, 334-347.	1.0	157
99	Ecological, morphological and genetic divergence of sympatric North Atlantic killer whale populations. Molecular Ecology, 2009, 18, 5207-5217.	3.9	156
100	The Origin of Insects. Science, 2006, 314, 1883-1884.	12.6	155
101	Ancient hepatitis B viruses from the Bronze Age to the Medieval period. Nature, 2018, 557, 418-423.	27.8	155
102	Statistical Evidence for Miscoding Lesions in Ancient DNA Templates. Molecular Biology and Evolution, 2001, 18, 262-265.	8.9	151
103	Extreme reversed sexual size dimorphism in the extinct New Zealand moa <i>Dinornis</i> . Nature, 2003, 425, 172-175.	27.8	151
104	The evolutionary history of the extinct ratite moa and New Zealand Neogene paleogeography. Proceedings of the National Academy of Sciences of the United States of America, 2009, 106, 20646-20651.	7.1	150
105	Screening mammal biodiversity using DNA from leeches. Current Biology, 2012, 22, R262-R263.	3.9	150
106	Geologically ancient DNA: fact or artefact?. Trends in Microbiology, 2005, 13, 212-220.	7.7	149
107	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
108	Beringian Paleoecology Inferred from Permafrost-Preserved Fungal DNA. Applied and Environmental Microbiology, 2005, 71, 1012-1017.	3.1	148

#	ARTICLE	IF	CITATIONS
109	Pre-Clovis Mastodon Hunting 13,800 Years Ago at the Manis Site, Washington. <i>Science</i> , 2011, 334, 351-353.	12.6	148
110	A comparative study of ancient sedimentary DNA, pollen and macrofossils from permafrost sediments of northern Siberia reveals long-term vegetational stability. <i>Molecular Ecology</i> , 2012, 21, 1989-2003.	3.9	144
111	Ancient mitochondrial DNA from hair. <i>Current Biology</i> , 2004, 14, R463-R464.	3.9	143
112	Population genomics of the Viking world. <i>Nature</i> , 2020, 585, 390-396.	27.8	143
113	Evolution, Systematics, and Phylogeography of Pleistocene Horses in the New World: A Molecular Perspective. <i>PLoS Biology</i> , 2005, 3, e241.	5.6	142
114	Ancient genomics. <i>Philosophical Transactions of the Royal Society B: Biological Sciences</i> , 2015, 370, 20130387.	4.0	142
115	The evolutionary history of dogs in the Americas. <i>Science</i> , 2018, 361, 81-85.	12.6	140
116	Tracking the origins of Yakutian horses and the genetic basis for their fast adaptation to subarctic environments. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2015, 112, E6889-97.	7.1	139
117	The origin and evolution of maize in the Southwestern United States. <i>Nature Plants</i> , 2015, 1, 14003.	9.3	138
118	Comparing Ancient DNA Preservation in Petrous Bone and Tooth Cementum. <i>PLoS ONE</i> , 2017, 12, e0170940.	2.5	136
119	Nuclear Gene Indicates Coat-Color Polymorphism in Mammoths. <i>Science</i> , 2006, 313, 62-62.	12.6	135
120	Early Pleistocene enamel proteome from Dmanisi resolves <i>Stephanorhinus</i> phylogeny. <i>Nature</i> , 2019, 574, 103-107.	27.8	135
121	A time transect of exomes from a Native American population before and after European contact. <i>Nature Communications</i> , 2016, 7, 13175.	12.8	134
122	The Genetic Origins of the Andaman Islanders. <i>American Journal of Human Genetics</i> , 2003, 72, 178-184.	6.2	133
123	Ancient DNA analysis. <i>Nature Reviews Methods Primers</i> , 2021, 1, .	21.2	133
124	Bayesian Inference of the Metazoan Phylogeny. <i>Current Biology</i> , 2004, 14, 1644-1649.	3.9	132
125	DNA in ancient bone – Where is it located and how should we extract it?. <i>Annals of Anatomy</i> , 2012, 194, 7-16.	1.9	132
126	Physiological and Genetic Adaptations to Diving in Sea Nomads. <i>Cell</i> , 2018, 173, 569-580.e15.	28.9	129



#	ARTICLE	IF	CITATIONS
127	Genome-Wide Analysis of Cold Adaptation in Indigenous Siberian Populations. PLoS ONE, 2014, 9, e98076.	2.5	128
128	Phylogenomics and Morphology of Extinct Paleognaths Reveal the Origin and Evolution of the Ratites. Current Biology, 2017, 27, 68-77.	3.9	123
129	Lake Sedimentary DNA Research on Past Terrestrial and Aquatic Biodiversity: Overview and Recommendations. Quaternary, 2021, 4, 6.	2.0	121
130	Blocking human contaminant DNA during PCR allows amplification of rare mammal species from sedimentary ancient DNA. Molecular Ecology, 2012, 21, 1806-1815.	3.9	120
131	A Selective Sweep on a Deleterious Mutation in CPT1A in Arctic Populations. American Journal of Human Genetics, 2014, 95, 584-589.	6.2	119
132	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.	7.1	119
133	Fungal palaeodiversity revealed using high-throughput metabarcoding of ancient <scp>DNA</scp> from arctic permafrost. Environmental Microbiology, 2013, 15, 1176-1189.	3.8	115
134	Evidence of human occupation in Mexico around the Last Glacial Maximum. Nature, 2020, 584, 87-92.	27.8	115
135	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
136	True single-molecule DNA sequencing of a pleistocene horse bone. Genome Research, 2011, 21, 1705-1719.	5.5	114
137	Tracing the dynamic life story of a Bronze Age Female. Scientific Reports, 2015, 5, 10431.	3.3	112
138	Evaluating the impact of domestication and captivity on the horse gut microbiome. Scientific Reports, 2017, 7, 15497.	3.3	112
139	Extensive Farming in Estonia Started through a Sex-Biased Migration from the Steppe. Current Biology, 2017, 27, 2185-2193.e6.	3.9	111
140	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.	7.1	110
141	Contaminating viral sequences in high-throughput sequencing viromics: a linkage study of 700 sequencing libraries. Clinical Microbiology and Infection, 2019, 25, 1277-1285.	6.0	109
142	Diverse variola virus (smallpox) strains were widespread in northern Europe in the Viking Age. Science, 2020, 369, .	12.6	108
143	Application and comparison of large-scale solution-based DNA capture-enrichment methods on ancient DNA. Scientific Reports, 2011, 1, 74.	3.3	106
144	Diversity of Holocene life forms in fossil glacier ice. Proceedings of the National Academy of Sciences of the United States of America, 1999, 96, 8017-8021.	7.1	105

#	ARTICLE	IF	CITATIONS
145	Fossil avian eggshell preserves ancient DNA. Proceedings of the Royal Society B: Biological Sciences, 2010, 277, 1991-2000.	2.6	103
146	Reconstructing genome evolution in historic samples of the Irish potato famine pathogen. Nature Communications, 2013, 4, 2172.	12.8	103
147	Crosslinks Rather Than Strand Breaks Determine Access to Ancient DNA Sequences From Frozen Sediments. Genetics, 2006, 173, 1175-1179.	2.9	100
148	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.	7.1	100
149	The dental proteome of Homo antecessor. Nature, 2020, 580, 235-238.	27.8	100
150	Non-Destructive Sampling of Ancient Insect DNA. PLoS ONE, 2009, 4, e5048.	2.5	99
151	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.	3.0	99
152	High-throughput sequencing of core STR loci for forensic genetic investigations using the Roche Genome Sequencer FLX platform. BioTechniques, 2011, 51, 127-133.	1.8	98
153	Positive selection on the killer whale mitogenome. Biology Letters, 2011, 7, 116-118.	2.3	97
154	Variola Virus in a 300-Year-Old Siberian Mummy. New England Journal of Medicine, 2012, 367, 2057-2059.	27.0	97
155	A large impact crater beneath Hiawatha Glacier in northwest Greenland. Science Advances, 2018, 4, eaar8173.	10.3	97
156	Assessing the Fidelity of Ancient DNA Sequences Amplified From Nuclear Genes. Genetics, 2006, 172, 733-741.	2.9	95
157	Identification of microsatellites from an extinct moa species using high-throughput (454) sequence data. BioTechniques, 2009, 46, 195-200.	1.8	94
158	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.	7.1	94
159	Biochemical and physical correlates of DNA contamination in archaeological human bones and teeth excavated at Matera, Italy. Journal of Archaeological Science, 2005, 32, 785-793.	2.4	92
160	Analysis of complete mitochondrial genomes from extinct and extant rhinoceroses reveals lack of phylogenetic resolution. BMC Evolutionary Biology, 2009, 9, 95.	3.2	92
161	Selection in Europeans on Fatty Acid Desaturases Associated with Dietary Changes. Molecular Biology and Evolution, 2017, 34, 1307-1318.	8.9	90
162	Damage and repair of ancient DNA. Mutation Research - Fundamental and Molecular Mechanisms of Mutagenesis, 2005, 571, 265-276.	1.0	89

#	ARTICLE	IF	CITATIONS
163	Lake sediment multi-taxon DNA from North Greenland records early post-glacial appearance of vascular plants and accurately tracks environmental changes. <i>Quaternary Science Reviews</i> , 2015, 117, 152-163.	3.0	88
164	Rodents of the Caribbean: origin and diversification of hutias unravelled by next-generation museomics. <i>Biology Letters</i> , 2014, 10, 20140266.	2.3	87
165	Genetic differentiation among North Atlantic killer whale populations. <i>Molecular Ecology</i> , 2011, 20, 629-641.	3.9	86
166	One Hundred Twenty Years of Koala Retrovirus Evolution Determined from Museum Skins. <i>Molecular Biology and Evolution</i> , 2013, 30, 299-304.	8.9	85
167	gargammel: a sequence simulator for ancient DNA. <i>Bioinformatics</i> , 2017, 33, 577-579.	4.1	85
168	Molecular- and pollen-based vegetation analysis in lake sediments from central Scandinavia. <i>Molecular Ecology</i> , 2013, 22, 3511-3524.	3.9	84
169	Mitogenome sequencing reveals shallow evolutionary histories and recent divergence time between morphologically and ecologically distinct European whitefish ( <i>Coregonus</i> spp.). <i>Molecular Ecology</i> , 2012, 21, 2727-2742.	3.9	83
170	A multidisciplinary study of archaeological grape seeds. <i>Die Naturwissenschaften</i> , 2010, 97, 205-217.	1.6	82
171	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
172	Aerial Photographs Reveal Late-20th-Century Dynamic Ice Loss in Northwestern Greenland. <i>Science</i> , 2012, 337, 569-573.	12.6	81
173	Late Quaternary dynamics of Arctic biota from ancient environmental genomics. <i>Nature</i> , 2021, 600, 86-92.	27.8	81
174	New data from an enigmatic phylum: evidence from molecular sequence data supports a sister-group relationship between Loricifera and Nematomorpha. <i>Journal of Zoological Systematics and Evolutionary Research</i> , 2008, 46, 231-239.	1.4	78
175	Mitogenomic phylogenetic analyses of the Delphinidae with an emphasis on the Globicephalinae. <i>BMC Evolutionary Biology</i> , 2011, 11, 65.	3.2	76
176	Ancient Biomolecules and Evolutionary Inference. <i>Annual Review of Biochemistry</i> , 2018, 87, 1029-1060.	11.1	76
177	Interordinal gene capture, the phylogenetic position of Steller's sea cow based on molecular and morphological data, and the macroevolutionary history of Sirenia. <i>Molecular Phylogenetics and Evolution</i> , 2015, 91, 178-193.	2.7	75
178	Human Disease Variation in the Light of Population Genomics. <i>Cell</i> , 2019, 177, 115-131.	28.9	75
179	Two ancient human genomes reveal Polynesian ancestry among the indigenous Botocudos of Brazil. <i>Current Biology</i> , 2014, 24, R1035-R1037.	3.9	73
180	Evolutionary Patterns and Processes: Lessons from Ancient DNA. <i>Systematic Biology</i> , 2017, 66, syw059.	5.6	73

#	ARTICLE	IF	CITATIONS
181	Discovery of lost diversity of paternal horse lineages using ancient DNA. <i>Nature Communications</i> , 2011, 2, 450.	12.8	72
182	Ancient DNA suggests modern wolves trace their origin to a Late Pleistocene expansion from Beringia. <i>Molecular Ecology</i> , 2020, 29, 1596-1610.	3.9	70
183	Ligation Bias in Illumina Next-Generation DNA Libraries: Implications for Sequencing Ancient Genomes. <i>PLoS ONE</i> , 2013, 8, e78575.	2.5	68
184	Islands in the ice: detecting past vegetation on Greenlandic nunataks using historical records and sedimentary ancient DNA Meta-barcoding. <i>Molecular Ecology</i> , 2012, 21, 1980-1988.	3.9	67
185	Experimental conditions improving in-solution target enrichment for ancient <scp>DNA</scp>. <i>Molecular Ecology Resources</i> , 2017, 17, 508-522.	4.8	67
186	The evolutionary history of cockatoos (Aves: Psittaciformes: Cacatuidae). <i>Molecular Phylogenetics and Evolution</i> , 2011, 59, 615-622.	2.7	66
187	Ancient DNA reveals that bowhead whale lineages survived Late Pleistocene climate change and habitat shifts. <i>Nature Communications</i> , 2013, 4, 1677.	12.8	66
188	Ancient mitochondrial DNA from the northern fringe of the Neolithic farming expansion in Europe sheds light on the dispersion process. <i>Philosophical Transactions of the Royal Society B: Biological Sciences</i> , 2015, 370, 20130373.	4.0	65
189	Fast phylogenetic DNA barcoding. <i>Philosophical Transactions of the Royal Society B: Biological Sciences</i> , 2008, 363, 3997-4002.	4.0	64
190	Origins and genetic legacies of the Caribbean Taino. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2018, 115, 2341-2346.	7.1	64
191	Ancient human parvovirus B19 in Eurasia reveals its long-term association with humans. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2018, 115, 7557-7562.	7.1	64
192	DNA evidence of bowhead whale exploitation by Greenlandic Paleo-Inuit 4,000 years ago. <i>Nature Communications</i> , 2016, 7, 13389.	12.8	63
193	Quantitative metaproteomics of medieval dental calculus reveals individual oral health status. <i>Nature Communications</i> , 2018, 9, 4744.	12.8	63
194	Ancient DNA from latrines in Northern Europe and the Middle East (500 BC–1700 AD) reveals past parasites and diet. <i>PLoS ONE</i> , 2018, 13, e0195481.	2.5	63
195	Peopling of the Americas as inferred from ancient genomics. <i>Nature</i> , 2021, 594, 356-364.	27.8	63
196	DNA from keratinous tissue. Part I: Hair and nail. <i>Annals of Anatomy</i> , 2012, 194, 17-25.	1.9	61
197	Pros and cons of methylation-based enrichment methods for ancient DNA. <i>Scientific Reports</i> , 2015, 5, 11826.	3.3	61
198	Joint Estimates of Heterozygosity and Runs of Homozygosity for Modern and Ancient Samples. <i>Genetics</i> , 2019, 212, 587-614.	2.9	61

#	ARTICLE	IF	CITATIONS
199	“The Farm Beneath the Sand” an archaeological case study on ancient “dirt” DNA. <i>Antiquity</i> , 2009, 83, 430-444.	83.10	60
200	A matter of months: High precision migration chronology of a Bronze Age female. <i>PLoS ONE</i> , 2017, 12, e0178834.	2.5	60
201	Arctic-adapted dogs emerged at the Pleistocene–Holocene transition. <i>Science</i> , 2020, 368, 1495-1499.	12.6	60
202	Insights into the processes behind the contamination of degraded human teeth and bone samples with exogenous sources of DNA. <i>International Journal of Osteoarchaeology</i> , 2006, 16, 156-164.	1.2	59
203	Ancient DNA sequences point to a large loss of mitochondrial genetic diversity in the saiga antelope ( <i>Saiga tatarica</i> ) since the Pleistocene. <i>Molecular Ecology</i> , 2010, 19, 4863-4875.	3.9	59
204	Human Origins and Ancient Human DNA. <i>Science</i> , 2001, 292, 1655-1656.	12.6	56
205	The Effect of Ancient DNA Damage on Inferences of Demographic Histories. <i>Molecular Biology and Evolution</i> , 2008, 25, 2181-2187.	8.9	56
206	Ancient DNA reveals traces of Iberian Neolithic and Bronze Age lineages in modern Iberian horses. <i>Molecular Ecology</i> , 2010, 19, 64-78.	3.9	56
207	Fast, Accurate and Automatic Ancient Nucleosome and Methylation Maps with epiPALEOMIX. <i>Molecular Biology and Evolution</i> , 2016, 33, 3284-3298.	8.9	53
208	Response to Comment by Goldberg <i>et al.</i> on “œDNA from Pre-Clovis Human Coprolites in Oregon, North America” <i>Science</i> , 2009, 325, 148-148.	12.6	52
209	Human evolution: a tale from ancient genomes. <i>Philosophical Transactions of the Royal Society B: Biological Sciences</i> , 2017, 372, 20150484.	4.0	51
210	Genome-wide Ancestry Patterns in Rapanui Suggest Pre-European Admixture with Native Americans. <i>Current Biology</i> , 2014, 24, 2518-2525.	3.9	50
211	Genomic insights into the origin and diversification of late maritime hunter-gatherers from the Chilean Patagonia. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2018, 115, E4006-E4012.	7.1	50
212	Fellow travellers: a concordance of colonization patterns between mice and men in the North Atlantic region. <i>BMC Evolutionary Biology</i> , 2012, 12, 35.	3.2	49
213	Grey wolf genomic history reveals a dual ancestry of dogs. <i>Nature</i> , 2022, 607, 313-320.	27.8	48
214	The late Pleistocene environment of the Eastern West Beringia based on the principal section at the Main River, Chukotka. <i>Quaternary Science Reviews</i> , 2011, 30, 2091-2106.	3.0	47
215	Paper II - Dirt, dates and DNA: OSL and radiocarbon chronologies of perennially frozen sediments in Siberia, and their implications for sedimentary ancient DNA studies. <i>Boreas</i> , 2011, 40, 417-445.	2.4	47
216	A simple method for the parallel deep sequencing of full influenza A genomes. <i>Journal of Virological Methods</i> , 2011, 178, 243-248.	2.1	46

#	ARTICLE	IF	CITATIONS
217	Disentangling Immediate Adaptive Introgression from Selection on Standing Introgressed Variation in Humans. <i>Molecular Biology and Evolution</i> , 2018, 35, 623-630.	8.9	46
218	Ancient Jomon genome sequence analysis sheds light on migration patterns of early East Asian populations. <i>Communications Biology</i> , 2020, 3, 437.	4.4	44
219	Optical dating of perennially frozen deposits associated with preserved ancient plant and animal DNA in north-central Siberia. <i>Quaternary Geochronology</i> , 2008, 3, 114-136.	1.4	42
220	Identification of Polynesian mtDNA haplogroups in remains of Botocudo Amerindians from Brazil. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2013, 110, 6465-6469.	7.1	42
221	Environmental genomics of Late Pleistocene black bears and giant short-faced bears. <i>Current Biology</i> , 2021, 31, 2728-2736.e8.	3.9	42
222	Woolly rhino discovery in the lower Kolyma River. <i>Quaternary Science Reviews</i> , 2011, 30, 2262-2272.	3.0	41
223	An epigenetic window into the past?. <i>Science</i> , 2014, 345, 511-512.	12.6	41
224	Ancient nuclear genomes enable repatriation of Indigenous human remains. <i>Science Advances</i> , 2018, 4, eaau5064.	10.3	41
225	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
226	Statistical Guidelines for Detecting Past Population Shifts Using Ancient DNA. <i>Molecular Biology and Evolution</i> , 2012, 29, 2241-2251.	8.9	40
227	<i>bammds</i> : a tool for assessing the ancestry of low-depth whole-genome data using multidimensional scaling (MDS). <i>Bioinformatics</i> , 2014, 30, 2962-2964.	4.1	40
228	Profiling the Dead: Generating Microsatellite Data from Fossil Bones of Extinct Megafauna—Protocols, Problems, and Prospects. <i>PLoS ONE</i> , 2011, 6, e16670.	2.5	39
229	Next-generation sequencing offers new insights into DNA degradation. <i>Trends in Biotechnology</i> , 2012, 30, 364-368.	9.3	39
230	The evolutionary and phylogeographic history of woolly mammoths: a comprehensive mitogenomic analysis. <i>Scientific Reports</i> , 2017, 7, 44585.	3.3	39
231	Influence of past climate change on phylogeography and demographic history of narwhals, <i>Monodon monoceros</i> . <i>Proceedings of the Royal Society B: Biological Sciences</i> , 2020, 287, 20192964.	2.6	39
232	Deep Sequencing of RNA from Ancient Maize Kernels. <i>PLoS ONE</i> , 2013, 8, e50961.	2.5	38
233	Ancient pathogen DNA in human teeth and petrous bones. <i>Ecology and Evolution</i> , 2018, 8, 3534-3542.	1.9	38
234	Major transitions in human evolution revisited: A tribute to ancient DNA. <i>Journal of Human Evolution</i> , 2015, 79, 4-20.	2.6	37

#	ARTICLE	IF	CITATIONS
235	Eight Millennia of Matrilineal Genetic Continuity in the South Caucasus. <i>Current Biology</i> , 2017, 27, 2023-2028.e7.	3.9	37
236	The Late Pleistocene distribution of vicuñas ( <i>Vicugna vicugna</i> ) and the “extinction” of the gracile llama (“ <i>Lama gracilis</i> ”): New molecular data. <i>Quaternary Science Reviews</i> , 2009, 28, 1369-1373.	3.0	36
237	Mitochondrial genomes reveal the extinct <i>Hippidion</i> as an outgroup to all living equids. <i>Biology Letters</i> , 2015, 11, 20141058.	2.3	36
238	Improving the performance of true single molecule sequencing for ancient DNA. <i>BMC Genomics</i> , 2012, 13, 177.	2.8	35
239	Response to Comment by Poinar et al. on “DNA from Pre-Clovis Human Coprolites in Oregon, North America”. <i>Science</i> , 2009, 325, 148-148.	12.6	34
240	Investigation of Human Cancers for Retrovirus by Low-Stringency Target Enrichment and High-Throughput Sequencing. <i>Scientific Reports</i> , 2015, 5, 13201.	3.3	34
241	mtDNA analysis of human remains from an early Danish Christian cemetery. <i>American Journal of Physical Anthropology</i> , 2005, 128, 424-429.	2.1	33
242	5'-Tailed sequencing primers improve sequencing quality of PCR products. <i>BioTechniques</i> , 2007, 42, 174-176.	1.8	33
243	Segregation distortion in chicken and the evolutionary consequences of female meiotic drive in birds. <i>Heredity</i> , 2010, 105, 290-298.	2.6	33
244	Out of the Pacific and Back Again: Insights into the Matrilineal History of Pacific Killer Whale Ecotypes. <i>PLoS ONE</i> , 2011, 6, e24980.	2.5	33
245	Characterisation of insect and plant origins using DNA extracted from small volumes of bee honey. <i>Arthropod-Plant Interactions</i> , 2010, 4, 107-116.	1.1	32
246	Characterising the potential of sheep wool for ancient DNA analyses. <i>Archaeological and Anthropological Sciences</i> , 2011, 3, 209-221.	1.8	32
247	Early Modern Humans from Tam Pã Ling, Laos. <i>Current Anthropology</i> , 2017, 58, S527-S538.	1.6	32
248	A preliminary analysis of the DNA and diet of the extinct Beothuk: A systematic approach to ancient human DNA. <i>American Journal of Physical Anthropology</i> , 2007, 132, 594-604.	2.1	30
249	50,000+ years of genetic uniformity in the critically endangered Iberian lynx. <i>Molecular Ecology</i> , 2011, 20, 3785-3795.	3.9	30
250	Target-Dependent Enrichment of Virions Determines the Reduction of High-Throughput Sequencing in Virus Discovery. <i>PLoS ONE</i> , 2015, 10, e0122636.	2.5	28
251	Ancient DNA Reveals Matrilineal Continuity in Present-Day Poland over the Last Two Millennia. <i>PLoS ONE</i> , 2014, 9, e110839.	2.5	27
252	Recovery of DNA from archaeological insect remains: first results, problems and potential. <i>Journal of Archaeological Science</i> , 2009, 36, 1179-1183.	2.4	26



#	ARTICLE	IF	CITATIONS
253	Transposable elements in cancer as a by-product of stress-induced evolvability. <i>Frontiers in Genetics</i> , 2014, 5, 156.	2.3	26
254	Ancient mtDNA sequences from the First Australians revisited. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2016, 113, 6892-6897.	7.1	26
255	Genomes of Pleistocene Siberian Wolves Uncover Multiple Extinct Wolf Lineages. <i>Current Biology</i> , 2021, 31, 198-206.e8.	3.9	26
256	Multidisciplinary medical identification of a French king's head (Henri IV). <i>BMJ, The</i> , 2010, 341, c6805-c6805.	6.0	24
257	Traces of ATCV-1 associated with laboratory component contamination. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2015, 112, E925-6.	7.1	24
258	Ancient environmental DNA reveals shifts in dominant mutualisms during the late Quaternary. <i>Nature Communications</i> , 2018, 9, 139.	12.8	24
259	Response to Comment on "Glacial Survival of Boreal Trees in Northern Scandinavia". <i>Science</i> , 2012, 338, 742-742.	12.6	23
260	Barking up the wrong tree: Modern northern European dogs fail to explain their origin. <i>BMC Evolutionary Biology</i> , 2008, 8, 71.	3.2	22
261	Horizontal transfer of short and degraded DNA has evolutionary implications for microbes and eukaryotic sexual reproduction. <i>BioEssays</i> , 2014, 36, 1005-1010.	2.5	22
262	Cutavirus in Cutaneous Malignant Melanoma. <i>Emerging Infectious Diseases</i> , 2017, 23, 363-365.	4.3	22
263	Number of endemic and native plant species in the Galápagos Archipelago in relation to geographical parameters. <i>Ecography</i> , 2002, 25, 109-119.	4.5	20
264	A Middle Pleistocene Denisovan molar from the Annamite Chain of northern Laos. <i>Nature Communications</i> , 2022, 13, 2557.	12.8	20
265	Ancient DNA: Would the Real Neandertal Please Stand up?. <i>Current Biology</i> , 2004, 14, R431-R433.	3.9	19
266	Demographic analysis of cyanobacteria based on the mutation rates estimated from an ancient ice core. <i>Heredity</i> , 2018, 120, 562-573.	2.6	19
267	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
268	800,000 year old mammoth DNA, modern elephant DNA or PCR artefact?. <i>Biology Letters</i> , 2007, 3, 55-57.	2.3	18
269	Evaluating Neanderthal Genetics and Phylogeny. <i>Journal of Molecular Evolution</i> , 2007, 64, 50-60.	1.8	18
270	The last Viking King: A royal maternity case solved by ancient DNA analysis. <i>Forensic Science International</i> , 2007, 166, 21-27.	2.2	18



#	ARTICLE	IF	CITATIONS
271	Retrotransposons and non-protein coding RNAs. Briefings in Functional Genomics & Proteomics, 2009, 8, 493-501.	3.8	18
272	Large-scale transcriptome data reveals transcriptional activity of fission yeast LTR retrotransposons. BMC Genomics, 2010, 11, 167.	2.8	18
273	Bone Marrow and Bone as a Source for Postmortem RNA*. Journal of Forensic Sciences, 2011, 56, 720-725.	1.6	18
274	Late Pleistocene paleoecology and phylogeography of woolly rhinoceroses. Quaternary Science Reviews, 2021, 263, 106993.	3.0	18
275	Clarification of the taxonomic relationship of the extant and extinct ovibovids, Ovibos, Praeovibos, Euceratherium and Bootherium. Quaternary Science Reviews, 2010, 29, 2123-2130.	3.0	17
276	Screening mammal biodiversity using DNA from leeches. Current Biology, 2012, 22, 1980.	3.9	17
277	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.	0.5	17
278	Contamination in the Draft of the Human Genome Masquerades As Lateral Gene Transfer. DNA Sequence, 2002, 13, 75-76.	0.7	15
279	An improved PCR method for endogenous DNA retrieval in contaminated Neandertal samples based on the use of blocking primers. Journal of Archaeological Science, 2009, 36, 2676-2679.	2.4	15
280	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.	2.5	14
281	High diversity of picornaviruses in rats from different continents revealed by deep sequencing. Emerging Microbes and Infections, 2016, 5, 1-8.	6.5	14
282	Mitogenomic diversity in Sacred Ibis Mummies sheds light on early Egyptian practices. PLoS ONE, 2019, 14, e0223964.	2.5	14
283	Multi-proxy analyses of a mid-15th century Middle Iron Age Bantu-speaker palaeo-faecal specimen elucidates the configuration of the "ancestral"™ sub-Saharan African intestinal microbiome. Microbiome, 2020, 8, 62.	11.1	14
284	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.	3.0	14
285	King Tutankhamun's Family and Demise. JAMA - Journal of the American Medical Association, 2010, 303, 2471.	7.4	13
286	High-Throughput Sequencing-Based Investigation of Viruses in Human Cancers by Multienrichment Approach. Journal of Infectious Diseases, 2019, 220, 1312-1324.	4.0	13
287	An Ancient Baboon Genome Demonstrates Long-Term Population Continuity in Southern Africa. Genome Biology and Evolution, 2020, 12, 407-412.	2.5	13
288	Finding the founder of Stockholm – A kinship study based on Y-chromosomal, autosomal and mitochondrial DNA. Annals of Anatomy, 2012, 194, 138-145.	1.9	12

#	ARTICLE	IF	CITATIONS
289	Amplification of TruSeq ancient DNA libraries with AccuPrime Pfx: consequences on nucleotide misincorporation and methylation patterns. <i>Science and Technology of Archaeological Research</i> , 2015, 1, 1-9.	2.4	12
290	Identification of Known and Novel Recurrent Viral Sequences in Data from Multiple Patients and Multiple Cancers. <i>Viruses</i> , 2016, 8, 53.	3.3	11
291	Genomic Steppe ancestry in skeletons from the Neolithic Single Grave Culture in Denmark. <i>PLoS ONE</i> , 2021, 16, e0244872.	2.5	11
292	Does Selection against Transcriptional Interference Shape Retroelement-Free Regions in Mammalian Genomes?. <i>PLoS ONE</i> , 2008, 3, e3760.	2.5	11
293	Application of full mitochondrial genome sequencing using 454 GS FLX pyrosequencing. <i>Forensic Science International: Genetics Supplement Series</i> , 2009, 2, 518-519.	0.3	10
294	Living at the margin of the retreating Fennoscandian Ice Sheet: The early Mesolithic sites at Aareavaara, northernmost Sweden. <i>Holocene</i> , 2013, 23, 104-116.	1.7	10
295	Can Identification of a Fourth Domain of Life Be Made from Sequence Data Alone, and Could It Be Done on Mars?. <i>Astrobiology</i> , 2007, 7, 801-814.	3.0	9
296	Rescuing ancient DNA. <i>Nature Biotechnology</i> , 2007, 25, 872-874.	17.5	9
297	Radiocarbon dating of Sacred Ibis mummies from ancient Egypt. <i>Journal of Archaeological Science: Reports</i> , 2015, 4, 355-361.	0.5	9
298	Vancomycin gene selection in the microbiome of urban <i>Rattus norvegicus</i> from hospital environment. <i>Evolution, Medicine and Public Health</i> , 2016, 2016, 219-226.	2.5	9
299	High Y-chromosomal Differentiation Among Ethnic Groups of Dir and Swat Districts, Pakistan. <i>Annals of Human Genetics</i> , 2017, 81, 234-248.	0.8	9
300	DNA from keratinous tissue. <i>Annals of Anatomy</i> , 2012, 194, 31-35.	1.9	8
301	Substitutions of short heterologous DNA segments of intragenomic or extragenomic origins produce clustered genomic polymorphisms. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2016, 113, 15066-15071.	7.1	8
302	Parasitic infections and resource economy of Danish Iron Age settlement through ancient DNA sequencing. <i>PLoS ONE</i> , 2018, 13, e0197399.	2.5	8
303	Ancient DNA reveals multiple origins and migration waves of extinct Japanese brown bear lineages. <i>Royal Society Open Science</i> , 2021, 8, 210518.	2.4	8
304	Panspermia—true or false?. <i>Lancet, The</i> , 2003, 362, 406.	13.7	5
305	Molecular identification of the extinct mountain goat, <i>Oreamnos harringtoni</i> (Bovidae). <i>Boreas</i> , 2010, 39, 18-23.	2.4	5
306	Identifying a living great-grandson of the Lakota Sioux leader Tatanka Iyotake (Sitting Bull). <i>Science Advances</i> , 2021, 7, eabh2013.	10.3	5

#	ARTICLE	IF	CITATIONS
307	Sequences of microvariant/â€œoff-ladderâ€•STR alleles. Forensic Science International: Genetics Supplement Series, 2011, 3, e204-e205.	0.3	4
308	Insights Into Aboriginal Australian Mortuary Practices: Perspectives From Ancient DNA. Frontiers in Ecology and Evolution, 2020, 8, .	2.2	4
309	Chiquihuite Cave and Americaâ€™s Hidden Limestone Industries: A Reply to Chatters et al.. PaleoAmerica, 2022, 8, 17-28.	1.5	3
310	Pathogenic microbial ancient DNA: a problem or an opportunity?. Proceedings of the Royal Society B: Biological Sciences, 2006, 273, 643-643.	2.6	2
311	Characterizing novel endogenous retroviruses from genetic variation inferred from short sequence reads. Scientific Reports, 2015, 5, 15644.	3.3	2
312	Data sharing: do scientists know best?. Nature, 2017, 548, 281-281.	27.8	2
313	Bayesian Inference of the Metazoan Phylogeny. Current Biology, 2005, 15, 392-393.	3.9	1
314	Isolation of DNA from Ancient Samples. , 2009, , .		1
315	Reply to Vigilant and Langergraber: Patrilocality in Neandertals is still the most plausible explanation. Proceedings of the National Academy of Sciences of the United States of America, 2011, 108, E88-E88.	7.1	1
316	Perspectives for DNA Studies on Polar Ice Cores. Series of the Centro De Estudios CientÃficos De Santiago, 2002, , 17-27.	0.2	1
317	Very Old DNA. Soil Biology, 2009, , 47-57.	0.8	1
318	One Hundred Twenty Years of Koala Retrovirus Evolution Determined from Museum Skins. Molecular Biology and Evolution, 2013, 30, 1237-1237.	8.9	0
319	Early Americans: Respecting ancestors. Science, 2014, 345, 390-390.	12.6	0
320	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.	0.5	0
321	Re-theorising mobility and the formation of culture and language among the Corded Ware Culture in Europeâ€™CORRIGENDUM. Antiquity, 2020, 94, 839-839.	1.0	0