

Ludovic Orlando

List of Publications by Year in Descending Order

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The third column is the impact factor (IF) of the journal, and the fourth column is the number of citations of the article.

202 papers	21,376 citations	72 h-index	144 g-index
221 ext. papers	27,746 ext. citations	13.9 avg, IF	6.52 L-index

#	Paper	IF	Citations
202	Sex in the city: Uncovering sex-specific management of equine resources from prehistoric times to the Modern Period in France. <i>Journal of Archaeological Science: Reports</i> , 2022 , 41, 103341	0.7	0
201	Modern human incursion into Neanderthal territories 54,000 years ago at Mandrin, France.. <i>Science Advances</i> , 2022 , 8, eabj9496	14.3	9
200	Ancient DNA refines taxonomic classification of Roman equids north of the Alps, elaborated with osteomorphology and geometric morphometrics. <i>Journal of Archaeological Science</i> , 2022 , 143, 105624	2.9	0
199	A single-nucleotide mutation within the TBX3 enhancer increased body size in Chinese horses.. <i>Current Biology</i> , 2021 ,	6.3	2
198	Historical management of equine resources in France from the Iron Age to the Modern Period. <i>Journal of Archaeological Science: Reports</i> , 2021 , 40, 103250	0.7	3
197	Late Quaternary dynamics of Arctic biota from ancient environmental genomics. <i>Nature</i> , 2021 , 600, 86-93	30.4	12
196	The origins and spread of domestic horses from the Western Eurasian steppes. <i>Nature</i> , 2021 , 598, 634-640	30.4	24
195	Heterogeneous Hunter-Gatherer and Steppe-Related Ancestries in Late Neolithic and Bell Beaker Genomes from Present-Day France. <i>Current Biology</i> , 2021 , 31, 1072-1083.e10	6.3	5
194	"Adopt-a-Tissue" Initiative Advances Efforts to Identify Tissue-Specific Histone Marks in the Mare. <i>Frontiers in Genetics</i> , 2021 , 12, 649959	4.5	1
193	No particular genomic features underpin the dramatic economic consequences of 17 century plague epidemics in Italy. <i>iScience</i> , 2021 , 24, 102383	6.1	4
192	Evidence for early dispersal of domestic sheep into Central Asia. <i>Nature Human Behaviour</i> , 2021 , 5, 1169-1179	11.9	11
191	Ancient horse genomes reveal the timing and extent of dispersals across the Bering Land Bridge. <i>Molecular Ecology</i> , 2021 , 30, 6144-6161	5.7	7
190	Assessing the predictive taxonomic power of the bony labyrinth 3D shape in horses, donkeys and their F1-hybrids. <i>Journal of Archaeological Science</i> , 2021 , 131, 105383	2.9	4
189	Genomics and the Evolutionary History of Equids. <i>Annual Review of Animal Biosciences</i> , 2021 , 9, 81-101	13.7	6
188	EVOSHEEP: the makeup of sheep breeds in the ancient Near East. <i>Antiquity</i> , 2021 , 95,	1	2
187	Ancient DNA analysis. <i>Nature Reviews Methods Primers</i> , 2021 , 1,		21
186	Performance and automation of ancient DNA capture with RNA hyRAD probes. <i>Molecular Ecology Resources</i> , 2021 ,	8.4	1

185	Horse males became over-represented in archaeological assemblages during the Bronze Age. <i>Journal of Archaeological Science: Reports</i> , 2020 , 31, 102364	0.7	3
184	Filling Important Gaps in the Genomic History of Southwest Asia. <i>Cell</i> , 2020 , 181, 966-968	56.2	0
183	Animal domestication in the era of ancient genomics. <i>Nature Reviews Genetics</i> , 2020 , 21, 449-460	30.1	61
182	Unveiling the Ecological Applications of Ancient DNA From Mollusk Shells. <i>Frontiers in Ecology and Evolution</i> , 2020 , 8,	3.7	15
181	CASCADE: A Custom-Made Archiving System for the Conservation of Ancient DNA Experimental Data. <i>Frontiers in Ecology and Evolution</i> , 2020 , 8,	3.7	1
180	Dairy pastoralism sustained eastern Eurasian steppe populations for 5,000 years. <i>Nature Ecology and Evolution</i> , 2020 , 4, 346-355	12.3	46
179	Museomics identifies genetic erosion in two butterfly species across the 20th century in Finland. <i>Molecular Ecology Resources</i> , 2020 , 20, 1191-1205	8.4	15
178	Uncovering Signatures of DNA Methylation in Ancient Plant Remains From Patterns of Post-mortem DNA Damage. <i>Frontiers in Ecology and Evolution</i> , 2020 , 8,	3.7	1
177	Ancient Genomes Reveal Unexpected Horse Domestication and Management Dynamics. <i>BioEssays</i> , 2020 , 42, e1900164	4.1	16
176	Genetic diversity, evolution and selection in the major histocompatibility complex DRB and DQB loci in the family Equidae. <i>BMC Genomics</i> , 2020 , 21, 677	4.5	2
175	The mules that are not mules - metrics, morphology, archaeogenomics and mtDNA d-loop diversity in equids from Roman Switzerland. <i>Journal of Archaeological Science</i> , 2020 , 123, 105253	2.9	4
174	The Evolutionary and Historical Foundation of the Modern Horse: Lessons from Ancient Genomics. <i>Annual Review of Genetics</i> , 2020 , 54, 563-581	14.5	4
173	Using paleo-archives to safeguard biodiversity under climate change. <i>Science</i> , 2020 , 369,	33.3	34
172	Population genomics of the Viking world. <i>Nature</i> , 2020 , 585, 390-396	50.4	35
171	Assessing DNA Sequence Alignment Methods for Characterizing Ancient Genomes and Methylomes. <i>Frontiers in Ecology and Evolution</i> , 2020 , 8,	3.7	13
170	Origin and Evolution of Deleterious Mutations in Horses. <i>Genes</i> , 2019 , 10,	4.2	13
169	Early Pleistocene enamel proteome from Dmanisi resolves Stephanorhinus phylogeny. <i>Nature</i> , 2019 , 574, 103-107	50.4	70
168	DamMet: ancient methylome mapping accounting for errors, true variants, and post-mortem DNA damage. <i>GigaScience</i> , 2019 , 8,	7.6	7

167	Joint Estimates of Heterozygosity and Runs of Homozygosity for Modern and Ancient Samples. <i>Genetics</i> , 2019 , 212, 587-614	4	26
166	Tracking Five Millennia of Horse Management with Extensive Ancient Genome Time Series. <i>Cell</i> , 2019 , 177, 1419-1435.e31	56.2	110
165	Authentication and Assessment of Contamination in Ancient DNA. <i>Methods in Molecular Biology</i> , 2019 , 1963, 163-194	1.4	7
164	EPAS1 gain-of-function mutation contributes to high-altitude adaptation in Tibetan horses. <i>Molecular Biology and Evolution</i> , 2019 ,	8.3	28
163	Investigating ancient animal economies and exchange in Kyrgyzstan & Alay Valley. <i>Antiquity</i> , 2019 , 93,	1	4
162	Paleogenomics: reconstruction of plant evolutionary trajectories from modern and ancient DNA. <i>Genome Biology</i> , 2019 , 20, 29	18.3	33
161	Sexing Viking Age horses from burial and non-burial sites in Iceland using ancient DNA. <i>Journal of Archaeological Science</i> , 2019 , 101, 115-122	2.9	12
160	Ancient genomes revisit the ancestry of domestic and Przewalski & horses. <i>Science</i> , 2018 , 360, 111-114	33.3	153
159	Convergent genomic signatures of domestication in sheep and goats. <i>Nature Communications</i> , 2018 , 9, 813	17.4	112
158	Decline of genetic diversity in ancient domestic stallions in Europe. <i>Science Advances</i> , 2018 , 4, eaap9691	14.3	17
157	Improved de novo genomic assembly for the domestic donkey. <i>Science Advances</i> , 2018 , 4, eaaq0392	14.3	24
156	High-Throughput DNA sequencing of ancient wood. <i>Molecular Ecology</i> , 2018 , 27, 1138-1154	5.7	45
155	A southern African origin and cryptic structure in the highly mobile plains zebra. <i>Nature Ecology and Evolution</i> , 2018 , 2, 491-498	12.3	21
154	Terminal Pleistocene Alaskan genome reveals first founding population of Native Americans. <i>Nature</i> , 2018 , 553, 203-207	50.4	178
153	Detecting Signatures of Positive Selection along Defined Branches of a Population Tree Using LSD. <i>Molecular Biology and Evolution</i> , 2018 , 35, 1520-1535	8.3	17
152	Ancient Epigenomics. <i>Population Genomics</i> , 2018 , 75-111	1.4	7
151	Late Quaternary horses in Eurasia in the face of climate and vegetation change. <i>Science Advances</i> , 2018 , 4, eaar5589	14.3	17
150	Horse Y chromosome assembly displays unique evolutionary features and putative stallion fertility genes. <i>Nature Communications</i> , 2018 , 9, 2945	17.4	35

149	Displays an Original Type IV Secretion System in Strains Pathogenic for Bivalve Molluscs. <i>Frontiers in Microbiology</i> , 2018 , 9, 227	5.7	10
148	137 ancient human genomes from across the Eurasian steppes. <i>Nature</i> , 2018 , 557, 369-374	50.4	197
147	Ancient hepatitis B viruses from the Bronze Age to the Medieval period. <i>Nature</i> , 2018 , 557, 418-423	50.4	112
146	The first horse herders and the impact of early Bronze Age steppe expansions into Asia. <i>Science</i> , 2018 , 360,	33.3	162
145	Oral health status in historic population: Macroscopic and metagenomic evidence. <i>PLoS ONE</i> , 2018 , 13, e0196482	3.7	11
144	Late Bronze Age cultural origins of dairy pastoralism in Mongolia. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2018 , 115, 12083-12085	11.5	4
143	Improved reference genome for the domestic horse increases assembly contiguity and composition. <i>Communications Biology</i> , 2018 , 1, 197	6.7	74
142	Early pastoral economies along the Ancient Silk Road: Biomolecular evidence from the Alay Valley, Kyrgyzstan. <i>PLoS ONE</i> , 2018 , 13, e0205646	3.7	26
141	An Ancient DNA Perspective on Horse Evolution. <i>Population Genomics</i> , 2018 , 325-351	1.4	3
140	The prehistoric peopling of Southeast Asia. <i>Science</i> , 2018 , 361, 88-92	33.3	174
139	Zonkey: A simple, accurate and sensitive pipeline to genetically identify equine F1-hybrids in archaeological assemblages. <i>Journal of Archaeological Science</i> , 2017 , 78, 147-157	2.9	27
138	Ancient DNA analysis identifies marine mollusc shells as new metagenomic archives of the past. <i>Molecular Ecology Resources</i> , 2017 , 17, 835-853	8.4	38
137	Less effective selection leads to larger genomes. <i>Genome Research</i> , 2017 , 27, 1016-1028	9.7	44
136	Detecting taxonomic and phylogenetic signals in equid cheek teeth: towards new palaeontological and archaeological proxies. <i>Royal Society Open Science</i> , 2017 , 4, 160997	3.3	38
135	A Robust Framework for Microbial Archaeology. <i>Annual Review of Genomics and Human Genetics</i> , 2017 , 18, 321-356	9.7	92
134	Ancient genomic changes associated with domestication of the horse. <i>Science</i> , 2017 , 356, 442-445	33.3	149
133	Human evolution: a tale from ancient genomes. <i>Philosophical Transactions of the Royal Society B: Biological Sciences</i> , 2017 , 372,	5.8	34
132	A communal catalogue reveals Earth@ multiscale microbial diversity. <i>Nature</i> , 2017 , 551, 457-463	50.4	1076

131	Genome-wide Ancestry and Demographic History of African-Descendant Maroon Communities from French Guiana and Suriname. <i>American Journal of Human Genetics</i> , 2017 , 101, 725-736	11	29
130	Ancient genomes show social and reproductive behavior of early Upper Paleolithic foragers. <i>Science</i> , 2017 , 358, 659-662	33.3	160
129	Survival and divergence in a small group: The extraordinary genomic history of the endangered Apennine brown bear stragglers. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2017 , 114, E9589-E9597	11.5	95
128	Developing a 670k genotyping array to tag ~2M SNPs across 24 horse breeds. <i>BMC Genomics</i> , 2017 , 18, 565	4.5	66
127	gargammel: a sequence simulator for ancient DNA. <i>Bioinformatics</i> , 2017 , 33, 577-579	7.2	37
126	The Effects of Captivity on the Mammalian Gut Microbiome. <i>Integrative and Comparative Biology</i> , 2017 , 57, 690-704	2.8	169
125	Evaluating the impact of domestication and captivity on the horse gut microbiome. <i>Scientific Reports</i> , 2017 , 7, 15497	4.9	64
124	The wolf reference genome sequence (<i>Canis lupus lupus</i>) and its implications for <i>Canis</i> spp. population genomics. <i>BMC Genomics</i> , 2017 , 18, 495	4.5	49
123	Taming the Past: Ancient DNA and the Study of Animal Domestication. <i>Annual Review of Animal Biosciences</i> , 2017 , 5, 329-351	13.7	78
122	Combining bleach and mild predigestion improves ancient DNA recovery from bones. <i>Molecular Ecology Resources</i> , 2017 , 17, 742-751	8.4	48
121	Experimental conditions improving in-solution target enrichment for ancient DNA. <i>Molecular Ecology Resources</i> , 2017 , 17, 508-522	8.4	48
120	Planktonic foraminifera-derived environmental DNA extracted from abyssal sediments preserves patterns of plankton macroecology. <i>Biogeosciences</i> , 2017 , 14, 2741-2754	4.6	17
119	A new genus of horse from Pleistocene North America. <i>ELife</i> , 2017 , 6,	8.9	42
118	Evolutionary Patterns and Processes: Lessons from Ancient DNA. <i>Systematic Biology</i> , 2017 , 66, e1-e29	8.4	53
117	Mitogenomic Phylogeny, Diversification, and Biogeography of South American Spiny Rats. <i>Molecular Biology and Evolution</i> , 2017 , 34, 613-633	8.3	33
116	Fast, Accurate and Automatic Ancient Nucleosome and Methylation Maps with epiPALEOMIX. <i>Molecular Biology and Evolution</i> , 2016 , 33, 3284-3298	8.3	36
115	Synergistic roles of climate warming and human occupation in Patagonian megafaunal extinctions during the Last Deglaciation. <i>Science Advances</i> , 2016 , 2, e1501682	14.3	81
114	Early cave art and ancient DNA record the origin of European bison. <i>Nature Communications</i> , 2016 , 7, 13158	17.4	63

113	AdapterRemoval v2: rapid adapter trimming, identification, and read merging. <i>BMC Research Notes</i> , 2016 , 9, 88	2.3	658
112	Accurate continuous geographic assignment from low- to high-density SNP data. <i>Bioinformatics</i> , 2016 , 32, 1106-8	7.2	9
111	Positive selection in the SLC11A1 gene in the family Equidae. <i>Immunogenetics</i> , 2016 , 68, 353-64	3.2	4
110	Regulatory mutations in TBX3 disrupt asymmetric hair pigmentation that underlies Dun camouflage color in horses. <i>Nature Genetics</i> , 2016 , 48, 152-8	36.3	45
109	Population characteristics of a large whale shark aggregation inferred from seawater environmental DNA. <i>Nature Ecology and Evolution</i> , 2016 , 1, 4	12.3	140
108	metaBIT, an integrative and automated metagenomic pipeline for analysing microbial profiles from high-throughput sequencing shotgun data. <i>Molecular Ecology Resources</i> , 2016 , 16, 1415-1427	8.4	30
107	Comparing the performance of three ancient DNA extraction methods for high-throughput sequencing. <i>Molecular Ecology Resources</i> , 2016 , 16, 459-69	8.4	98
106	Spotted phenotypes in horses lost attractiveness in the Middle Ages. <i>Scientific Reports</i> , 2016 , 6, 38548	4.9	21
105	The Evolutionary Origin and Genetic Makeup of Domestic Horses. <i>Genetics</i> , 2016 , 204, 423-434	4	39
104	The origin of ambling horses. <i>Current Biology</i> , 2016 , 26, R697-R699	6.3	16
103	Postglacial viability and colonization in North America@ ice-free corridor. <i>Nature</i> , 2016 , 537, 45-49	50.4	213
102	A genomewide catalogue of single nucleotide polymorphisms in white-beaked and Atlantic white-sided dolphins. <i>Molecular Ecology Resources</i> , 2016 , 16, 266-76	8.4	13
101	The ancestry and affiliations of Kennewick Man. <i>Nature</i> , 2015 , 523, 455-458	50.4	157
100	Improving access to endogenous DNA in ancient bones and teeth. <i>Scientific Reports</i> , 2015 , 5, 11184	4.9	135
99	Planning tiger recovery: Understanding intraspecific variation for effective conservation. <i>Science Advances</i> , 2015 , 1, e1400175	14.3	45
98	Population Demography and Genetic Diversity in the Pleistocene Cave Lion. <i>Open Quaternary</i> , 2015 , 1, 4	1.1	34
97	Ancient proteins resolve the evolutionary history of Darwin@ South American ungulates. <i>Nature</i> , 2015 , 522, 81-4	50.4	210
96	Mitochondrial genomes reveal the extinct Hippidion as an outgroup to all living equids. <i>Biology Letters</i> , 2015 , 11,	3.6	26

95	Early divergent strains of <i>Yersinia pestis</i> in Eurasia 5,000 years ago. <i>Cell</i> , 2015 , 163, 571-82	56.2	294
94	Equids. <i>Current Biology</i> , 2015 , 25, R973-8	6.3	16
93	Evolutionary Genomics and Conservation of the Endangered Przewalski Horse. <i>Current Biology</i> , 2015 , 25, 2577-83	6.3	115
92	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	11.5	89
91	Mitochondrial Genetic Diversity of Eurasian Red Squirrels (<i>Sciurus vulgaris</i>) from Denmark. <i>Journal of Heredity</i> , 2015 , 106, 719-27	2.4	5
90	Major transitions in human evolution revisited: a tribute to ancient DNA. <i>Journal of Human Evolution</i> , 2015 , 79, 4-20	3.1	35
89	Ancient and modern environmental DNA. <i>Philosophical Transactions of the Royal Society B: Biological Sciences</i> , 2015 , 370, 20130383	5.8	184
88	Pros and cons of methylation-based enrichment methods for ancient DNA. <i>Scientific Reports</i> , 2015 , 5, 11826	4.9	40
87	The first aurochs genome reveals the breeding history of British and European cattle. <i>Genome Biology</i> , 2015 , 16, 225	18.3	17
86	Annotation of the Protein Coding Regions of the Equine Genome. <i>PLoS ONE</i> , 2015 , 10, e0124375	3.7	17
85	Comparison of the Equine Reference Sequence with Its Sanger Source Data and New Illumina Reads. <i>PLoS ONE</i> , 2015 , 10, e0126852	3.7	6
84	New insights on single-stranded versus double-stranded DNA library preparation for ancient DNA. <i>BioTechniques</i> , 2015 , 59, 368-71	2.5	33
83	Population genomics of Bronze Age Eurasia. <i>Nature</i> , 2015 , 522, 167-72	50.4	827
82	Reconstructing ancient genomes and epigenomes. <i>Nature Reviews Genetics</i> , 2015 , 16, 395-408	30.1	151
81	Genome-wide ancestry of 17th-century enslaved Africans from the Caribbean. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2015 , 112, 3669-73	11.5	82
80	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	1.2	9
79	Ancient genomics. <i>Philosophical Transactions of the Royal Society B: Biological Sciences</i> , 2015 , 370, 20130387	5.8	107
78	The genome of a Late Pleistocene human from a Clovis burial site in western Montana. <i>Nature</i> , 2014 , 506, 225-9	50.4	357

77	Characterization of ancient and modern genomes by SNP detection and phylogenomic and metagenomic analysis using PALEOMIX. <i>Nature Protocols</i> , 2014 , 9, 1056-82	18.8	231
76	Population genomics reveal recent speciation and rapid evolutionary adaptation in polar bears. <i>Cell</i> , 2014 , 157, 785-94	56.2	242
75	Fifty thousand years of Arctic vegetation and megafaunal diet. <i>Nature</i> , 2014 , 506, 47-51	50.4	351
74	Upper Palaeolithic Siberian genome reveals dual ancestry of Native Americans. <i>Nature</i> , 2014 , 505, 87-91	50.4	581
73	Paleogenomics. Genomic structure in Europeans dating back at least 36,200 years. <i>Science</i> , 2014 , 346, 1113-8	33.3	232
72	Two ancient human genomes reveal Polynesian ancestry among the indigenous Botocudos of Brazil. <i>Current Biology</i> , 2014 , 24, R1035-7	6.3	62
71	Evolution. An epigenetic window into the past?. <i>Science</i> , 2014 , 345, 511-2	33.3	32
70	A 400,000-year-old mitochondrial genome questions phylogenetic relationships amongst archaic hominins: using the latest advances in ancient genomics, the mitochondrial genome sequence of a 400,000-year-old hominin has been deciphered. <i>BioEssays</i> , 2014 , 36, 598-605	4.1	9
69	Rodents of the Caribbean: origin and diversification of hutias unravelled by next-generation museomics. <i>Biology Letters</i> , 2014 , 10,	3.6	71
68	The genetic prehistory of the New World Arctic. <i>Science</i> , 2014 , 345, 1255832	33.3	204
67	Genome-wide nucleosome map and cytosine methylation levels of an ancient human genome. <i>Genome Research</i> , 2014 , 24, 454-66	9.7	113
66	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	11.5	197
65	Shotgun microbial profiling of fossil remains. <i>Molecular Ecology</i> , 2014 , 23, 1780-98	5.7	43
64	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, 18655-60	11.5	133
63	Whole-genome analyses resolve early branches in the tree of life of modern birds. <i>Science</i> , 2014 , 346, 1320-31	33.3	1182
62	Comparative genomics reveals insights into avian genome evolution and adaptation. <i>Science</i> , 2014 , 346, 1311-20	33.3	628
61	Using Ancient DNA to Understand Evolutionary and Ecological Processes. <i>Annual Review of Ecology, Evolution, and Systematics</i> , 2014 , 45, 573-598	13.5	60
60	First evidence of <i>Equus asinus</i> L. in the Chalcolithic disputes the Phoenicians as the first to introduce donkeys into the Iberian Peninsula. <i>Journal of Archaeological Science</i> , 2013 , 40, 4483-4490	2.9	14

59	A comparative study of ancient environmental DNA to pollen and macrofossils from lake sediments reveals taxonomic overlap and additional plant taxa. <i>Quaternary Science Reviews</i> , 2013 , 75, 161-168	3.9	72
58	Morphological and genetic evidence for early Holocene cattle management in northeastern China. <i>Nature Communications</i> , 2013 , 4, 2755	17.4	59
57	Bacterial natural transformation by highly fragmented and damaged DNA. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2013 , 110, 19860-5	11.5	111
56	Recalibrating Equus evolution using the genome sequence of an early Middle Pleistocene horse. <i>Nature</i> , 2013 , 499, 74-8	50.4	563
55	Reconstructing genome evolution in historic samples of the Irish potato famine pathogen. <i>Nature Communications</i> , 2013 , 4, 2172	17.4	79
54	mapDamage2.0: fast approximate Bayesian estimates of ancient DNA damage parameters. <i>Bioinformatics</i> , 2013 , 29, 1682-4	7.2	725
53	Mitochondrial phylogenomics of modern and ancient equids. <i>PLoS ONE</i> , 2013 , 8, e55950	3.7	99
52	Ligation bias in illumina next-generation DNA libraries: implications for sequencing ancient genomes. <i>PLoS ONE</i> , 2013 , 8, e78575	3.7	57
51	Meta-barcoding of QIIME DNA from soil reflects vertebrate biodiversity. <i>Molecular Ecology</i> , 2012 , 21, 1966-79	5.7	180
50	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, 1980-8	5.7	54
49	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	5.7	103
48	Monitoring endangered freshwater biodiversity using environmental DNA. <i>Molecular Ecology</i> , 2012 , 21, 2565-73	5.7	669
47	DNA from soil mirrors plant taxonomic and growth form diversity. <i>Molecular Ecology</i> , 2012 , 21, 3647-55	5.7	170
46	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, 2727-42	5.7	67
45	Next-generation sequencing offers new insights into DNA degradation. <i>Trends in Biotechnology</i> , 2012 , 30, 364-8	15.1	32
44	Statistical guidelines for detecting past population shifts using ancient DNA. <i>Molecular Biology and Evolution</i> , 2012 , 29, 2241-51	8.3	33
43	Improving the performance of true single molecule sequencing for ancient DNA. <i>BMC Genomics</i> , 2012 , 13, 177	4.5	32
42	Improving ancient DNA read mapping against modern reference genomes. <i>BMC Genomics</i> , 2012 , 13, 1784.5	4.5	178

41	Glacial survival of boreal trees in northern Scandinavia. <i>Science</i> , 2012 , 335, 1083-6	33.3	239
40	Variola virus in a 300-year-old Siberian mummy. <i>New England Journal of Medicine</i> , 2012 , 367, 2057-9	59.2	71
39	Investigating the potential use of environmental DNA (eDNA) for genetic monitoring of marine mammals. <i>PLoS ONE</i> , 2012 , 7, e41781	3.7	218
38	Proteomic analysis of a pleistocene mammoth femur reveals more than one hundred ancient bone proteins. <i>Journal of Proteome Research</i> , 2012 , 11, 917-26	5.6	150
37	Genomic affinities of two 7,000-year-old Iberian hunter-gatherers. <i>Current Biology</i> , 2012 , 22, 1494-9	6.3	129
36	Partial genetic turnover in neandertals: continuity in the East and population replacement in the West. <i>Molecular Biology and Evolution</i> , 2012 , 29, 1893-7	8.3	59
35	Species-specific responses of Late Quaternary megafauna to climate and humans. <i>Nature</i> , 2011 , 479, 359-64	50.4	483
34	Out of the Pacific and back again: insights into the matrilineal history of Pacific killer whale ecotypes. <i>PLoS ONE</i> , 2011 , 6, e24980	3.7	28
33	Twelve Years of Neandertal Genetic Discoveries: State-of-the-Art and Future Challenges. <i>Vertebrate Paleobiology and Paleoanthropology</i> , 2011 , 223-238	0.8	
32	An Aboriginal Australian genome reveals separate human dispersals into Asia. <i>Science</i> , 2011 , 334, 94-8	33.3	528
31	Mitogenomic phylogenetic analyses of the Delphinidae with an emphasis on the Globicephalinae. <i>BMC Evolutionary Biology</i> , 2011 , 11, 65	3	65
30	True single-molecule DNA sequencing of a pleistocene horse bone. <i>Genome Research</i> , 2011 , 21, 1705-19	9.7	99
29	mapDamage: testing for damage patterns in ancient DNA sequences. <i>Bioinformatics</i> , 2011 , 27, 2153-5	7.2	209
28	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, 4863-75	5.7	45
27	Ancient human genome sequence of an extinct Palaeo-Eskimo. <i>Nature</i> , 2010 , 463, 757-62	50.4	567
26	The microcephalin ancestral allele in a Neanderthal individual. <i>PLoS ONE</i> , 2010 , 5, e10648	3.7	26
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24	Using classical population genetics tools with heterochroneous data: time matters!. <i>PLoS ONE</i> , 2009 , 4, e5541	3.7	36

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22	DNA from extinct giant lemurs links archaeolemurids to extant indriids. <i>BMC Evolutionary Biology</i> , 2008 , 8, 121	3	32
21	Ancient DNA clarifies the evolutionary history of American Late Pleistocene equids. <i>Journal of Molecular Evolution</i> , 2008 , 66, 533-8	3.1	27
20	Surprising migration and population size dynamics in ancient Iberian brown bears (<i>Ursus arctos</i>). <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2008 , 105, 5123-8	11.5	80
19	Does the 43 bp sequence from an 800,000 year old cretan dwarf elephantid really rewrite the textbook on mammoths?. <i>Biology Letters</i> , 2007 , 3, 57-9; discussion 60-3	3.6	5
18	Neanderthals in central Asia and Siberia. <i>Nature</i> , 2007 , 449, 902-4	50.4	243
17	Conceptual bases for quantifying the role of the environment on gene evolution: the participation of positive selection and neutral evolution. <i>Biological Reviews</i> , 2007 , 82, 551-72	13.5	26
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15	Mammoth and Elephant Phylogenetic Relationships: <i>Mammot Americanum</i> , the Missing Outgroup. <i>Evolutionary Bioinformatics</i> , 2007 , 3, 117693430700300	1.9	5
14	Mammoth and elephant phylogenetic relationships: <i>Mammot americanum</i> , the missing outgroup. <i>Evolutionary Bioinformatics</i> , 2007 , 3, 45-51	1.9	2
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12	Geographic distribution of an extinct equid (<i>Equus hydruntinus</i> : Mammalia, Equidae) revealed by morphological and genetical analyses of fossils. <i>Molecular Ecology</i> , 2006 , 15, 2083-93	5.7	61
11	Morphological convergence in Hippidion and Equus (<i>Amerhippus</i>) South American equids elucidated by ancient DNA analysis. <i>Journal of Molecular Evolution</i> , 2003 , 57 Suppl 1, S29-40	3.1	21
10	Napoleon Bonaparte and the fate of an Amazonian rat: new data on the taxonomy of <i>Mesomys hispidus</i> (Rodentia: Echimyidae). <i>Molecular Phylogenetics and Evolution</i> , 2003 , 27, 113-20	4.1	8
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8	Ancient DNA and the population genetics of cave bears (<i>Ursus spelaeus</i>) through space and time. <i>Molecular Biology and Evolution</i> , 2002 , 19, 1920-33	8.3	78
7	Ancient DNA analysis reveals divergence of the cave bear, <i>Ursus spelaeus</i> , and brown bear, <i>Ursus arctos</i> , lineages. <i>Current Biology</i> , 2001 , 11, 200-3	6.3	141
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5	Ancient Genomics Reveals Four Prehistoric Migration Waves into Southeast Asia	2
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