

# Ludovic Orlando

## List of Publications by Citations

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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	Whole-genome analyses resolve early branches in the tree of life of modern birds. <i>Science</i> , <b>2014</b> , 346, 1320-31	33.3	1182
201	A communal catalogue reveals Earth's multiscale microbial diversity. <i>Nature</i> , <b>2017</b> , 551, 457-463	50.4	1076
200	Population genomics of Bronze Age Eurasia. <i>Nature</i> , <b>2015</b> , 522, 167-72	50.4	827
199	mapDamage2.0: fast approximate Bayesian estimates of ancient DNA damage parameters. <i>Bioinformatics</i> , <b>2013</b> , 29, 1682-4	7.2	725
198	Monitoring endangered freshwater biodiversity using environmental DNA. <i>Molecular Ecology</i> , <b>2012</b> , 21, 2565-73	5.7	669
197	AdapterRemoval v2: rapid adapter trimming, identification, and read merging. <i>BMC Research Notes</i> , <b>2016</b> , 9, 88	2.3	658
196	Comparative genomics reveals insights into avian genome evolution and adaptation. <i>Science</i> , <b>2014</b> , 346, 1311-20	33.3	628
195	Upper Palaeolithic Siberian genome reveals dual ancestry of Native Americans. <i>Nature</i> , <b>2014</b> , 505, 87-91	50.4	581
194	Ancient human genome sequence of an extinct Palaeo-Eskimo. <i>Nature</i> , <b>2010</b> , 463, 757-62	50.4	567
193	Recalibrating Equus evolution using the genome sequence of an early Middle Pleistocene horse. <i>Nature</i> , <b>2013</b> , 499, 74-8	50.4	563
192	An Aboriginal Australian genome reveals separate human dispersals into Asia. <i>Science</i> , <b>2011</b> , 334, 94-8	33.3	528
191	Species-specific responses of Late Quaternary megafauna to climate and humans. <i>Nature</i> , <b>2011</b> , 479, 359-64	50.4	483
190	The derived FOXP2 variant of modern humans was shared with Neandertals. <i>Current Biology</i> , <b>2007</b> , 17, 1908-12	6.3	376
189	The genome of a Late Pleistocene human from a Clovis burial site in western Montana. <i>Nature</i> , <b>2014</b> , 506, 225-9	50.4	357
188	Fifty thousand years of Arctic vegetation and megafaunal diet. <i>Nature</i> , <b>2014</b> , 506, 47-51	50.4	351
187	Early divergent strains of <i>Yersinia pestis</i> in Eurasia 5,000 years ago. <i>Cell</i> , <b>2015</b> , 163, 571-82	56.2	294
186	Neanderthals in central Asia and Siberia. <i>Nature</i> , <b>2007</b> , 449, 902-4	50.4	243

185	Population genomics reveal recent speciation and rapid evolutionary adaptation in polar bears. <i>Cell</i> , <b>2014</b> , 157, 785-94	56.2	242
184	Glacial survival of boreal trees in northern Scandinavia. <i>Science</i> , <b>2012</b> , 335, 1083-6	33.3	239
183	Paleogenomics. Genomic structure in Europeans dating back at least 36,200 years. <i>Science</i> , <b>2014</b> , 346, 1113-8	33.3	232
182	Characterization of ancient and modern genomes by SNP detection and phylogenomic and metagenomic analysis using PALEOMIX. <i>Nature Protocols</i> , <b>2014</b> , 9, 1056-82	18.8	231
181	Investigating the potential use of environmental DNA (eDNA) for genetic monitoring of marine mammals. <i>PLoS ONE</i> , <b>2012</b> , 7, e41781	3.7	218
180	Postglacial viability and colonization in North America@ ice-free corridor. <i>Nature</i> , <b>2016</b> , 537, 45-49	50.4	213
179	Ancient proteins resolve the evolutionary history of Darwin@ South American ungulates. <i>Nature</i> , <b>2015</b> , 522, 81-4	50.4	210
178	mapDamage: testing for damage patterns in ancient DNA sequences. <i>Bioinformatics</i> , <b>2011</b> , 27, 2153-5	7.2	209
177	The genetic prehistory of the New World Arctic. <i>Science</i> , <b>2014</b> , 345, 1255832	33.3	204
176	137 ancient human genomes from across the Eurasian steppes. <i>Nature</i> , <b>2018</b> , 557, 369-374	50.4	197
175	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> , <b>2014</b> , 111, E5661-9	11.5	197
174	Ancient and modern environmental DNA. <i>Philosophical Transactions of the Royal Society B: Biological Sciences</i> , <b>2015</b> , 370, 20130383	5.8	184
173	Meta-barcoding of Qirt@DNA from soil reflects vertebrate biodiversity. <i>Molecular Ecology</i> , <b>2012</b> , 21, 1966-79	5.7	180
172	Terminal Pleistocene Alaskan genome reveals first founding population of Native Americans. <i>Nature</i> , <b>2018</b> , 553, 203-207	50.4	178
171	Improving ancient DNA read mapping against modern reference genomes. <i>BMC Genomics</i> , <b>2012</b> , 13, 1784.5		178
170	Ancient DNA analyses exclude humans as the driving force behind late Pleistocene musk ox ( <i>Ovibos moschatus</i> ) population dynamics. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , <b>2010</b> , 107, 5675-80	11.5	175
169	The prehistoric peopling of Southeast Asia. <i>Science</i> , <b>2018</b> , 361, 88-92	33.3	174
168	DNA from soil mirrors plant taxonomic and growth form diversity. <i>Molecular Ecology</i> , <b>2012</b> , 21, 3647-55	5.7	170

167	The Effects of Captivity on the Mammalian Gut Microbiome. <i>Integrative and Comparative Biology</i> , <b>2017</b> , 57, 690-704	2.8	169
166	The first horse herders and the impact of early Bronze Age steppe expansions into Asia. <i>Science</i> , <b>2018</b> , 360,	33.3	162
165	Ancient genomes show social and reproductive behavior of early Upper Paleolithic foragers. <i>Science</i> , <b>2017</b> , 358, 659-662	33.3	160
164	The ancestry and affiliations of Kennewick Man. <i>Nature</i> , <b>2015</b> , 523, 455-458	50.4	157
163	Ancient genomes revisit the ancestry of domestic and Przewalski's horses. <i>Science</i> , <b>2018</b> , 360, 111-114	33.3	153
162	Reconstructing ancient genomes and epigenomes. <i>Nature Reviews Genetics</i> , <b>2015</b> , 16, 395-408	30.1	151
161	Proteomic analysis of a pleistocene mammoth femur reveals more than one hundred ancient bone proteins. <i>Journal of Proteome Research</i> , <b>2012</b> , 11, 917-26	5.6	150
160	Ancient genomic changes associated with domestication of the horse. <i>Science</i> , <b>2017</b> , 356, 442-445	33.3	149
159	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> , <b>2001</b> , 11, 200-3	6.3	141
158	Population characteristics of a large whale shark aggregation inferred from seawater environmental DNA. <i>Nature Ecology and Evolution</i> , <b>2016</b> , 1, 4	12.3	140
157	Improving access to endogenous DNA in ancient bones and teeth. <i>Scientific Reports</i> , <b>2015</b> , 5, 11184	4.9	135
156	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> , <b>2014</b> , 111, 18655-60	11.5	133
155	Genomic affinities of two 7,000-year-old Iberian hunter-gatherers. <i>Current Biology</i> , <b>2012</b> , 22, 1494-9	6.3	129
154	Evolutionary Genomics and Conservation of the Endangered Przewalski's Horse. <i>Current Biology</i> , <b>2015</b> , 25, 2577-83	6.3	115
153	Genome-wide nucleosome map and cytosine methylation levels of an ancient human genome. <i>Genome Research</i> , <b>2014</b> , 24, 454-66	9.7	113
152	Convergent genomic signatures of domestication in sheep and goats. <i>Nature Communications</i> , <b>2018</b> , 9, 813	17.4	112
151	Ancient hepatitis B viruses from the Bronze Age to the Medieval period. <i>Nature</i> , <b>2018</b> , 557, 418-423	50.4	112
150	Revising the recent evolutionary history of equids using ancient DNA. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , <b>2009</b> , 106, 21754-9	11.5	112

149	Bacterial natural transformation by highly fragmented and damaged DNA. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , <b>2013</b> , 110, 19860-5	11.5	111
148	Tracking Five Millennia of Horse Management with Extensive Ancient Genome Time Series. <i>Cell</i> , <b>2019</b> , 177, 1419-1435.e31	56.2	110
147	Ancient genomics. <i>Philosophical Transactions of the Royal Society B: Biological Sciences</i> , <b>2015</b> , 370, 20130387	38.7	107
146	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> , <b>2012</b> , 21, 1989-2003	5.7	103
145	Mitochondrial phylogenomics of modern and ancient equids. <i>PLoS ONE</i> , <b>2013</b> , 8, e55950	3.7	99
144	True single-molecule DNA sequencing of a pleistocene horse bone. <i>Genome Research</i> , <b>2011</b> , 21, 1705-19	9.7	99
143	Comparing the performance of three ancient DNA extraction methods for high-throughput sequencing. <i>Molecular Ecology Resources</i> , <b>2016</b> , 16, 459-69	8.4	98
142	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> , <b>2017</b> , 114, E9589-E9597	11.5	95
141	A Robust Framework for Microbial Archaeology. <i>Annual Review of Genomics and Human Genetics</i> , <b>2017</b> , 18, 321-356	9.7	92
140	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> , <b>2015</b> , 112, E6889-97	11.5	89
139	Revisiting Neandertal diversity with a 100,000 year old mtDNA sequence. <i>Current Biology</i> , <b>2006</b> , 16, R400-3	6.3	86
138	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> , <b>2015</b> , 112, 3669-73	11.5	82
137	Synergistic roles of climate warming and human occupation in Patagonian megafaunal extinctions during the Last Deglaciation. <i>Science Advances</i> , <b>2016</b> , 2, e1501682	14.3	81
136	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> , <b>2008</b> , 105, 5123-8	11.5	80
135	Reconstructing genome evolution in historic samples of the Irish potato famine pathogen. <i>Nature Communications</i> , <b>2013</b> , 4, 2172	17.4	79
134	Taming the Past: Ancient DNA and the Study of Animal Domestication. <i>Annual Review of Animal Biosciences</i> , <b>2017</b> , 5, 329-351	13.7	78
133	Ancient DNA and the population genetics of cave bears ( <i>Ursus spelaeus</i> ) through space and time. <i>Molecular Biology and Evolution</i> , <b>2002</b> , 19, 1920-33	8.3	78
132	Improved reference genome for the domestic horse increases assembly contiguity and composition. <i>Communications Biology</i> , <b>2018</b> , 1, 197	6.7	74

131	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> , <b>2013</b> , 75, 161-168	3.9	72
130	Rodents of the Caribbean: origin and diversification of hutias unravelled by next-generation museomics. <i>Biology Letters</i> , <b>2014</b> , 10,	3.6	71
129	Variola virus in a 300-year-old Siberian mummy. <i>New England Journal of Medicine</i> , <b>2012</b> , 367, 2057-9	59.2	71
128	Early Pleistocene enamel proteome from Dmanisi resolves <i>Stephanorhinus</i> phylogeny. <i>Nature</i> , <b>2019</b> , 574, 103-107	50.4	70
127	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> , <b>2012</b> , 21, 2727-42	5.7	67
126	Developing a 670k genotyping array to tag ~2M SNPs across 24 horse breeds. <i>BMC Genomics</i> , <b>2017</b> , 18, 565	4.5	66
125	Mitogenomic phylogenetic analyses of the Delphinidae with an emphasis on the Globicephalinae. <i>BMC Evolutionary Biology</i> , <b>2011</b> , 11, 65	3	65
124	Evaluating the impact of domestication and captivity on the horse gut microbiome. <i>Scientific Reports</i> , <b>2017</b> , 7, 15497	4.9	64
123	Early cave art and ancient DNA record the origin of European bison. <i>Nature Communications</i> , <b>2016</b> , 7, 13158	17.4	63
122	Two ancient human genomes reveal Polynesian ancestry among the indigenous Botocudos of Brazil. <i>Current Biology</i> , <b>2014</b> , 24, R1035-7	6.3	62
121	Animal domestication in the era of ancient genomics. <i>Nature Reviews Genetics</i> , <b>2020</b> , 21, 449-460	30.1	61
120	Geographic distribution of an extinct equid ( <i>Equus hydruntinus</i> : Mammalia, Equidae) revealed by morphological and genetical analyses of fossils. <i>Molecular Ecology</i> , <b>2006</b> , 15, 2083-93	5.7	61
119	Using Ancient DNA to Understand Evolutionary and Ecological Processes. <i>Annual Review of Ecology, Evolution, and Systematics</i> , <b>2014</b> , 45, 573-598	13.5	60
118	Morphological and genetic evidence for early Holocene cattle management in northeastern China. <i>Nature Communications</i> , <b>2013</b> , 4, 2755	17.4	59
117	Partial genetic turnover in neandertals: continuity in the East and population replacement in the West. <i>Molecular Biology and Evolution</i> , <b>2012</b> , 29, 1893-7	8.3	59
116	Ancient DNA analysis reveals woolly rhino evolutionary relationships. <i>Molecular Phylogenetics and Evolution</i> , <b>2003</b> , 28, 485-99	4.1	59
115	Ligation bias in illumina next-generation DNA libraries: implications for sequencing ancient genomes. <i>PLoS ONE</i> , <b>2013</b> , 8, e78575	3.7	57
114	Islands in the ice: detecting past vegetation on Greenlandic nunataks using historical records and sedimentary ancient DNA meta-barcoding. <i>Molecular Ecology</i> , <b>2012</b> , 21, 1980-8	5.7	54

113	Evolutionary Patterns and Processes: Lessons from Ancient DNA. <i>Systematic Biology</i> , <b>2017</b> , 66, e1-e29	8.4	53
112	The wolf reference genome sequence ( <i>Canis lupus lupus</i> ) and its implications for <i>Canis</i> spp. population genomics. <i>BMC Genomics</i> , <b>2017</b> , 18, 495	4.5	49
111	Combining bleach and mild predigestion improves ancient DNA recovery from bones. <i>Molecular Ecology Resources</i> , <b>2017</b> , 17, 742-751	8.4	48
110	Experimental conditions improving in-solution target enrichment for ancient DNA. <i>Molecular Ecology Resources</i> , <b>2017</b> , 17, 508-522	8.4	48
109	Dairy pastoralism sustained eastern Eurasian steppe populations for 5,000 years. <i>Nature Ecology and Evolution</i> , <b>2020</b> , 4, 346-355	12.3	46
108	Planning tiger recovery: Understanding intraspecific variation for effective conservation. <i>Science Advances</i> , <b>2015</b> , 1, e1400175	14.3	45
107	High-Throughput DNA sequencing of ancient wood. <i>Molecular Ecology</i> , <b>2018</b> , 27, 1138-1154	5.7	45
106	Regulatory mutations in <i>TBX3</i> disrupt asymmetric hair pigmentation that underlies Dun camouflage color in horses. <i>Nature Genetics</i> , <b>2016</b> , 48, 152-8	36.3	45
105	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> , <b>2010</b> , 19, 4863-75	5.7	45
104	Less effective selection leads to larger genomes. <i>Genome Research</i> , <b>2017</b> , 27, 1016-1028	9.7	44
103	Shotgun microbial profiling of fossil remains. <i>Molecular Ecology</i> , <b>2014</b> , 23, 1780-98	5.7	43
102	A new genus of horse from Pleistocene North America. <i>ELife</i> , <b>2017</b> , 6,	8.9	42
101	Pros and cons of methylation-based enrichment methods for ancient DNA. <i>Scientific Reports</i> , <b>2015</b> , 5, 11826	4.9	40
100	The Evolutionary Origin and Genetic Makeup of Domestic Horses. <i>Genetics</i> , <b>2016</b> , 204, 423-434	4	39
99	Ancient DNA analysis identifies marine mollusc shells as new metagenomic archives of the past. <i>Molecular Ecology Resources</i> , <b>2017</b> , 17, 835-853	8.4	38
98	Detecting taxonomic and phylogenetic signals in equid cheek teeth: towards new palaeontological and archaeological proxies. <i>Royal Society Open Science</i> , <b>2017</b> , 4, 160997	3.3	38
97	gargammel: a sequence simulator for ancient DNA. <i>Bioinformatics</i> , <b>2017</b> , 33, 577-579	7.2	37
96	Fast, Accurate and Automatic Ancient Nucleosome and Methylation Maps with epiPALEOMIX. <i>Molecular Biology and Evolution</i> , <b>2016</b> , 33, 3284-3298	8.3	36

95	Using classical population genetics tools with heterochroneous data: time matters!. <i>PLoS ONE</i> , <b>2009</b> , 4, e5541	3.7	36
94	Major transitions in human evolution revisited: a tribute to ancient DNA. <i>Journal of Human Evolution</i> , <b>2015</b> , 79, 4-20	3.1	35
93	Horse Y chromosome assembly displays unique evolutionary features and putative stallion fertility genes. <i>Nature Communications</i> , <b>2018</b> , 9, 2945	17.4	35
92	Population genomics of the Viking world. <i>Nature</i> , <b>2020</b> , 585, 390-396	50.4	35
91	Human evolution: a tale from ancient genomes. <i>Philosophical Transactions of the Royal Society B: Biological Sciences</i> , <b>2017</b> , 372,	5.8	34
90	Population Demography and Genetic Diversity in the Pleistocene Cave Lion. <i>Open Quaternary</i> , <b>2015</b> , 1, 4	1.1	34
89	Using paleo-archives to safeguard biodiversity under climate change. <i>Science</i> , <b>2020</b> , 369,	33.3	34
88	New insights on single-stranded versus double-stranded DNA library preparation for ancient DNA. <i>BioTechniques</i> , <b>2015</b> , 59, 368-71	2.5	33
87	Statistical guidelines for detecting past population shifts using ancient DNA. <i>Molecular Biology and Evolution</i> , <b>2012</b> , 29, 2241-51	8.3	33
86	Mitogenomic Phylogeny, Diversification, and Biogeography of South American Spiny Rats. <i>Molecular Biology and Evolution</i> , <b>2017</b> , 34, 613-633	8.3	33
85	Paleogenomics: reconstruction of plant evolutionary trajectories from modern and ancient DNA. <i>Genome Biology</i> , <b>2019</b> , 20, 29	18.3	33
84	Evolution. An epigenetic window into the past?. <i>Science</i> , <b>2014</b> , 345, 511-2	33.3	32
83	Next-generation sequencing offers new insights into DNA degradation. <i>Trends in Biotechnology</i> , <b>2012</b> , 30, 364-8	15.1	32
82	Improving the performance of true single molecule sequencing for ancient DNA. <i>BMC Genomics</i> , <b>2012</b> , 13, 177	4.5	32
81	DNA from extinct giant lemurs links archaeolemurids to extant indriids. <i>BMC Evolutionary Biology</i> , <b>2008</b> , 8, 121	3	32
80	metaBIT, an integrative and automated metagenomic pipeline for analysing microbial profiles from high-throughput sequencing shotgun data. <i>Molecular Ecology Resources</i> , <b>2016</b> , 16, 1415-1427	8.4	30
79	Genome-wide Ancestry and Demographic History of African-Descendant Maroon Communities from French Guiana and Suriname. <i>American Journal of Human Genetics</i> , <b>2017</b> , 101, 725-736	11	29
78	EPAS1 gain-of-function mutation contributes to high-altitude adaptation in Tibetan horses. <i>Molecular Biology and Evolution</i> , <b>2019</b> ,	8.3	28



77	Out of the Pacific and back again: insights into the matrilineal history of Pacific killer whale ecotypes. <i>PLoS ONE</i> , <b>2011</b> , 6, e24980	3.7	28
76	Zonkey: A simple, accurate and sensitive pipeline to genetically identify equine F1-hybrids in archaeological assemblages. <i>Journal of Archaeological Science</i> , <b>2017</b> , 78, 147-157	2.9	27
75	Ancient DNA clarifies the evolutionary history of American Late Pleistocene equids. <i>Journal of Molecular Evolution</i> , <b>2008</b> , 66, 533-8	3.1	27
74	Joint Estimates of Heterozygosity and Runs of Homozygosity for Modern and Ancient Samples. <i>Genetics</i> , <b>2019</b> , 212, 587-614	4	26
73	Mitochondrial genomes reveal the extinct Hippidion as an outgroup to all living equids. <i>Biology Letters</i> , <b>2015</b> , 11,	3.6	26
72	The microcephalin ancestral allele in a Neanderthal individual. <i>PLoS ONE</i> , <b>2010</b> , 5, e10648	3.7	26
71	Conceptual bases for quantifying the role of the environment on gene evolution: the participation of positive selection and neutral evolution. <i>Biological Reviews</i> , <b>2007</b> , 82, 551-72	13.5	26
70	Early pastoral economies along the Ancient Silk Road: Biomolecular evidence from the Alay Valley, Kyrgyzstan. <i>PLoS ONE</i> , <b>2018</b> , 13, e0205646	3.7	26
69	Improved de novo genomic assembly for the domestic donkey. <i>Science Advances</i> , <b>2018</b> , 4, eaaq0392	14.3	24
68	The origins and spread of domestic horses from the Western Eurasian steppes. <i>Nature</i> , <b>2021</b> , 598, 634-640	30.4	24
67	A southern African origin and cryptic structure in the highly mobile plains zebra. <i>Nature Ecology and Evolution</i> , <b>2018</b> , 2, 491-498	12.3	21
66	Morphological convergence in Hippidion and Equus (Amerhippus) South American equids elucidated by ancient DNA analysis. <i>Journal of Molecular Evolution</i> , <b>2003</b> , 57 Suppl 1, S29-40	3.1	21
65	Spotted phenotypes in horses lost attractiveness in the Middle Ages. <i>Scientific Reports</i> , <b>2016</b> , 6, 38548	4.9	21
64	Ancient DNA analysis. <i>Nature Reviews Methods Primers</i> , <b>2021</b> , 1,		21
63	Decline of genetic diversity in ancient domestic stallions in Europe. <i>Science Advances</i> , <b>2018</b> , 4, eaap9691	14.3	17
62	Detecting Signatures of Positive Selection along Defined Branches of a Population Tree Using LSD. <i>Molecular Biology and Evolution</i> , <b>2018</b> , 35, 1520-1535	8.3	17
61	Late Quaternary horses in Eurasia in the face of climate and vegetation change. <i>Science Advances</i> , <b>2018</b> , 4, eaar5589	14.3	17
60	Planktonic foraminifera-derived environmental DNA extracted from abyssal sediments preserves patterns of plankton macroecology. <i>Biogeosciences</i> , <b>2017</b> , 14, 2741-2754	4.6	17

59	The first aurochs genome reveals the breeding history of British and European cattle. <i>Genome Biology</i> , <b>2015</b> , 16, 225	18.3	17
58	Annotation of the Protein Coding Regions of the Equine Genome. <i>PLoS ONE</i> , <b>2015</b> , 10, e0124375	3.7	17
57	Equids. <i>Current Biology</i> , <b>2015</b> , 25, R973-8	6.3	16
56	Ancient Genomes Reveal Unexpected Horse Domestication and Management Dynamics. <i>BioEssays</i> , <b>2020</b> , 42, e1900164	4.1	16
55	The origin of ambling horses. <i>Current Biology</i> , <b>2016</b> , 26, R697-R699	6.3	16
54	Unveiling the Ecological Applications of Ancient DNA From Mollusk Shells. <i>Frontiers in Ecology and Evolution</i> , <b>2020</b> , 8,	3.7	15
53	Museomics identifies genetic erosion in two butterfly species across the 20th century in Finland. <i>Molecular Ecology Resources</i> , <b>2020</b> , 20, 1191-1205	8.4	15
52	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> , <b>2013</b> , 40, 4483-4490	2.9	14
51	Origin and Evolution of Deleterious Mutations in Horses. <i>Genes</i> , <b>2019</b> , 10,	4.2	13
50	A genomewide catalogue of single nucleotide polymorphisms in white-beaked and Atlantic white-sided dolphins. <i>Molecular Ecology Resources</i> , <b>2016</b> , 16, 266-76	8.4	13
49	Assessing DNA Sequence Alignment Methods for Characterizing Ancient Genomes and Methylomes. <i>Frontiers in Ecology and Evolution</i> , <b>2020</b> , 8,	3.7	13
48	Late Quaternary dynamics of Arctic biota from ancient environmental genomics. <i>Nature</i> , <b>2021</b> , 600, 86-93	30.4	12
47	Sexing Viking Age horses from burial and non-burial sites in Iceland using ancient DNA. <i>Journal of Archaeological Science</i> , <b>2019</b> , 101, 115-122	2.9	12
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