

Beth Shapiro

List of Publications by Year in descending order

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Version: 2024-02-01

179
papers

18,085
citations

13827

67
h-index

17546

121
g-index

198
all docs

198
docs citations

198
times ranked

19513
citing authors

#	ARTICLE	IF	CITATIONS
1	Whole-genome analyses resolve early branches in the tree of life of modern birds. <i>Science</i> , 2014, 346, 1320-1331.	6.0	1,583
2	Towards complete and error-free genome assemblies of all vertebrate species. <i>Nature</i> , 2021, 592, 737-746.	13.7	1,139
3	Recalibrating Equus evolution using the genome sequence of an early Middle Pleistocene horse. <i>Nature</i> , 2013, 499, 74-78.	13.7	717
4	Rise and Fall of the Beringian Steppe Bison. <i>Science</i> , 2004, 306, 1561-1565.	6.0	601
5	Species-specific responses of Late Quaternary megafauna to climate and humans. <i>Nature</i> , 2011, 479, 359-364.	13.7	586
6	Diverse Plant and Animal Genetic Records from Holocene and Pleistocene Sediments. <i>Science</i> , 2003, 300, 791-795.	6.0	571
7	Metagenomics to Paleogenomics: Large-Scale Sequencing of Mammoth DNA. <i>Science</i> , 2006, 311, 392-394.	6.0	519
8	Improving Bayesian Population Dynamics Inference: A Coalescent-Based Model for Multiple Loci. <i>Molecular Biology and Evolution</i> , 2013, 30, 713-724.	3.5	449
9	Skyline plot methods for estimating demographic history from nucleotide sequences. <i>Molecular Ecology Resources</i> , 2011, 11, 423-434.	2.2	393
10	The earliest evidence for anatomically modern humans in northwestern Europe. <i>Nature</i> , 2011, 479, 521-524.	13.7	285
11	Using Time-Structured Data to Estimate Evolutionary Rates of Double-Stranded DNA Viruses. <i>Molecular Biology and Evolution</i> , 2010, 27, 2038-2051.	3.5	279
12	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.	3.3	260
13	Evidence for Time Dependency of Molecular Rate Estimates. <i>Systematic Biology</i> , 2007, 56, 515-522.	2.7	257
14	Ancient Hybridization and an Irish Origin for the Modern Polar Bear Matriline. <i>Current Biology</i> , 2011, 21, 1251-1258.	1.8	257
15	Dense sampling of bird diversity increases power of comparative genomics. <i>Nature</i> , 2020, 587, 252-257.	13.7	251
16	Mitochondrial DNA analysis shows a Near Eastern Neolithic origin for domestic cattle and no indication of domestication of European aurochs. <i>Proceedings of the Royal Society B: Biological Sciences</i> , 2007, 274, 1377-1385.	1.2	209
17	Insights into the Evolutionary History of an Emerging Livestock Pathogen: Porcine Circovirus 2. <i>Journal of Virology</i> , 2009, 83, 12813-12821.	1.5	208
18	Ancient DNA analyses exclude humans as the driving force behind late Pleistocene musk ox (<i>Ovibos</i>) in the United States of America, 2010, 107, 5675-5680.	3.3	208

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19	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.	3.5	202
20	Conservation of biodiversity in the genomics era. <i>Genome Biology</i> , 2018, 19, 131.	3.8	202
21	The Effect of Inappropriate Calibration: Three Case Studies in Molecular Ecology. <i>PLoS ONE</i> , 2008, 3, e1615.	1.1	201
22	Tracking Five Millennia of Horse Management with Extensive Ancient Genome Time Series. <i>Cell</i> , 2019, 177, 1419-1435.e31.	13.5	195
23	Genomic Evidence for Island Population Conversion Resolves Conflicting Theories of Polar Bear Evolution. <i>PLoS Genetics</i> , 2013, 9, e1003345.	1.5	181
24	Million-year-old DNA sheds light on the genomic history of mammoths. <i>Nature</i> , 2021, 591, 265-269.	13.7	179
25	The Global Spread of Hepatitis C Virus 1a and 1b: A Phylodynamic and Phylogeographic Analysis. <i>PLoS Medicine</i> , 2009, 6, e1000198.	3.9	177
26	Timing and causes of mid-Holocene mammoth extinction on St. Paul Island, Alaska. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2016, 113, 9310-9314.	3.3	162
27	Minimizing polymerase biases in metabarcoding. <i>Molecular Ecology Resources</i> , 2018, 18, 927-939.	2.2	160
28	Genome-wide Evidence Reveals that African and Eurasian Golden Jackals Are Distinct Species. <i>Current Biology</i> , 2015, 25, 2158-2165.	1.8	156
29	Highly accurate long-read HiFi sequencing data for five complex genomes. <i>Scientific Data</i> , 2020, 7, 399.	2.4	155
30	Synonymous Substitution Rates Predict HIV Disease Progression as a Result of Underlying Replication Dynamics. <i>PLoS Computational Biology</i> , 2007, 3, e29.	1.5	152
31	Ancient papillomavirus-host co-speciation in Felidae. <i>Genome Biology</i> , 2007, 8, R57.	13.9	152
32	Whole-genome sequence analysis shows that two endemic species of North American wolf are admixtures of the coyote and gray wolf. <i>Science Advances</i> , 2016, 2, e1501714.	4.7	150
33	Genomic evidence of geographically widespread effect of gene flow from polar bears into brown bears. <i>Molecular Ecology</i> , 2015, 24, 1205-1217.	2.0	148
34	863 genomes reveal the origin and domestication of chicken. <i>Cell Research</i> , 2020, 30, 693-701.	5.7	144
35	Flight of the Dodo. <i>Science</i> , 2002, 295, 1683-1683.	6.0	143
36	Ancient mitochondrial DNA from hair. <i>Current Biology</i> , 2004, 14, R463-R464.	1.8	143

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37	Phylogeography of lions (<i>Panthera leo</i> ssp.) reveals three distinct taxa and a late Pleistocene reduction in genetic diversity. <i>Molecular Ecology</i> , 2009, 18, 1668-1677.	2.0	142
38	The origins and spread of domestic horses from the Western Eurasian steppes. <i>Nature</i> , 2021, 598, 634-640.	13.7	142
39	Bison phylogeography constrains dispersal and viability of the Ice Free Corridor in western Canada. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2016, 113, 8057-8063.	3.3	140
40	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.	3.3	140
41	Early Pleistocene enamel proteome from Dmanisi resolves <i>Stephanorhinus</i> phylogeny. <i>Nature</i> , 2019, 574, 103-107.	13.7	135
42	Partial genomic survival of cave bears in living brown bears. <i>Nature Ecology and Evolution</i> , 2018, 2, 1563-1570.	3.4	132
43	Ancient genomes from North Africa evidence prehistoric migrations to the Maghreb from both the Levant and Europe. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2018, 115, 6774-6779.	3.3	131
44	Comment on "Protein Sequences from Mastodon and <i>Tyrannosaurus rex</i> Revealed by Mass Spectrometry". <i>Science</i> , 2008, 319, 33-33.	6.0	127
45	Mitochondrial Phylogenomics of Modern and Ancient Equids. <i>PLoS ONE</i> , 2013, 8, e55950.	1.1	123
46	A Bayesian Phylogenetic Method to Estimate Unknown Sequence Ages. <i>Molecular Biology and Evolution</i> , 2011, 28, 879-887.	3.5	119
47	True single-molecule DNA sequencing of a pleistocene horse bone. <i>Genome Research</i> , 2011, 21, 1705-1719.	2.4	114
48	Genetic Structure and Extinction of the Woolly Mammoth, <i>Mammuthus primigenius</i> . <i>Current Biology</i> , 2007, 17, 1072-1075.	1.8	109
49	Transoceanic drift and the domestication of African bottle gourds in the Americas. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2014, 111, 2937-2941.	3.3	108
50	Preservation of viral genomes in 700-y-old caribou feces from a subarctic ice patch. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2014, 111, 16842-16847.	3.3	107
51	Natural selection shaped the rise and fall of passenger pigeon genomic diversity. <i>Science</i> , 2017, 358, 951-954.	6.0	105
52	Conserving intraspecific variation for nature's contributions to people. <i>Nature Ecology and Evolution</i> , 2021, 5, 574-582.	3.4	97
53	Reintroduction of the archaic variant of <i>NOVA1</i> in cortical organoids alters neurodevelopment. <i>Science</i> , 2021, 371, .	6.0	96
54	Genomic Evidence of Widespread Admixture from Polar Bears into Brown Bears during the Last Ice Age. <i>Molecular Biology and Evolution</i> , 2018, 35, 1120-1129.	3.5	91

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55	Accommodating the Effect of Ancient DNA Damage on Inferences of Demographic Histories. <i>Molecular Biology and Evolution</i> , 2009, 26, 245-248.	3.5	86
56	Fossil and genomic evidence constrains the timing of bison arrival in North America. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2017, 114, 3457-3462.	3.3	84
57	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.	3.5	82
58	Early cave art and ancient DNA record the origin of European bison. <i>Nature Communications</i> , 2016, 7, 13158.	5.8	81
59	Life and extinction of megafauna in the ice-age Arctic. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2015, 112, 14301-14306.	3.3	78
60	Ancient DNA Provides New Insights into the Evolutionary History of New Zealand's Extinct Giant Eagle. <i>PLoS Biology</i> , 2005, 3, e9.	2.6	77
61	The Origin of the "Mycoplasma mycoides Cluster" Coincides with Domestication of Ruminants. <i>PLoS ONE</i> , 2012, 7, e36150.	1.1	76
62	Bayesian Estimation of Substitution Rates from Ancient DNA Sequences with Low Information Content. <i>Systematic Biology</i> , 2011, 60, 366-375.	2.7	75
63	Pathways to de-extinction: how close can we get to resurrection of an extinct species?. <i>Functional Ecology</i> , 2017, 31, 996-1002.	1.7	75
64	A Complete Mitochondrial Genome Sequence from a Mesolithic Wild Aurochs (<i>Bos primigenius</i>). <i>PLoS ONE</i> , 2010, 5, e9255.	1.1	73
65	Discovery of lost diversity of paternal horse lineages using ancient DNA. <i>Nature Communications</i> , 2011, 2, 450.	5.8	72
66	Genomic Data from Extinct North American <i>Camelops</i> Revise Camel Evolutionary History. <i>Molecular Biology and Evolution</i> , 2015, 32, 2433-2440.	3.5	72
67	Is amino acid racemization a useful tool for screening for ancient DNA in bone?. <i>Proceedings of the Royal Society B: Biological Sciences</i> , 2009, 276, 2971-2977.	1.2	71
68	Correlating Bayesian date estimates with climatic events and domestication using a bovine case study. <i>Biology Letters</i> , 2008, 4, 370-374.	1.0	70
69	A Fast and Efficient Single-stranded Genomic Library Preparation Method Optimized for Ancient DNA. <i>Journal of Heredity</i> , 2021, 112, 241-249.	1.0	68
70	Pros and cons of methylation-based enrichment methods for ancient DNA. <i>Scientific Reports</i> , 2015, 5, 11826.	1.6	61
71	A new genus of horse from Pleistocene North America. <i>ELife</i> , 2017, 6, .	2.8	61
72	Time-dependent estimates of molecular evolutionary rates: evidence and causes. <i>Molecular Ecology</i> , 2015, 24, 6007-6012.	2.0	59

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73	Landscape Genomics to Enable Conservation Actions: The California Conservation Genomics Project. <i>Journal of Heredity</i> , 2022, 113, 577-588.	1.0	59
74	Museum Genomics. <i>Annual Review of Genetics</i> , 2021, 55, 633-659.	3.2	58
75	Revealing the maternal demographic history of <i>Panthera leo</i> using ancient DNA and a spatially explicit genealogical analysis. <i>BMC Evolutionary Biology</i> , 2014, 14, 70.	3.2	57
76	Mid-Holocene vertebrate bone Concentration-Lagerstätte on oceanic island Mauritius provides a window into the ecosystem of the dodo (<i>Raphus cucullatus</i>). <i>Quaternary Science Reviews</i> , 2009, 28, 14-24.	1.4	56
77	Mammoth Population Dynamics in Late Pleistocene North America: Divergence, Phylogeography, and Introgression. <i>Frontiers in Ecology and Evolution</i> , 2016, 4, .	1.1	56
78	Mammoth 2.0: will genome engineering resurrect extinct species?. <i>Genome Biology</i> , 2015, 16, 228.	3.8	55
79	Puma genomes from North and South America provide insights into the genomic consequences of inbreeding. <i>Nature Communications</i> , 2019, 10, 4769.	5.8	55
80	Inferring species divergence times using pairwise sequential Markovian coalescent modelling and low-coverage genomic data. <i>Philosophical Transactions of the Royal Society B: Biological Sciences</i> , 2016, 371, 20150138.	1.8	54
81	Mitogenomes illuminate the origin and migration patterns of the indigenous people of the Canary Islands. <i>PLoS ONE</i> , 2019, 14, e0209125.	1.1	54
82	Setting Up an Ancient DNA Laboratory. <i>Methods in Molecular Biology</i> , 2019, 1963, 1-13.	0.4	54
83	Why sequence all eukaryotes?. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2022, 119, .	3.3	51
84	Palaeogenomes of Eurasian straight-tusked elephants challenge the current view of elephant evolution. <i>ELife</i> , 2017, 6, .	2.8	50
85	Genomic Analysis of Hepatitis B Virus Reveals Antigen State and Genotype as Sources of Evolutionary Rate Variation. <i>Viruses</i> , 2011, 3, 83-101.	1.5	49
86	A ligation-based single-stranded library preparation method to analyze cell-free DNA and synthetic oligos. <i>BMC Genomics</i> , 2019, 20, 1023.	1.2	49
87	Ancient and modern genomes unravel the evolutionary history of the rhinoceros family. <i>Cell</i> , 2021, 184, 4874-4885.e16.	13.5	49
88	Bayesian Estimation of Sequence Damage in Ancient DNA. <i>Molecular Biology and Evolution</i> , 2007, 24, 1416-1422.	3.5	48
89	Grey wolf genomic history reveals a dual ancestry of dogs. <i>Nature</i> , 2022, 607, 313-320.	13.7	48
90	An ancestral recombination graph of human, Neanderthal, and Denisovan genomes. <i>Science Advances</i> , 2021, 7, .	4.7	47

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91	A Phylogenetic Method for Detecting Positive Epistasis in Gene Sequences and Its Application to RNA Virus Evolution. <i>Molecular Biology and Evolution</i> , 2006, 23, 1724-1730.	3.5	46
92	Ancient Hybridization with an Unknown Population Facilitated High-Altitude Adaptation of Canids. <i>Molecular Biology and Evolution</i> , 2020, 37, 2616-2629.	3.5	46
93	Rapid range shifts and megafaunal extinctions associated with late Pleistocene climate change. <i>Nature Communications</i> , 2020, 11, 2770.	5.8	46
94	Modern and ancient DNA reveal recent partial replacement of caribou in the southwest Yukon. <i>Molecular Ecology</i> , 2010, 19, 1312-1323.	2.0	43
95	Dire wolves were the last of an ancient New World canid lineage. <i>Nature</i> , 2021, 591, 87-91.	13.7	43
96	Environmental genomics of Late Pleistocene black bears and giant short-faced bears. <i>Current Biology</i> , 2021, 31, 2728-2736.e8.	1.8	42
97	Pre-extinction Demographic Stability and Genomic Signatures of Adaptation in the Woolly Rhinoceros. <i>Current Biology</i> , 2020, 30, 3871-3879.e7.	1.8	41
98	A late Pleistocene steppe bison (<i>Bison priscus</i>) partial carcass from Tsiigehtchic, Northwest Territories, Canada. <i>Quaternary Science Reviews</i> , 2009, 28, 2734-2742.	1.4	39
99	The evolutionary and phylogeographic history of woolly mammoths: a comprehensive mitogenomic analysis. <i>Scientific Reports</i> , 2017, 7, 44585.	1.6	39
100	Climate impacts on transoceanic dispersal and habitat in gray whales from the Pleistocene to 2100. <i>Molecular Ecology</i> , 2015, 24, 1510-1522.	2.0	38
101	Complete mitochondrial genomes of living and extinct pigeons revise the timing of the columbiform radiation. <i>BMC Evolutionary Biology</i> , 2016, 16, 230.	3.2	38
102	Detecting hybridization using ancient <sc>DNA</sc>. <i>Molecular Ecology</i> , 2016, 25, 2398-2412.	2.0	37
103	The Late Pleistocene distribution of vicuñas (<i>Vicugna vicugna</i>) and the "extinction" of the gracile llama ("Lama gracilis"): New molecular data. <i>Quaternary Science Reviews</i> , 2009, 28, 1369-1373.	1.4	36
104	Improving the performance of true single molecule sequencing for ancient DNA. <i>BMC Genomics</i> , 2012, 13, 177.	1.2	35
105	Revisiting the effect of PCR replication and sequencing depth on biodiversity metrics in environmental DNA metabarcoding. <i>Ecology and Evolution</i> , 2021, 11, 15766-15779.	0.8	35
106	Late Pleistocene northward-dispersing <i>Bison antiquus</i> from the Bighill Creek Formation, Gallelli Gravel Pit, Alberta, Canada, and the fate of <i>Bison occidentalis</i> . <i>Canadian Journal of Earth Sciences</i> , 2008, 45, 827-859.	0.6	34
107	Phylogenetic Estimation of Timescales Using Ancient DNA: The Effects of Temporal Sampling Scheme and Uncertainty in Sample Ages. <i>Molecular Biology and Evolution</i> , 2012, 30, 253-262.	3.5	34
108	Multiple losses of flight and recent speciation in steamer ducks. <i>Proceedings of the Royal Society B: Biological Sciences</i> , 2012, 279, 2339-2346.	1.2	34

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109	The southern coastal Beringian land bridge: cryptic refugium or pseudorefugium for woody plants during the Last Glacial Maximum?. <i>Journal of Biogeography</i> , 2017, 44, 1559-1571.	1.4	34
110	Ancient DNA confirms a local origin of domesticated chenopod in eastern North America. <i>Journal of Archaeological Science</i> , 2011, 38, 3549-3554.	1.2	33
111	<i>Chomotherium serum</i> and <i>Cervalces</i> from the Great Lakes Region, USA: geochronology, morphology and ancient DNA. <i>Boreas</i> , 2012, 41, 546-556.	1.2	32
112	Complex Admixture Preceded and Followed the Extinction of Wisent in the Wild. <i>Molecular Biology and Evolution</i> , 2017, 34, msw254.	3.5	30
113	Ancient horse genomes reveal the timing and extent of dispersals across the Bering Land Bridge. <i>Molecular Ecology</i> , 2021, 30, 6144-6161.	2.0	30
114	An ancient bison from the mouth of the Rauchua River (Chukotka, Russia). <i>Quaternary Research</i> , 2015, 84, 232-245.	1.0	29
115	Ancient plant DNA reveals High Arctic greening during the Last Interglacial. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2021, 118, .	3.3	29
116	Lifetime mobility of an Arctic woolly mammoth. <i>Science</i> , 2021, 373, 806-808.	6.0	27
117	Mitogenomics of the Extinct Cave Lion, <i>Panthera spelaea</i> (Goldfuss, 1810), Resolve its Position within the Panthera Cats. <i>Open Quaternary</i> , 2016, 2, .	0.5	27
118	An Evolutionary Insertion in the Mxra8 Receptor-Binding Site Confers Resistance to Alphavirus Infection and Pathogenesis. <i>Cell Host and Microbe</i> , 2020, 27, 428-440.e9.	5.1	26
119	A Reference Genome Assembly of Simmental Cattle, <i>Bos taurus taurus</i> . <i>Journal of Heredity</i> , 2021, 112, 184-191.	1.0	25
120	Ancient mitochondrial DNA and the genetic history of Eurasian beaver (<i>Castor fiber</i>) in Europe. <i>Molecular Ecology</i> , 2014, 23, 1717-1729.	2.0	24
121	Depletion of Hemoglobin Transcripts and Long-Read Sequencing Improves the Transcriptome Annotation of the Polar Bear (<i>Ursus maritimus</i>). <i>Frontiers in Genetics</i> , 2019, 10, 643.	1.1	23
122	Landscape analyses using eDNA metabarcoding and Earth observation predict community biodiversity in California. <i>Ecological Applications</i> , 2021, 31, e02379.	1.8	23
123	Beringia as an Ice Age genetic museum. <i>Quaternary Research</i> , 2003, 60, 94-100.	1.0	22
124	Large-scale genomic analysis reveals the genetic cost of chicken domestication. <i>BMC Biology</i> , 2021, 19, 118.	1.7	22
125	Ancient DNA supports southern survival of Richardson's collared lemming (<i>Dicrostonyx richardsoni</i>) during the last glacial maximum. <i>Molecular Ecology</i> , 2013, 22, 2540-2548.	2.0	20
126	Discovery of the skull of <i>Stephanorhinus kirchbergensis</i> (Jäger, 1839) above the Arctic Circle. <i>Quaternary Research</i> , 2017, 88, 537-550.	1.0	20

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127	The Zhenya Mammoth (<i>Mammuthus primigenius</i> (Blum.)): Taphonomy, geology, age, morphology and ancient DNA of a 48,000 year old frozen mummy from western Taimyr, Russia. <i>Quaternary International</i> , 2017, 445, 104-134.	0.7	20
128	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.	1.8	20
129	The CALeDNA program: Citizen scientists and researchers inventory California's biodiversity. <i>California Agriculture</i> , 2021, 75, 20-32.	0.5	20
130	Analysis of ancient human genomes. <i>BioEssays</i> , 2010, 32, 388-391.	1.2	19
131	Empirical calibrated radiocarbon sampler: a tool for incorporating radiocarbon date and calibration error into Bayesian phylogenetic analyses of ancient DNA. <i>Molecular Ecology Resources</i> , 2015, 15, 81-86.	2.2	19
132	A method for positive forensic identification of samples from extremely low-coverage sequence data. <i>BMC Genomics</i> , 2015, 16, 1034.	1.2	18
133	Glacial ice supports a distinct and undocumented polar bear subpopulation persisting in late 21st-century sea-ice conditions. <i>Science</i> , 2022, 376, 1333-1338.	6.0	18
134	Engineered polymerases amplify the potential of ancient DNA. <i>Trends in Biotechnology</i> , 2008, 26, 285-287.	4.9	17
135	Case Study: Recovery of Ancient Nuclear DNA from Toe Pads of the Extinct Passenger Pigeon. <i>Methods in Molecular Biology</i> , 2012, 840, 29-35.	0.4	17
136	Nuclear DNA from the extinct Passenger Pigeon (<i>Ectopistes migratorius</i>) confirms a single origin of New World pigeons. <i>Annals of Anatomy</i> , 2012, 194, 52-57.	1.0	17
137	Genetic relatedness in two-tiered plains zebra societies suggests that females choose to associate with kin. <i>Behaviour</i> , 2015, 152, 2059-2078.	0.4	17
138	A probable prehistoric case of meningococcal disease from San Francisco Bay: Next generation sequencing of <i>Neisseria meningitidis</i> from dental calculus and osteological evidence. <i>International Journal of Paleopathology</i> , 2018, 22, 173-180.	0.8	17
139	Horseshoe-based Bayesian nonparametric estimation of effective population size trajectories. <i>Biometrics</i> , 2020, 76, 677-690.	0.8	16
140	Post-glacial dispersal patterns of Northern pike inferred from an 8800 year old pike (<i>Esox cf. lucius</i>) skull from interior Alaska. <i>Quaternary Science Reviews</i> , 2015, 120, 118-125.	1.4	15
141	A review of the dodo and its ecosystem: insights from a vertebrate concentration Lagerstätte in Mauritius. <i>Journal of Vertebrate Paleontology</i> , 2015, 35, 3-20.	0.4	15
142	Demographic reconstruction from ancient DNA supports rapid extinction of the great auk. <i>ELife</i> , 2019, 8, .	2.8	15
143	Human Evolution: Turning Back the Clock. <i>Current Biology</i> , 2013, 23, R286-R288.	1.8	14
144	Ancient DNA Resolves the History of Tetragnatha (Araneae, Tetragnathidae) Spiders on Rapa Nui. <i>Genes</i> , 2017, 8, 403.	1.0	14

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145	A Reference Genome Assembly of American Bison, <i>Bison bison bison</i> . <i>Journal of Heredity</i> , 2021, 112, 174-183.	1.0	14
146	Ancient DNA analysis indicates the first English lions originated from North Africa. <i>Contributions To Zoology</i> , 2008, 77, 7-16.	0.2	13
147	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
148	Using ancient DNA and coalescent-based methods to infer extinction. <i>Biology Letters</i> , 2016, 12, 20150822.	1.0	12
149	Sedimentary DNA and molecular evidence for early human occupation of the Faroe Islands. <i>Communications Earth & Environment</i> , 2021, 2, .	2.6	11
150	Ancient DNA typing of archaeological pig remains corroborates historical records. <i>Journal of Archaeological Science</i> , 2010, 37, 174-177.	1.2	10
151	Bermuda 2.0: reflections from Santa Cruz. <i>GigaScience</i> , 2016, 5, 1-4.	3.3	10
152	A middle Holocene steppe bison and paleoenvironments from the Versleuce Meadows, Whitehorse, Yukon, Canada. <i>Canadian Journal of Earth Sciences</i> , 2017, 54, 1138-1152.	0.6	10
153	Metabarcoding meiofauna biodiversity assessment in four beaches of Northern Colombia: effects of sampling protocols and primer choice. <i>Hydrobiologia</i> , 2021, 848, 3407.	1.0	10
154	A polar bear paleogenome reveals extensive ancient gene flow from polar bears into brown bears. <i>Nature Ecology and Evolution</i> , 2022, 6, 936-944.	3.4	10
155	A detailed life history of a pleistocene steppe bison (<i>Bison priscus</i>) skeleton unearthed in Arctic Alaska. <i>Quaternary Science Reviews</i> , 2020, 249, 106578.	1.4	9
156	Genomic basis for skin phenotype and cold adaptation in the extinct Steller's sea cow. <i>Science Advances</i> , 2022, 8, eabl6496.	4.7	9
157	The case of an arctic wild ass highlights the utility of ancient DNA for validating problematic identifications in museum collections. <i>Molecular Ecology Resources</i> , 2020, 20, 1182-1190.	2.2	8
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