

M Thomas P Gilbert

List of Publications by Year in descending order

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Version: 2024-02-01

406
papers

44,946
citations

1981

104
h-index

3782

185
g-index

445
all docs

445
docs citations

445
times ranked

42624
citing authors

#	ARTICLE	IF	CITATIONS
1	The potential of aquatic bloodfeeding and nonbloodfeeding leeches as a tool for iDNA characterisation. <i>Molecular Ecology Resources</i> , 2022, 22, 539-553.	2.2	8
2	Disentangling hostâ€microbiota complexity through hologenomics. <i>Nature Reviews Genetics</i> , 2022, 23, 281-297.	7.7	44
3	The Earth BioGenome Project 2020: Starting the clock. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2022, 119, .	3.3	124
4	The era of reference genomes in conservation genomics. <i>Trends in Ecology and Evolution</i> , 2022, 37, 197-202.	4.2	138
5	A multi-omics approach unravels metagenomic and metabolic alterations of a probiotic and synbiotic additive in rainbow trout (<i>Oncorhynchus mykiss</i>). <i>Microbiome</i> , 2022, 10, 21.	4.9	25
6	Ancient and historical DNA in conservation policy. <i>Trends in Ecology and Evolution</i> , 2022, 37, 420-429.	4.2	31
7	Probing the genomic limits of de-extinction in the Christmas Island rat. <i>Current Biology</i> , 2022, , .	1.8	8
8	The Australian dingo is an early offshoot of modern breed dogs. <i>Science Advances</i> , 2022, 8, eabm5944.	4.7	14
9	Archival influenza virus genomes from Europe reveal genomic variability during the 1918 pandemic. <i>Nature Communications</i> , 2022, 13, 2314.	5.8	25
10	Ancient proteins resolve controversy over the identity of <i>Genyornis</i> eggshell. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2022, 119, .	3.3	14
11	Grey wolf genomic history reveals a dual ancestry of dogs. <i>Nature</i> , 2022, 607, 313-320.	13.7	48
12	Phylogenomics of the worldâ€™s otters. <i>Current Biology</i> , 2022, 32, 3650-3658.e4.	1.8	14
13	Leech bloodâ€meal invertebrateâ€derived DNA reveals differences in Bornean mammal diversity across habitats. <i>Molecular Ecology</i> , 2021, 30, 3299-3312.	2.0	24
14	Ancient microRNA profiles of 14,300-yr-old canid samples confirm taxonomic origin and provide glimpses into tissue-specific gene regulation from the Pleistocene. <i>Rna</i> , 2021, 27, 324-334.	1.6	7
15	Tracking the history of grapevine cultivation in Georgia by combining geometric morphometrics and ancient DNA. <i>Vegetation History and Archaeobotany</i> , 2021, 30, 63-76.	1.0	29
16	Genomes of Pleistocene Siberian Wolves Uncover Multiple Extinct Wolf Lineages. <i>Current Biology</i> , 2021, 31, 198-206.e8.	1.8	26
17	Mitochondrial genomes of Danish vertebrate species generated for the national DNA reference database, DNAMark. <i>Environmental DNA</i> , 2021, 3, 472-480.	3.1	24
18	eDNAâ€based biomonitoring at an experimental German vineyard to characterize how management regimes shape ecosystem diversity. <i>Environmental DNA</i> , 2021, 3, 70-82.	3.1	14

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19	Dire wolves were the last of an ancient New World canid lineage. <i>Nature</i> , 2021, 591, 87-91.	13.7	43
20	Extended survival of Pleistocene Siberian wolves into the early 20th century on the island of HonshÅ«. <i>IScience</i> , 2021, 24, 101904.	1.9	9
21	Molecular parallelisms between pigmentation in the avian iris and the integument of ectothermic vertebrates. <i>PLoS Genetics</i> , 2021, 17, e1009404.	1.5	8
22	A towering genome: Experimentally validated adaptations to high blood pressure and extreme stature in the giraffe. <i>Science Advances</i> , 2021, 7, .	4.7	31
23	Salmon gut microbiota correlates with disease infection status: potential for monitoring health in farmed animals. <i>Animal Microbiome</i> , 2021, 3, 30.	1.5	84
24	Towards complete and error-free genome assemblies of all vertebrate species. <i>Nature</i> , 2021, 592, 737-746.	13.7	1,139
25	Genomic insights into the conservation status of the worldâ€™s last remaining Sumatran rhinoceros populations. <i>Nature Communications</i> , 2021, 12, 2393.	5.8	39
26	Ancient and modern stickleback genomes reveal the demographic constraints on adaptation. <i>Current Biology</i> , 2021, 31, 2027-2036.e8.	1.8	33
27	Genome-resolved metagenomics suggests a mutualistic relationship between <i>Mycoplasma</i> and salmonid hosts. <i>Communications Biology</i> , 2021, 4, 579.	2.0	55
28	The genomic origin of Zana of Abkhazia. <i>Genetics & Genomics Next</i> , 2021, 2, e10051.	0.8	0
29	A genomic exploration of the early evolution of extant cats and their sabre-toothed relatives. <i>Open Research Europe</i> , 2021, 1, 25.	2.0	2
30	Feasibility of applying shotgun metagenomic analyses to grapevine leaf, rhizosphere and soil microbiome characterisation. <i>Australian Journal of Grape and Wine Research</i> , 2021, 27, 519-526.	1.0	4
31	Historical population declines prompted significant genomic erosion in the northern and southern white rhinoceros (<i>Ceratotherium simum</i>). <i>Molecular Ecology</i> , 2021, 30, 6355-6369.	2.0	39
32	Contrasting genetic signal of recolonization after rainforest fragmentation in African trees with different dispersal abilities. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2021, 118, .	3.3	4
33	Nonâ€™invasive surveys of mammalian viruses using environmental DNA. <i>Methods in Ecology and Evolution</i> , 2021, 12, 1941-1952.	2.2	10
34	Reconsidering domestication from a process archaeology perspective. <i>World Archaeology</i> , 2021, 53, 56-77.	0.5	36
35	Runs of homozygosity in killer whale genomes provide a global record of demographic histories. <i>Molecular Ecology</i> , 2021, 30, 6162-6177.	2.0	39
36	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, .	3.3	19

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37	Ancient and modern genomes unravel the evolutionary history of the rhinoceros family. <i>Cell</i> , 2021, 184, 4874-4885.e16.	13.5	49
38	Evolutionary history of the extinct Sardinian dhole. <i>Current Biology</i> , 2021, 31, 5571-5579.e6.	1.8	7
39	Kouprey (<i>Bos sauveli</i>) genomes unveil polytomic origin of wild Asian Bos. <i>IScience</i> , 2021, 24, 103226.	1.9	8
40	The role of the gut microbiota in the dietary niche expansion of fishing bats. <i>Animal Microbiome</i> , 2021, 3, 76.	1.5	8
41	The genome sequence of the grey wolf, <i>Canis lupus</i> Linnaeus 1758. <i>Wellcome Open Research</i> , 2021, 6, 310.	0.9	9
42	To bee, or not to bee? One leg is the question. <i>Molecular Ecology Resources</i> , 2021, , .	2.2	3
43	Gut Microbiota Linked with Reduced Fear of Humans in Red Junglefowl Has Implications for Early Domestication. <i>Genetics & Genomics Next</i> , 2021, 2, .	0.8	7
44	<i>Plasmodium vivax</i> Malaria Viewed through the Lens of an Eradicated European Strain. <i>Molecular Biology and Evolution</i> , 2020, 37, 773-785.	3.5	38
45	Near-Random Distribution of Chromosome-Derived Circular DNA in the Condensed Genome of Pigeons and the Larger, More Repeat-Rich Human Genome. <i>Genome Biology and Evolution</i> , 2020, 12, 3762-3777.	1.1	52
46	Ancient DNA suggests modern wolves trace their origin to a Late Pleistocene expansion from Beringia. <i>Molecular Ecology</i> , 2020, 29, 1596-1610.	2.0	70
47	Evolutionary History, Genomic Adaptation to Toxic Diet, and Extinction of the Carolina Parakeet. <i>Current Biology</i> , 2020, 30, 108-114.e5.	1.8	24
48	Genomic Adaptations and Evolutionary History of the Extinct Scimitar-Toothed Cat, <i>Homotherium latidens</i> . <i>Current Biology</i> , 2020, 30, 5018-5025.e5.	1.8	34
49	Releasing the microbes from old bones: the effect of different DNA extraction protocols on microbial community profiling. <i>Science and Technology of Archaeological Research</i> , 2020, 6, 1-15.	2.4	2
50	Dense sampling of bird diversity increases power of comparative genomics. <i>Nature</i> , 2020, 587, 252-257.	13.7	251
51	Holo-Omics: Integrated Host-Microbiota Multi-omics for Basic and Applied Biological Research. <i>IScience</i> , 2020, 23, 101414.	1.9	80
52	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
53	Molecular identification and phylogenetic analysis of a <i>Callosciurus notatus</i> complete mitogenome from Peninsular Malaysia. <i>Mitochondrial DNA Part B: Resources</i> , 2020, 5, 3004-3006.	0.2	2
54	Multi-omic detection of <i>Mycobacterium leprae</i> in archaeological human dental calculus. <i>Philosophical Transactions of the Royal Society B: Biological Sciences</i> , 2020, 375, 20190584.	1.8	31

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55	Using paleo-archives to safeguard biodiversity under climate change. <i>Science</i> , 2020, 369, .	6.0	98
56	Population genomics of the Viking world. <i>Nature</i> , 2020, 585, 390-396.	13.7	143
57	Hi-C chromosome conformation capture sequencing of avian genomes using the BGISEQ-500 platform. <i>GigaScience</i> , 2020, 9, .	3.3	6
58	DNA-Based Arthropod Diversity Assessment in Amazonian Iron Mine Lands Show Ecological Succession Towards Undisturbed Reference Sites. <i>Frontiers in Ecology and Evolution</i> , 2020, 8, .	1.1	5
59	Using in silico predicted ancestral genomes to improve the efficiency of paleogenome reconstruction. <i>Ecology and Evolution</i> , 2020, 10, 12700-12709.	0.8	4
60	The secrets of Sobek – A crocodile mummy mitogenome from ancient Egypt. <i>Journal of Archaeological Science: Reports</i> , 2020, 33, 102483.	0.2	4
61	The evolutionary history of extinct and living lions. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2020, 117, 10927-10934.	3.3	70
62	Darwin’s Fancy Revised: An Updated Understanding of the Genomic Constitution of Pigeon Breeds. <i>Genome Biology and Evolution</i> , 2020, 12, 136-150.	1.1	13
63	The first complete mitochondrial genome data of <i>Hippocampus kuda</i> originating from Malaysia. <i>Data in Brief</i> , 2020, 31, 105721.	0.5	8
64	Beyond DNA barcoding: The unrealized potential of genome skim data in sample identification. <i>Molecular Ecology</i> , 2020, 29, 2521-2534.	2.0	58
65	Rapid loss of endogenous DNA in pig bone buried in five different environments. <i>Archaeometry</i> , 2020, 62, 827-846.	0.6	2
66	Recent mitochondrial lineage extinction in the critically endangered Javan rhinoceros. <i>Zoological Journal of the Linnean Society</i> , 2020, 190, 372-383.	1.0	13
67	DNA metabarcoding and spatial modelling link diet diversification with distribution homogeneity in European bats. <i>Nature Communications</i> , 2020, 11, 1154.	5.8	35
68	Arctic-adapted dogs emerged at the Pleistocene–Holocene transition. <i>Science</i> , 2020, 368, 1495-1499.	6.0	60
69	GC bias affects genomic and metagenomic reconstructions, underrepresenting GC-poor organisms. <i>GigaScience</i> , 2020, 9, .	3.3	91
70	Phylogeny of Neotropical Seirinae (Collembola, Entomobryidae) based on mitochondrial genomes. <i>Zoologica Scripta</i> , 2020, 49, 329-339.	0.7	11
71	Adaptive venom evolution and toxicity in octopods is driven by extensive novel gene formation, expansion, and loss. <i>GigaScience</i> , 2020, 9, .	3.3	15
72	Bone biodeterioration – The effect of marine and terrestrial depositional environments on early diagenesis and bone bacterial community. <i>PLoS ONE</i> , 2020, 15, e0240512.	1.1	22

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73	Avian Binocularity and Adaptation to Nocturnal Environments: Genomic Insights from a Highly Derived Visual Phenotype. <i>Genome Biology and Evolution</i> , 2019, 11, 2244-2255.	1.1	12
74	Ancient pigs reveal a near-complete genomic turnover following their introduction to Europe. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2019, 116, 17231-17238.	3.3	101
75	31° South: Dietary niche of an arid-zone endemic passerine. <i>Environmental DNA</i> , 2019, 1, 109-118.	3.1	5
76	31° South: The physiology of adaptation to arid conditions in a passerine bird. <i>Molecular Ecology</i> , 2019, 28, 3709-3721.	2.0	11
77	The discovery of Neotropical <i>Lepidosira</i> (Collembola, Entomobryidae) and its systematic position. <i>Zoologica Scripta</i> , 2019, 48, 783-800.	0.7	6
78	Ancient RNA from Late Pleistocene permafrost and historical canids shows tissue-specific transcriptome survival. <i>PLoS Biology</i> , 2019, 17, e3000166.	2.6	33
79	The Vertebrate TLR Supergene Family Evolved Dynamically by Gene Gain/Loss and Positive Selection Revealing a Host-Pathogen Arms Race in Birds. <i>Diversity</i> , 2019, 11, 131.	0.7	25
80	Early Pleistocene enamel proteome from Dmanisi resolves <i>Stephanorhinus</i> phylogeny. <i>Nature</i> , 2019, 574, 103-107.	13.7	135
81	High-coverage genomes to elucidate the evolution of penguins. <i>GigaScience</i> , 2019, 8, .	3.3	18
82	Resolving a clinical tuberculosis outbreak using palaeogenomic genome reconstruction methodologies. <i>Tuberculosis</i> , 2019, 119, 101865.	0.8	1
83	Killer whale genomes reveal a complex history of recurrent admixture and vicariance. <i>Molecular Ecology</i> , 2019, 28, 3427-3444.	2.0	46
84	Postglacial Colonization of Northern Coastal Habitat by Bottlenose Dolphins: A Marine Leading-Edge Expansion?. <i>Journal of Heredity</i> , 2019, 110, 662-674.	1.0	16
85	Large-scale ruminant genome sequencing provides insights into their evolution and distinct traits. <i>Science</i> , 2019, 364, .	6.0	266
86	Biological adaptations in the Arctic cervid, the reindeer (<i>Rangifer tarandus</i>). <i>Science</i> , 2019, 364, .	6.0	58
87	A simplified DNA extraction protocol for unsorted bulk arthropod samples that maintains exoskeletal integrity. <i>Environmental DNA</i> , 2019, 1, 144-154.	3.1	34
88	Palaeogenomic insights into the origins of French grapevine diversity. <i>Nature Plants</i> , 2019, 5, 595-603.	4.7	85
89	DNA metabarcoding—Need for robust experimental designs to draw sound ecological conclusions. <i>Molecular Ecology</i> , 2019, 28, 1857-1862.	2.0	300
90	Taxonomic and Functional Characterization of the Microbial Community During Spontaneous in vitro Fermentation of Riesling Must. <i>Frontiers in Microbiology</i> , 2019, 10, 697.	1.5	30

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91	Diabetic cats have decreased gut microbial diversity and a lack of butyrate producing bacteria. <i>Scientific Reports</i> , 2019, 9, 4822.	1.6	40
92	A comparison of storage methods for gut microbiome studies in teleosts: Insights from rainbow trout (<i>Oncorhynchus mykiss</i>). <i>Journal of Microbiological Methods</i> , 2019, 160, 42-48.	0.7	10
93	DNA Extraction from Keratin and Chitin. <i>Methods in Molecular Biology</i> , 2019, 1963, 57-63.	0.4	7
94	A guide to the application of Hill numbers to DNA-based diversity analyses. <i>Molecular Ecology Resources</i> , 2019, 19, 804-817.	2.2	125
95	Skmer: assembly-free and alignment-free sample identification using genome skims. <i>Genome Biology</i> , 2019, 20, 34.	3.8	70
96	Mitogenomic evidence of close relationships between New Zealand's extinct giant raptors and small-sized Australian sister-taxa. <i>Molecular Phylogenetics and Evolution</i> , 2019, 134, 122-128.	1.2	17
97	Parallel adaptation of rabbit populations to myxoma virus. <i>Science</i> , 2019, 363, 1319-1326.	6.0	124
98	Specialized sledge dogs accompanied Inuit dispersal across the North American Arctic. <i>Proceedings of the Royal Society B: Biological Sciences</i> , 2019, 286, 20191929.	1.2	38
99	A 5700 year-old human genome and oral microbiome from chewed birch pitch. <i>Nature Communications</i> , 2019, 10, 5520.	5.8	61
100	Using metabarcoding to compare the suitability of two blood-feeding leech species for sampling mammalian diversity in North Borneo. <i>Molecular Ecology Resources</i> , 2019, 19, 105-117.	2.2	31
101	Host-derived population genomics data provides insights into bacterial and diatom composition of the killer whale skin. <i>Molecular Ecology</i> , 2019, 28, 484-502.	2.0	42
102	MobiSeq: De novo SNP discovery in model and non-model species through sequencing the flanking region of transposable elements. <i>Molecular Ecology Resources</i> , 2019, 19, 512-525.	2.2	4
103	The Genomic Footprints of the Fall and Recovery of the Crested Ibis. <i>Current Biology</i> , 2019, 29, 340-349.e7.	1.8	94
104	Promises and pitfalls of using high-throughput sequencing for diet analysis. <i>Molecular Ecology Resources</i> , 2019, 19, 327-348.	2.2	138
105	Multi-omics and potential applications in wine production. <i>Current Opinion in Biotechnology</i> , 2019, 56, 172-178.	3.3	45
106	Ancient <i>scp</i> DNA reveals the timing and persistence of organellar genetic bottlenecks over 3,000 years of sunflower domestication and improvement. <i>Evolutionary Applications</i> , 2019, 12, 38-53.	1.5	27
107	Genetic affinities of an eradicated European <i>Plasmodium falciparum</i> strain. <i>Microbial Genomics</i> , 2019, 5, .	1.0	9
108	Demographic reconstruction from ancient DNA supports rapid extinction of the great auk. <i>ELife</i> , 2019, 8, .	2.8	15

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109	Ancient RNA. <i>Population Genomics</i> , 2018, , 53-74.	0.2	7
110	No longer locally extinct? Tracing the origins of a lion (<i>Panthera leo</i>) living in Gabon. <i>Conservation Genetics</i> , 2018, 19, 611-618.	0.8	11
111	Improved Genome Assembly and Annotation for the Rock Pigeon (<i>Columba livia</i>). <i>G3: Genes, Genomes, Genetics</i> , 2018, 8, 1391-1398.	0.8	62
112	Using <i>DNA</i> metabarcoding for simultaneous inference of common vampire bat diet and population structure. <i>Molecular Ecology Resources</i> , 2018, 18, 1050-1063.	2.2	70
113	Earth BioGenome Project: Sequencing life for the future of life. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2018, 115, 4325-4333.	3.3	652
114	Scrutinizing key steps for reliable metabarcoding of environmental samples. <i>Methods in Ecology and Evolution</i> , 2018, 9, 134-147.	2.2	425
115	Hologenomic adaptations underlying the evolution of sanguivory in the common vampire bat. <i>Nature Ecology and Evolution</i> , 2018, 2, 659-668.	3.4	124
116	Applied Hologenomics: Feasibility and Potential in Aquaculture. <i>Trends in Biotechnology</i> , 2018, 36, 252-264.	4.9	51
117	Quantifying Temporal Genomic Erosion in Endangered Species. <i>Trends in Ecology and Evolution</i> , 2018, 33, 176-185.	4.2	162
118	Agriculture shapes the trophic niche of a bat preying on multiple pest arthropods across Europe: Evidence from <i>DNA</i> metabarcoding. <i>Molecular Ecology</i> , 2018, 27, 815-825.	2.0	110
119	Whole-Genome Sequencing of African Dogs Provides Insights into Adaptations against Tropical Parasites. <i>Molecular Biology and Evolution</i> , 2018, 35, 287-298.	3.5	41
120	Single-tube library preparation for degraded <i>DNA</i> . <i>Methods in Ecology and Evolution</i> , 2018, 9, 410-419.	2.2	261
121	Bat Biology, Genomes, and the Bat1K Project: To Generate Chromosome-Level Genomes for All Living Bat Species. <i>Annual Review of Animal Biosciences</i> , 2018, 6, 23-46.	3.6	166
122	Identification of transcription factor genes involved in anthocyanin biosynthesis in carrot (<i>Daucus</i>). <i>PLoS Genetics</i> , 2018, 14, e1007745.	1.2	38
123	Population genomics of grey wolves and wolf-like canids in North America. <i>PLoS Genetics</i> , 2018, 14, e1007745.	1.5	54
124	Multiproxy evidence highlights a complex evolutionary legacy of maize in South America. <i>Science</i> , 2018, 362, 1309-1313.	6.0	172
125	Protective role of the vulture facial skin and gut microbiomes aid adaptation to scavenging. <i>Acta Veterinaria Scandinavica</i> , 2018, 60, 61.	0.5	40
126	Interspecific Gene Flow Shaped the Evolution of the Genus <i>Canis</i> . <i>Current Biology</i> , 2018, 28, 3441-3449.e5.	1.8	110

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127	Ancient DNA analysis of Scandinavian medieval drinking horns and the horn of the last aurochs bull. <i>Journal of Archaeological Science</i> , 2018, 99, 47-54.	1.2	11
128	Testosterone in ancient hair from an extinct species. <i>Palaeontology</i> , 2018, 61, 797-802.	1.0	11
129	Ancient genomes from Iceland reveal the making of a human population. <i>Science</i> , 2018, 360, 1028-1032.	6.0	62
130	The evolutionary history of dogs in the Americas. <i>Science</i> , 2018, 361, 81-85.	6.0	140
131	Pan-genome Analysis of Ancient and Modern <i>Salmonella enterica</i> Demonstrates Genomic Stability of the Invasive Para C Lineage for Millennia. <i>Current Biology</i> , 2018, 28, 2420-2428.e10.	1.8	65
132	Mind the gut: genomic insights to population divergence and gut microbial composition of two marine keystone species. <i>Microbiome</i> , 2018, 6, 82.	4.9	28
133	Recent Asian origin of chytrid fungi causing global amphibian declines. <i>Science</i> , 2018, 360, 621-627.	6.0	389
134	Greenland sled dogs at risk of extinction. <i>Science</i> , 2018, 360, 1080-1080.	6.0	8
135	Debugging diversity – a pancontinental exploration of the potential of terrestrial blood-feeding leeches as a vertebrate monitoring tool. <i>Molecular Ecology Resources</i> , 2018, 18, 1282-1298.	2.2	45
136	Characterizing restriction enzyme-associated loci in historic ragweed (<i>Ambrosia artemisiifolia</i>) voucher specimens using custom-designed <i>scRNA</i> probes. <i>Molecular Ecology Resources</i> , 2017, 17, 209-220.	2.2	31
137	Eggshell palaeogenomics: Palaeognath evolutionary history revealed through ancient nuclear and mitochondrial DNA from Madagascan elephant bird (<i>Aepyornis</i> sp.) eggshell. <i>Molecular Phylogenetics and Evolution</i> , 2017, 109, 151-163.	1.2	65
138	Molecular clocks indicate turnover and diversification of modern coleoid cephalopods during the Mesozoic Marine Revolution. <i>Proceedings of the Royal Society B: Biological Sciences</i> , 2017, 284, 20162818.	1.2	86
139	Functional roles of Aves class-specific cis-regulatory elements on macroevolution of bird-specific features. <i>Nature Communications</i> , 2017, 8, 14229.	5.8	61
140	Connecting Earth observation to high-throughput biodiversity data. <i>Nature Ecology and Evolution</i> , 2017, 1, 176.	3.4	156
141	Leeches as a source of mammalian viral DNA and RNA – a study in medicinal leeches. <i>European Journal of Wildlife Research</i> , 2017, 63, 1.	0.7	9
142	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.	2.6	50
143	Evolutionary History of Saber-Toothed Cats Based on Ancient Mitogenomics. <i>Current Biology</i> , 2017, 27, 3330-3336.e5.	1.8	45
144	An expanded mammal mitogenome dataset from Southeast Asia. <i>GigaScience</i> , 2017, 6, 1-8.	3.3	27

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145	Documenting DNA in the dust. <i>Molecular Ecology</i> , 2017, 26, 969-971.	2.0	5
146	Natural selection shaped the rise and fall of passenger pigeon genomic diversity. <i>Science</i> , 2017, 358, 951-954.	6.0	105
147	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.	1.2	73
148	Comparative performance of the BGISEQ-500 vs Illumina HiSeq2500 sequencing platforms for palaeogenomic sequencing. <i>GigaScience</i> , 2017, 6, 1-13.	3.3	137
149	Relative performance of two DNA extraction and library preparation methods on archaeological human teeth samples. <i>Science and Technology of Archaeological Research</i> , 2017, 3, 80-88.	2.4	6
150	An "Aukward" Tale: A Genetic Approach to Discover the Whereabouts of the Last Great Auks. <i>Genes</i> , 2017, 8, 164.	1.0	11
151	The population genomic basis of geographic differentiation in North American common ragweed (<i>Ambrosia artemisiifolia</i> L.). <i>Ecology and Evolution</i> , 2016, 6, 3760-3771.	0.8	35
152	Bone-associated gene evolution and the origin of flight in birds. <i>BMC Genomics</i> , 2016, 17, 371.	1.2	12
153	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
154	Genomic population structure of freshwater-resident and anadromous ide (<i>Leuciscus idus</i>) in northwestern Europe. <i>Ecology and Evolution</i> , 2016, 6, 1064-1074.	0.8	20
155	Mitochondrial DNA from the eradicated European <i>Plasmodium vivax</i> and <i>P. falciparum</i> from 70-year-old slides from the Ebro Delta in Spain. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2016, 113, 11495-11500.	3.3	41
156	Do Vertebrate Gut Metagenomes Confer Rapid Ecological Adaptation?. <i>Trends in Ecology and Evolution</i> , 2016, 31, 689-699.	4.2	235
157	Genome Sequence of a 5,310-Year-Old Maize Cob Provides Insights into the Early Stages of Maize Domestication. <i>Current Biology</i> , 2016, 26, 3195-3201.	1.8	130
158	Genome-culture coevolution promotes rapid divergence of killer whale ecotypes. <i>Nature Communications</i> , 2016, 7, 11693.	5.8	222
159	The potential and pitfalls of de-extinction. <i>Zoologica Scripta</i> , 2016, 45, 22-36.	0.7	25
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