M Thomas P Gilbert

List of Publications by Year
in descending order

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406 papers	44,946 citations	1697 104 h-index	3257 185 g-index
445 all docs	445 docs citations	445 times ranked	38459 citing authors

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

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

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37	Ancient and modern genomes unravel the evolutionary history of the rhinoceros family. Cell, 2021, 184, 4874-4885.e16.	13.5	49
38	Evolutionary history of the extinct Sardinian dhole. Current Biology, 2021, 31, 5571-5579.e6.	1.8	7
39	Kouprey (Bos sauveli) genomes unveil polytomic origin of wild Asian Bos. IScience, 2021, 24, 103226.	1.9	8
40	The role of the gut microbiota in the dietary niche expansion of fishing bats. Animal Microbiome, 2021, 3, 76.	1.5	8
41	The genome sequence of the grey wolf, Canis lupus Linnaeus 1758. Wellcome Open Research, 2021, 6, 310.	0.9	9
42	To bee, or not to bee? One leg is the question. Molecular Ecology Resources, 2021, , .	2.2	3
43	Gut Microbiota Linked with Reduced Fear of Humans in Red Junglefowl Has Implications for Early Domestication. Genetics & Genomics Next, 2021, 2, .	0.8	7
44	Plasmodium vivax Malaria Viewed through the Lens of an Eradicated European Strain. Molecular Biology and Evolution, 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. Genome Biology and Evolution, 2020, 12, 3762-3777.	1.1	52
46	Ancient DNA suggests modern wolves trace their origin to a Late Pleistocene expansion from Beringia. Molecular Ecology, 2020, 29, 1596-1610.	2.0	70
47	Evolutionary History, Genomic Adaptation to Toxic Diet, and Extinction of the Carolina Parakeet. Current Biology, 2020, 30, 108-114.e5.	1.8	24
48	Genomic Adaptations and Evolutionary History of the Extinct Scimitar-Toothed Cat, Homotherium latidens. Current Biology, 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. Science and Technology of Archaeological Research, 2020, 6, 1-15.	2.4	2
50	Dense sampling of bird diversity increases power of comparative genomics. Nature, 2020, 587, 252-257.	13.7	251
51	Holo-Omics: Integrated Host-Microbiota Multi-omics for Basic and Applied Biological Research. IScience, 2020, 23, 101414.	1.9	80
52	Pre-extinction Demographic Stability and Genomic Signatures of Adaptation in the Woolly Rhinoceros. Current Biology, 2020, 30, 3871-3879.e7.	1.8	41
53	Molecular identification and phylogenetic analysis of a Callosciurus notatus complete mitogenome from Peninsular Malaysia. Mitochondrial DNA Part B: Resources, 2020, 5, 3004-3006.	0.2	2
54	Multi-omic detection ofMycobacterium lepraein archaeological human dental calculus. Philosophical Transactions of the Royal Society B: Biological Sciences, 2020, 375, 20190584.	1.8	31

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55	Using paleo-archives to safeguard biodiversity under climate change. Science, 2020, 369, .	6.0	98
56	Population genomics of the Viking world. Nature, 2020, 585, 390-396.	13.7	143
57	Hi-C chromosome conformation capture sequencing of avian genomes using the BGISEQ-500 platform. GigaScience, 2020, 9, .	3.3	6
58	DNA-Based Arthropod Diversity Assessment in Amazonian Iron Mine Lands Show Ecological Succession Towards Undisturbed Reference Sites. Frontiers in Ecology and Evolution, 2020, 8, .	1.1	5
59	Using in silico predicted ancestral genomes to improve the efficiency of paleogenome reconstruction. Ecology and Evolution, 2020, 10, 12700-12709.	0.8	4
60	The secrets of Sobek â€“ A crocodile mummy mitogenome from ancient Egypt. Journal of Archaeological Science: Reports, 2020, 33, 102483.	0.2	4
61	The evolutionary history of extinct and living lions. Proceedings of the National Academy of Sciences of the United States of America, 2020, 117, 10927-10934.	3.3	70
62	Darwinâ€™s Fancy Revised: An Updated Understanding of the Genomic Constitution of Pigeon Breeds. Genome Biology and Evolution, 2020, 12, 136-150.	1.1	13
63	The first complete mitochondrial genome data of Hippocampus kuda originating from Malaysia. Data in Brief, 2020, 31, 105721.	0.5	8
64	Beyond DNA barcoding: The unrealized potential of genome skim data in sample identification. Molecular Ecology, 2020, 29, 2521-2534.	2.0	58
65	Rapid loss of endogenous DNA in pig bone buried in five different environments. Archaeometry, 2020, 62, 827-846.	0.6	2
66	Recent mitochondrial lineage extinction in the critically endangered Javan rhinoceros. Zoological Journal of the Linnean Society, 2020, 190, 372-383.	1.0	13
67	DNA metabarcoding and spatial modelling link diet diversification with distribution homogeneity in European bats. Nature Communications, 2020, 11, 1154.	5.8	35
68	Arctic-adapted dogs emerged at the Pleistoceneâ€“Holocene transition. Science, 2020, 368, 1495-1499.	6.0	60
69	GC bias affects genomic and metagenomic reconstructions, underrepresenting GC-poor organisms. GigaScience, 2020, 9, .	3.3	91
70	Phylogeny of Neotropical Seirinae (Collembola, Entomobryidae) based on mitochondrial genomes. Zoologica Scripta, 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. GigaScience, 2020, 9, .	3.3	15
72	Bone biodeteriorationâ€”The effect of marine and terrestrial depositional environments on early diagenesis and bone bacterial community. PLoS ONE, 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. Genome Biology and Evolution, 2019, 11, 2244-2255.	1.1	12
74	Ancient pigs reveal a near-complete genomic turnover following their introduction to Europe. Proceedings of the National Academy of Sciences of the United States of America, 2019, 116, 17231-17238.	3.3	101
75	31Â° South: Dietary niche of an aridâ€zone endemic passerine. Environmental DNA, 2019, 1, 109-118.	3.1	5
76	31Â° South: The physiology of adaptation to arid conditions in a passerine bird. Molecular Ecology, 2019, 28, 3709-3721.	2.0	11
77	The discovery of Neotropical Lepidosira (Collembola, Entomobryidae) and its systematic position. Zoologica Scripta, 2019, 48, 783-800.	0.7	6
78	Ancient RNA from Late Pleistocene permafrost and historical canids shows tissue-specific transcriptome survival. PLoS Biology, 2019, 17, e3000166.	2.6	33
79	The Vertebrate TLR Supergene Family Evolved Dynamically by Gene Gain/Loss and Positive Selection Revealing a Hostâ€"Pathogen Arms Race in Birds. Diversity, 2019, 11, 131.	0.7	25
80	Early Pleistocene enamel proteome from Dmanisi resolves Stephanorhinus phylogeny. Nature, 2019, 574, 103-107.	13.7	135
81	High-coverage genomes to elucidate the evolution of penguins. GigaScience, 2019, 8, .	3.3	18
82	Resolving a clinical tuberculosis outbreak using palaeogenomic genome reconstruction methodologies. Tuberculosis, 2019, 119, 101865.	0.8	1
83	Killer whale genomes reveal a complex history of recurrent admixture and vicariance. Molecular Ecology, 2019, 28, 3427-3444.	2.0	46
84	Postglacial Colonization of Northern Coastal Habitat by Bottlenose Dolphins: A Marine Leading-Edge Expansion?. Journal of Heredity, 2019, 110, 662-674.	1.0	16
85	Large-scale ruminant genome sequencing provides insights into their evolution and distinct traits. Science, 2019, 364, .	6.0	266
86	Biological adaptations in the Arctic cervid, the reindeer (Rangifer tarandus). Science, 2019, 364, .	6.0	58
87	A simplified DNA extraction protocol for unsorted bulk arthropod samples that maintains exoskeletal integrity. Environmental DNA, 2019, 1, 144-154.	3.1	34
88	Palaeogenomic insights into the origins of French grapevine diversity. Nature Plants, 2019, 5, 595-603.	4.7	85
89	DNA metabarcodingâ€"Need for robust experimental designs to draw sound ecological conclusions. Molecular Ecology, 2019, 28, 1857-1862.	2.0	300
90	Taxonomic and Functional Characterization of the Microbial Community During Spontaneous in vitro Fermentation of Riesling Must. Frontiers in Microbiology, 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. Scientific Reports, 2019, 9, 4822.	1.6	40
92	A comparison of storage methods for gut microbiome studies in teleosts: Insights from rainbow trout (Oncorhynchus mykiss). Journal of Microbiological Methods, 2019, 160, 42-48.	0.7	10
93	DNA Extraction from Keratin and Chitin. Methods in Molecular Biology, 2019, 1963, 57-63.	0.4	7
94	A guide to the application of Hill numbers to DNAâ€based diversity analyses. Molecular Ecology Resources, 2019, 19, 804-817.	2.2	125
95	Skmer: assembly-free and alignment-free sample identification using genome skims. Genome Biology, 2019, 20, 34.	3.8	70
96	Mitogenomic evidence of close relationships between New Zealandâ€™s extinct giant raptors and small-sized Australian sister-taxa. Molecular Phylogenetics and Evolution, 2019, 134, 122-128.	1.2	17
97	Parallel adaptation of rabbit populations to myxoma virus. Science, 2019, 363, 1319-1326.	6.0	124
98	Specialized sledge dogs accompanied Inuit dispersal across the North American Arctic. Proceedings of the Royal Society B: Biological Sciences, 2019, 286, 20191929.	1.2	38
99	A 5700 year-old human genome and oral microbiome from chewed birch pitch. Nature Communications, 2019, 10, 5520.	5.8	61
100	Using metabarcoding to compare the suitability of two bloodâ€feeding leech species for sampling mammalian diversity in North Borneo. Molecular Ecology Resources, 2019, 19, 105-117.	2.2	31
101	Hostâ€derived population genomics data provides insights into bacterial and diatom composition of the killer whale skin. Molecular Ecology, 2019, 28, 484-502.	2.0	42
102	MobiSeq: De novo SNP discovery in model and nonâ€model species through sequencing the flanking region of transposable elements. Molecular Ecology Resources, 2019, 19, 512-525.	2.2	4
103	The Genomic Footprints of the Fall and Recovery of the Crested Ibis. Current Biology, 2019, 29, 340-349.e7.	1.8	94
104	Promises and pitfalls of using highâ€throughput sequencing for diet analysis. Molecular Ecology Resources, 2019, 19, 327-348.	2.2	138
105	Multi-omics and potential applications in wine production. Current Opinion in Biotechnology, 2019, 56, 172-178.	3.3	45
106	Ancient <scp>DNA</scp> reveals the timing and persistence of organellar genetic bottlenecks over 3,000Âyears of sunflower domestication and improvement. Evolutionary Applications, 2019, 12, 38-53.	1.5	27
107	Genetic affinities of an eradicated European Plasmodium falciparum strain. Microbial Genomics, 2019, 5, .	1.0	9
108	Demographic reconstruction from ancient DNA supports rapid extinction of the great auk. ELife, 2019, 8, .	2.8	15

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109	Ancient RNA. Population Genomics, 2018, , 53-74.	0.2	7
110	No longer locally extinct? Tracing the origins of a lion (Panthera leo) living in Gabon. Conservation Genetics, 2018, 19, 611-618.	0.8	11
111	Improved Genome Assembly and Annotation for the Rock Pigeon (Columba livia). G3: Genes, Genomes, Genetics, 2018, 8, 1391-1398.	0.8	62
112	Using <scp>DNA</scp> metabarcoding for simultaneous inference of common vampire bat diet and population structure. Molecular Ecology Resources, 2018, 18, 1050-1063.	2.2	70
113	Earth BioGenome Project: Sequencing life for the future of life. Proceedings of the National Academy of Sciences of the United States of America, 2018, 115, 4325-4333.	3.3	652
114	Scrutinizing key steps for reliable metabarcoding of environmental samples. Methods in Ecology and Evolution, 2018, 9, 134-147.	2.2	425
115	Hologenomic adaptations underlying the evolution of sanguivory in the common vampire bat. Nature Ecology and Evolution, 2018, 2, 659-668.	3.4	124
116	Applied Hologenomics: Feasibility and Potential in Aquaculture. Trends in Biotechnology, 2018, 36, 252-264.	4.9	51
117	Quantifying Temporal Genomic Erosion in Endangered Species. Trends in Ecology and Evolution, 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 <scp>DNA</scp> metabarcoding. Molecular Ecology, 2018, 27, 815-825.	2.0	110
119	Whole-Genome Sequencing of African Dogs Provides Insights into Adaptations against Tropical Parasites. Molecular Biology and Evolution, 2018, 35, 287-298.	3.5	41
120	Singleâ€tube library preparation for degraded <scp>DNA</scp>. Methods in Ecology and Evolution, 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. Annual Review of Animal Biosciences, 2018, 6, 23-46.	3.6	166
122	Identification of transcription factor genes involved in anthocyanin biosynthesis in carrot (Daucus) Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50	1.2	39
123	Population genomics of grey wolves and wolf-like canids in North America. PLoS Genetics, 2018, 14, e1007745.	1.5	54
124	Multiproxy evidence highlights a complex evolutionary legacy of maize in South America. Science, 2018, 362, 1309-1313.	6.0	172
125	Protective role of the vulture facial skin and gut microbiomes aid adaptation to scavenging. Acta Veterinaria Scandinavica, 2018, 60, 61.	0.5	40
126	Interspecific Gene Flow Shaped the Evolution of the Genus Canis. Current Biology, 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. Journal of Archaeological Science, 2018, 99, 47-54.	1.2	11
128	Testosterone in ancient hair from an extinct species. Palaeontology, 2018, 61, 797-802.	1.0	11
129	Ancient genomes from Iceland reveal the making of a human population. Science, 2018, 360, 1028-1032.	6.0	62
130	The evolutionary history of dogs in the Americas. Science, 2018, 361, 81-85.	6.0	140
131	Pan-genome Analysis of Ancient and Modern Salmonella enterica Demonstrates Genomic Stability of the Invasive Para C Lineage for Millennia. Current Biology, 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. Microbiome, 2018, 6, 82.	4.9	28
133	Recent Asian origin of chytrid fungi causing global amphibian declines. Science, 2018, 360, 621-627.	6.0	389
134	Greenland sled dogs at risk of extinction. Science, 2018, 360, 1080-1080.	6.0	8
135	Debugging diversity â€“ a panâ€continental exploration of the potential of terrestrial bloodâ€feeding leeches as a vertebrate monitoring tool. Molecular Ecology Resources, 2018, 18, 1282-1298.	2.2	45
136	Characterizing restriction enzymeâ€associated loci in historic ragweed (Ambrosia artemisiifolia) voucher specimens using customâ€designed <scp>RNA</scp> probes. Molecular Ecology Resources, 2017, 17, 209-220.	2.2	31
137	Eggshell palaeogenomics: Palaeognath evolutionary history revealed through ancient nuclear and mitochondrial DNA from Madagascan elephant bird (Aepyornis sp.) eggshell. Molecular Phylogenetics and Evolution, 2017, 109, 151-163.	1.2	65
138	Molecular clocks indicate turnover and diversification of modern coleoid cephalopods during the Mesozoic Marine Revolution. Proceedings of the Royal Society B: Biological Sciences, 2017, 284, 20162818.	1.2	86
139	Functional roles of Aves class-specific cis-regulatory elements on macroevolution of bird-specific features. Nature Communications, 2017, 8, 14229.	5.8	61
140	Connecting Earth observation to high-throughput biodiversity data. Nature Ecology and Evolution, 2017, 1, 176.	3.4	156
141	Leeches as a source of mammalian viral DNA and RNAâ€"a study in medicinal leeches. European Journal of Wildlife Research, 2017, 63, 1.	0.7	9
142	Genome-wide Ancestry and Demographic History of African-Descendant Maroon Communities from French Guiana and Suriname. American Journal of Human Genetics, 2017, 101, 725-736.	2.6	50
143	Evolutionary History of Saber-Toothed Cats Based on Ancient Mitogenomics. Current Biology, 2017, 27, 3330-3336.e5.	1.8	45
144	An expanded mammal mitogenome dataset from Southeast Asia. GigaScience, 2017, 6, 1-8.	3.3	27

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145	Documenting DNA in the dust. Molecular Ecology, 2017, 26, 969-971.	2.0	5
146	Natural selection shaped the rise and fall of passenger pigeon genomic diversity. Science, 2017, 358, 951-954.	6.0	105
147	The wolf reference genome sequence (Canis lupus lupus) and its implications for Canis spp. population genomics. BMC Genomics, 2017, 18, 495.	1.2	73
148	Comparative performance of the BGISEQ-500 vs Illumina HiSeq2500 sequencing platforms for palaeogenomic sequencing. GigaScience, 2017, 6, 1-13.	3.3	137
149	Relative performance of two DNA extraction and library preparation methods on archaeological human teeth samples. Science and Technology of Archaeological Research, 2017, 3, 80-88.	2.4	6
150	An â€›Aukwardâ€™ Tale: A Genetic Approach to Discover the Whereabouts of the Last Great Auks. Genes, 2017, 8, 164.	1.0	11
151	The population genomic basis of geographic differentiation in <scp>N</scp>orth <scp>A</scp>merican common ragweed (<scp>A</scp>mbrosia artemisiifolia <scp>L</scp>.). Ecology and Evolution, 2016, 6, 3760-3771.	0.8	35
152	Bone-associated gene evolution and the origin of flight in birds. BMC Genomics, 2016, 17, 371.	1.2	12
153	Complete mitochondrial genomes of living and extinct pigeons revise the timing of the columbiform radiation. BMC Evolutionary Biology, 2016, 16, 230.	3.2	38
154	Genomic population structure of freshwaterâ€resident and anadromous ide (Leuciscus idus) in northâ€western Europe. Ecology and Evolution, 2016, 6, 1064-1074.	0.8	20
155	Mitochondrial DNA from the eradicated European Plasmodium vivax and P. falciparum from 70-year-old slides from the Ebro Delta in Spain. Proceedings of the National Academy of Sciences of the United States of America, 2016, 113, 11495-11500.	3.3	41
156	Do Vertebrate Gut Metagenomes Confer Rapid Ecological Adaptation?. Trends in Ecology and Evolution, 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. Current Biology, 2016, 26, 3195-3201.	1.8	130
158	Genome-culture coevolution promotes rapid divergence of killer whale ecotypes. Nature Communications, 2016, 7, 11693.	5.8	222
159	The potential and pitfalls of deâ€extinction. Zoologica Scripta, 2016, 45, 22-36.	0.7	25
160	DAMe: a toolkit for the initial processing of datasets with PCR replicates of double-tagged amplicons for DNA metabarcoding analyses. BMC Research Notes, 2016, 9, 255.	0.6	45
161	The limits and potential of paleogenomic techniques for reconstructing grapevine domestication. Journal of Archaeological Science, 2016, 72, 57-70.	1.2	43
162	Whole-Genome Identification, Phylogeny, and Evolution of the Cytochrome P450 Family 2 (CYP2) Subfamilies in Birds. Genome Biology and Evolution, 2016, 8, 1115-1131.	1.1	20

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163	Genomic Characterization of a South AmericanPhytophthoraHybrid Mandates Reassessment of the Geographic Origins ofPhytophthora infestans. Molecular Biology and Evolution, 2016, 33, 478-491.	3.5	48
164	Mitogenomics of the Extinct Cave Lion, Panthera spelaea (Goldfuss, 1810), Resolve its Position within the Panthera Cats. Open Quaternary, 2016, 2, .	0.5	27
165	The Draft Genome of Extinct European Aurochs and its Implications for De-Extinction. Open Quaternary, 2016, 2, .	0.5	12
166	Further evidence of Chelonid herpesvirus 5 (ChHV5) latency: high levels of ChHV5 DNA detected in clinically healthy marine turtles. PeerJ, 2016, 4, e2274.	0.9	27
167	The origin and evolution of maize in the Southwestern United States. Nature Plants, 2015, 1, 14003.	4.7	138
168	Gene loss, adaptive evolution and the co-evolution of plumage coloration genes with opsins in birds. BMC Genomics, 2015, 16, 751.	1.2	58
169	iDNA from terrestrial haematophagous leeches as a wildlife surveying and monitoring tool â€“ prospects, pitfalls and avenues to be developed. Frontiers in Zoology, 2015, 12, 24.	0.9	89
170	Comparative performance of two wholeâ€genome capture methodologies on ancient <scp>DNA</scp> Illumina libraries. Methods in Ecology and Evolution, 2015, 6, 725-734.	2.2	43
171	Contrasting populationâ€level responses to Pleistocene climatic oscillations in anÂalpine bat revealed by complete mitochondrial genomes and evolutionary history inference. Journal of Biogeography, 2015, 42, 1689-1700.	1.4	23
172	Geographic and temporal dynamics of a global radiation and diversification in the killer whale. Molecular Ecology, 2015, 24, 3964-3979.	2.0	74
173	New insights on single-stranded versus double-stranded DNA library preparation for ancient DNA. BioTechniques, 2015, 59, 368-371.	0.8	43
174	Bird sequencing project takes off. Nature, 2015, 522, 34-34.	13.7	136
175	Reconstructing ancient genomes and epigenomes. Nature Reviews Genetics, 2015, 16, 395-408.	7.7	197
176	Genome-wide ancestry of 17th-century enslaved Africans from the Caribbean. Proceedings of the National Academy of Sciences of the United States of America, 2015, 112, 3669-3673.	3.3	110
177	A refined model of the genomic basis for phenotypic variation in vertebrate hemostasis. BMC Evolutionary Biology, 2015, 15, 124.	3.2	16
178	Convergent evolution of the genomes of marine mammals. Nature Genetics, 2015, 47, 272-275.	9.4	392
179	Ancient genomics. Philosophical Transactions of the Royal Society B: Biological Sciences, 2015, 370, 20130387.	1.8	142
180	Penile density and globally used chemicals in Canadian and Greenland polar bears. Environmental Research, 2015, 137, 287-291.	3.7	34

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181	Environmental genes and genomes: understanding the differences and challenges in the approaches and software for their analyses. Briefings in Bioinformatics, 2015, 16, 745-758.	3.2	66
182	The Genome 10K Project: A Way Forward. Annual Review of Animal Biosciences, 2015, 3, 57-111.	3.6	294
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