

M Thomas P Gilbert

List of Publications by Year in Descending Order

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

407
papers

31,273
citations

96
h-index

165
g-index

444
ext. papers

39,301
ext. citations

10.6
avg, IF

6.89
L-index

#	Paper	IF	Citations
407	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,	11.5	15
406	The era of reference genomes in conservation genomics.. <i>Trends in Ecology and Evolution</i> , 2022 ,	10.9	8
405	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	16.6	2
404	Ancient and historical DNA in conservation policy.. <i>Trends in Ecology and Evolution</i> , 2022 ,	10.9	3
403	Probing the genomic limits of de-extinction in the Christmas Island rat.. <i>Current Biology</i> , 2022 ,	6.3	1
402	The Australian dingo is an early offshoot of modern breed dogs.. <i>Science Advances</i> , 2022 , 8, eabm5944	14.3	2
401	Archival influenza virus genomes from Europe reveal genomic variability during the 1918 pandemic.. <i>Nature Communications</i> , 2022 , 13, 2314	17.4	2
400	The genome sequence of the grey wolf, Linnaeus 1758.. <i>Wellcome Open Research</i> , 2021 , 6, 310	4.8	2
399	Evolutionary history of the extinct Sardinian dhole. <i>Current Biology</i> , 2021 ,	6.3	2
398	Kouprey () genomes unveil polytomic origin of wild Asian. <i>IScience</i> , 2021 , 24, 103226	6.1	0
397	The role of the gut microbiota in the dietary niche expansion of fishing bats. <i>Animal Microbiome</i> , 2021 , 3, 76	4.1	1
396	A towering genome: Experimentally validated adaptations to high blood pressure and extreme stature in the giraffe. <i>Science Advances</i> , 2021 , 7,	14.3	10
395	Salmon gut microbiota correlates with disease infection status: potential for monitoring health in farmed animals. <i>Animal Microbiome</i> , 2021 , 3, 30	4.1	14
394	Towards complete and error-free genome assemblies of all vertebrate species. <i>Nature</i> , 2021 , 592, 737-746	46.4	161
393	Genomic insights into the conservation status of the world's last remaining Sumatran rhinoceros populations. <i>Nature Communications</i> , 2021 , 12, 2393	17.4	10
392	Ancient and modern stickleback genomes reveal the demographic constraints on adaptation. <i>Current Biology</i> , 2021 , 31, 2027-2036.e8	6.3	5
391	Genome-resolved metagenomics suggests a mutualistic relationship between <i>Mycoplasma</i> and salmonid hosts. <i>Communications Biology</i> , 2021 , 4, 579	6.7	12

390	The genomic origin of Zana of Abkhazia. <i>Genetics & Genomics Next</i> , 2021 , 2, e10051	1.2	
389	A genomic exploration of the early evolution of extant cats and their sabre-toothed relatives [version 2; peer review: 2 approved].. <i>Open Research Europe</i> , 2021 , 1, 25		
388	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	2.4	1
387	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	5.7	5
386	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,	11.5	1
385	Leech blood-meal invertebrate-derived DNA reveals differences in Bornean mammal diversity across habitats. <i>Molecular Ecology</i> , 2021 , 30, 3299-3312	5.7	3
384	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	2.6	8
383	Genomes of Pleistocene Siberian Wolves Uncover Multiple Extinct Wolf Lineages. <i>Current Biology</i> , 2021 , 31, 198-206.e8	6.3	7
382	Mitochondrial genomes of Danish vertebrate species generated for the national DNA reference database, DNAMark. <i>Environmental DNA</i> , 2021 , 3, 472-480	7.6	8
381	eDNA-based biomonitoring at an experimental German vineyard to characterize how management regimes shape ecosystem diversity. <i>Environmental DNA</i> , 2021 , 3, 70-82	7.6	3
380	Dire wolves were the last of an ancient New World canid lineage. <i>Nature</i> , 2021 , 591, 87-91	50.4	18
379	Extended survival of Pleistocene Siberian wolves into the early 20th century on the island of Honshu. <i>Science</i> , 2021 , 24, 101904	6.1	3
378	Molecular parallelisms between pigmentation in the avian iris and the integument of ectothermic vertebrates. <i>PLoS Genetics</i> , 2021 , 17, e1009404	6	5
377	Non-invasive surveys of mammalian viruses using environmental DNA. <i>Methods in Ecology and Evolution</i> , 2021 , 12, 1941	7.7	2
376	Runs of homozygosity in killer whale genomes provide a global record of demographic histories. <i>Molecular Ecology</i> , 2021 , 30, 6162-6177	5.7	6
375	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,	11.5	4
374	Ancient and modern genomes unravel the evolutionary history of the rhinoceros family. <i>Cell</i> , 2021 , 184, 4874-4885.e16	56.2	6
373	Gut Microbiota Linked with Reduced Fear of Humans in Red Junglefowl Has Implications for Early Domestication. <i>Genetics & Genomics Next</i> , 2021 , 2, 2100018	1.2	1

372	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,	3.7	1
371	Using in silico predicted ancestral genomes to improve the efficiency of paleogenome reconstruction. <i>Ecology and Evolution</i> , 2020 , 10, 12700-12709	2.8	2
370	The secrets of Sobek I A crocodile mummy mitogenome from ancient Egypt. <i>Journal of Archaeological Science: Reports</i> , 2020 , 33, 102483	0.7	1
369	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	11.5	31
368	Darwin's Fancy Revised: An Updated Understanding of the Genomic Constitution of Pigeon Breeds. <i>Genome Biology and Evolution</i> , 2020 , 12, 136-150	3.9	5
367	The first complete mitochondrial genome data of originating from Malaysia. <i>Data in Brief</i> , 2020 , 31, 105721	1.2	7
366	Rapid loss of endogenous DNA in pig bone buried in five different environments. <i>Archaeometry</i> , 2020 , 62, 827-846	1.6	0
365	Recent mitochondrial lineage extinction in the critically endangered Javan rhinoceros. <i>Zoological Journal of the Linnean Society</i> , 2020 , 190, 372-383	2.4	4
364	DNA metabarcoding and spatial modelling link diet diversification with distribution homogeneity in European bats. <i>Nature Communications</i> , 2020 , 11, 1154	17.4	11
363	Arctic-adapted dogs emerged at the Pleistocene-Holocene transition. <i>Science</i> , 2020 , 368, 1495-1499	33.3	28
362	GC bias affects genomic and metagenomic reconstructions, underrepresenting GC-poor organisms. <i>GigaScience</i> , 2020 , 9,	7.6	35
361	Phylogeny of Neotropical Seirinae (Collembola, Entomobryidae) based on mitochondrial genomes. <i>Zoologica Scripta</i> , 2020 , 49, 329-339	2.5	5
360	Bone biodeterioration-The effect of marine and terrestrial depositional environments on early diagenesis and bone bacterial community. <i>PLoS ONE</i> , 2020 , 15, e0240512	3.7	5
359	Adaptive venom evolution and toxicity in octopods is driven by extensive novel gene formation, expansion, and loss. <i>GigaScience</i> , 2020 , 9,	7.6	4
358	Plasmodium vivax Malaria Viewed through the Lens of an Eradicated European Strain. <i>Molecular Biology and Evolution</i> , 2020 , 37, 773-785	8.3	21
357	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	3.9	19
356	Ancient DNA suggests modern wolves trace their origin to a Late Pleistocene expansion from Beringia. <i>Molecular Ecology</i> , 2020 , 29, 1596-1610	5.7	33
355	Evolutionary History, Genomic Adaptation to Toxic Diet, and Extinction of the Carolina Parakeet. <i>Current Biology</i> , 2020 , 30, 108-114.e5	6.3	16

354	Genomic Adaptations and Evolutionary History of the Extinct Scimitar-Toothed Cat, <i>Homotherium latidens</i> . <i>Current Biology</i> , 2020 , 30, 5018-5025.e5	6.3	18
353	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	1.2	1
352	Dense sampling of bird diversity increases power of comparative genomics. <i>Nature</i> , 2020 , 587, 252-257	50.4	89
351	Holo-Omics: Integrated Host-Microbiota Multi-omics for Basic and Applied Biological Research. <i>iScience</i> , 2020 , 23, 101414	6.1	27
350	Pre-extinction Demographic Stability and Genomic Signatures of Adaptation in the Woolly Rhinoceros. <i>Current Biology</i> , 2020 , 30, 3871-3879.e7	6.3	16
349	Molecular identification and phylogenetic analysis of a complete mitogenome from Peninsular Malaysia. <i>Mitochondrial DNA Part B: Resources</i> , 2020 , 5, 3004-3006	0.5	2
348	Multi-omic detection of in archaeological human dental calculus. <i>Philosophical Transactions of the Royal Society B: Biological Sciences</i> , 2020 , 375, 20190584	5.8	13
347	Using paleo-archives to safeguard biodiversity under climate change. <i>Science</i> , 2020 , 369,	33.3	34
346	Population genomics of the Viking world. <i>Nature</i> , 2020 , 585, 390-396	50.4	35
345	Hi-C chromosome conformation capture sequencing of avian genomes using the BGISEQ-500 platform. <i>GigaScience</i> , 2020 , 9,	7.6	2
344	Ancient microRNA profiles of a 14,300-year-old canid samples confirm taxonomic origin and give glimpses into tissue-specific gene regulation from the Pleistocene. <i>Rna</i> , 2020 ,	5.8	2
343	Early Pleistocene enamel proteome from Dmanisi resolves <i>Stephanorhinus</i> phylogeny. <i>Nature</i> , 2019 , 574, 103-107	50.4	70
342	High-coverage genomes to elucidate the evolution of penguins. <i>GigaScience</i> , 2019 , 8,	7.6	6
341	Resolving a clinical tuberculosis outbreak using palaeogenomic genome reconstruction methodologies. <i>Tuberculosis</i> , 2019 , 119, 101865	2.6	0
340	Killer whale genomes reveal a complex history of recurrent admixture and vicariance. <i>Molecular Ecology</i> , 2019 , 28, 3427-3444	5.7	25
339	Postglacial Colonization of Northern Coastal Habitat by Bottlenose Dolphins: A Marine Leading-Edge Expansion?. <i>Journal of Heredity</i> , 2019 , 110, 662-674	2.4	8
338	Large-scale ruminant genome sequencing provides insights into their evolution and distinct traits. <i>Science</i> , 2019 , 364,	33.3	120
337	Biological adaptations in the Arctic cervid, the reindeer (). <i>Science</i> , 2019 , 364,	33.3	22

336	A simplified DNA extraction protocol for unsorted bulk arthropod samples that maintains exoskeletal integrity. <i>Environmental DNA</i> , 2019 , 1, 144-154	7.6	20
335	Palaeogenomic insights into the origins of French grapevine diversity. <i>Nature Plants</i> , 2019 , 5, 595-603	11.5	54
334	Taxonomic and Functional Characterization of the Microbial Community During Spontaneous Fermentation of Riesling Must. <i>Frontiers in Microbiology</i> , 2019 , 10, 697	5.7	18
333	Diabetic cats have decreased gut microbial diversity and a lack of butyrate producing bacteria. <i>Scientific Reports</i> , 2019 , 9, 4822	4.9	26
332	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	2.8	3
331	DNA Extraction from Keratin and Chitin. <i>Methods in Molecular Biology</i> , 2019 , 1963, 57-63	1.4	3
330	A guide to the application of Hill numbers to DNA-based diversity analyses. <i>Molecular Ecology Resources</i> , 2019 , 19, 804-817	8.4	51
329	Skmer: assembly-free and alignment-free sample identification using genome skims. <i>Genome Biology</i> , 2019 , 20, 34	18.3	37
328	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	4.1	7
327	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	3.9	6
326	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 ^{11.5}	42	
325	31°South: Dietary niche of an arid-zone endemic passerine. <i>Environmental DNA</i> , 2019 , 1, 109-118	7.6	1
324	31°South: The physiology of adaptation to arid conditions in a passerine bird. <i>Molecular Ecology</i> , 2019 , 28, 3709-3721	5.7	6
323	The discovery of Neotropical <i>Lepidosira</i> (Collembola, Entomobryidae) and its systematic position. <i>Zoologica Scripta</i> , 2019 , 48, 783-800	2.5	3
322	Ancient RNA from Late Pleistocene permafrost and historical canids shows tissue-specific transcriptome survival. <i>PLoS Biology</i> , 2019 , 17, e3000166	9.7	17
321	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	2.5	9
320	Demographic reconstruction from ancient DNA supports rapid extinction of the great auk. <i>ELife</i> , 2019 , 8,	8.9	6
319	Genetic affinities of an eradicated European strain. <i>Microbial Genomics</i> , 2019 , 5,	4.4	5

318	Parallel adaptation of rabbit populations to myxoma virus. <i>Science</i> , 2019 , 363, 1319-1326	33.3	66
317	Specialized sledge dogs accompanied Inuit dispersal across the North American Arctic. <i>Proceedings of the Royal Society B: Biological Sciences</i> , 2019 , 286, 20191929	4.4	19
316	A 5700 year-old human genome and oral microbiome from chewed birch pitch. <i>Nature Communications</i> , 2019 , 10, 5520	17.4	31
315	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	8.4	24
314	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	5.7	26
313	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	8.4	2
312	The Genomic Footprints of the Fall and Recovery of the Crested Ibis. <i>Current Biology</i> , 2019 , 29, 340-349. 673	6.3	42
311	Promises and pitfalls of using high-throughput sequencing for diet analysis. <i>Molecular Ecology Resources</i> , 2019 , 19, 327-348	8.4	77
310	Multi-omics and potential applications in wine production. <i>Current Opinion in Biotechnology</i> , 2019 , 56, 172-178	11.4	27
309	Ancient 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	4.8	19
308	Ancient RNA. <i>Population Genomics</i> , 2018 , 53-74	1.4	4
307	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	2.6	7
306	Improved Genome Assembly and Annotation for the Rock Pigeon (<i>Columba rockii</i>). <i>G3: Genes, Genomes, Genetics</i> , 2018 , 8, 1391-1398	3.2	34
305	Using DNA metabarcoding for simultaneous inference of common vampire bat diet and population structure. <i>Molecular Ecology Resources</i> , 2018 , 18, 1050	8.4	42
304	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	11.5	334
303	Scrutinizing key steps for reliable metabarcoding of environmental samples. <i>Methods in Ecology and Evolution</i> , 2018 , 9, 134-147	7.7	246
302	Hologenomic adaptations underlying the evolution of sanguivory in the common vampire bat. <i>Nature Ecology and Evolution</i> , 2018 , 2, 659-668	12.3	64
301	Applied Hologenomics: Feasibility and Potential in Aquaculture. <i>Trends in Biotechnology</i> , 2018 , 36, 252-264. 4.1	4.1	25

300	Quantifying Temporal Genomic Erosion in Endangered Species. <i>Trends in Ecology and Evolution</i> , 2018 , 33, 176-185	10.9	66
299	Agriculture shapes the trophic niche of a bat preying on multiple pest arthropods across Europe: Evidence from DNA metabarcoding. <i>Molecular Ecology</i> , 2018 , 27, 815-825	5.7	62
298	Whole-Genome Sequencing of African Dogs Provides Insights into Adaptations against Tropical Parasites. <i>Molecular Biology and Evolution</i> , 2018 , 35, 287-298	8.3	24
297	Single-tube library preparation for degraded DNA. <i>Methods in Ecology and Evolution</i> , 2018 , 9, 410-419	7.7	122
296	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	6.3	44
295	Mind the gut: genomic insights to population divergence and gut microbial composition of two marine keystone species. <i>Microbiome</i> , 2018 , 6, 82	16.6	16
294	Recent Asian origin of chytrid fungi causing global amphibian declines. <i>Science</i> , 2018 , 360, 621-627	33.3	229
293	Greenland sled dogs at risk of extinction. <i>Science</i> , 2018 , 360, 1080	33.3	4
292	Debugging diversity - a pan-continental exploration of the potential of terrestrial blood-feeding leeches as a vertebrate monitoring tool. <i>Molecular Ecology Resources</i> , 2018 , 18, 1282-1298	8.4	35
291	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	13.7	88
290	Identification of transcription factor genes involved in anthocyanin biosynthesis in carrot (<i>Daucus carota</i> L.) using RNA-Seq. <i>BMC Genomics</i> , 2018 , 19, 811	4.5	23
289	Population genomics of grey wolves and wolf-like canids in North America. <i>PLoS Genetics</i> , 2018 , 14, e1007745	26	
288	Multiproxy evidence highlights a complex evolutionary legacy of maize in South America. <i>Science</i> , 2018 , 362, 1309-1313	33.3	97
287	Protective role of the vulture facial skin and gut microbiomes aid adaptation to scavenging. <i>Acta Veterinaria Scandinavica</i> , 2018 , 60, 61	2	21
286	Interspecific Gene Flow Shaped the Evolution of the Genus <i>Canis</i> . <i>Current Biology</i> , 2018 , 28, 3441-3449.e6.3	58	
285	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	2.9	6
284	Testosterone in ancient hair from an extinct species. <i>Palaeontology</i> , 2018 , 61, 797-802	2.9	7
283	Ancient genomes from Iceland reveal the making of a human population. <i>Science</i> , 2018 , 360, 1028-1032	33.3	37

282	The evolutionary history of dogs in the Americas. <i>Science</i> , 2018 , 361, 81-85	33.3	73
281	Characterizing restriction enzyme-associated loci in historic ragweed (<i>Ambrosia artemisiifolia</i>) voucher specimens using custom-designed RNA probes. <i>Molecular Ecology Resources</i> , 2017 , 17, 209-220	8.4	14
280	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	4.1	42
279	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,	4.4	56
278	Functional roles of Aves class-specific cis-regulatory elements on macroevolution of bird-specific features. <i>Nature Communications</i> , 2017 , 8, 14229	17.4	44
277	Connecting Earth observation to high-throughput biodiversity data. <i>Nature Ecology and Evolution</i> , 2017 , 1, 176	12.3	117
276	Leeches as a source of mammalian viral DNA and RNA \bar{B} study in medicinal leeches. <i>European Journal of Wildlife Research</i> , 2017 , 63, 1	2	9
275	Genome-wide Ancestry and Demographic History of African-Descendant Maroon Communities from French Guiana and Suriname. <i>American Journal of Human Genetics</i> , 2017 , 101, 725-736	11	29
274	Evolutionary History of Saber-Toothed Cats Based on Ancient Mitogenomics. <i>Current Biology</i> , 2017 , 27, 3330-3336.e5	6.3	29
273	An expanded mammal mitogenome dataset from Southeast Asia. <i>GigaScience</i> , 2017 , 6, 1-8	7.6	20
272	Natural selection shaped the rise and fall of passenger pigeon genomic diversity. <i>Science</i> , 2017 , 358, 951-954	33.3	68
271	The wolf reference genome sequence (<i>Canis lupus lupus</i>) and its implications for <i>Canis</i> spp. population genomics. <i>BMC Genomics</i> , 2017 , 18, 495	4.5	49
270	Comparative performance of the BGISEQ-500 vs Illumina HiSeq2500 sequencing platforms for palaeogenomic sequencing. <i>GigaScience</i> , 2017 , 6, 1-13	7.6	88
269	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	1.2	3
268	An 'Aukward' Tale: A Genetic Approach to Discover the Whereabouts of the Last Great Auks. <i>Genes</i> , 2017 , 8,	4.2	4
267	Do Vertebrate Gut Metagenomes Confer Rapid Ecological Adaptation?. <i>Trends in Ecology and Evolution</i> , 2016 , 31, 689-699	10.9	122
266	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	6.3	95
265	Genome-culture coevolution promotes rapid divergence of killer whale ecotypes. <i>Nature Communications</i> , 2016 , 7, 11693	17.4	161

264	The potential and pitfalls of de-extinction. <i>Zoologica Scripta</i> , 2016 , 45, 22-36	2.5	22
263	DAME: a toolkit for the initial processing of datasets with PCR replicates of double-tagged amplicons for DNA metabarcoding analyses. <i>BMC Research Notes</i> , 2016 , 9, 255	2.3	36
262	The limits and potential of paleogenomic techniques for reconstructing grapevine domestication. <i>Journal of Archaeological Science</i> , 2016 , 72, 57-70	2.9	31
261	Whole-Genome Identification, Phylogeny, and Evolution of the Cytochrome P450 Family 2 (CYP2) Subfamilies in Birds. <i>Genome Biology and Evolution</i> , 2016 , 8, 1115-31	3.9	15
260	Genomic Characterization of a South American Phytophthora Hybrid Mandates Reassessment of the Geographic Origins of Phytophthora infestans. <i>Molecular Biology and Evolution</i> , 2016 , 33, 478-91	8.3	33
259	Mitogenomics of the Extinct Cave Lion, Panthera spelaea (Goldfuss, 1810), Resolve its Position within the Panthera Cats. <i>Open Quaternary</i> , 2016 , 2,	1.1	15
258	The Draft Genome of Extinct European Aurochs and its Implications for De-Extinction. <i>Open Quaternary</i> , 2016 , 2,	1.1	6
257	Further evidence of Chelonid herpesvirus 5 (ChHV5) latency: high levels of ChHV5 DNA detected in clinically healthy marine turtles. <i>PeerJ</i> , 2016 , 4, e2274	3.1	19
256	The population genomic basis of geographic differentiation in North American common ragweed (L.). <i>Ecology and Evolution</i> , 2016 , 6, 3760-3771	2.8	17
255	Bone-associated gene evolution and the origin of flight in birds. <i>BMC Genomics</i> , 2016 , 17, 371	4.5	5
254	Complete mitochondrial genomes of living and extinct pigeons revise the timing of the columbiform radiation. <i>BMC Evolutionary Biology</i> , 2016 , 16, 230	3	25
253	Genomic population structure of freshwater-resident and anadromous ide (Leuciscus idus) in north-western Europe. <i>Ecology and Evolution</i> , 2016 , 6, 1064-74	2.8	14
252	Mitochondrial DNA from the eradicated European Plasmodium vivax and P. falciparum 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	11.5	31
251	Environmental genes and genomes: understanding the differences and challenges in the approaches and software for their analyses. <i>Briefings in Bioinformatics</i> , 2015 , 16, 745-58	13.4	44
250	The Genome 10K Project: a way forward. <i>Annual Review of Animal Biosciences</i> , 2015 , 3, 57-111	13.7	223
249	Avianbase: a community resource for bird genomics. <i>Genome Biology</i> , 2015 , 16, 21	18.3	22
248	Olfactory Receptor Subgenomes Linked with Broad Ecological Adaptations in Sauropsida. <i>Molecular Biology and Evolution</i> , 2015 , 32, 2832-43	8.3	47
247	Tag jumps illuminated--reducing sequence-to-sample misidentifications in metabarcoding studies. <i>Molecular Ecology Resources</i> , 2015 , 15, 1289-303	8.4	280

246	Response to Comment on "Whole-genome analyses resolve early branches in the tree of life of modern birds". <i>Science</i> , 2015 , 349, 1460	33.3	37
245	Viral meningitis epidemics and a single, recent, recombinant and anthroponotic origin of swine vesicular disease virus. <i>Evolution, Medicine and Public Health</i> , 2015 , 2015, 289-303	3	10
244	Odintifier--A computational method for identifying insertions of organellar origin from modern and ancient high-throughput sequencing data based on haplotype phasing. <i>BMC Bioinformatics</i> , 2015 , 16, 232	3.6	5
243	A Common Genetic Origin for Early Farmers from Mediterranean Cardial and Central European LBK Cultures. <i>Molecular Biology and Evolution</i> , 2015 , 32, 3132-42	8.3	120
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14	Non-invasive surveys of mammalian viruses using environmental DNA		3
13	Runs of homozygosity in killer whale genomes provide a global record of demographic histories		4

12	Historical population declines prompted significant genomic erosion in the northern and southern white rhinoceros (<i>Ceratotherium simum</i>)	1
11	Towards complete and error-free genome assemblies of all vertebrate species	38
10	Rapid discovery of novel prophages using biological feature engineering and machine learning	2
9	Assembly-free and alignment-free sample identification using genome skims	1
8	Modern wolves trace their origin to a late Pleistocene expansion from Beringia	2
7	Early Pleistocene enamel proteome sequences from Dmanisi resolve <i>Stephanorhinus</i> phylogeny	5
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