M Thomas P Gilbert

List of Publications by Citations

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	Whole-genome analyses resolve early branches in the tree of life of modern birds. *Science*, **2014**, 346, 1320-31	33.3	1182
406	Monitoring endangered freshwater biodiversity using environmental DNA. *Molecular Ecology*, **2012**, 21, 2565-73	5.7	669
405	Comparative genomics reveals insights into avian genome evolution and adaptation. *Science*, **2014**, 346, 1311-20	33.3	628
404	Environmental DNA for wildlife biology and biodiversity monitoring. *Trends in Ecology and Evolution* , **2014**, 29, 358-67	10.9	623
403	Ancient human genome sequence of an extinct Palaeo-Eskimo. *Nature*, **2010**, 463, 757-62	50.4	567
402	Recalibrating Equus evolution using the genome sequence of an early Middle Pleistocene horse. *Nature*, **2013**, 499, 74-8	50.4	563
401	An Aboriginal Australian genome reveals separate human dispersals into Asia. *Science*, **2011**, 334, 94-8	33.3	528
400	Rise and fall of the Beringian steppe bison. *Science*, **2004**, 306, 1561-5	33.3	518
399	Species-specific responses of Late Quaternary megafauna to climate and humans. *Nature*, **2011**, 479, 359-64	50.4	483
398	Assessing ancient DNA studies. *Trends in Ecology and Evolution*, **2005**, 20, 541-4	10.9	442
397	Diverse plant and animal genetic records from Holocene and Pleistocene sediments. *Science*, **2003**, 300, 791-5	33.3	424
396	Genetic evidence for local retention of pelagic larvae in a Caribbean reef fish. *Science*, **2003**, 299, 107-9	33.3	422
395	Current perspectives and the future of domestication studies. *Proceedings of the National Academy of Sciences of the United States of America*, **2014**, 111, 6139-46	11.5	414
394	Origins and genetic legacy of Neolithic farmers and hunter-gatherers in Europe. *Science*, **2012**, 336, 466-9	33.3	410
393	The use of coded PCR primers enables high-throughput sequencing of multiple homolog amplification products by 454 parallel sequencing. *PLoS ONE*, **2007**, 2, e197	3.7	402
392	Direct evidence of extensive diversity of HIV-1 in Kinshasa by 1960. *Nature*, **2008**, 455, 661-4	50.4	379
391	Pathogens and host immunity in the ancient human oral cavity. *Nature Genetics*, **2014**, 46, 336-44	36.3	353

390	Fifty thousand years of Arctic vegetation and megafaunal diet. *Nature*, **2014**, 506, 47-51	50.4	351
389	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	11.5	334
388	The half-life of DNA in bone: measuring decay kinetics in 158 dated fossils. *Proceedings of the Royal Society B: Biological Sciences*, **2012**, 279, 4724-33	4.4	331
387	Ancient biomolecules from deep ice cores reveal a forested southern Greenland. *Science*, **2007**, 317, 111-4	33.3	319
386	Convergent transcriptional specializations in the brains of humans and song-learning birds. *Science*, **2014**, 346, 1256846	33.3	283
385	Tag jumps illuminated--reducing sequence-to-sample misidentifications in metabarcoding studies. *Molecular Ecology Resources*, **2015**, 15, 1289-303	8.4	280
384	Complete mitochondrial genome phylogeographic analysis of killer whales (Orcinus orca) indicates multiple species. *Genome Research*, **2010**, 20, 908-16	9.7	274
383	The isolation of nucleic acids from fixed, paraffin-embedded tissues-which methods are useful when?. *PLoS ONE*, **2007**, 2, e537	3.7	274
382	Convergent evolution of the genomes of marine mammals. *Nature Genetics*, **2015**, 47, 272-5	36.3	263
381	Scrutinizing key steps for reliable metabarcoding of environmental samples. *Methods in Ecology and Evolution*, **2018**, 9, 134-147	7.7	246
380	Most of the extant mtDNA boundaries in south and southwest Asia were likely shaped during the initial settlement of Eurasia by anatomically modern humans. *BMC Genetics*, **2004**, 5, 26	2.6	244
379	Glacial survival of boreal trees in northern Scandinavia. *Science*, **2012**, 335, 1083-6	33.3	239
378	Recent Asian origin of chytrid fungi causing global amphibian declines. *Science*, **2018**, 360, 621-627	33.3	229
377	DNA from pre-Clovis human coprolites in Oregon, North America. *Science*, **2008**, 320, 786-9	33.3	225
376	Early allelic selection in maize as revealed by ancient DNA. *Science*, **2003**, 302, 1206-8	33.3	224
375	The Genome 10K Project: a way forward. *Annual Review of Animal Biosciences*, **2015**, 3, 57-111	13.7	223
374	Pulling out the 1%: whole-genome capture for the targeted enrichment of ancient DNA sequencing libraries. *American Journal of Human Genetics*, **2013**, 93, 852-64	11	221
373	The emergence of HIV/AIDS in the Americas and beyond. *Proceedings of the National Academy of Sciences of the United States of America*, **2007**, 104, 18566-70	11.5	219

372	Investigating the potential use of environmental DNA (eDNA) for genetic monitoring of marine mammals. *PLoS ONE*, **2012**, 7, e41781	3.7	218
371	mapDamage: testing for damage patterns in ancient DNA sequences. *Bioinformatics*, **2011**, 27, 2153-5	7.2	209
370	The genetic prehistory of the New World Arctic. *Science*, **2014**, 345, 1255832	33.3	204
369	Ancient bacteria show evidence of DNA repair. *Proceedings of the National Academy of Sciences of the United States of America*, **2007**, 104, 14401-5	11.5	204
368	Prehistoric genomes reveal the genetic foundation and cost of horse domestication. *Proceedings of the National Academy of Sciences of the United States of America*, **2014**, 111, E5661-9	11.5	197
367	Characterization of genetic miscoding lesions caused by postmortem damage. *American Journal of Human Genetics*, **2003**, 72, 48-61	11	193
366	Plasmodium falciparum erythrocyte membrane protein 1 domain cassettes 8 and 13 are associated with severe malaria in children. *Proceedings of the National Academy of Sciences of the United States of America*, **2012**, 109, E1791-800	11.5	192
365	Whole-genome shotgun sequencing of mitochondria from ancient hair shafts. *Science*, **2007**, 317, 1927-30	33.3	191
364	Ancient and modern environmental DNA. *Philosophical Transactions of the Royal Society B: Biological Sciences*, **2015**, 370, 20130383	5.8	184
363	Complex evolutionary trajectories of sex chromosomes across bird taxa. *Science*, **2014**, 346, 1246338	33.3	184
362	Critical review of host specificity and its coevolutionary implications in the fig/fig-wasp mutualism. *Proceedings of the National Academy of Sciences of the United States of America*, **2005**, 102 Suppl 1, 6558-65	11.5	184
361	Meta-barcoding of 'dirt' DNA from soil reflects vertebrate biodiversity. *Molecular Ecology*, **2012**, 21, 1966-79	5.7	180
360	Distribution patterns of postmortem damage in human mitochondrial DNA. *American Journal of Human Genetics*, **2003**, 72, 32-47	11	178
359	The microbiome of New World vultures. *Nature Communications*, **2014**, 5, 5498	17.4	177
358	Ancient DNA reveals lack of continuity between neolithic hunter-gatherers and contemporary Scandinavians. *Current Biology*, **2009**, 19, 1758-62	6.3	177
357	Ancient DNA analyses exclude humans as the driving force behind late Pleistocene musk ox (Ovibos moschatus) population dynamics. *Proceedings of the National Academy of Sciences of the United States of America*, **2010**, 107, 5675-80	11.5	175
356	DNA extraction from dry museum beetles without conferring external morphological damage. *PLoS ONE*, **2007**, 2, e272	3.7	171
355	DNA from soil mirrors plant taxonomic and growth form diversity. *Molecular Ecology*, **2012**, 21, 3647-55	5.7	170

354	Ancient DNA reveals late survival of mammoth and horse in interior Alaska. *Proceedings of the National Academy of Sciences of the United States of America*, **2009**, 106, 22352-7	11.5	170
353	Genomic diversity and evolution of the head crest in the rock pigeon. *Science*, **2013**, 339, 1063-7	33.3	169
352	Historical mammal extinction on Christmas Island (Indian Ocean) correlates with introduced infectious disease. *PLoS ONE*, **2008**, 3, e3602	3.7	162
351	Genome-culture coevolution promotes rapid divergence of killer whale ecotypes. *Nature Communications*, **2016**, 7, 11693	17.4	161
350	Towards complete and error-free genome assemblies of all vertebrate species. *Nature*, **2021**, 592, 737-746	36.4	161
349	Molecular diet analysis of two african free-tailed bats (molossidae) using high throughput sequencing. *PLoS ONE*, **2011**, 6, e21441	3.7	154
348	Reconstructing ancient genomes and epigenomes. *Nature Reviews Genetics*, **2015**, 16, 395-408	30.1	151
347	Proteomic analysis of a pleistocene mammoth femur reveals more than one hundred ancient bone proteins. *Journal of Proteome Research*, **2012**, 11, 917-26	5.6	150
346	Clovis age Western Stemmed projectile points and human coprolites at the Paisley Caves. *Science*, **2012**, 337, 223-8	33.3	150
345	Paleo-Eskimo mtDNA genome reveals matrilineal discontinuity in Greenland. *Science*, **2008**, 320, 1787-9	33.3	146
344	Ancient DNA chronology within sediment deposits: are paleobiological reconstructions possible and is DNA leaching a factor?. *Molecular Biology and Evolution*, **2007**, 24, 982-9	8.3	145
343	Absence of Yersinia pestis-specific DNA in human teeth from five European excavations of putative plague victims. *Microbiology (United Kingdom)*, **2004**, 150, 341-354	2.9	141
342	Ecological, morphological and genetic divergence of sympatric North Atlantic killer whale populations. *Molecular Ecology*, **2009**, 18, 5207-17	5.7	140
341	Transcriptomes of the desiccation-tolerant resurrection plant Craterostigma plantagineum. *Plant Journal*, **2010**, 63, 212-28	6.9	138
340	Genetic evidence for patrilocal mating behavior among Neandertal groups. *Proceedings of the National Academy of Sciences of the United States of America*, **2011**, 108, 250-3	11.5	136
339	Recharacterization of ancient DNA miscoding lesions: insights in the era of sequencing-by-synthesis. *Nucleic Acids Research*, **2007**, 35, 1-10	20.1	136
338	Intraspecific phylogenetic analysis of Siberian woolly mammoths using complete mitochondrial genomes. *Proceedings of the National Academy of Sciences of the United States of America*, **2008**, 105, 8327-32	11.5	130
337	Genomic affinities of two 7,000-year-old Iberian hunter-gatherers. *Current Biology*, **2012**, 22, 1494-9	6.3	129

336	Pre-Clovis mastodon hunting 13,800 years ago at the Manis site, Washington. *Science*, **2011**, 334, 351-3	33.3	129
335	Macroevolution of complex retroviruses. *Science*, **2009**, 325, 1512	33.3	128
334	Direct evidence of milk consumption from ancient human dental calculus. *Scientific Reports*, **2014**, 4, 7104	4.9	125
333	Single-tube library preparation for degraded DNA. *Methods in Ecology and Evolution*, **2018**, 9, 410-419	7.7	122
332	Do Vertebrate Gut Metagenomes Confer Rapid Ecological Adaptation?. *Trends in Ecology and Evolution*, **2016**, 31, 689-699	10.9	122
331	High-throughput sequencing offers insight into mechanisms of resource partitioning in cryptic bat species. *Ecology and Evolution*, **2011**, 1, 556-70	2.8	122
330	Beringian paleoecology inferred from permafrost-preserved fungal DNA. *Applied and Environmental Microbiology*, **2005**, 71, 1012-7	4.8	121
329	Large-scale ruminant genome sequencing provides insights into their evolution and distinct traits. *Science*, **2019**, 364,	33.3	120
328	A Common Genetic Origin for Early Farmers from Mediterranean Cardial and Central European LBK Cultures. *Molecular Biology and Evolution*, **2015**, 32, 3132-42	8.3	120
327	Connecting Earth observation to high-throughput biodiversity data. *Nature Ecology and Evolution*, **2017**, 1, 176	12.3	117
326	Genome-wide nucleosome map and cytosine methylation levels of an ancient human genome. *Genome Research*, **2014**, 24, 454-66	9.7	113
325	The genetic origins of the Andaman Islanders. *American Journal of Human Genetics*, **2003**, 72, 178-84	11	108
324	Ancient genomics. *Philosophical Transactions of the Royal Society B: Biological Sciences*, **2015**, 370, 20130387	5.8	107
323	Comment on "Protein sequences from mastodon and Tyrannosaurus rex revealed by mass spectrometry". *Science*, **2008**, 319, 33; author reply 33	33.3	106
322	Screening mammal biodiversity using DNA from leeches. *Current Biology*, **2012**, 22, R262-3	6.3	105
321	Ancient mitochondrial DNA from hair. *Current Biology*, **2004**, 14, R463-4	6.3	105
320	DNA in ancient bone - where is it located and how should we extract it?. *Annals of Anatomy*, **2012**, 194, 7-16	2.9	104
319	A comparative study of ancient sedimentary DNA, pollen and macrofossils from permafrost sediments of northern Siberia reveals long-term vegetational stability. *Molecular Ecology*, **2012**, 21, 1989-2003	5.7	103

318	More on contamination: the use of asymmetric molecular behavior to identify authentic ancient human DNA. *Molecular Biology and Evolution*, **2007**, 24, 998-1004	8.3	103
317	The origin and evolution of maize in the Southwestern United States. *Nature Plants*, **2015**, 1, 14003	11.5	99
316	True single-molecule DNA sequencing of a pleistocene horse bone. *Genome Research*, **2011**, 21, 1705-19	9.7	99
315	Genomics: Bird sequencing project takes off. *Nature*, **2015**, 522, 34	50.4	97
314	Stable isotope and DNA evidence for ritual sequences in Inca child sacrifice. *Proceedings of the National Academy of Sciences of the United States of America*, **2007**, 104, 16456-61	11.5	97
313	Multiproxy evidence highlights a complex evolutionary legacy of maize in South America. *Science*, **2018**, 362, 1309-1313	33.3	97
312	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	6.3	95
311	Tracking down human contamination in ancient human teeth. *Molecular Biology and Evolution*, **2006**, 23, 1801-7	8.3	95
310	Comparative genomic data of the Avian Phylogenomics Project. *GigaScience*, **2014**, 3, 26	7.6	91
309	Identification of microsatellites from an extinct moa species using high-throughput (454) sequence data. *BioTechniques*, **2009**, 46, 195-200	2.5	91
308	Dense sampling of bird diversity increases power of comparative genomics. *Nature*, **2020**, 587, 252-257	50.4	89
307	Comparative performance of the BGISEQ-500 vs Illumina HiSeq2500 sequencing platforms for palaeogenomic sequencing. *GigaScience*, **2017**, 6, 1-13	7.6	88
306	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	13.7	88
305	Positive selection on the killer whale mitogenome. *Biology Letters*, **2011**, 7, 116-8	3.6	87
304	Application and comparison of large-scale solution-based DNA capture-enrichment methods on ancient DNA. *Scientific Reports*, **2011**, 1, 74	4.9	87
303	Fossil avian eggshell preserves ancient DNA. *Proceedings of the Royal Society B: Biological Sciences*, **2010**, 277, 1991-2000	4.4	86
302	High-throughput sequencing of core STR loci for forensic genetic investigations using the Roche Genome Sequencer FLX platform. *BioTechniques*, **2011**, 51, 127-33	2.5	85
301	Assessing the fidelity of ancient DNA sequences amplified from nuclear genes. *Genetics*, **2006**, 172, 733-41		85

300	The mitochondrial genome sequence of the Tasmanian tiger (Thylacinus cynocephalus). *Genome Research*, **2009**, 19, 213-20	9.7	83
299	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, 3669-73	11.5	82
298	Biochemical and physical correlates of DNA contamination in archaeological human bones and teeth excavated at Matera, Italy. *Journal of Archaeological Science*, **2005**, 32, 785-793	2.9	82
297	Storytelling and story testing in domestication. *Proceedings of the National Academy of Sciences of the United States of America*, **2014**, 111, 6159-64	11.5	80
296	Reconstructing genome evolution in historic samples of the Irish potato famine pathogen. *Nature Communications*, **2013**, 4, 2172	17.4	79
295	One Hundred Twenty Years of Koala Retrovirus Evolution Determined from Museum Skins. *Molecular Biology and Evolution*, **2013**, 30, 1237-1237	8.3	78
294	Reply to Vigilant and Langergraber: Patrilocality in Neandertals is still the most plausible explanation. *Proceedings of the National Academy of Sciences of the United States of America*, **2011**, 108, E88-E88	11.5	78
293	Analysis of complete mitochondrial genomes from extinct and extant rhinoceroses reveals lack of phylogenetic resolution. *BMC Evolutionary Biology*, **2009**, 9, 95	3	77
292	Promises and pitfalls of using high-throughput sequencing for diet analysis. *Molecular Ecology Resources*, **2019**, 19, 327-348	8.4	77
291	Non-destructive sampling of ancient insect DNA. *PLoS ONE*, **2009**, 4, e5048	3.7	75
290	Unravelling migrations in the steppe: mitochondrial DNA sequences from ancient central Asians. *Proceedings of the Royal Society B: Biological Sciences*, **2004**, 271, 941-7	4.4	75
289	Evidence for a single loss of mineralized teeth in the common avian ancestor. *Science*, **2014**, 346, 1254390	33.3	74
288	Genetic differentiation among North Atlantic killer whale populations. *Molecular Ecology*, **2011**, 20, 629-41	5.7	73
287	The evolutionary history of dogs in the Americas. *Science*, **2018**, 361, 81-85	33.3	73
286	Early Pleistocene enamel proteome from Dmanisi resolves Stephanorhinus phylogeny. *Nature*, **2019**, 574, 103-107	50.4	70
285	Natural selection shaped the rise and fall of passenger pigeon genomic diversity. *Science*, **2017**, 358, 951-954	33.3	68
284	Extinct New Zealand megafauna were not in decline before human colonization. *Proceedings of the National Academy of Sciences of the United States of America*, **2014**, 111, 4922-7	11.5	67
283	Mitogenome sequencing reveals shallow evolutionary histories and recent divergence time between morphologically and ecologically distinct European whitefish (Coregonus spp.). *Molecular Ecology*, **2012**, 21, 2727-42	5.7	67

282	Quantifying Temporal Genomic Erosion in Endangered Species. *Trends in Ecology and Evolution*, **2018**, 33, 176-185	10.9	66
281	Dynamic evolution of the alpha (α) and beta (β) keratins has accompanied integument diversification and the adaptation of birds into novel lifestyles. *BMC Evolutionary Biology*, **2014**, 14, 249	3	66
280	Parallel adaptation of rabbit populations to myxoma virus. *Science*, **2019**, 363, 1319-1326	33.3	66
279	One hundred twenty years of koala retrovirus evolution determined from museum skins. *Molecular Biology and Evolution*, **2013**, 30, 299-304	8.3	65
278	Mitogenomic phylogenetic analyses of the Delphinidae with an emphasis on the Globicephalinae. *BMC Evolutionary Biology*, **2011**, 11, 65	3	65
277	A multidisciplinary study of archaeological grape seeds. *Die Naturwissenschaften*, **2010**, 97, 205-17	2	65
276	Hologenomic adaptations underlying the evolution of sanguivory in the common vampire bat. *Nature Ecology and Evolution*, **2018**, 2, 659-668	12.3	64
275	Recent diversification of a marine genus (Tursiops spp.) tracks habitat preference and environmental change. *Systematic Biology*, **2013**, 62, 865-77	8.4	64
274	iDNA from terrestrial haematophagous leeches as a wildlife surveying and monitoring tool - prospects, pitfalls and avenues to be developed. *Frontiers in Zoology*, **2015**, 12, 24	2.8	64
273	Marine turtle mitogenome phylogenetics and evolution. *Molecular Phylogenetics and Evolution*, **2012**, 65, 241-50	4.1	64
272	Agriculture shapes the trophic niche of a bat preying on multiple pest arthropods across Europe: Evidence from DNA metabarcoding. *Molecular Ecology*, **2018**, 27, 815-825	5.7	62
271	Ancient mitogenomics. *Mitochondrion*, **2010**, 10, 1-11	4.9	60
270	Partial genetic turnover in neandertals: continuity in the East and population replacement in the West. *Molecular Biology and Evolution*, **2012**, 29, 1893-7	8.3	59
269	Second generation sequencing and morphological faecal analysis reveal unexpected foraging behaviour by Myotis nattereri (Chiroptera, Vespertilionidae) in winter. *Frontiers in Zoology*, **2014**, 11, 39	2.8	58
268	Interspecific Gene Flow Shaped the Evolution of the Genus Canis. *Current Biology*, **2018**, 28, 3441-3449.e6	6.3	58
267	Mitochondrial DNA from pre-Columbian Ciboneys from Cuba and the prehistoric colonization of the Caribbean. *American Journal of Physical Anthropology*, **2003**, 121, 97-108	2.5	57
266	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,	4.4	56
265	Biochemistry. Unlocking ancient protein palimpsests. *Science*, **2014**, 343, 1320-2	33.3	56

264	Genomic signatures of near-extinction and rebirth of the crested ibis and other endangered bird species. *Genome Biology*, **2014**, 15, 557	18.3	56
263	Palaeogenomic insights into the origins of French grapevine diversity. *Nature Plants*, **2019**, 5, 595-603	11.5	54
262	Islands in the ice: detecting past vegetation on Greenlandic nunataks using historical records and sedimentary ancient DNA meta-barcoding. *Molecular Ecology*, **2012**, 21, 1980-8	5.7	54
261	Geographic and temporal dynamics of a global radiation and diversification in the killer whale. *Molecular Ecology*, **2015**, 24, 3964-79	5.7	54
260	Ancient DNA reveals that bowhead whale lineages survived Late Pleistocene climate change and habitat shifts. *Nature Communications*, **2013**, 4, 1677	17.4	53
259	Resistance of degraded hair shafts to contaminant DNA. *Forensic Science International*, **2006**, 156, 208-12	2.6	52
258	A guide to the application of Hill numbers to DNA-based diversity analyses. *Molecular Ecology Resources*, **2019**, 19, 804-817	8.4	51
257	Insights into the processes behind the contamination of degraded human teeth and bone samples with exogenous sources of DNA. *International Journal of Osteoarchaeology*, **2006**, 16, 156-164	1.1	51
256	No proof that typhoid caused the Plague of Athens (a reply to Papagrigorakis et al.). *International Journal of Infectious Diseases*, **2006**, 10, 334-5; author reply 335-6	10.5	51
255	Two Antarctic penguin genomes reveal insights into their evolutionary history and molecular changes related to the Antarctic environment. *GigaScience*, **2014**, 3, 27	7.6	50
254	DNA extraction from formalin-fixed material. *Methods in Molecular Biology*, **2012**, 840, 81-5	1.4	50
253	Estimation of population divergence times from non-overlapping genomic sequences: examples from dogs and wolves. *Molecular Biology and Evolution*, **2011**, 28, 1505-17	8.3	50
252	The Farm Beneath the Sand: an archaeological case study on ancient 'dirt' DNA. *Antiquity*, **2009**, 83, 430-444	1	50
251	The wolf reference genome sequence (Canis lupus lupus) and its implications for Canis spp. population genomics. *BMC Genomics*, **2017**, 18, 495	4.5	49
250	The evolutionary history of cockatoos (Aves: Psittaciformes: Cacatuidae). *Molecular Phylogenetics and Evolution*, **2011**, 59, 615-22	4.1	49
249	Ancient mitochondrial DNA from the northern fringe of the Neolithic farming expansion in Europe sheds light on the dispersion process. *Philosophical Transactions of the Royal Society B: Biological Sciences*, **2015**, 370, 20130373	5.8	48
248	Ancient DNA reveals traces of Iberian Neolithic and Bronze Age lineages in modern Iberian horses. *Molecular Ecology*, **2010**, 19, 64-78	5.7	48
247	Olfactory Receptor Subgenomes Linked with Broad Ecological Adaptations in Sauropsida. *Molecular Biology and Evolution*, **2015**, 32, 2832-43	8.3	47

246	Mitochondrial genome diversity and population structure of the giant squid Architeuthis: genetics sheds new light on one of the most enigmatic marine species. *Proceedings of the Royal Society B: Biological Sciences*, **2013**, 280, 20130273	4.4	47
245	DNA from keratinous tissue. Part I: hair and nail. *Annals of Anatomy*, **2012**, 194, 17-25	2.9	47
244	Mitogenomic analyses from ancient DNA. *Molecular Phylogenetics and Evolution*, **2013**, 69, 404-16	4.1	46
243	Ancient DNA sequences point to a large loss of mitochondrial genetic diversity in the saiga antelope (Saiga tatarica) since the Pleistocene. *Molecular Ecology*, **2010**, 19, 4863-75	5.7	45
242	Optimization of DNA recovery and amplification from non-carbonized archaeobotanical remains. *PLoS ONE*, **2014**, 9, e86827	3.7	45
241	Functional roles of Aves class-specific cis-regulatory elements on macroevolution of bird-specific features. *Nature Communications*, **2017**, 8, 14229	17.4	44
240	Environmental genes and genomes: understanding the differences and challenges in the approaches and software for their analyses. *Briefings in Bioinformatics*, **2015**, 16, 745-58	13.4	44
239	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	6.3	44
238	Low frequency of paleoviral infiltration across the avian phylogeny. *Genome Biology*, **2014**, 15, 539	18.3	43
237	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	4.1	42
236	Using DNA metabarcoding for simultaneous inference of common vampire bat diet and population structure. *Molecular Ecology Resources*, **2018**, 18, 1050	8.4	42
235	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	11.5	42
234	The Genomic Footprints of the Fall and Recovery of the Crested Ibis. *Current Biology*, **2019**, 29, 340-349.e7	6.3	42
233	Global distribution of Chelonid fibropapilloma-associated herpesvirus among clinically healthy sea turtles. *BMC Evolutionary Biology*, **2014**, 14, 206	3	41
232	The effect of ancient DNA damage on inferences of demographic histories. *Molecular Biology and Evolution*, **2008**, 25, 2181-7	8.3	41
231	An invertebrate stomach's view on vertebrate ecology: certain invertebrates could be used as "vertebrate samplers" and deliver DNA-based information on many aspects of vertebrate ecology. *BioEssays*, **2013**, 35, 1004-13	4.1	40
230	Fellow travellers: a concordance of colonization patterns between mice and men in the North Atlantic region. *BMC Evolutionary Biology*, **2012**, 12, 35	3	40
229	Avian genomes. A flock of genomes. Introduction. *Science*, **2014**, 346, 1308-9	33.3	39

228	Profiling the dead: generating microsatellite data from fossil bones of extinct megafauna--protocols, problems, and prospects. *PLoS ONE*, **2011**, 6, e16670	3.7	38
227	The survival of PCR-amplifiable DNA in cow leather. *Journal of Archaeological Science*, **2007**, 34, 823-829	2.9	38
226	Towards complete and error-free genome assemblies of all vertebrate species		38
225	Skmer: assembly-free and alignment-free sample identification using genome skims. *Genome Biology*, **2019**, 20, 34	18.3	37
224	Response to Comment on "Whole-genome analyses resolve early branches in the tree of life of modern birds". *Science*, **2015**, 349, 1460	33.3	37
223	Herbarium specimens reveal a historical shift in phylogeographic structure of common ragweed during native range disturbance. *Molecular Ecology*, **2014**, 23, 1701-16	5.7	37
222	Gene loss, adaptive evolution and the co-evolution of plumage coloration genes with opsins in birds. *BMC Genomics*, **2015**, 16, 751	4.5	37
221	Ancient genomes from Iceland reveal the making of a human population. *Science*, **2018**, 360, 1028-1032	33.3	37
220	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	2.3	36
219	Long-term RNA persistence in postmortem contexts. *Investigative Genetics*, **2013**, 4, 7		36
218	Comparative performance of two whole-genome capture methodologies on ancient DNA Illumina libraries. *Methods in Ecology and Evolution*, **2015**, 6, 725-734	7.7	36
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