Alan J Cooper

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.

80 24,562 150 297 h-index g-index citations papers 6.71 29,271 10.4 315 L-index avg, IF ext. citations ext. papers

#	Paper	IF	Citations
297	An age-depth model and revised stratigraphy of vertebrate-bearing units in Natural Trap Cave, Wyoming. <i>Quaternary International</i> , 2022 ,	2	2
296	Lions and brown bears colonized North America in multiple synchronous waves of dispersal across the Bering Land Bridge. <i>Molecular Ecology</i> , 2021 ,	5.7	3
295	Response to Comment on "A global environmental crisis 42,000 years ago". <i>Science</i> , 2021 , 374, eabi975	633.3	2
294	Evidence for Pleistocene gene flow through the ice-free corridor from extinct horses and camels from Natural Trap Cave, Wyoming. <i>Quaternary International</i> , 2021 ,	2	1
293	Response to Comment on "A global environmental crisis 42,000 years ago". <i>Science</i> , 2021 , 374, eabh365	5 5 3.3	
292	Characterizing porous microaggregates and soil organic matter sequestered in allophanic paleosols on Holocene tephras using synchrotron-based X-ray microscopy and spectroscopy. <i>Scientific Reports</i> , 2021 , 11, 21310	4.9	2
291	Widespread Denisovan ancestry in Island Southeast Asia but no evidence of substantial super-archaic hominin admixture. <i>Nature Ecology and Evolution</i> , 2021 , 5, 616-624	12.3	15
29 0	Systematic benchmark of ancient DNA read mapping. Briefings in Bioinformatics, 2021, 22,	13.4	3
289	Mitogenomes Reveal Two Major Influxes of Papuan Ancestry across Wallacea Following the Last Glacial Maximum and Austronesian Contact. <i>Genes</i> , 2021 , 12,	4.2	3
288	A global environmental crisis 42,000 years ago. <i>Science</i> , 2021 , 371, 811-818	33.3	28
287	Origin, extinction and ancient DNA of a new fossil insular viper: molecular clues of overseas immigration. <i>Zoological Journal of the Linnean Society</i> , 2021 , 192, 144-168	2.4	2
286	Dire wolves were the last of an ancient New World canid lineage. <i>Nature</i> , 2021 , 591, 87-91	50.4	18
285	Ancient and modern genomes unravel the evolutionary history of the rhinoceros family. <i>Cell</i> , 2021 , 184, 4874-4885.e16	56.2	6
284	A new extinct species of Polynesian sandpiper (Charadriiformes: Scolopacidae: Prosobonia) from Henderson Island, Pitcairn Group, and the phylogenetic relationships of Prosobonia. <i>Zoological Journal of the Linnean Society</i> , 2020 ,	2.4	3
283	A Paleogenomic Reconstruction of the Deep Population History of the Andes. <i>Cell</i> , 2020 , 181, 1131-114	l55 é2 1	33
282	Palaeomicrobiology: Application of Ancient DNA Sequencing to Better Understand Bacterial Genome Evolution and Adaptation. <i>Frontiers in Ecology and Evolution</i> , 2020 , 8,	3.7	3
281	Early Last Interglacial ocean warming drove substantial ice mass loss from Antarctica. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2020 , 117, 3996-4006	11.5	30

280	Toxic Epidermal Necrolysis and Steven-Johnson Syndrome: A Comprehensive Review. <i>Advances in Wound Care</i> , 2020 , 9, 426-439	4.8	13
279	An optimized method for the extraction of ancient eukaryote DNA from marine sediments. <i>Molecular Ecology Resources</i> , 2020 , 20, 906-919	8.4	8
278	Ancient DNA from an extinct Mediterranean micromammal Hypnomys morpheus (Rodentia: Gliridae) Provides insight into the biogeographic history of insular dormice. <i>Journal of Zoological Systematics and Evolutionary Research</i> , 2020 , 58, 427-438	1.9	2
277	Widespread male sex bias in mammal fossil and museum collections. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2019 , 116, 19019-19024	11.5	16
276	Mitogenomes Uncover Extinct Penguin Taxa and Reveal Island Formation as a Key Driver of Speciation. <i>Molecular Biology and Evolution</i> , 2019 , 36, 784-797	8.3	23
275	Ancient DNA from marine sediments: Precautions and considerations for seafloor coring, sample handling and data generation. <i>Earth-Science Reviews</i> , 2019 , 196, 102887	10.2	25
274	Unraveling the phylogenetic relationships of the extinct bovid Myotragus balearicus Bate 1909 from the Balearic Islands. <i>Quaternary Science Reviews</i> , 2019 , 215, 185-195	3.9	6
273	Laboratory contamination over time during low-biomass sample analysis. <i>Molecular Ecology Resources</i> , 2019 , 19, 982-996	8.4	79
272	The Dogma of Dingoes-Taxonomic status of the dingo: A reply to Smith et al. <i>Zootaxa</i> , 2019 , 4564, zoo	taøaş45	66 4 51.7
271	Low-cost cross-taxon enrichment of mitochondrial DNA using in-house synthesised RNA probes. <i>PLoS ONE</i> , 2019 , 14, e0209499	3.7	5
270	Retrospective eDNA assessment of potentially harmful algae in historical ship ballast tank and marine port sediments. <i>Molecular Ecology</i> , 2019 , 28, 2476-2485	5.7	17
269	Broadening the taxonomic scope of coral reef palaeoecological studies using ancient DNA. <i>Molecular Ecology</i> , 2019 , 28, 2636-2652	5.7	3
268	Mitochondrial Genomes from New Zealand Extinct Adzebills (Aves: Aptornithidae: Aptornis) Support a Sister-Taxon Relationship with the Afro-Madagascan Sarothruridae. <i>Diversity</i> , 2019 , 11, 24	2.5	12
267	Using hominin introgression to trace modern human dispersals. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2019 , 116, 15327-15332	11.5	10
266	Contamination in Low Microbial Biomass Microbiome Studies: Issues and Recommendations. <i>Trends in Microbiology</i> , 2019 , 27, 105-117	12.4	340
265	Reconstructing the Evolution of Giant Extinct Kangaroos: Comparing the Utility of DNA, Morphology, and Total Evidence. <i>Systematic Biology</i> , 2019 , 68, 520-537	8.4	12
264	Evolution and extinction of the giant rhinoceros Elasmotherium sibiricum sheds light on late Quaternary megafaunal extinctions. <i>Nature Ecology and Evolution</i> , 2019 , 3, 31-38	12.3	39
263	Ancient Microbial DNA in Dental Calculus: A New method for Studying Rapid Human Migration Events. <i>Journal of Island and Coastal Archaeology</i> , 2019 , 14, 149-162	1.2	9

262	Genetic diversity and drivers of dwarfism in extinct island emu populations. <i>Biology Letters</i> , 2018 , 14,	3.6	14
261	Coprolites reveal ecological interactions lost with the extinction of New Zealand birds. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2018 , 115, 1546-1551	11.5	38
260	Molecular phylogenetics supports the origin of an endemic Balearic shrew lineage (Nesiotites) coincident with the Messinian Salinity Crisis. <i>Molecular Phylogenetics and Evolution</i> , 2018 , 125, 188-195	4.1	6
259	When did first reach Southeast Asia and Sahul?. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2018 , 115, 8482-8490	11.5	100
258	Ancient DNA from Giant Panda (Ailuropoda melanoleuca) of South-Western China Reveals Genetic Diversity Loss during the Holocene. <i>Genes</i> , 2018 , 9,	4.2	8
257	Molecular resolution to a morphological controversy: The case of North American fossil muskoxen Bootherium and Symbos. <i>Molecular Phylogenetics and Evolution</i> , 2018 , 129, 70-76	4.1	10
256	Ancient plant DNA in the genomic era. <i>Nature Plants</i> , 2018 , 4, 394-396	11.5	19
255	Genome of the Tasmanian tiger provides insights into the evolution and demography of an extinct marsupial carnivore. <i>Nature Ecology and Evolution</i> , 2018 , 2, 182-192	12.3	48
254	Connecting the Greenland ice-core and UII timescales via cosmogenic radionuclides: testing the synchroneity of Dansgaard Deschger events. <i>Climate of the Past</i> , 2018 , 14, 1755-1781	3.9	38
253	Reconstructing the Deep Population History of Central and South America. <i>Cell</i> , 2018 , 175, 1185-1197.6	2 3 6.2	143
252	Consequences of colonialism: A microbial perspective to contemporary Indigenous health. <i>American Journal of Physical Anthropology</i> , 2018 , 167, 423-437	2.5	7
251	Palaeogeography and voyage modeling indicates early human colonization of Australia was likely from Timor-Roti. <i>Quaternary Science Reviews</i> , 2018 , 191, 431-439	3.9	33
250	Using environmental (e)DNA sequencing for aquatic biodiversity surveys: a beginner guide. <i>Marine and Freshwater Research</i> , 2017 , 68, 20	2.2	27
249	From the field to the laboratory: Controlling DNA contamination in human ancient DNA research in the high-throughput sequencing era. <i>Science and Technology of Archaeological Research</i> , 2017 , 3, 1-14	1.2	83
248	A primer to metabarcoding surveys of Antarctic terrestrial biodiversity. <i>Antarctic Science</i> , 2017 , 29, 3-15	1.7	6
247	Aboriginal mitogenomes reveal 50,000 years of regionalism in Australia. <i>Nature</i> , 2017 , 544, 180-184	50.4	122
246	Neanderthal behaviour, diet, and disease inferred from ancient DNA in dental calculus. <i>Nature</i> , 2017 , 544, 357-361	50.4	263
245	Megafaunal isotopes reveal role of increased moisture on rangeland during late Pleistocene extinctions. <i>Nature Ecology and Evolution</i> , 2017 , 1, 125	12.3	26

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226	DNA adsorption by nanocrystalline allophane spherules and nanoaggregates, and implications for carbon sequestration in Andisols. <i>Applied Clay Science</i> , 2016 , 120, 40-50	5.2	27
225	Comparison of environmental DNA metabarcoding and conventional fish survey methods in a river system. <i>Biological Conservation</i> , 2016 , 197, 131-138	6.2	143
224	Climate change not to blame for late Quaternary megafauna extinctions in Australia. <i>Nature Communications</i> , 2016 , 7, 10511	17.4	91
223	Antarctic eukaryotic soil diversity of the Prince Charles Mountains revealed by high-throughput sequencing. <i>Soil Biology and Biochemistry</i> , 2016 , 95, 112-121	7.5	30
222	Response to Comment on "Abrupt warming events drove Late Pleistocene Holarctic megafaunal turnover". <i>Science</i> , 2016 , 351, 927	33.3	
221	Ancient DNA Analysis Suggests Negligible Impact of the Wari Empire Expansion in Peru's Central Coast during the Middle Horizon. <i>PLoS ONE</i> , 2016 , 11, e0155508	3.7	10
220	Age-related environmental gradients influence invertebrate distribution in the Prince Charles Mountains, East Antarctica. <i>Royal Society Open Science</i> , 2016 , 3, 160296	3.3	5
219	Exploring Relationships between Host Genome and Microbiome: New Insights from Genome-Wide Association Studies. <i>Frontiers in Microbiology</i> , 2016 , 7, 1611	5.7	14
218	Review of Toxic Epidermal Necrolysis. International Journal of Molecular Sciences, 2016, 17,	6.3	32
217	High-throughput Sequencing of Trace Quantities of Soil Provides Reproducible and Discriminative Fungal DNA Profiles. <i>Journal of Forensic Sciences</i> , 2016 , 61, 478-484	1.8	14
216	A new method to extract and purify DNA from allophanic soils and paleosols, and potential for paleoenvironmental reconstruction and other applications. <i>Geoderma</i> , 2016 , 274, 114-125	6.7	10
215	Ancient mitochondrial genomes clarify the evolutionary history of New Zealand's enigmatic acanthisittid wrens. <i>Molecular Phylogenetics and Evolution</i> , 2016 , 102, 295-304	4.1	18
214	Closing the gap: New data on the last documented Myotragus and the first human evidence on Mallorca (Balearic Islands, Western Mediterranean Sea). <i>Holocene</i> , 2016 , 26, 1887-1891	2.6	27
213	Ancient mitochondrial DNA reveals convergent evolution of giant short-faced bears (Tremarctinae) in North and South America. <i>Biology Letters</i> , 2016 , 12,	3.6	57
212	Phylogenetic relationships and terrestrial adaptations of the extinct laughing owl, Sceloglaux albifacies (Aves: Strigidae). <i>Zoological Journal of the Linnean Society</i> , 2016 ,	2.4	4
211	The skin microbiome: Associations between altered microbial communities and disease. <i>Australasian Journal of Dermatology</i> , 2015 , 56, 268-74	1.3	63
210	Massive migration from the steppe was a source for Indo-European languages in Europe. <i>Nature</i> , 2015 , 522, 207-11	50.4	968
209	PALEOECOLOGY. Abrupt warming events drove Late Pleistocene Holarctic megafaunal turnover. <i>Science</i> , 2015 , 349, 602-6	33.3	217

(2014-2015)

208	Using Amplicon Sequencing To Characterize and Monitor Bacterial Diversity in Drinking Water Distribution Systems. <i>Applied and Environmental Microbiology</i> , 2015 , 81, 6463-73	4.8	42
207	Residual soil DNA extraction increases the discriminatory power between samples. <i>Forensic Science, Medicine, and Pathology</i> , 2015 , 11, 268-72	1.5	7
206	Predicting the origin of soil evidence: High throughput eukaryote sequencing and MIR spectroscopy applied to a crime scene scenario. <i>Forensic Science International</i> , 2015 , 251, 22-31	2.6	29
205	Comment on "Whole-genome analyses resolve early branches in the tree of life of modern birds". <i>Science</i> , 2015 , 349, 1460	33.3	29
204	New Zealand Passerines Help Clarify the Diversification of Major Songbird Lineages during the Oligocene. <i>Genome Biology and Evolution</i> , 2015 , 7, 2983-95	3.9	29
203	Criteria for assessing the quality of Middle Pleistocene to Holocene vertebrate fossil ages. <i>Quaternary Geochronology</i> , 2015 , 30, 69-79	2.7	27
202	Genome-wide patterns of selection in 230 ancient Eurasians. <i>Nature</i> , 2015 , 528, 499-503	50.4	774
201	Ancient DNA analysis of dental calculus. <i>Journal of Human Evolution</i> , 2015 , 79, 119-24	3.1	76
200	Treatment of chronic diabetic lower leg ulcers with activated protein C: a randomised placebo-controlled, double-blind pilot clinical trial. <i>International Wound Journal</i> , 2015 , 12, 422-7	2.6	18
199	Role of nanocrystalline silver dressings in the management of toxic epidermal necrolysis (TEN) and TEN/Stevens-Johnson syndrome overlap. <i>Australasian Journal of Dermatology</i> , 2015 , 56, 298-302	1.3	9
198	The Biarzo case in northern Italy: is the temporal dynamic of swine mitochondrial DNA lineages in Europe related to domestication?. <i>Scientific Reports</i> , 2015 , 5, 16514	4.9	11
197	Reintroduction of locally extinct vertebrates impacts arid soil fungal communities. <i>Molecular Ecology</i> , 2015 , 24, 3194-205	5.7	16
196	Obliquity-driven expansion of North Atlantic sea ice during the last glacial. <i>Geophysical Research Letters</i> , 2015 , 42, 10,382	4.9	10
195	Amplification of TruSeq ancient DNA libraries with AccuPrime Pfx: consequences on nucleotide misincorporation and methylation patterns. <i>Science and Technology of Archaeological Research</i> , 2015 , 1, 1-9	1.2	9
194	Uncertainties in dating constrain model choice for inferring extinction time from fossil records. <i>Quaternary Science Reviews</i> , 2015 , 112, 128-137	3.9	34
193	Late pleistocene Australian marsupial DNA clarifies the affinities of extinct megafaunal kangaroos and wallabies. <i>Molecular Biology and Evolution</i> , 2015 , 32, 574-84	8.3	22
192	A Re-Appraisal of the Early Andean Human Remains from Lauricocha in Peru. PLoS ONE, 2015 , 10, e0127	′3.4 ⁄1	34
191	Limitations and recommendations for successful DNA extraction from forensic soil samples: a review. <i>Science and Justice - Journal of the Forensic Science Society</i> , 2014 , 54, 238-44	2	57

190	Integrating multiple lines of evidence into historical biogeography hypothesis testing: a Bison bison case study. <i>Proceedings of the Royal Society B: Biological Sciences</i> , 2014 , 281, 20132782	4.4	29
189	Pleistocene Chinese cave hyenas and the recent Eurasian history of the spotted hyena, Crocuta crocuta. <i>Molecular Ecology</i> , 2014 , 23, 522-33	5.7	21
188	Environmental metabarcodes for insects: in silico PCR reveals potential for taxonomic bias. <i>Molecular Ecology Resources</i> , 2014 , 14, 1160-70	8.4	195
187	Using ancient DNA to study the origins and dispersal of ancestral Polynesian chickens across the Pacific. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2014 , 111, 4826	5- 31 ·5	110
186	Reply to Santiago-Rodriguez et al.: Was luxS really isolated from 25- to 40-million-year-old bacteria?. <i>FEMS Microbiology Letters</i> , 2014 , 353, 85-6	2.9	10
185	Ancient DNA reveals elephant birds and kiwi are sister taxa and clarifies ratite bird evolution. <i>Science</i> , 2014 , 344, 898-900	33.3	189
184	Fifty thousand years of Arctic vegetation and megafaunal diet. <i>Nature</i> , 2014 , 506, 47-51	50.4	351
183	Using palaeoenvironmental DNA to reconstruct past environments: progress and prospects. <i>Journal of Quaternary Science</i> , 2014 , 29, 610-626	2.3	64
182	Assessing the impact of water treatment on bacterial biofilms in drinking water distribution systems using high-throughput DNA sequencing. <i>Chemosphere</i> , 2014 , 117, 185-92	8.4	29
181	An extinct nestorid parrot (Aves, Psittaciformes, Nestoridae) from the Chatham Islands, New Zealand. <i>Zoological Journal of the Linnean Society</i> , 2014 , 172, 185-199	2.4	14
180	Ancient human genomes suggest three ancestral populations for present-day Europeans. <i>Nature</i> , 2014 , 513, 409-13	50.4	812
179	Forensic soil DNA analysis using high-throughput sequencing: a comparison of four molecular markers. <i>Forensic Science International: Genetics</i> , 2014 , 13, 176-84	4.3	42
178	Reply to Beavan, Bryant, and Storey and Matisoo-Smith: Ancestral Polynesian Dhaplotypes reflect authentic Pacific chicken lineages. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2014 , 111, E3585-6	11.5	8
177	Molecular phylogeny, biogeography, and habitat preference evolution of marsupials. <i>Molecular Biology and Evolution</i> , 2014 , 31, 2322-30	8.3	137
176	Molecular genetic evidence for the place of origin of the Pacific rat, Rattus exulans. <i>PLoS ONE</i> , 2014 , 9, e91356	3.7	25
175	Genotyping single nucleotide polymorphisms using different molecular beacon multiplexed within a suspended core optical fiber. <i>Sensors</i> , 2014 , 14, 14488-99	3.8	6
174	Using Ancient DNA to Understand Evolutionary and Ecological Processes. <i>Annual Review of Ecology, Evolution, and Systematics</i> , 2014 , 45, 573-598	13.5	60
173	Ancient mitochondrial genome reveals unsuspected taxonomic affinity of the extinct Chatham duck (Pachyanas chathamica) and resolves divergence times for New Zealand and sub-Antarctic brown teals. <i>Molecular Phylogenetics and Evolution</i> , 2014 , 70, 420-8	4.1	38

(2013-2014)

172	Modular tagging of amplicons using a single PCR for high-throughput sequencing. <i>Molecular Ecology Resources</i> , 2014 , 14, 117-21	8.4	25
171	Mitochondrial genome sequencing in Mesolithic North East Europe Unearths a new sub-clade within the broadly distributed human haplogroup C1. <i>PLoS ONE</i> , 2014 , 9, e87612	3.7	15
170	AmericaPlex26: a SNaPshot multiplex system for genotyping the main human mitochondrial founder lineages of the Americas. <i>PLoS ONE</i> , 2014 , 9, e93292	3.7	14
169	Carbon Storage and DNA Adsorption in Allophanic Soils and Paleosols 2014 , 163-172		4
168	Rapid megafaunal extinction following human arrival throughout the New World. <i>Quaternary International</i> , 2013 , 308-309, 273-277	2	37
167	Resolving lost herbivore community structure using coprolites of four sympatric moa species (Aves: Dinornithiformes). <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2013 , 110, 16910-5	11.5	47
166	Ancient DNA reveals key stages in the formation of central European mitochondrial genetic diversity. <i>Science</i> , 2013 , 342, 257-61	33.3	237
165	Youngest reported radiocarbon age of a moa (Aves: Dinornithiformes) dated from a natural site in New Zealand. <i>Journal of the Royal Society of New Zealand</i> , 2013 , 43, 100-107	2	10
164	DNA capture and next-generation sequencing can recover whole mitochondrial genomes from highly degraded samples for human identification. <i>Investigative Genetics</i> , 2013 , 4, 26		78
163	A quantitative assessment of a reliable screening technique for the STR analysis of telogen hair roots. <i>Forensic Science International: Genetics</i> , 2013 , 7, 180-8	4.3	23
162	Sequencing ancient calcified dental plaque shows changes in oral microbiota with dietary shifts of the Neolithic and Industrial revolutions. <i>Nature Genetics</i> , 2013 , 45, 450-5, 455e1	36.3	366
161	The origins of the enigmatic Falkland Islands wolf. <i>Nature Communications</i> , 2013 , 4, 1552	17.4	33
160	Ancient DNA reveals prehistoric gene-flow from siberia in the complex human population history of North East Europe. <i>PLoS Genetics</i> , 2013 , 9, e1003296	6	66
159	Neolithic mitochondrial haplogroup H genomes and the genetic origins of Europeans. <i>Nature Communications</i> , 2013 , 4, 1764	17.4	141
158	Paleontology. Did the Denisovans cross Wallace's Line?. <i>Science</i> , 2013 , 342, 321-3	33.3	74
157	Ancient DNA identifies post-glacial recolonisation, not recent bottlenecks, as the primary driver of contemporary mtDNA phylogeography and diversity in Scandinavian brown bears. <i>Diversity and Distributions</i> , 2013 , 19, 245-256	5	52
156	Mitochondrial phylogenomics of modern and ancient equids. PLoS ONE, 2013, 8, e55950	3.7	99
155	Lack of chronological support for stepwise prehuman extinctions of Australian megafauna. Proceedings of the National Academy of Sciences of the United States of America, 2013, 110, E3368	11.5	18

154	A megafauna's microfauna: gastrointestinal parasites of New Zealand's extinct moa (Aves: Dinornithiformes). <i>PLoS ONE</i> , 2013 , 8, e57315	3.7	51
153	Y-chromosome and mtDNA genetics reveal significant contrasts in affinities of modern Middle Eastern populations with European and African populations. <i>PLoS ONE</i> , 2013 , 8, e54616	3.7	39
152	Historical stocking data and 19th century DNA reveal human-induced changes to native diversity and distribution of cutthroat trout. <i>Molecular Ecology</i> , 2012 , 21, 5194-207	5.7	29
151	Recombination gives a new insight in the effective population size and the history of the old world human populations. <i>Molecular Biology and Evolution</i> , 2012 , 29, 25-30	8.3	24
150	Mitochondrial origin of the matrilocal Mosuo people in China. Mitochondrial DNA, 2012, 23, 13-9		10
149	Evidence of pre-Roman tribal genetic structure in Basques from uniparentally inherited markers. <i>Molecular Biology and Evolution</i> , 2012 , 29, 2211-22	8.3	32
148	A lost link between a flightless parrot and a parasitic plant and the potential role of coprolites in conservation paleobiology. <i>Conservation Biology</i> , 2012 , 26, 1091-9	6	28
147	Robust estimates of extinction time in the geological record. <i>Quaternary Science Reviews</i> , 2012 , 33, 14-	· 19 .9	48
146	Man and megafauna in Tasmania: closing the gap. Quaternary Science Reviews, 2012, 37, 38-47	3.9	25
145	The effect of climate and environmental change on the megafaunal moa of New Zealand in the absence of humans. <i>Quaternary Science Reviews</i> , 2012 , 50, 141-153	3.9	35
144	High-resolution analysis of cytosine methylation in ancient DNA. PLoS ONE, 2012, 7, e30226	3.7	61
143	Y-chromosome analysis in individuals bearing the Basarab name of the first dynasty of Wallachian kings. <i>PLoS ONE</i> , 2012 , 7, e41803	3.7	9
142	Clan, language, and migration history has shaped genetic diversity in Haida and Tlingit populations from Southeast Alaska. <i>American Journal of Physical Anthropology</i> , 2012 , 148, 422-35	2.5	30
141	The Basque paradigm: genetic evidence of a maternal continuity in the Franco-Cantabrian region since pre-Neolithic times. <i>American Journal of Human Genetics</i> , 2012 , 90, 486-93	11	47
140	Y-chromosome O3 haplogroup diversity in Sino-Tibetan populations reveals two migration routes into the eastern Himalayas. <i>Annals of Human Genetics</i> , 2012 , 76, 92-9	2.2	24
139	The influence of rate heterogeneity among sites on the time dependence of molecular rates. <i>Molecular Biology and Evolution</i> , 2012 , 29, 3345-58	8.3	140
138	Molecular beacons immobilized within suspended core optical fiber for specific DNA detection. <i>Optics Express</i> , 2012 , 20, 29378-85	3.3	27
137	Afghanistan's ethnic groups share a Y-chromosomal heritage structured by historical events. <i>PLoS ONE</i> , 2012 , 7, e34288	3.7	35

(2011-2012)

136	High-resolution coproecology: using coprolites to reconstruct the habits and habitats of New Zealand's extinct upland moa (Megalapteryx didinus). <i>PLoS ONE</i> , 2012 , 7, e40025	3.7	60
135	Population differentiation of southern Indian male lineages correlates with agricultural expansions predating the caste system. <i>PLoS ONE</i> , 2012 , 7, e50269	3.7	34
134	Multiple geographic origins of commensalism and complex dispersal history of Black Rats. <i>PLoS ONE</i> , 2011 , 6, e26357	3.7	189
133	Discovery of lost diversity of paternal horse lineages using ancient DNA. <i>Nature Communications</i> , 2011 , 2, 450	17.4	62
132	Species-specific responses of Late Quaternary megafauna to climate and humans. <i>Nature</i> , 2011 , 479, 359-64	50.4	483
131	Survival and recovery of DNA from ancient teeth and bones. <i>Journal of Archaeological Science</i> , 2011 , 38, 956-964	2.9	114
130	Late-Quaternary biogeographic scenarios for the brown bear (Ursus arctos), a wild mammal model species. <i>Quaternary Science Reviews</i> , 2011 , 30, 418-430	3.9	121
129	Sporormiella as a proxy for non-mammalian herbivores in island ecosystems. <i>Quaternary Science Reviews</i> , 2011 , 30, 915-920	3.9	42
128	Human migration through bottlenecks from Southeast Asia into East Asia during Last Glacial Maximum revealed by Y chromosomes. <i>PLoS ONE</i> , 2011 , 6, e24282	3.7	58
127	Time-dependent rates of molecular evolution. <i>Molecular Ecology</i> , 2011 , 20, 3087-101	5.7	383
126	Influences of history, geography, and religion on genetic structure: the Maronites in Lebanon. <i>European Journal of Human Genetics</i> , 2011 , 19, 334-40	5.3	37
125	An updated tree of Y-chromosome Haplogroup O and revised phylogenetic positions of mutations P164 and PK4. <i>European Journal of Human Genetics</i> , 2011 , 19, 1013-5	5.3	62
124	Parallel evolution of genes and languages in the Caucasus region. <i>Molecular Biology and Evolution</i> , 2011 , 28, 2905-20	8.3	107
123	The complete mitochondrial genome of an 11,450-year-old aurochsen (Bos primigenius) from Central Italy. <i>BMC Evolutionary Biology</i> , 2011 , 11, 32	3	36
122	A new subhaplogroup of native American Y-Chromosomes from the Andes. <i>American Journal of Physical Anthropology</i> , 2011 , 146, 553-9	2.5	34
121	Genetic ancestry and indigenous heritage in a Native American descendant community in Bermuda. <i>American Journal of Physical Anthropology</i> , 2011 , 146, 392-405	2.5	16
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4	Population size history from short genomic scaffolds: how short is too short?		2
3	Parallel paleogenomic transects reveal complex genetic history of early European farmers		7
2	Ancient human genomes reveal a hidden history of strong selection in Eurasia		1
1	Laboratory contamination over time during low-biomass sample analysis		1