

Simon Y W Ho

List of Publications by Year in descending order

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237
papers

30,234
citations

10986

71
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5394

164
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257
all docs

257
docs citations

257
times ranked

30168
citing authors

#	ARTICLE	IF	CITATIONS
1	Relaxed Phylogenetics and Dating with Confidence. PLoS Biology, 2006, 4, e88.	5.6	5,566
2	PartitionFinder: Combined Selection of Partitioning Schemes and Substitution Models for Phylogenetic Analyses. Molecular Biology and Evolution, 2012, 29, 1695-1701.	8.9	5,083
3	Whole-genome analyses resolve early branches in the tree of life of modern birds. Science, 2014, 346, 1320-1331.	12.6	1,583
4	Time Dependency of Molecular Rate Estimates and Systematic Overestimation of Recent Divergence Times. Molecular Biology and Evolution, 2005, 22, 1561-1568.	8.9	933
5	Accounting for Calibration Uncertainty in Phylogenetic Estimation of Evolutionary Divergence Times. Systematic Biology, 2009, 58, 367-380.	5.6	789
6	Species-specific responses of Late Quaternary megafauna to climate and humans. Nature, 2011, 479, 359-364.	27.8	586
7	Time-dependent rates of molecular evolution. Molecular Ecology, 2011, 20, 3087-3101.	3.9	473
8	Rethinking dog domestication by integrating genetics, archeology, and biogeography. Proceedings of the National Academy of Sciences of the United States of America, 2012, 109, 8878-8883.	7.1	412
9	Skylineâ€plot methods for estimating demographic history from nucleotide sequences. Molecular Ecology Resources, 2011, 11, 423-434.	4.8	393
10	Molecular clocks: when times are a-changin'. Trends in Genetics, 2006, 22, 79-83.	6.7	357
11	Testing the Impact of Calibration on Molecular Divergence Times Using a Fossil-Rich Group: The Case of Nothofagus (Fagales). Systematic Biology, 2012, 61, 289-313.	5.6	351
12	Radiation of Extant Cetaceans Driven by Restructuring of the Oceans. Systematic Biology, 2009, 58, 573-585.	5.6	315
13	Ancient mitochondrial DNA provides high-resolution time scale of the peopling of the Americas. Science Advances, 2016, 2, e1501385.	10.3	306
14	EasyCodeML: A visual tool for analysis of selection using CodeML. Ecology and Evolution, 2019, 9, 3891-3898.	1.9	291
15	Molecularâ€clock methods for estimating evolutionary rates and timescales. Molecular Ecology, 2014, 23, 5947-5965.	3.9	290
16	Comparison of Methods for Molecular Species Delimitation Across a Range of Speciation Scenarios. Systematic Biology, 2018, 67, 830-846.	5.6	277
17	The Influence of Rate Heterogeneity among Sites on the Time Dependence of Molecular Rates. Molecular Biology and Evolution, 2012, 29, 3345-3358.	8.9	275
18	Evidence for Time Dependency of Molecular Rate Estimates. Systematic Biology, 2007, 56, 515-522.	5.6	257

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19	Estimating the phylogeny and divergence times of primates using a supermatrix approach. BMC Evolutionary Biology, 2009, 9, 259.	3.2	253
20	The Biasing Effect of Compositional Heterogeneity on Phylogenetic Estimates May be Underestimated. Systematic Biology, 2004, 53, 638-643.	5.6	234
21	Mitochondrial DNA analysis shows a Near Eastern Neolithic origin for domestic cattle and no indication of domestication of European aurochs. Proceedings of the Royal Society B: Biological Sciences, 2007, 274, 1377-1385.	2.6	209
22	Ancient DNA Chronology within Sediment Deposits: Are Paleobiological Reconstructions Possible and Is DNA Leaching a Factor?. Molecular Biology and Evolution, 2007, 24, 982-989.	8.9	202
23	The Effect of Inappropriate Calibration: Three Case Studies in Molecular Ecology. PLoS ONE, 2008, 3, e1615.	2.5	201
24	Using genetic evidence to evaluate four palaeoanthropological hypotheses for the timing of Neanderthal and modern human origins. Journal of Human Evolution, 2010, 59, 87-95.	2.6	190
25	Neolithic mitochondrial haplogroup H genomes and the genetic origins of Europeans. Nature Communications, 2013, 4, 1764.	12.8	180
26	Taller plants have lower rates of molecular evolution. Nature Communications, 2013, 4, 1879.	12.8	179
27	The Global Spread of Hepatitis C Virus 1a and 1b: A Phylodynamic and Phylogeographic Analysis. PLoS Medicine, 2009, 6, e1000198.	8.4	177
28	The Performance of the Date-Randomization Test in Phylogenetic Analyses of Time-Structured Virus Data. Molecular Biology and Evolution, 2015, 32, 1895-1906.	8.9	172
29	Accuracy of Rate Estimation Using Relaxed-Clock Models with a Critical Focus on the Early Metazoan Radiation. Molecular Biology and Evolution, 2005, 22, 1355-1363.	8.9	169
30	Analyses of evolutionary dynamics in viruses are hindered by a time-dependent bias in rate estimates. Proceedings of the Royal Society B: Biological Sciences, 2014, 281, 20140732.	2.6	166
31	Adaptation and conservation insights from the koala genome. Nature Genetics, 2018, 50, 1102-1111.	21.4	163
32	Tracing the Decay of the Historical Signal in Biological Sequence Data. Systematic Biology, 2004, 53, 623-637.	5.6	154
33	Interpreting the modern distribution of Myrtaceae using a dated molecular phylogeny. Molecular Phylogenetics and Evolution, 2015, 93, 29-43.	2.7	153
34	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, 8327-8332.	7.1	149
35	Late-Quaternary biogeographic scenarios for the brown bear (Ursus arctos), a wild mammal model species. Quaternary Science Reviews, 2011, 30, 418-430.	3.0	143
36	Evolution, Systematics, and Phylogeography of Pleistocene Horses in the New World: A Molecular Perspective. PLoS Biology, 2005, 3, e241.	5.6	142

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37	Phylogeography of lions (<i>Panthera leo</i> ssp.) reveals three distinct taxa and a late Pleistocene reduction in genetic diversity. <i>Molecular Ecology</i> , 2009, 18, 1668-1677.	3.9	142
38	Performance of criteria for selecting evolutionary models in phylogenetics: a comprehensive study based on simulated datasets. <i>BMC Evolutionary Biology</i> , 2010, 10, 242.	3.2	141
39	The impact of calibration and clock-model choice on molecular estimates of divergence times. <i>Molecular Phylogenetics and Evolution</i> , 2014, 78, 277-289.	2.7	135
40	Dating the origin and dispersal of hepatitis B virus infection in humans and primates. <i>Hepatology</i> , 2013, 57, 908-916.	7.3	131
41	Bayesian molecular dating: opening up the black box. <i>Biological Reviews</i> , 2018, 93, 1165-1191.	10.4	128
42	Comment on "Protein Sequences from Mastodon and <i>Tyrannosaurus rex</i> Revealed by Mass Spectrometry". <i>Science</i> , 2008, 319, 33-33.	12.6	127
43	Mutation rate is linked to diversification in birds. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2010, 107, 20423-20428.	7.1	126
44	Sudden expansion of a single brown bear maternal lineage across northern continental Eurasia after the last ice age: a general demographic model for mammals?. <i>Molecular Ecology</i> , 2009, 18, 1963-1979.	3.9	119
45	A Bayesian Phylogenetic Method to Estimate Unknown Sequence Ages. <i>Molecular Biology and Evolution</i> , 2011, 28, 879-887.	8.9	119
46	Mitogenetic structure of brown bears (<i>Ursus arctos</i> L.) in northeastern Europe and a new time frame for the formation of European brown bear lineages. <i>Molecular Ecology</i> , 2006, 16, 401-413.	3.9	118
47	Evaluating the Impact of Genomic Data and Priors on Bayesian Estimates of the Angiosperm Evolutionary Timescale. <i>Systematic Biology</i> , 2017, 66, syw086.	5.6	117
48	The extremophile <i>Nicotiana benthamiana</i> has traded viral defence for early vigour. <i>Nature Plants</i> , 2015, 1, 15165.	9.3	114
49	The changing face of the molecular evolutionary clock. <i>Trends in Ecology and Evolution</i> , 2014, 29, 496-503.	8.7	110
50	Adaptive radiation of chemosymbiotic deep-sea mussels. <i>Proceedings of the Royal Society B: Biological Sciences</i> , 2013, 280, 20131243.	2.6	109
51	Evaluating the mitochondrial timescale of human evolution. <i>Trends in Ecology and Evolution</i> , 2009, 24, 515-521.	8.7	106
52	Reconstructing genome evolution in historic samples of the Irish potato famine pathogen. <i>Nature Communications</i> , 2013, 4, 2172.	12.8	103
53	Uplift of the Tibetan plateau: Evidence from divergence times of glyptosternoid catfishes. <i>Molecular Phylogenetics and Evolution</i> , 2006, 39, 568-572.	2.7	96
54	Assessing the Fidelity of Ancient DNA Sequences Amplified From Nuclear Genes. <i>Genetics</i> , 2006, 172, 733-741.	2.9	95

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55	The Light Skin Allele of SLC24A5 in South Asians and Europeans Shares Identity by Descent. PLoS Genetics, 2013, 9, e1003912.	3.5	93
56	Biogeographic calibrations for the molecular clock. Biology Letters, 2015, 11, 20150194.	2.3	93
57	Analysis of complete mitochondrial genomes from extinct and extant rhinoceroses reveals lack of phylogenetic resolution. BMC Evolutionary Biology, 2009, 9, 95.	3.2	92
58	Divergent evolutionary processes associated with colonization of offshore islands. Molecular Ecology, 2013, 22, 5205-5220.	3.9	92
59	A Bayesian Evaluation of Human Mitochondrial Substitution Rates. American Journal of Human Genetics, 2008, 82, 895-902.	6.2	90
60	Mitochondrial Phylogenomics Resolves the Global Spread of Higher Termites, Ecosystem Engineers of the Tropics. Molecular Biology and Evolution, 2017, 34, msw253.	8.9	89
61	Elevated substitution rates estimated from ancient DNA sequences. Biology Letters, 2007, 3, 702-705.	2.3	87
62	Simulating and detecting autocorrelation of molecular evolutionary rates among lineages. Molecular Ecology Resources, 2015, 15, 688-696.	4.8	87
63	Accommodating the Effect of Ancient DNA Damage on Inferences of Demographic Histories. Molecular Biology and Evolution, 2009, 26, 245-248.	8.9	86
64	Improving the Analysis of Dinoflagellate Phylogeny based on rDNA. Protist, 2005, 156, 269-286.	1.5	85
65	One Hundred Twenty Years of Koala Retrovirus Evolution Determined from Museum Skins. Molecular Biology and Evolution, 2013, 30, 299-304.	8.9	85
66	Analysis of Phylogenomic Tree Space Resolves Relationships Among Marsupial Families. Systematic Biology, 2018, 67, 400-412.	5.6	85
67	Tracing the Temporal and Spatial Origins of Island Endemics in the Mediterranean Region: A Case Study from the Citrus Family (Ruta L., Rutaceae). Systematic Biology, 2010, 59, 705-722.	5.6	83
68	Disulfide Bond Acquisition through Eukaryotic Protein Evolution. Molecular Biology and Evolution, 2011, 28, 327-334.	8.9	83
69	Potential efficacy of mitochondrial genes for animal DNA barcoding: a case study using eutherian mammals. BMC Genomics, 2011, 12, 84.	2.8	83
70	Early cave art and ancient DNA record the origin of European bison. Nature Communications, 2016, 7, 13158.	12.8	81
71	Bayesian Evaluation of Temporal Signal in Measurably Evolving Populations. Molecular Biology and Evolution, 2020, 37, 3363-3379.	8.9	81
72	Turnip Mosaic Potyvirus Probably First Spread to Eurasian Brassica Crops from Wild Orchids about 1000 Years Ago. PLoS ONE, 2013, 8, e55336.	2.5	81

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73	The Impact of the Tree Prior on Molecular Dating of Data Sets Containing a Mixture of Inter- and Intraspecies Sampling. <i>Systematic Biology</i> , 2017, 66, syw095.	5.6	80
74	An examination of phylogenetic models of substitution rate variation among lineages. <i>Biology Letters</i> , 2009, 5, 421-424.	2.3	79
75	Mitogenomic phylogenetic analyses of the Delphinidae with an emphasis on the Globicephalinae. <i>BMC Evolutionary Biology</i> , 2011, 11, 65.	3.2	76
76	Bayesian Estimation of Substitution Rates from Ancient DNA Sequences with Low Information Content. <i>Systematic Biology</i> , 2011, 60, 366-375.	5.6	75
77	Geographic and temporal dynamics of a global radiation and diversification in the killer whale. <i>Molecular Ecology</i> , 2015, 24, 3964-3979.	3.9	74
78	A practical introduction to sequentially Markovian coalescent methods for estimating demographic history from genomic data. <i>Ecology and Evolution</i> , 2020, 10, 579-589.	1.9	74
79	Complete mitochondrial genomes and a novel spatial genetic method reveal cryptic phylogeographical structure and migration patterns among brown bears in northwestern Eurasia. <i>Journal of Biogeography</i> , 2013, 40, 915-927.	3.0	73
80	Declining transition/transversion ratios through time reveal limitations to the accuracy of nucleotide substitution models. <i>BMC Evolutionary Biology</i> , 2015, 15, 36.	3.2	73
81	Transoceanic Dispersal and Plate Tectonics Shaped Global Cockroach Distributions: Evidence from Mitochondrial Phylogenomics. <i>Molecular Biology and Evolution</i> , 2018, 35, 970-983.	8.9	73
82	Two Antarctic penguin genomes reveal insights into their evolutionary history and molecular changes related to the Antarctic environment. <i>GigaScience</i> , 2014, 3, 27.	6.4	72
83	Phylogenomic analyses data of the avian phylogenomics project. <i>GigaScience</i> , 2015, 4, 4.	6.4	72
84	Correlating Bayesian date estimates with climatic events and domestication using a bovine case study. <i>Biology Letters</i> , 2008, 4, 370-374.	2.3	70
85	Comment on "Phylogenomics resolves the timing and pattern of insect evolution". <i>Science</i> , 2015, 349, 487-487.	12.6	69
86	Improved characterisation of among-lineage rate variation in cetacean mitogenomes using codon-partitioned relaxed clocks. <i>Mitochondrial DNA</i> , 2010, 21, 138-146.	0.6	67
87	Phylogeographical analyses of domestic and wild yaks based on mitochondrial DNA: new data and reappraisal. <i>Journal of Biogeography</i> , 2010, 37, 2332-2344.	3.0	66
88	Ancient DNA reveals that bowhead whale lineages survived Late Pleistocene climate change and habitat shifts. <i>Nature Communications</i> , 2013, 4, 1677.	12.8	66
89	Ancient mitogenomics. <i>Mitochondrion</i> , 2010, 10, 1-11.	3.4	65
90	Are pollen fossils useful for calibrating relaxed molecular clock dating of phylogenies? A comparative study using Myrtaceae. <i>Molecular Phylogenetics and Evolution</i> , 2012, 63, 15-27.	2.7	65

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91	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.	3.9	65
92	A Potentially Fatal Mix of Herpes in Zoos. <i>Current Biology</i> , 2012, 22, 1727-1731.	3.9	61
93	Mitochondrial DNA diversity and evolution of the Pleistocene cave bear complex. <i>Quaternary International</i> , 2014, 339-340, 224-231.	1.5	60
94	Time-dependent estimates of molecular evolutionary rates: evidence and causes. <i>Molecular Ecology</i> , 2015, 24, 6007-6012.	3.9	59
95	Large-scale migrations of brown bears in Eurasia and to North America during the Late Pleistocene. <i>Journal of Biogeography</i> , 2018, 45, 394-405.	3.0	59
96	The Crucial Role of Calibration in Molecular Date Estimates for the Peopling of the Americas. <i>American Journal of Human Genetics</i> , 2008, 83, 142-146.	6.2	57
97	Revealing the maternal demographic history of <i>Panthera leo</i> using ancient DNA and a spatially explicit genealogical analysis. <i>BMC Evolutionary Biology</i> , 2014, 14, 70.	3.2	57
98	The genetic legacy of aridification: Climate cycling fostered lizard diversification in Australian montane refugia and left low-lying deserts genetically depauperate. <i>Molecular Phylogenetics and Evolution</i> , 2011, 61, 750-759.	2.7	56
99	Accounting for Uncertainty in the Evolutionary Timescale of Green Plants Through Clock-Partitioning and Fossil Calibration Strategies. <i>Systematic Biology</i> , 2020, 69, 1-16.	5.6	55
100	Evidence for Permo-Triassic colonization of the deep sea by isopods. <i>Biology Letters</i> , 2012, 8, 979-982.	2.3	54
101	ClockstaR: choosing the number of relaxed-clock models in molecular phylogenetic analysis. <i>Bioinformatics</i> , 2014, 30, 1017-1019.	4.1	54
102	The Timescale of Emergence and Spread of Turnip Mosaic Potyvirus. <i>Scientific Reports</i> , 2017, 7, 4240.	3.3	54
103	Founder-specific inbreeding depression affects racing performance in Thoroughbred horses. <i>Scientific Reports</i> , 2018, 8, 6167.	3.3	54
104	Comparative dating of <i>Acacia</i> : combining fossils and multiple phylogenies to infer ages of clades with poor fossil records. <i>Australian Journal of Botany</i> , 2013, 61, 436.	0.6	53
105	Response to Comment on "Whole-genome analyses resolve early branches in the tree of life of modern birds". <i>Science</i> , 2015, 349, 1460-1460.	12.6	53
106	Rethinking the evolution of extant sub-Saharan African suids (Suidae, Artiodactyla). <i>Zoologica Scripta</i> , 2011, 40, 327-335.	1.7	51
107	The Temporal Evolution and Global Spread of Cauliflower mosaic virus, a Plant Pararetrovirus. <i>PLoS ONE</i> , 2014, 9, e85641.	2.5	51
108	The Mitochondrial Genome of <i>Elodia flavipalpis</i> Aldrich (Diptera: Tachinidae) and the Evolutionary Timescale of Tachinid Flies. <i>PLoS ONE</i> , 2013, 8, e61814.	2.5	51

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109	Multiple migrations to the Philippines during the last 50,000 years. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2021, 118, .	7.1	50
110	Global and Local Persistence of Influenza A(H5N1) Virus. <i>Emerging Infectious Diseases</i> , 2014, 20, 1287-1295.	4.3	49
111	Phylogeography, Genetic Diversity, and Management Units of Hawksbill Turtles in the Indo-Pacific. <i>Journal of Heredity</i> , 2016, 107, 199-213.	2.4	49
112	Bayesian Estimation of Sequence Damage in Ancient DNA. <i>Molecular Biology and Evolution</i> , 2007, 24, 1416-1422.	8.9	48
113	Positive selection on hemagglutinin and neuraminidase genes of H1N1 influenza viruses. <i>Virology Journal</i> , 2011, 8, 183.	3.4	48
114	The Impact of Modelling Rate Heterogeneity among Sites on Phylogenetic Estimates of Intraspecific Evolutionary Rates and Timescales. <i>PLoS ONE</i> , 2014, 9, e95722.	2.5	48
115	Genomic Characterization of a South American <i>Phytophthora</i> Hybrid Mandates Reassessment of the Geographic Origins of <i>Phytophthora infestans</i> . <i>Molecular Biology and Evolution</i> , 2016, 33, 478-491.	8.9	48
116	Evaluating the Adequacy of Molecular Clock Models Using Posterior Predictive Simulations. <i>Molecular Biology and Evolution</i> , 2015, 32, 2986-2995.	8.9	46
117	PhyloMAd: efficient assessment of phylogenomic model adequacy. <i>Bioinformatics</i> , 2018, 34, 2300-2301.	4.1	46
118	The insect molecular clock. <i>Australian Journal of Entomology</i> , 2013, 52, 101-105.	1.1	45
119	Detailed mtDNA genotypes permit a reassessment of the settlement and population structure of the Andaman Islands. <i>American Journal of Physical Anthropology</i> , 2008, 136, 19-27.	2.1	44
120	Increased Mutation Rate Is Linked to Genome Reduction in Prokaryotes. <i>Current Biology</i> , 2020, 30, 3848-3855.e4.	3.9	44
121	Dating the origin of hepatitis B virus reveals higher substitution rate and adaptation on the branch leading to F/H genotypes. <i>Molecular Phylogenetics and Evolution</i> , 2015, 93, 44-54.	2.7	43
122	An evolutionary timescale for terrestrial isopods and a lack of molecular support for the monophyly of Oniscidea (Crustacea: Isopoda). <i>Organisms Diversity and Evolution</i> , 2017, 17, 813-820.	1.6	43
123	Temporal genetic variation of the red fox, <i>Vulpes vulpes</i> , across western Europe and the British Isles. <i>Quaternary Science Reviews</i> , 2012, 57, 95-104.	3.0	42
124	Tracing the epidemic history of HIV-1 CRF01_AE clusters using near-complete genome sequences. <i>Scientific Reports</i> , 2017, 7, 4024.	3.3	42
125	Linking Branch Lengths across Sets of Loci Provides the Highest Statistical Support for Phylogenetic Inference. <i>Molecular Biology and Evolution</i> , 2020, 37, 1202-1210.	8.9	42
126	Statistical Guidelines for Detecting Past Population Shifts Using Ancient DNA. <i>Molecular Biology and Evolution</i> , 2012, 29, 2241-2251.	8.9	40

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127	Persistence of the Mitochondrial Lineage Responsible for the Irish Potato Famine in Extant New World <i>Phytophthora infestans</i> . <i>Molecular Biology and Evolution</i> , 2014, 31, 1414-1420.	8.9	39
128	Tree imbalance causes a bias in phylogenetic estimation of evolutionary timescales using heterochronous sequences. <i>Molecular Ecology Resources</i> , 2015, 15, 785-794.	4.8	39
129	A Simulation-Based Evaluation of Tip-Dating Under the Fossilized Birth-Death Process. <i>Systematic Biology</i> , 2020, 69, 325-344.	5.6	39
130	Estimating evolutionary rates using time-structured data: a general comparison of phylogenetic methods. <i>Bioinformatics</i> , 2016, 32, 3375-3379.	4.1	38
131	Philippine <i>Ayta</i> possess the highest level of Denisovan ancestry in the world. <i>Current Biology</i> , 2021, 31, 4219-4230.e10.	3.9	37
132	Cryptic diversity, diversification and vicariance in two species complexes of <i>Homocerus</i> (<i>Homocerus</i> <i>collembola</i> , <i>Homocerus</i> <i>hina</i>). <i>Zoologica Scripta</i> , 2014, 43, 393-404.	1.7	36
133	Prolonged decay of molecular rate estimates for metazoan mitochondrial DNA. <i>PeerJ</i> , 2015, 3, e821.	2.0	36
134	Molecular phylogeny of Australian <i>Helicarionidae</i> , <i>Euconulidae</i> and related groups (Gastropoda: Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50 4 2007, 45, 792-812.	2.7	35
135	New Statistical Criteria Detect Phylogenetic Bias Caused by Compositional Heterogeneity. <i>Molecular Biology and Evolution</i> , 2017, 34, 1529-1534.	8.9	35
136	Phylogenetic Estimation of Timescales Using Ancient DNA: The Effects of Temporal Sampling Scheme and Uncertainty in Sample Ages. <i>Molecular Biology and Evolution</i> , 2012, 30, 253-262.	8.9	34
137	Diversification and Demography of the Oriental Garden Lizard (<i>Calotes versicolor</i>) on Hainan Island and the Adjacent Mainland. <i>PLoS ONE</i> , 2013, 8, e64754.	2.5	34
138	Temporal analysis of reassortment and molecular evolution of Cucumber mosaic virus: Extra clues from its segmented genome. <i>Virology</i> , 2016, 487, 188-197.	2.4	34
139	Mitogenomic analysis of a 50-generation chicken pedigree reveals a rapid rate of mitochondrial evolution and evidence for paternal mtDNA inheritance. <i>Biology Letters</i> , 2015, 11, .	2.3	33
140	Phylogenetic evidence of the migration of turnip mosaic potyvirus from Europe to Australia and New Zealand. <i>Journal of General Virology</i> , 2015, 96, 701-713.	2.9	33
141	The Recovery, Interpretation and Use of Ancient Pathogen Genomes. <i>Current Biology</i> , 2020, 30, R1215-R1231.	3.9	33
142	Genomic analysis of the brassica pathogen turnip mosaic potyvirus reveals its spread along the former trade routes of the Silk Road. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2021, 118, .	7.1	32
143	The evolutionary history of Stomatopoda (Crustacea: Malacostraca) inferred from molecular data. <i>PeerJ</i> , 2017, 5, e3844.	2.0	29
144	Evaluating the Impact of Post-Mortem Damage in Ancient DNA: A Theoretical Approach. <i>Journal of Molecular Evolution</i> , 2011, 73, 244-255.	1.8	28

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145	Using multiple relaxed-clock models to estimate evolutionary timescales from DNA sequence data. <i>Molecular Phylogenetics and Evolution</i> , 2014, 77, 65-70.	2.7	28
146	A simulation study of sample size for DNA barcoding. <i>Ecology and Evolution</i> , 2015, 5, 5869-5879.	1.9	28
147	Mitogenomics of the Extinct Cave Lion, <i>Panthera spelaea</i> (Goldfuss, 1810), Resolve its Position within the <i>Panthera</i> Cats. <i>Open Quaternary</i> , 2016, 2, .	1.0	27
148	ACCOUNTING FOR RATE VARIATION AMONG LINEAGES IN COMPARATIVE DEMOGRAPHIC ANALYSES. <i>Evolution; International Journal of Organic Evolution</i> , 2014, 68, 2689-2700.	2.3	25
149	The origins and radiation of Australian <i>Coptotermes</i> termites: From rainforest to desert dwellers. <i>Molecular Phylogenetics and Evolution</i> , 2015, 82, 234-244.	2.7	25
150	Recalibration of the insect evolutionary time scale using Monte San Giorgio fossils suggests survival of key lineages through the End-Permian Extinction. <i>Proceedings of the Royal Society B: Biological Sciences</i> , 2019, 286, 20191854.	2.6	24
151	Genetic structure and phylogeography of platypuses revealed by mitochondrial <i>cytb</i> DNA. <i>Journal of Zoology</i> , 2012, 286, 110-119.	1.7	23
152	A comparison of methods for estimating substitution rates from ancient DNA sequence data. <i>BMC Evolutionary Biology</i> , 2018, 18, 70.	3.2	23
153	Plastome sequences and exploration of tree-space help to resolve the phylogeny of riceflowers (<i>Thymelaeaceae: Pimelea</i>). <i>Molecular Phylogenetics and Evolution</i> , 2018, 127, 156-167.	2.7	23
154	Molecular phylogeny and the underestimated species diversity of the endemic white-bellied rat (<i>Rodentia: Muridae: Niviventer</i>) in Southeast Asia and China. <i>Zoologica Scripta</i> , 2015, 44, 475-494.	1.7	22
155	Investigating the origins of eastern Polynesians using genome-wide data from the Leeward Society Isles. <i>Scientific Reports</i> , 2018, 8, 1823.	3.3	22
156	Parallel evolution of mound-building and grass-feeding in Australian nasute termites. <i>Biology Letters</i> , 2017, 13, 20160665.	2.3	20
157	Empirical calibrated radiocarbon sampler: a tool for incorporating radiocarbon date and calibration error into Bayesian phylogenetic analyses of ancient <i>cytb</i> DNA. <i>Molecular Ecology Resources</i> , 2015, 15, 81-86.	4.8	19
158	Zebra Alpha herpesviruses (EHV-1 and EHV-9): Genetic Diversity, Latency and Co-Infections. <i>Viruses</i> , 2016, 8, 262.	3.3	19
159	Cross-validation to select Bayesian hierarchical models in phylogenetics. <i>BMC Evolutionary Biology</i> , 2016, 16, 115.	3.2	19
160	Molecular clocks. <i>Current Biology</i> , 2016, 26, R399-R402.	3.9	19
161	Strategies for Partitioning Clock Models in Phylogenomic Dating: Application to the Angiosperm Evolutionary Timescale. <i>Genome Biology and Evolution</i> , 2017, 9, 2752-2763.	2.5	19
162	Angels in disguise: sympatric hybridization in the marine angelfishes is widespread and occurs between deeply divergent lineages. <i>Proceedings of the Royal Society B: Biological Sciences</i> , 2020, 287, 20201459.	2.6	18

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