

# Simon Y W Ho

## List of Publications by Year in descending order

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237  
papers

30,234  
citations

10956

71  
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5364

164  
g-index

257  
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257  
docs citations

257  
times ranked

30168  
citing authors

#	ARTICLE	IF	CITATIONS
1	Relaxed Phylogenetics and Dating with Confidence. <i>PLoS Biology</i> , 2006, 4, e88.	2.6	5,566
2	PartitionFinder: Combined Selection of Partitioning Schemes and Substitution Models for Phylogenetic Analyses. <i>Molecular Biology and Evolution</i> , 2012, 29, 1695-1701.	3.5	5,083
3	Whole-genome analyses resolve early branches in the tree of life of modern birds. <i>Science</i> , 2014, 346, 1320-1331.	6.0	1,583
4	Time Dependency of Molecular Rate Estimates and Systematic Overestimation of Recent Divergence Times. <i>Molecular Biology and Evolution</i> , 2005, 22, 1561-1568.	3.5	933
5	Accounting for Calibration Uncertainty in Phylogenetic Estimation of Evolutionary Divergence Times. <i>Systematic Biology</i> , 2009, 58, 367-380.	2.7	789
6	Species-specific responses of Late Quaternary megafauna to climate and humans. <i>Nature</i> , 2011, 479, 359-364.	13.7	586
7	Time-dependent rates of molecular evolution. <i>Molecular Ecology</i> , 2011, 20, 3087-3101.	2.0	473
8	Rethinking dog domestication by integrating genetics, archeology, and biogeography. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2012, 109, 8878-8883.	3.3	412
9	Skyline plot methods for estimating demographic history from nucleotide sequences. <i>Molecular Ecology Resources</i> , 2011, 11, 423-434.	2.2	393
10	Molecular clocks: when times are a-changin'. <i>Trends in Genetics</i> , 2006, 22, 79-83.	2.9	357
11	Testing the Impact of Calibration on Molecular Divergence Times Using a Fossil-Rich Group: The Case of <i>Nothofagus</i> (Fagales). <i>Systematic Biology</i> , 2012, 61, 289-313.	2.7	351
12	Radiation of Extant Cetaceans Driven by Restructuring of the Oceans. <i>Systematic Biology</i> , 2009, 58, 573-585.	2.7	315
13	Ancient mitochondrial DNA provides high-resolution time scale of the peopling of the Americas. <i>Science Advances</i> , 2016, 2, e1501385.	4.7	306
14	EasyCodeML: A visual tool for analysis of selection using CodeML. <i>Ecology and Evolution</i> , 2019, 9, 3891-3898.	0.8	291
15	Molecular clock methods for estimating evolutionary rates and timescales. <i>Molecular Ecology</i> , 2014, 23, 5947-5965.	2.0	290
16	Comparison of Methods for Molecular Species Delimitation Across a Range of Speciation Scenarios. <i>Systematic Biology</i> , 2018, 67, 830-846.	2.7	277
17	The Influence of Rate Heterogeneity among Sites on the Time Dependence of Molecular Rates. <i>Molecular Biology and Evolution</i> , 2012, 29, 3345-3358.	3.5	275
18	Evidence for Time Dependency of Molecular Rate Estimates. <i>Systematic Biology</i> , 2007, 56, 515-522.	2.7	257

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19	Estimating the phylogeny and divergence times of primates using a supermatrix approach. <i>BMC Evolutionary Biology</i> , 2009, 9, 259.	3.2	253
20	The Biasing Effect of Compositional Heterogeneity on Phylogenetic Estimates May be Underestimated. <i>Systematic Biology</i> , 2004, 53, 638-643.	2.7	234
21	Mitochondrial DNA analysis shows a Near Eastern Neolithic origin for domestic cattle and no indication of domestication of European aurochs. <i>Proceedings of the Royal Society B: Biological Sciences</i> , 2007, 274, 1377-1385.	1.2	209
22	Ancient DNA Chronology within Sediment Deposits: Are Paleobiological Reconstructions Possible and Is DNA Leaching a Factor?. <i>Molecular Biology and Evolution</i> , 2007, 24, 982-989.	3.5	202
23	The Effect of Inappropriate Calibration: Three Case Studies in Molecular Ecology. <i>PLoS ONE</i> , 2008, 3, e1615.	1.1	201
24	Using genetic evidence to evaluate four palaeoanthropological hypotheses for the timing of Neanderthal and modern human origins. <i>Journal of Human Evolution</i> , 2010, 59, 87-95.	1.3	190
25	Neolithic mitochondrial haplogroup H genomes and the genetic origins of Europeans. <i>Nature Communications</i> , 2013, 4, 1764.	5.8	180
26	Taller plants have lower rates of molecular evolution. <i>Nature Communications</i> , 2013, 4, 1879.	5.8	179
27	The Global Spread of Hepatitis C Virus 1a and 1b: A Phylodynamic and Phylogeographic Analysis. <i>PLoS Medicine</i> , 2009, 6, e1000198.	3.9	177
28	The Performance of the Date-Randomization Test in Phylogenetic Analyses of Time-Structured Virus Data. <i>Molecular Biology and Evolution</i> , 2015, 32, 1895-1906.	3.5	172
29	Accuracy of Rate Estimation Using Relaxed-Clock Models with a Critical Focus on the Early Metazoan Radiation. <i>Molecular Biology and Evolution</i> , 2005, 22, 1355-1363.	3.5	169
30	Analyses of evolutionary dynamics in viruses are hindered by a time-dependent bias in rate estimates. <i>Proceedings of the Royal Society B: Biological Sciences</i> , 2014, 281, 20140732.	1.2	166
31	Adaptation and conservation insights from the koala genome. <i>Nature Genetics</i> , 2018, 50, 1102-1111.	9.4	163
32	Tracing the Decay of the Historical Signal in Biological Sequence Data. <i>Systematic Biology</i> , 2004, 53, 623-637.	2.7	154
33	Interpreting the modern distribution of Myrtaceae using a dated molecular phylogeny. <i>Molecular Phylogenetics and Evolution</i> , 2015, 93, 29-43.	1.2	153
34	Intraspecific phylogenetic analysis of Siberian woolly mammoths using complete mitochondrial genomes. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2008, 105, 8327-8332.	3.3	149
35	Late-Quaternary biogeographic scenarios for the brown bear ( <i>Ursus arctos</i> ), a wild mammal model species. <i>Quaternary Science Reviews</i> , 2011, 30, 418-430.	1.4	143
36	Evolution, Systematics, and Phylogeography of Pleistocene Horses in the New World: A Molecular Perspective. <i>PLoS Biology</i> , 2005, 3, e241.	2.6	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.	2.0	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.	1.2	135
40	Dating the origin and dispersal of hepatitis B virus infection in humans and primates. <i>Hepatology</i> , 2013, 57, 908-916.	3.6	131
41	Bayesian molecular dating: opening up the black box. <i>Biological Reviews</i> , 2018, 93, 1165-1191.	4.7	128
42	Comment on "Protein Sequences from Mastodon and <i>Tyrannosaurus rex</i> Revealed by Mass Spectrometry". <i>Science</i> , 2008, 319, 33-33.	6.0	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.	3.3	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.	2.0	119
45	A Bayesian Phylogenetic Method to Estimate Unknown Sequence Ages. <i>Molecular Biology and Evolution</i> , 2011, 28, 879-887.	3.5	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.	2.0	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.	2.7	117
48	The extremophile <i>Nicotiana benthamiana</i> has traded viral defence for early vigour. <i>Nature Plants</i> , 2015, 1, 15165.	4.7	114
49	The changing face of the molecular evolutionary clock. <i>Trends in Ecology and Evolution</i> , 2014, 29, 496-503.	4.2	110
50	Adaptive radiation of chemosymbiotic deep-sea mussels. <i>Proceedings of the Royal Society B: Biological Sciences</i> , 2013, 280, 20131243.	1.2	109
51	Evaluating the mitochondrial timescale of human evolution. <i>Trends in Ecology and Evolution</i> , 2009, 24, 515-521.	4.2	106
52	Reconstructing genome evolution in historic samples of the Irish potato famine pathogen. <i>Nature Communications</i> , 2013, 4, 2172.	5.8	103
53	Uplift of the Tibetan plateau: Evidence from divergence times of glyptosternoid catfishes. <i>Molecular Phylogenetics and Evolution</i> , 2006, 39, 568-572.	1.2	96
54	Assessing the Fidelity of Ancient DNA Sequences Amplified From Nuclear Genes. <i>Genetics</i> , 2006, 172, 733-741.	1.2	95

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55	The Light Skin Allele of SLC24A5 in South Asians and Europeans Shares Identity by Descent. <i>PLoS Genetics</i> , 2013, 9, e1003912.	1.5	93
56	Biogeographic calibrations for the molecular clock. <i>Biology Letters</i> , 2015, 11, 20150194.	1.0	93
57	Analysis of complete mitochondrial genomes from extinct and extant rhinoceroses reveals lack of phylogenetic resolution. <i>BMC Evolutionary Biology</i> , 2009, 9, 95.	3.2	92
58	Divergent evolutionary processes associated with colonization of offshore islands. <i>Molecular Ecology</i> , 2013, 22, 5205-5220.	2.0	92
59	A Bayesian Evaluation of Human Mitochondrial Substitution Rates. <i>American Journal of Human Genetics</i> , 2008, 82, 895-902.	2.6	90
60	Mitochondrial Phylogenomics Resolves the Global Spread of Higher Termites, Ecosystem Engineers of the Tropics. <i>Molecular Biology and Evolution</i> , 2017, 34, msw253.	3.5	89
61	Elevated substitution rates estimated from ancient DNA sequences. <i>Biology Letters</i> , 2007, 3, 702-705.	1.0	87
62	Simulating and detecting autocorrelation of molecular evolutionary rates among lineages. <i>Molecular Ecology Resources</i> , 2015, 15, 688-696.	2.2	87
63	Accommodating the Effect of Ancient DNA Damage on Inferences of Demographic Histories. <i>Molecular Biology and Evolution</i> , 2009, 26, 245-248.	3.5	86
64	Improving the Analysis of Dinoflagellate Phylogeny based on rDNA. <i>Protist</i> , 2005, 156, 269-286.	0.6	85
65	One Hundred Twenty Years of Koala Retrovirus Evolution Determined from Museum Skins. <i>Molecular Biology and Evolution</i> , 2013, 30, 299-304.	3.5	85
66	Analysis of Phylogenomic Tree Space Resolves Relationships Among Marsupial Families. <i>Systematic Biology</i> , 2018, 67, 400-412.	2.7	85
67	Tracing the Temporal and Spatial Origins of Island Endemics in the Mediterranean Region: A Case Study from the Citrus Family ( <i>Ruta</i> L., Rutaceae). <i>Systematic Biology</i> , 2010, 59, 705-722.	2.7	83
68	Disulfide Bond Acquisition through Eukaryotic Protein Evolution. <i>Molecular Biology and Evolution</i> , 2011, 28, 327-334.	3.5	83
69	Potential efficacy of mitochondrial genes for animal DNA barcoding: a case study using eutherian mammals. <i>BMC Genomics</i> , 2011, 12, 84.	1.2	83
70	Early cave art and ancient DNA record the origin of European bison. <i>Nature Communications</i> , 2016, 7, 13158.	5.8	81
71	Bayesian Evaluation of Temporal Signal in Measurably Evolving Populations. <i>Molecular Biology and Evolution</i> , 2020, 37, 3363-3379.	3.5	81
72	Turnip Mosaic Potyvirus Probably First Spread to Eurasian Brassica Crops from Wild Orchids about 1000 Years Ago. <i>PLoS ONE</i> , 2013, 8, e55336.	1.1	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.	2.7	80
74	An examination of phylogenetic models of substitution rate variation among lineages. <i>Biology Letters</i> , 2009, 5, 421-424.	1.0	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.	2.7	75
77	Geographic and temporal dynamics of a global radiation and diversification in the killer whale. <i>Molecular Ecology</i> , 2015, 24, 3964-3979.	2.0	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.	0.8	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.	1.4	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.	3.5	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.	3.3	72
83	Phylogenomic analyses data of the avian phylogenomics project. <i>GigaScience</i> , 2015, 4, 4.	3.3	72
84	Correlating Bayesian date estimates with climatic events and domestication using a bovine case study. <i>Biology Letters</i> , 2008, 4, 370-374.	1.0	70
85	Comment on "Phylogenomics resolves the timing and pattern of insect evolution". <i>Science</i> , 2015, 349, 487-487.	6.0	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.	1.4	66
88	Ancient DNA reveals that bowhead whale lineages survived Late Pleistocene climate change and habitat shifts. <i>Nature Communications</i> , 2013, 4, 1677.	5.8	66
89	Ancient mitogenomics. <i>Mitochondrion</i> , 2010, 10, 1-11.	1.6	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.	1.2	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.	1.8	65
92	A Potentially Fatal Mix of Herpes in Zoos. <i>Current Biology</i> , 2012, 22, 1727-1731.	1.8	61
93	Mitochondrial DNA diversity and evolution of the Pleistocene cave bear complex. <i>Quaternary International</i> , 2014, 339-340, 224-231.	0.7	60
94	Time-dependent estimates of molecular evolutionary rates: evidence and causes. <i>Molecular Ecology</i> , 2015, 24, 6007-6012.	2.0	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.	1.4	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.	2.6	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.	1.2	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.	2.7	55
100	Evidence for Permo-Triassic colonization of the deep sea by isopods. <i>Biology Letters</i> , 2012, 8, 979-982.	1.0	54
101	ClockstaR: choosing the number of relaxed-clock models in molecular phylogenetic analysis. <i>Bioinformatics</i> , 2014, 30, 1017-1019.	1.8	54
102	The Timescale of Emergence and Spread of Turnip Mosaic Potyvirus. <i>Scientific Reports</i> , 2017, 7, 4240.	1.6	54
103	Founder-specific inbreeding depression affects racing performance in Thoroughbred horses. <i>Scientific Reports</i> , 2018, 8, 6167.	1.6	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.	0.3	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.	6.0	53
106	Rethinking the evolution of extant sub-Saharan African suids (Suidae, Artiodactyla). <i>Zoologica Scripta</i> , 2011, 40, 327-335.	0.7	51
107	The Temporal Evolution and Global Spread of Cauliflower mosaic virus, a Plant Pararetrovirus. <i>PLoS ONE</i> , 2014, 9, e85641.	1.1	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.	1.1	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, .	3.3	50
110	Global and Local Persistence of Influenza A(H5N1) Virus. <i>Emerging Infectious Diseases</i> , 2014, 20, 1287-1295.	2.0	49
111	Phylogeography, Genetic Diversity, and Management Units of Hawksbill Turtles in the Indo-Pacific. <i>Journal of Heredity</i> , 2016, 107, 199-213.	1.0	49
112	Bayesian Estimation of Sequence Damage in Ancient DNA. <i>Molecular Biology and Evolution</i> , 2007, 24, 1416-1422.	3.5	48
113	Positive selection on hemagglutinin and neuraminidase genes of H1N1 influenza viruses. <i>Virology Journal</i> , 2011, 8, 183.	1.4	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.	1.1	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.	3.5	48
116	Evaluating the Adequacy of Molecular Clock Models Using Posterior Predictive Simulations. <i>Molecular Biology and Evolution</i> , 2015, 32, 2986-2995.	3.5	46
117	PhyloMAd: efficient assessment of phylogenomic model adequacy. <i>Bioinformatics</i> , 2018, 34, 2300-2301.	1.8	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.	1.8	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.	1.2	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.	0.7	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.	1.4	42
124	Tracing the epidemic history of HIV-1 CRF01_AE clusters using near-complete genome sequences. <i>Scientific Reports</i> , 2017, 7, 4024.	1.6	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.	3.5	42
126	Statistical Guidelines for Detecting Past Population Shifts Using Ancient DNA. <i>Molecular Biology and Evolution</i> , 2012, 29, 2241-2251.	3.5	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.	3.5	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.	2.2	39
129	A Simulation-Based Evaluation of Tip-Dating Under the Fossilized Birth-Death Process. <i>Systematic Biology</i> , 2020, 69, 325-344.	2.7	39
130	Estimating evolutionary rates using time-structured data: a general comparison of phylogenetic methods. <i>Bioinformatics</i> , 2016, 32, 3375-3379.	1.8	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.	1.8	37
132	Cryptic diversity, diversification and vicariance in two species complexes of <i>Tomocerus</i> ( <i>Tomocerus</i> ( <i>Tomocerus</i> ) <i>collembola</i> , <i>Tomocerus</i> ( <i>Tomocerus</i> ) <i>hina</i> ). <i>Zoologica Scripta</i> , 2014, 43, 393-404.	0.7	36
133	Prolonged decay of molecular rate estimates for metazoan mitochondrial DNA. <i>PeerJ</i> , 2015, 3, e821.	0.9	36
134	Molecular phylogeny of Australian Helicarionidae, Euconulidae and related groups (Gastropoda: Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50 4 2007, 45, 792-812.	1.2	35
135	New Statistical Criteria Detect Phylogenetic Bias Caused by Compositional Heterogeneity. <i>Molecular Biology and Evolution</i> , 2017, 34, 1529-1534.	3.5	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.	3.5	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.	1.1	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.	1.1	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, .	1.0	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.	1.3	33
141	The Recovery, Interpretation and Use of Ancient Pathogen Genomes. <i>Current Biology</i> , 2020, 30, R1215-R1231.	1.8	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, .	3.3	32
143	The evolutionary history of Stomatopoda (Crustacea: Malacostraca) inferred from molecular data. <i>PeerJ</i> , 2017, 5, e3844.	0.9	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.	0.8	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.	1.2	28
146	A simulation study of sample size for DNA barcoding. <i>Ecology and Evolution</i> , 2015, 5, 5869-5879.	0.8	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, .	0.5	27
148	ACCOUNTING FOR RATE VARIATION AMONG LINEAGES IN COMPARATIVE DEMOGRAPHIC ANALYSES. <i>Evolution; International Journal of Organic Evolution</i> , 2014, 68, 2689-2700.	1.1	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.	1.2	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.	1.2	24
151	Genetic structure and phylogeography of platypuses revealed by mitochondrial <i>cytb</i> DNA. <i>Journal of Zoology</i> , 2012, 286, 110-119.	0.8	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.	1.2	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.	0.7	22
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