

Robert C Thomson

List of Publications by Year in descending order

Source: <https://exaly.com/author-pdf/1440049/publications.pdf>

Version: 2024-02-01

45
papers

2,227
citations

236612

25
h-index

233125

45
g-index

51
all docs

51
docs citations

51
times ranked

3229
citing authors

#	ARTICLE	IF	CITATIONS
1	The western painted turtle genome, a model for the evolution of extreme physiological adaptations in a slowly evolving lineage. <i>Genome Biology</i> , 2013, 14, R28.	13.9	276
2	Delimiting Species in Recent Radiations. <i>Systematic Biology</i> , 2007, 56, 896-906.	2.7	178
3	Sparse Supermatrices for Phylogenetic Inference: Taxonomy, Alignment, Rogue Taxa, and the Phylogeny of Living Turtles. <i>Systematic Biology</i> , 2010, 59, 42-58.	2.7	155
4	Phylogenomics Reveals Ancient Gene Tree Discordance in the Amphibian Tree of Life. <i>Systematic Biology</i> , 2021, 70, 49-66.	2.7	124
5	Genome-enabled development of DNA markers for ecology, evolution and conservation. <i>Molecular Ecology</i> , 2010, 19, 2184-2195.	2.0	114
6	A global phylogeny of turtles reveals a burst of climate-associated diversification on continental margins. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2021, 118, .	3.3	98
7	Bayes factors unmask highly variable information content, bias, and extreme influence in phylogenomic analyses. <i>Systematic Biology</i> , 2017, 66, syw101.	2.7	97
8	Fourteen nuclear genes provide phylogenetic resolution for difficult nodes in the turtle tree of life. <i>Molecular Phylogenetics and Evolution</i> , 2010, 55, 1189-1194.	1.2	81
9	Impact of Model Violations on the Inference of Species Boundaries Under the Multispecies Coalescent. <i>Systematic Biology</i> , 2018, 67, 269-284.	2.7	76
10	A critical appraisal of the use of microRNA data in phylogenetics. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2014, 111, E3659-68.	3.3	63
11	Phylogenomics and species delimitation in the knob-scaled lizards of the genus <i>Xenosaurus</i> (Squamata: Xenosauridae) using ddRADseq data reveal a substantial underestimation of diversity. <i>Molecular Phylogenetics and Evolution</i> , 2017, 106, 241-253.	1.2	63
12	Developing markers for multilocus phylogenetics in non-model organisms: A test case with turtles. <i>Molecular Phylogenetics and Evolution</i> , 2008, 49, 514-525.	1.2	57
13	The advantages of going large: genome-wide <i>scn</i> SNP <i>s</i> clarify the complex population history and systematics of the threatened western pond turtle. <i>Molecular Ecology</i> , 2014, 23, 2228-2241.	2.0	56
14	Biomechanical trade-offs bias rates of evolution in the feeding apparatus of fishes. <i>Proceedings of the Royal Society B: Biological Sciences</i> , 2012, 279, 1287-1292.	1.2	55
15	Assessing what is needed to resolve a molecular phylogeny: simulations and empirical data from emydid turtles. <i>BMC Evolutionary Biology</i> , 2009, 9, 56.	3.2	51
16	Variation Across Mitochondrial Gene Trees Provides Evidence for Systematic Error: How Much Gene Tree Variation Is Biological?. <i>Systematic Biology</i> , 2018, 67, 847-860.	2.7	51
17	Nuclear gene phylogeography reveals the historical legacy of an ancient inland sea on lineages of the western pond turtle, <i>Emys marmorata</i> in California. <i>Molecular Ecology</i> , 2010, 19, 542-556.	2.0	44
18	Misleading phylogenetic inferences based on single-exemplar sampling in the turtle genus <i>Pseudemys</i> . <i>Molecular Phylogenetics and Evolution</i> , 2013, 68, 269-281.	1.2	43

#	ARTICLE	IF	CITATIONS
19	Assessing the performance of <sc>DNA</sc> barcoding using posterior predictive simulations. <i>Molecular Ecology</i> , 2016, 25, 1944-1957.	2.0	40
20	Evaluating Model Performance in Evolutionary Biology. <i>Annual Review of Ecology, Evolution, and Systematics</i> , 2018, 49, 95-114.	3.8	39
21	Phylogeny and temporal diversification of the New World pond turtles (Emydidae). <i>Molecular Phylogenetics and Evolution</i> , 2016, 103, 85-97.	1.2	34
22	Species boundaries and phylogenetic relationships in the critically endangered Asian box turtle genus <i>Cuora</i> . <i>Molecular Phylogenetics and Evolution</i> , 2012, 63, 656-667.	1.2	33
23	Model-Based Species Delimitation: Are Coalescent Species Reproductively Isolated?. <i>Systematic Biology</i> , 2020, 69, 708-721.	2.7	33
24	The origin of tiger salamander (<i>Ambystoma tigrinum</i>) populations in California, Oregon, and Nevada: introductions or relicts?. <i>Conservation Genetics</i> , 2011, 12, 355-370.	0.8	32
25	Sun skink landscape genomics: assessing the roles of microevolutionary processes in shaping genetic and phenotypic diversity across a heterogeneous and fragmented landscape. <i>Molecular Ecology</i> , 2015, 24, 1696-1712.	2.0	32
26	P3: Phylogenetic Posterior Prediction in RevBayes. <i>Molecular Biology and Evolution</i> , 2018, 35, 1028-1034.	3.5	28
27	Rapid progress on the vertebrate tree of life. <i>BMC Biology</i> , 2010, 8, 19.	1.7	27
28	Revised classification of the righteye flounders (Teleostei: Pleuronectidae) based on multilocus phylogeny with complete taxon sampling. <i>Molecular Phylogenetics and Evolution</i> , 2018, 125, 147-162.	1.2	26
29	Complex patterns of hybridization and introgression across evolutionary timescales in Mexican whiptail lizards (<i>Aspidoscelis</i>). <i>Molecular Phylogenetics and Evolution</i> , 2019, 132, 284-295.	1.2	25
30	Phylogeography of a widespread lizard complex reflects patterns of both geographic and ecological isolation. <i>Molecular Ecology</i> , 2019, 28, 644-657.	2.0	23
31	Multilocus phylogeny of the New-World mud turtles (Kinosternidae) supports the traditional classification of the group. <i>Molecular Phylogenetics and Evolution</i> , 2014, 76, 254-260.	1.2	21
32	Habitat Features Determine the Basking Distribution of Introduced Red-Eared Sliders and Native Western Pond Turtles. <i>Chelonian Conservation and Biology</i> , 2013, 12, 192-199.	0.1	19
33	Molecular phylogeny and divergence of the map turtles (Emydidae: Graptemys). <i>Molecular Phylogenetics and Evolution</i> , 2018, 121, 61-70.	1.2	19
34	Cryptic variation and the tragedy of unrecognized taxa: the case of international trade in the spiny turtle <i>Heosemys spinosa</i> (Testudines: Geoemydidae). <i>Zoological Journal of the Linnean Society</i> , 2012, 164, 811-824.	1.0	18
35	Distribution and Abundance of Invasive Red-Eared Sliders (<i>Trachemys scripta elegans</i>) in California's Sacramento River Basin and Possible Impacts on Native Western Pond Turtles (<i>Emys marmorata</i>). <i>Chelonian Conservation and Biology</i> , 2010, 9, 297-302.	0.1	17
36	Properties of Markov Chain Monte Carlo Performance across Many Empirical Alignments. <i>Molecular Biology and Evolution</i> , 2021, 38, 1627-1640.	3.5	13

#	ARTICLE	IF	CITATIONS
37	Genetic diversity and the origins of parthenogenesis in the teiid lizard <i>Aspidoscelis laredoensis</i> . <i>Molecular Ecology</i> , 2022, 31, 266-278.	2.0	10
38	Ecological variability is associated with functional trait diversity in the western fence lizard (<i>Sceloporus occidentalis</i>). <i>Biological Journal of the Linnean Society</i> , 2020, 129, 414-424.	0.7	9
39	A New Diploid Parthenogenetic Whiptail Lizard from Sonora, Mexico, Is the "Missing Link" in the Evolutionary Transition to Polyploidy. <i>American Naturalist</i> , 2021, 198, 295-309.	1.0	9
40	On the Need for New Measures of Phylogenomic Support. <i>Systematic Biology</i> , 2022, 71, 917-920.	2.7	9
41	Testing avian, squamate, and mammalian nuclear markers for cross amplification in turtles. <i>Conservation Genetics Resources</i> , 2010, 2, 127-129.	0.4	8
42	A time-calibrated phylogeny of the butterfly tribe Melitaeini. <i>Molecular Phylogenetics and Evolution</i> , 2014, 79, 69-81.	1.2	8
43	The Behavior of Metropolis-Coupled Markov Chains When Sampling Rugged Phylogenetic Distributions. <i>Systematic Biology</i> , 2018, 67, 729-734.	2.7	6
44	PhyLIS: A Simple GNU/Linux Distribution for Phylogenetics and Phyloinformatics. <i>Evolutionary Bioinformatics</i> , 2009, 5, EBO.S3169.	0.6	4
45	Origins of softshell turtles in Hawaii with implications for conservation. <i>Conservation Genetics</i> , 2016, 17, 207-220.	0.8	1