

Jack Sullivan

List of Publications by Year in descending order

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Version: 2024-02-01

54
papers

4,066
citations

147726

31
h-index

175177

52
g-index

55
all docs

55
docs citations

55
times ranked

3784
citing authors

#	ARTICLE	IF	CITATIONS
1	Genomic evidence of an ancient inland temperate rainforest in the Pacific Northwest of North America. <i>Molecular Ecology</i> , 2022, , .	2.0	4
2	The role of multiple Pleistocene refugia in promoting diversification in the Pacific Northwest. <i>Molecular Ecology</i> , 2022, 31, 4402-4416.	2.0	4
3	Genomic resolution of cryptic species diversity in chipmunks. <i>Evolution; International Journal of Organic Evolution</i> , 2022, 76, 2004-2019.	1.1	2
4	Diversification, Introgression, and Rampant Cytonuclear Discordance in Rocky Mountains Chipmunks (<i>Sciuridae: <i>Tamias</i></i>). <i>Systematic Biology</i> , 2021, 70, 908-921.	2.7	20
5	GENETIC STRUCTURE NOT DETECTED IN NORTHERN IDAHO AND NORTHEAST WASHINGTON WESTERN TOAD (<i>ANAXYRUS BOREAS</i>) POPULATIONS. , 2021, 102, .		2
6	Comparative phylogeography of two Northern Rocky Mountain endemics: the widespread <i>Anguispira kochi occidentalis</i> and the narrow-range <i>Anguispira nimapuna</i> (Gastropoda: Discidae). <i>Biological Journal of the Linnean Society</i> , 2021, 133, 817-834.	0.7	2
7	No evidence for phyllosymbiosis in western chipmunk species. <i>FEMS Microbiology Ecology</i> , 2020, 96, .	1.3	22
8	Carnivore Contact: A Species Fracture Zone Delineated Amongst Genetically Structured North American Marten Populations (<i>Martes americana</i> and <i>Martes caurina</i>). <i>Frontiers in Genetics</i> , 2020, 11, 735.	1.1	8
9	Integrating life history traits into predictive phylogeography. <i>Molecular Ecology</i> , 2019, 28, 2062-2073.	2.0	11
10	Complex interplay of ancient vicariance and recent patterns of geographical speciation in north-western North American temperate rainforests explains the phylogeny of jumping slugs (<i>Hemphillia</i> spp.). <i>Biological Journal of the Linnean Society</i> , 2019, 127, 876-889.	0.7	10
11	Combining allele frequency and tree-based approaches improves phylogeographic inference from natural history collections. <i>Molecular Ecology</i> , 2018, 27, 1012-1024.	2.0	9
12	Predicting plant conservation priorities on a global scale. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2018, 115, 13027-13032.	3.3	92
13	Testing for the presence of cryptic diversity in tail-dropper slugs (<i>Prophysaon</i>) using molecular data. <i>Biological Journal of the Linnean Society</i> , 2018, 124, 518-532.	0.7	10
14	Demographic model selection using random forests and the site frequency spectrum. <i>Molecular Ecology</i> , 2017, 26, 4562-4573.	2.0	49
15	Comparative Phylogenomic Assessment of Mitochondrial Introgression among Several Species of Chipmunks (<i>TAMIAS</i>). <i>Genome Biology and Evolution</i> , 2016, 9, evw254.	1.1	12
16	Identifying cryptic diversity with predictive phylogeography. <i>Proceedings of the Royal Society B: Biological Sciences</i> , 2016, 283, 20161529.	1.2	45
17	Genetic Structure across Broad Spatial and Temporal Scales: Rocky Mountain Tailed Frogs (<i>Ascaphus</i>)	1.0	11
18	Model selection as a tool for phylogeographic inference: an example from the willow <i><i>Salix melanopsis</i></i> . <i>Molecular Ecology</i> , 2013, 22, 4014-4028.	2.0	58

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19	Inferring the Evolutionary History of IncP-1 Plasmids Despite Incongruence among Backbone Gene Trees. <i>Molecular Biology and Evolution</i> , 2013, 30, 154-166.	3.5	63
20	Phylogeny Estimation of the Radiation of Western North American Chipmunks (<i>Tamias</i>) in the Face of Introgression Using Reproductive Protein Genes. <i>Systematic Biology</i> , 2012, 61, 44.	2.7	55
21	Species limits and integrated taxonomy of the Idaho ground squirrel (<i>Urocyon</i>): genetic and ecological differentiation. <i>Journal of Mammalogy</i> , 2012, 93, 589-604.	0.6	13
22	Approximating Model Probabilities in Bayesian Information Criterion and Decision-Theoretic Approaches to Model Selection in Phylogenetics. <i>Molecular Biology and Evolution</i> , 2011, 28, 343-349.	3.5	8
23	Introgression at differentially aged hybrid zones in red-tailed chipmunks. <i>Genetica</i> , 2010, 138, 869-883.	0.5	15
24	Effects of parameter estimation on maximum-likelihood bootstrap analysis. <i>Molecular Phylogenetics and Evolution</i> , 2010, 56, 642-648.	1.2	2
25	Assessment of Substitution Model Adequacy Using Frequentist and Bayesian Methods. <i>Molecular Biology and Evolution</i> , 2010, 27, 2790-2803.	3.5	45
26	Examination of nuclear loci across a zone of mitochondrial introgression between <i>Tamias ruficaudus</i> and <i>T. amoenus</i> . <i>Journal of Mammalogy</i> , 2010, 91, 1389-1400.	0.6	14
27	Assessment of gene flow across a hybrid zone in red-tailed chipmunks (<i>Tamias ruficaudus</i>). <i>Molecular Ecology</i> , 2009, 18, 3097-3109.	2.0	42
28	Ancient hybridization and mitochondrial capture between two species of chipmunks. <i>Molecular Ecology</i> , 2008, 17, 1313-1327.	2.0	162
29	Does Choice in Model Selection Affect Maximum Likelihood Analysis?. <i>Systematic Biology</i> , 2008, 57, 76-85.	2.7	108
30	The complete nuclear estrogen receptor family in the rainbow trout: Discovery of the novel ER β 2 and both ER α 2 isoforms. <i>Gene</i> , 2007, 392, 164-173.	1.0	149
31	A multi-compartmented glacial refugium in the northern Rocky Mountains: Evidence from the phylogeography of <i>Cardamine constancei</i> (Brassicaceae). <i>Conservation Genetics</i> , 2006, 6, 895-904.	0.8	48
32	ALLOZYME AND MITOCHONDRIAL DNA VARIATION IN THE TAILED FROG (ANURA: ASCAPHUS): THE INFLUENCE OF GEOGRAPHY AND GENE FLOW. <i>Herpetologica</i> , 2006, 62, 235-258.	0.2	23
33	Testing hypotheses of speciation timing in <i>Dicamptodon copei</i> and <i>Dicamptodon aterrimus</i> (Caudata: Tj ETQq1 1 0,784314 48 BT /Over	1.2	14
34	INVESTIGATING THE EVOLUTIONARY HISTORY OF THE PACIFIC NORTHWEST MESIC FOREST ECOSYSTEM: HYPOTHESIS TESTING WITHIN A COMPARATIVE PHYLOGEOGRAPHIC FRAMEWORK. <i>Evolution; International Journal of Organic Evolution</i> , 2005, 59, 1639-1652.	1.1	183
35	Accounting for Uncertainty in the Tree Topology Has Little Effect on the Decision-Theoretic Approach to Model Selection in Phylogeny Estimation. <i>Molecular Biology and Evolution</i> , 2005, 22, 691-703.	3.5	68
36	INVESTIGATING THE EVOLUTIONARY HISTORY OF THE PACIFIC NORTHWEST MESIC FOREST ECOSYSTEM: HYPOTHESIS TESTING WITHIN A COMPARATIVE PHYLOGEOGRAPHIC FRAMEWORK. <i>Evolution; International Journal of Organic Evolution</i> , 2005, 59, 1639.	1.1	170

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37	Evaluating the Performance of a Successive-Approximations Approach to Parameter Optimization in Maximum-Likelihood Phylogeny Estimation. <i>Molecular Biology and Evolution</i> , 2005, 22, 1386-1392.	3.5	115
38	Maximum-Likelihood Methods for Phylogeny Estimation. <i>Methods in Enzymology</i> , 2005, 395, 757-779.	0.4	22
39	Model Selection in Phylogenetics. <i>Annual Review of Ecology, Evolution, and Systematics</i> , 2005, 36, 445-466.	3.8	349
40	Investigating the evolutionary history of the Pacific Northwest mesic forest ecosystem: hypothesis testing within a comparative phylogeographic framework. <i>Evolution; International Journal of Organic Evolution</i> , 2005, 59, 1639-52.	1.1	36
41	Testing Nested Phylogenetic and Phylogeographic Hypotheses in the <i>Plethodon vandykei</i> Species Group. <i>Systematic Biology</i> , 2004, 53, 781-792.	2.7	85
42	Extensive mtDNA variation within the yellow-pine chipmunk, <i>Tamias amoenus</i> (Rodentia: Sciuridae), and phylogeographic inferences for northwest North America. <i>Molecular Phylogenetics and Evolution</i> , 2003, 26, 389-408.	1.2	62
43	PHYLOGEOGRAPHY AND INTROGRESSIVE HYBRIDIZATION: CHIPMUNKS (GENUS <i>TAMIAS</i>) IN THE NORTHERN ROCKY MOUNTAINS. <i>Evolution; International Journal of Organic Evolution</i> , 2003, 57, 1900-1916.	1.1	76
44	Performance-Based Selection of Likelihood Models for Phylogeny Estimation. <i>Systematic Biology</i> , 2003, 52, 674-683.	2.7	386
45	Phylogeography of the red-tailed chipmunk (<i>Tamias ruficaudus</i>), a northern Rocky Mountain endemic. <i>Molecular Ecology</i> , 2001, 10, 2683-2695.	2.0	57
46	PHYLOGEOGRAPHY OF THE TAILED FROG (<i>ASCAPHUS TRUEI</i>): IMPLICATIONS FOR THE BIOGEOGRAPHY OF THE PACIFIC NORTHWEST. <i>Evolution; International Journal of Organic Evolution</i> , 2001, 55, 147-160.	1.1	140
47	Should We Use Model-Based Methods for Phylogenetic Inference When We Know That Assumptions About Among-Site Rate Variation and Nucleotide Substitution Pattern Are Violated?. <i>Systematic Biology</i> , 2001, 50, 723-729.	2.7	170
48	Phylogeography of <i>Peromyscus furvus</i> (Rodentia; Muridae) based on cytochrome b sequence data. <i>Molecular Ecology</i> , 2000, 9, 2129-2135.	2.0	34
49	Comparative Phylogeography of Mesoamerican Highland Rodents: Concerted versus Independent Response to Past Climatic Fluctuations. <i>American Naturalist</i> , 2000, 155, 755-768.	1.0	180
50	Phylogeography and Molecular Systematics of the <i>Peromyscus aztecus</i> Species Group (Rodentia: Muridae). <i>Molecular Ecology</i> , 2000, 9, 2129-2135.	2.7	236
51	Are Guinea Pigs Rodents? The Importance of Adequate Models in Molecular Phylogenetics. <i>Journal of Mammalian Evolution</i> , 1997, 4, 77-86.	1.0	266
52	Evolution of the Mitochondrial Cytochrome Oxidase II Gene in Collembola. <i>Journal of Molecular Evolution</i> , 1997, 44, 145-158.	0.8	177
53	The effect of topology on estimates of among-site rate variation. <i>Journal of Molecular Evolution</i> , 1996, 42, 308-312.	0.8	87
54	Genomic Resources for the North American Water Vole (<i>Microtus richardsoni</i>) and the Montane Vole (<i>Microtus montanus</i>). <i>GigaByte</i> , 0, 2021, 1-13.	0.0	1