

Keith A Crandall

List of Publications by Year in descending order

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Version: 2024-02-01

350
papers

59,688
citations

8755

75
h-index

1009

236
g-index

395
all docs

395
docs citations

395
times ranked

42554
citing authors

#	ARTICLE	IF	CITATIONS
1	MODELTEST: testing the model of DNA substitution.. <i>Bioinformatics</i> , 1998, 14, 817-818.	4.1	18,761
2	TCS: a computer program to estimate gene genealogies. <i>Molecular Ecology</i> , 2000, 9, 1657-1659.	3.9	8,515
3	A cladistic analysis of phenotypic associations with haplotypes inferred from restriction endonuclease mapping and DNA sequence data. III. Cladogram estimation.. <i>Genetics</i> , 1992, 132, 619-633.	2.9	2,593
4	Considering evolutionary processes in conservation biology. <i>Trends in Ecology and Evolution</i> , 2000, 15, 290-295.	8.7	1,567
5	Intraspecific gene genealogies: trees grafting into networks. <i>Trends in Ecology and Evolution</i> , 2001, 16, 37-45.	8.7	1,359
6	Evaluation of methods for detecting recombination from DNA sequences: Computer simulations. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2001, 98, 13757-13762.	7.1	1,330
7	GeoDis: a program for the cladistic nested analysis of the geographical distribution of genetic haplotypes. <i>Molecular Ecology</i> , 2000, 9, 487-488.	3.9	1,205
8	PHYLOGENY ESTIMATION AND HYPOTHESIS TESTING USING MAXIMUM LIKELIHOOD. <i>Annual Review of Ecology, Evolution, and Systematics</i> , 1997, 28, 437-466.	6.7	896
9	Multiple and Ancient Origins of the Domestic Dog. <i>Science</i> , 1997, 276, 1687-1689.	12.6	878
10	Many species in one: DNA barcoding overestimates the number of species when nuclear mitochondrial pseudogenes are coamplified. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2008, 105, 13486-13491.	7.1	842
11	Empirical tests of some predictions from coalescent theory with applications to intraspecific phylogeny reconstruction.. <i>Genetics</i> , 1993, 134, 959-969.	2.9	777
12	A Modified Bootscan Algorithm for Automated Identification of Recombinant Sequences and Recombination Breakpoints. <i>AIDS Research and Human Retroviruses</i> , 2005, 21, 98-102.	1.1	746
13	Selecting the Best-Fit Model of Nucleotide Substitution. <i>Systematic Biology</i> , 2001, 50, 580-601.	5.6	714
14	Earth BioGenome Project: Sequencing life for the future of life. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2018, 115, 4325-4333.	7.1	652
15	Synthesis of phylogeny and taxonomy into a comprehensive tree of life. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2015, 112, 12764-12769.	7.1	584
16	Phylogeography's past, present, and future: 10 years after Avise, 2000. <i>Molecular Phylogenetics and Evolution</i> , 2010, 54, 291-301.	2.7	535
17	The Impact of Species Concept on Biodiversity Studies. <i>Quarterly Review of Biology</i> , 2004, 79, 161-179.	0.1	483
18	The causes and consequences of HIV evolution. <i>Nature Reviews Genetics</i> , 2004, 5, 52-61.	16.3	444

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19	Selecting the Best-Fit Model of Nucleotide Substitution. <i>Systematic Biology</i> , 2001, 50, 580-601.	5.6	438
20	The Effect of Recombination on the Accuracy of Phylogeny Estimation. <i>Journal of Molecular Evolution</i> , 2002, 54, 396-402.	1.8	421
21	Crayfish Molecular Systematics: Using a Combination of Procedures to Estimate Phylogeny. <i>Systematic Biology</i> , 1996, 45, 1-26.	5.6	390
22	TCS: estimating gene genealogies. , 2002, , .		338
23	Mitochondrial DNA phylogeography and population history of the grey wolf <i>Canis lupus</i> . <i>Molecular Ecology</i> , 1999, 8, 2089-2103.	3.9	314
24	Beyond FST: Analysis of population genetic data for conservation. <i>Conservation Genetics</i> , 2004, 5, 585-602.	1.5	309
25	TreeSAAP: Selection on Amino Acid Properties using phylogenetic trees. <i>Bioinformatics</i> , 2003, 19, 671-672.	4.1	269
26	Recombination in Evolutionary Genomics. <i>Annual Review of Genetics</i> , 2002, 36, 75-97.	7.6	266
27	Genome-wide analysis of SARS-CoV-2 virus strains circulating worldwide implicates heterogeneity. <i>Scientific Reports</i> , 2020, 10, 14004.	3.3	242
28	Intragenomic Variation Within ITS1 and ITS2 of Freshwater Crayfishes (Decapoda: Cambaridae): Implications for Phylogenetic and Microsatellite Studies. <i>Molecular Biology and Evolution</i> , 2000, 17, 284-291.	8.9	238
29	Multiple drivers of decline in the global status of freshwater crayfish (Decapoda: Astacidea). <i>Philosophical Transactions of the Royal Society B: Biological Sciences</i> , 2015, 370, 20140060.	4.0	225
30	Beyond FST: Analysis of population genetic data for conservation. <i>Conservation Genetics</i> , 2004, 5, 585-602.	1.5	223
31	Model-based multi-locus estimation of decapod phylogeny and divergence times. <i>Molecular Phylogenetics and Evolution</i> , 2005, 37, 355-369.	2.7	223
32	Composition, taxonomy and functional diversity of the oropharynx microbiome in individuals with schizophrenia and controls. <i>PeerJ</i> , 2015, 3, e1140.	2.0	222
33	Global diversity of crayfish (Astacidae, Cambaridae, and Parastacidae "Decapoda) in freshwater. <i>Hydrobiologia</i> , 2008, 595, 295-301.	2.0	217
34	Multiple interspecies transmissions of human and simian T-cell leukemia/lymphoma virus type I sequences. <i>Molecular Biology and Evolution</i> , 1996, 13, 115-131.	8.9	214
35	Selecting the best-fit model of nucleotide substitution. <i>Systematic Biology</i> , 2001, 50, 580-601.	5.6	212
36	PathoScope 2.0: a complete computational framework for strain identification in environmental or clinical sequencing samples. <i>Microbiome</i> , 2014, 2, 33.	11.1	206

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37	Targeted Amplicon Sequencing (TAS): A Scalable Next-Gen Approach to Multilocus, Multitaxa Phylogenetics. <i>Genome Biology and Evolution</i> , 2011, 3, 1312-1323.	2.5	196
38	An updated classification of the freshwater crayfishes (Decapoda: Astacidea) of the world, with a complete species list. <i>Journal of Crustacean Biology</i> , 2017, 37, 615-653.	0.8	196
39	Clinical Characterization and Prediction of Clinical Severity of SARS-CoV-2 Infection Among US Adults Using Data From the US National COVID Cohort Collaborative. <i>JAMA Network Open</i> , 2021, 4, e2116901.	5.9	179
40	Lost along the way: the significance of evolution in reverse. <i>Trends in Ecology and Evolution</i> , 2003, 18, 541-547.	8.7	174
41	Testing Species Boundaries in Biodiversity Studies. <i>Conservation Biology</i> , 1997, 11, 1289-1297.	4.7	165
42	The Cancer Microbiome: Distinguishing Direct and Indirect Effects Requires a Systemic View. <i>Trends in Cancer</i> , 2020, 6, 192-204.	7.4	162
43	Pathogen typing in the genomics era: MLST and the future of molecular epidemiology. <i>Infection, Genetics and Evolution</i> , 2013, 16, 38-53.	2.3	157
44	Parallel evolution of drug resistance in HIV: failure of nonsynonymous/synonymous substitution rate ratio to detect selection. <i>Molecular Biology and Evolution</i> , 1999, 16, 372-382.	8.9	153
45	The monophyletic origin of freshwater crayfish estimated from nuclear and mitochondrial DNA sequences. <i>Proceedings of the Royal Society B: Biological Sciences</i> , 2000, 267, 1679-1686.	2.6	153
46	Selecting Models of Nucleotide Substitution: An Application to Human Immunodeficiency Virus 1 (HIV-1). <i>Molecular Biology and Evolution</i> , 2001, 18, 897-906.	8.9	139
47	Population genetics of microbial pathogens estimated from multilocus sequence typing (MLST) data. <i>Infection, Genetics and Evolution</i> , 2006, 6, 97-112.	2.3	135
48	Human Immunodeficiency Virus Type 1 Quasi Species That Rebound after Discontinuation of Highly Active Antiretroviral Therapy Are Similar to the Viral Quasi Species Present before Initiation of Therapy. <i>Journal of Infectious Diseases</i> , 2001, 183, 36-50.	4.0	134
49	Baseline human gut microbiota profile in healthy people and standard reporting template. <i>PLoS ONE</i> , 2019, 14, e0206484.	2.5	133
50	Characterization of the Follicular Dendritic Cell Reservoir of Human Immunodeficiency Virus Type 1. <i>Journal of Virology</i> , 2008, 82, 5548-5561.	3.4	132
51	<i>Pathoscope</i>: Species identification and strain attribution with unassembled sequencing data. <i>Genome Research</i> , 2013, 23, 1721-1729.	5.5	132
52	The tempo and mode of barnacle evolution. <i>Molecular Phylogenetics and Evolution</i> , 2008, 46, 328-346.	2.7	127
53	A phylogenomic framework, evolutionary timeline and genomic resources for comparative studies of decapod crustaceans. <i>Proceedings of the Royal Society B: Biological Sciences</i> , 2019, 286, 20190079.	2.6	126
54	The Emergence of Lobsters: Phylogenetic Relationships, Morphological Evolution and Divergence Time Comparisons of an Ancient Group (Decapoda: Achelata, Astacidea, Glypheidea, Polychelida). <i>Systematic Biology</i> , 2014, 63, 457-479.	5.6	124

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55	The Earth BioGenome Project 2020: Starting the clock. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2022, 119, .	7.1	124
56	Intraspecific Cladogram Estimation: Accuracy at Higher Levels of Divergence. <i>Systematic Biology</i> , 1994, 43, 222-235.	5.6	118
57	Molecular Systematics and Biogeography of the Southern South American Freshwater Crabs (Decapoda: Anomura: Aegliidae) Using Multiple Heuristic Tree Search Approaches. <i>Systematic Biology</i> , 2004, 53, 767-780.	5.6	113
58	A comprehensive and integrative reconstruction of evolutionary history for Anomura (Crustacea: Tj ETQq0 0 0 rgBT (Overlock 10 Tf 50	3.2	113
59	Unraveling the Evolutionary Radiation of the Thoracican Barnacles Using Molecular and Morphological Evidence: A Comparison of Several Divergence Time Estimation Approaches. <i>Systematic Biology</i> , 2004, 53, 244-264.	5.6	112
60	Epitope-based chimeric peptide vaccine design against S, M and E proteins of SARS-CoV-2 etiologic agent of global pandemic COVID-19: an in silico approach. <i>PeerJ</i> , 2020, 8, e9572.	2.0	108
61	Associations between HIV infection and clinical spectrum of COVID-19: a population level analysis based on US National COVID Cohort Collaborative (N3C) data. <i>Lancet HIV</i> , the, 2021, 8, e690-e700.	4.7	106
62	Subterranean phylogeography of freshwater crayfishes shows extensive gene flow and surprisingly large population sizes. <i>Molecular Ecology</i> , 2005, 14, 4259-4273.	3.9	105
63	Telescope: Characterization of the retrotranscriptome by accurate estimation of transposable element expression. <i>PLoS Computational Biology</i> , 2019, 15, e1006453.	3.2	99
64	A Comparison of Phylogenetic Network Methods Using Computer Simulation. <i>PLoS ONE</i> , 2008, 3, e1913.	2.5	98
65	Independent Evolution of HIV Type 1 in Different Brain Regions. <i>AIDS Research and Human Retroviruses</i> , 1999, 15, 811-820.	1.1	97
66	Testing hypotheses of population structuring in the Northeast Atlantic Ocean and Mediterranean Sea using the common cuttlefish <i>Sepia officinalis</i> . <i>Molecular Ecology</i> , 2007, 16, 2667-2679.	3.9	97
67	Metagenomic deep sequencing reveals association of microbiome signature with functional biases in bovine mastitis. <i>Scientific Reports</i> , 2019, 9, 13536.	3.3	97
68	Gut microbiome differences between wild and captive black rhinoceros " implications for rhino health. <i>Scientific Reports</i> , 2019, 9, 7570.	3.3	97
69	Phylogenetic relationships among the Australian and New Zealand genera of freshwater crayfishes (Decapoda : Parastacidae). <i>Australian Journal of Zoology</i> , 1999, 47, 199.	1.0	96
70	The Global Invertebrate Genomics Alliance (GIGA): Developing Community Resources to Study Diverse Invertebrate Genomes. <i>Journal of Heredity</i> , 2014, 105, 1-18.	2.4	96
71	Effective population sizes: missing measures and missing concepts. <i>Animal Conservation</i> , 1999, 2, 317-319.	2.9	89
72	EVOLUTIONARY BIOLOGY IN BIODIVERSITY SCIENCE, CONSERVATION, AND POLICY: A CALL TO ACTION. Evolution; <i>International Journal of Organic Evolution</i> , 2010, 64, 1517-28.	2.3	87

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73	Dual Transcriptomic Profiling of Host and Microbiota during Health and Disease in Pediatric Asthma. PLoS ONE, 2015, 10, e0131819.	2.5	87
74	Molecular taxonomy in the dark: Evolutionary history, phylogeography, and diversity of cave crayfish in the subgenus Aviticambarus, genus Cambarus. Molecular Phylogenetics and Evolution, 2007, 42, 435-448.	2.7	83
75	Kisspeptin/GPR54 System: What Do We Know About Its Role in Human Reproduction?. Cellular Physiology and Biochemistry, 2018, 49, 1259-1276.	1.6	83
76	Pleistocene glaciation leaves deep signature on the freshwater crab <i>Aegla alacalufi</i> in Chilean Patagonia. Molecular Ecology, 2009, 18, 904-918.	3.9	81
77	Molecular Characterization of Crustacean Visual Pigments and the Evolution of Pancrustacean Opsins. Molecular Biology and Evolution, 2006, 24, 253-268.	8.9	79
78	The evolution of HIV: Inferences using phylogenetics. Molecular Phylogenetics and Evolution, 2012, 62, 777-792.	2.7	79
79	LINEAR HABITATS AND THE NESTED CLADE ANALYSIS: AN EMPIRICAL EVALUATION OF GEOGRAPHIC VERSUS RIVER DISTANCES USING AN OZARK CRAYFISH (DECAPODA: CAMBARIDAE). Evolution; International Journal of Organic Evolution, 2003, 57, 2101-2118.	2.3	78
80	Metataxonomic and Metagenomic Approaches vs. Culture-Based Techniques for Clinical Pathology. Frontiers in Microbiology, 2016, 7, 484.	3.5	78
81	Opsin Phylogeny and Evolution: A Model for Blue Shifts in Wavelength Regulation. Molecular Phylogenetics and Evolution, 1995, 4, 31-43.	2.7	77
82	Cryptic species of Clavelina (Asciacea) in two different habitats: harbours and rocky littoral zones in the northwestern Mediterranean. Marine Biology, 2001, 139, 455-462.	1.5	77
83	Interspecies physiological variation as a tool for cross-species assessments of global warming-induced endangerment: validation of an intrinsic determinant of macroecological and phylogeographic structure. Biology Letters, 2007, 3, 695-699.	2.3	75
84	Nested clade analysis statistics. Molecular Ecology Notes, 2006, 6, 590-593.	1.7	73
85	Evaluating the performance of likelihood methods for detecting population structure and migration. Molecular Ecology, 2004, 13, 837-851.	3.9	72
86	Phylogeography and speciation of colour morphs in the colonial ascidian <i>Pseudodistoma crucigaster</i> . Molecular Ecology, 2004, 13, 3125-3136.	3.9	72
87	Comparing Phylogenetic Codivergence between Polyomaviruses and Their Hosts. Journal of Virology, 2006, 80, 5663-5669.	3.4	71
88	Gondwanan radiation of the Southern Hemisphere crayfishes (Decapoda: Parastacidae): evidence from fossils and molecules. Journal of Biogeography, 2010, 37, 2275-2290.	3.0	71
89	Cocaine abuse and HIV-1 infection: Epidemiology and neuropathogenesis. Journal of Neuroimmunology, 1998, 83, 88-101.	2.3	70
90	Biogeographic regionalization of Australia: assigning conservation priorities based on endemic freshwater crayfish phylogenetics. Animal Conservation, 2000, 3, 155-163.	2.9	70

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91	Evolution of Afrotropical freshwater crab lineages obscured by morphological convergence. <i>Molecular Phylogenetics and Evolution</i> , 2006, 40, 227-235.	2.7	70
92	Single-Molecule Long-Read 16S Sequencing To Characterize the Lung Microbiome from Mechanically Ventilated Patients with Suspected Pneumonia. <i>Journal of Clinical Microbiology</i> , 2014, 52, 3913-3921.	3.9	69
93	Global diversity of crabs (Aeglidae: Anomura: Decapoda) in freshwater. <i>Hydrobiologia</i> , 2008, 595, 267-273.	2.0	68
94	Sampling bias and incorrect rooting make phylogenetic network tracing of SARS-COV-2 infections unreliable. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2020, 117, 12522-12523.	7.1	68
95	Life in extreme environments: microbial diversity in Great Salt Lake, Utah. <i>Extremophiles</i> , 2014, 18, 525-535.	2.3	67
96	SYSTEMATICS OF THE EUROPEAN ENDANGERED CRAYFISH SPECIES AUSTROPOTAMOBIVUS PALLIPES (DECAPODA: ASTACIDAE). <i>Journal of Crustacean Biology</i> , 2000, 20, 522-529.	0.8	65
97	Phylogenetic relationships between spiny, slipper and coral lobsters (Crustacea, Decapoda, Achelata). <i>Molecular Phylogenetics and Evolution</i> , 2009, 50, 152-162.	2.7	65
98	Rhodopsin evolution in the dark. <i>Nature</i> , 1997, 387, 667-668.	27.8	63
99	Integrating microbial and host transcriptomics to characterize asthma-associated microbial communities. <i>BMC Medical Genomics</i> , 2015, 8, 50.	1.5	63
100	Phylogeographic patterning in a freshwater crab species (Decapoda: Potamonautidae: Potamonautes) reveals the signature of historical climatic oscillations. <i>Journal of Biogeography</i> , 2006, 33, 1538-1549.	3.0	62
101	Using phylogenetically-informed annotation (PIA) to search for light-interacting genes in transcriptomes from non-model organisms. <i>BMC Bioinformatics</i> , 2014, 15, 350.	2.6	62
102	The evolutionary diversity of barnacles, with an updated classification of fossil and living forms. <i>Zoological Journal of the Linnean Society</i> , 2021, 193, 789-846.	2.3	62
103	Incorporating gaps as phylogenetic characters across eight DNA regions: Ramifications for North American Psoraleeae (Leguminosae). <i>Molecular Phylogenetics and Evolution</i> , 2008, 46, 532-546.	2.7	61
104	Phylogeny and biogeography of the freshwater crayfish <i>Euastacus</i> (Decapoda: Parastacidae) based on nuclear and mitochondrial DNA. <i>Molecular Phylogenetics and Evolution</i> , 2005, 37, 249-263.	2.7	60
105	Somatic Mitochondrial DNA Mutations in Prostate Cancer and Normal Appearing Adjacent Glands in Comparison to Age-Matched Prostate Samples without Malignant Histology. <i>Journal of Molecular Diagnostics</i> , 2006, 8, 312-319.	2.8	60
106	Environmental DNA survey captures patterns of fish and invertebrate diversity across a tropical seascape. <i>Scientific Reports</i> , 2020, 10, 6729.	3.3	60
107	Lost Branches on the Tree of Life. <i>PLoS Biology</i> , 2013, 11, e1001636.	5.6	58
108	Machine learning approaches to predict lupus disease activity from gene expression data. <i>Scientific Reports</i> , 2019, 9, 9617.	3.3	58

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109	Conservation phylogenetics of Chilean freshwater crabs <i>Aegla</i> (Anomura, Aeglididae): assigning priorities for aquatic habitat protection. <i>Biological Conservation</i> , 2002, 105, 345-353.	4.1	56
110	Insights Into the Resistome of Bovine Clinical Mastitis Microbiome, a Key Factor in Disease Complication. <i>Frontiers in Microbiology</i> , 2020, 11, 860.	3.5	56
111	Simple (Wrong) Models for Complex Trees: A Case from Retroviridae. <i>Molecular Biology and Evolution</i> , 2001, 18, 271-275.	8.9	55
112	Phylogenetic position, systematic status, and divergence time of the Procarididea (Crustacea: Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50 622	1.7	55
113	Clinical PathoScope: rapid alignment and filtration for accurate pathogen identification in clinical samples using unassembled sequencing data. <i>BMC Bioinformatics</i> , 2014, 15, 262.	2.6	55
114	Nasopharyngeal Microbiome Diversity Changes over Time in Children with Asthma. <i>PLoS ONE</i> , 2017, 12, e0170543.	2.5	55
115	Conservation Assessment of Southern South American Freshwater Ecoregions on the Basis of the Distribution and Genetic Diversity of Crabs from the Genus <i>Aegla</i> . <i>Conservation Biology</i> , 2009, 23, 692-702.	4.7	53
116	All the better to see you with: a review of odonate color vision with transcriptomic insight into the odonate eye. <i>Organisms Diversity and Evolution</i> , 2012, 12, 241-250.	1.6	51
117	Why sequence all eukaryotes?. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2022, 119, .	7.1	51
118	DNA EVIDENCE FOR NONHYBRID ORIGINS OF PARTHENOGENESIS IN NATURAL POPULATIONS OF VERTEBRATES. <i>Evolution; International Journal of Organic Evolution</i> , 2009, 64, 1346-57.	2.3	50
119	THE ZOOGEOGRAPHY AND CENTERS OF ORIGIN OF THE CRAYFISH SUBGENUS <i>PROCERICAMBARUS</i> (DECAPODA: CAMBARIDAE). <i>Evolution; International Journal of Organic Evolution</i> , 1999, 53, 123-134.	2.3	49
120	Phylogeny, extinction and conservation: embracing uncertainties in a time of urgency. <i>Philosophical Transactions of the Royal Society B: Biological Sciences</i> , 2015, 370, 20140002.	4.0	49
121	Different Models, Different Trees: The Geographic Origin of PTLV-I. <i>Molecular Phylogenetics and Evolution</i> , 1999, 13, 336-347.	2.7	47
122	Empirical tests for ecological exchangeability. <i>Animal Conservation</i> , 2005, 8, 239-247.	2.9	47
123	Mutated CEACAMs Disrupt Transforming Growth Factor Beta Signaling and Alter the Intestinal Microbiome to Promote Colorectal Carcinogenesis. <i>Gastroenterology</i> , 2020, 158, 238-252.	1.3	46
124	Pediatric asthma comprises different phenotypic clusters with unique nasal microbiotas. <i>Microbiome</i> , 2018, 6, 179.	11.1	45
125	HIV-1 Heterogeneity and Cytokines. <i>Advances in Experimental Medicine and Biology</i> , 1995, 373, 225-238.	1.6	45
126	Conservation phylogenetics of Ozark crayfishes: Assigning priorities for aquatic habitat protection. <i>Biological Conservation</i> , 1998, 84, 107-117.	4.1	44

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127	Recombination favors the evolution of drug resistance in HIV-1 during antiretroviral therapy. <i>Infection, Genetics and Evolution</i> , 2007, 7, 476-483.	2.3	44
128	Fish-T1K (Transcriptomes of 1,000 Fishes) Project: large-scale transcriptome data for fish evolution studies. <i>GigaScience</i> , 2016, 5, 18.	6.4	44
129	Testing Species Boundaries in an Ancient Species Complex with Deep Phylogeographic History: Genus <i>Xantusia</i> (Squamata: Xantusiidae). <i>American Naturalist</i> , 2004, 164, 396-414.	2.1	42
130	Remarkable convergent evolution in specialized parasitic Thecostraca (Crustacea). <i>BMC Biology</i> , 2009, 7, 15.	3.8	42
131	The evolution of foot-and-mouth disease virus: Impacts of recombination and selection. <i>Infection, Genetics and Evolution</i> , 2008, 8, 786-798.	2.3	41
132	Decapod Phylogenetics and Molecular Evolution. <i>Crustacean Issues</i> , 2009, , 15-29.	0.9	41
133	Microbiome dynamics and genomic determinants of bovine mastitis. <i>Genomics</i> , 2020, 112, 5188-5203.	2.9	41
134	Population Genetics of <i>Neisseria gonorrhoeae</i> in a High-Prevalence Community Using a Hypervariable Outer Membrane porB and 13 Slowly Evolving Housekeeping Genes. <i>Molecular Biology and Evolution</i> , 2005, 22, 1887-1902.	8.9	40
135	Multi-locus DNA sequence data reveal a history of deep cryptic vicariance and habitat-driven convergence in the desert night lizard <i>Xantusia vigilis</i> species complex (Squamata: Xantusiidae). <i>Molecular Ecology</i> , 2007, 16, 4455-4481.	3.9	40
136	Molecular phylogeny, systematics and morphological evolution of the acorn barnacles (Thoracica: Tj ETQq0 0 0 rgBT / Overlock 10 Tf 50	2.7	40
137	On the Phylogenetic Positioning of the South American Freshwater Crayfish Genera (Decapoda: Tj ETQq1 1 0.784314 rgBT / Overlock 10 Tf 50	0.8	39
138	Population Genetics of the porB Gene of <i>Neisseria gonorrhoeae</i> : Different Dynamics in Different Homology Groups. <i>Molecular Biology and Evolution</i> , 2000, 17, 423-436.	8.9	39
139	Recombination Estimation Under Complex Evolutionary Models with the Coalescent Composite-Likelihood Method. <i>Molecular Biology and Evolution</i> , 2006, 23, 817-827.	8.9	39
140	Transcriptome patterns in hidradenitis suppurativa: support for the role of antimicrobial peptides and interferon pathways in disease pathogenesis. <i>Clinical and Experimental Dermatology</i> , 2019, 44, 882-892.	1.3	39
141	The Molecular Evolution of Visual Pigments of Freshwater Crayfishes (Decapoda: Cambaridae). <i>Journal of Molecular Evolution</i> , 1997, 45, 524-534.	1.8	38
142	Evolution underground: A molecular phylogenetic investigation of Australian burrowing freshwater crayfish (Decapoda: Parastacidae) with particular focus on <i>Engaeus</i> Erichson. <i>Molecular Phylogenetics and Evolution</i> , 2009, 50, 580-598.	2.7	38
143	A synthetic phylogeny of freshwater crayfish: insights for conservation. <i>Philosophical Transactions of the Royal Society B: Biological Sciences</i> , 2015, 370, 20140009.	4.0	38
144	Phylogenetic evidence from freshwater crayfishes that cave adaptation is not an evolutionary dead-end. <i>Evolution; International Journal of Organic Evolution</i> , 2017, 71, 2522-2532.	2.3	38

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145	Gene flow estimates in Utah's cougars imply management beyond Utah. <i>Animal Conservation</i> , 2001, 4, 257-264.	2.9	37
146	Phylogenetics links monster larva to deep-sea shrimp. <i>Ecology and Evolution</i> , 2012, 2, 2367-2373.	1.9	37
147	Intraspecific phylogenetics: support for dental transmission of human immunodeficiency virus. <i>Journal of Virology</i> , 1995, 69, 2351-2356.	3.4	37
148	Squamate relationships based on C-mos nuclear DNA sequences: increased taxon sampling improves bootstrap support. <i>Amphibia - Reptilia</i> , 2001, 22, 235-242.	0.5	36
149	Temporal trends in gonococcal population genetics in a high prevalence urban community. <i>Infection, Genetics and Evolution</i> , 2007, 7, 271-278.	2.3	36
150	Population Genomics and Phylogeography of an Australian Dairy Factory Derived Lytic Bacteriophage. <i>Genome Biology and Evolution</i> , 2012, 4, 382-393.	2.5	36
151	The ecology and conservation status of Madagascar's endemic freshwater crayfish (Parastacidae; <i>Tj ETQq1 1 0.784314 rgBT /Overlock 10 Tf 50</i>)	2.4	35
152	Divergence and diversification in North American Psoraleeae (Fabaceae) due to climate change. <i>BMC Biology</i> , 2008, 6, 55.	3.8	35
153	Unlocking capacities of genomics for the COVID-19 response and future pandemics. <i>Nature Methods</i> , 2022, 19, 374-380.	19.0	35
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