

Keith A Crandall

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353
papers

50,598
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69
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223
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395
ext. papers

55,086
ext. citations

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7.84
L-index

#	Paper	IF	Citations
353	MODELTEST: testing the model of DNA substitution. <i>Bioinformatics</i> , 1998 , 14, 817-8	7.2	17513
352	TCS: a computer program to estimate gene genealogies. <i>Molecular Ecology</i> , 2000 , 9, 1657-9	5.7	7618
351	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, 619-33	4	2150
350	Considering evolutionary processes in conservation biology. <i>Trends in Ecology and Evolution</i> , 2000 , 15, 290-295	10.9	1352
349	Intraspecific gene genealogies: trees grafting into networks. <i>Trends in Ecology and Evolution</i> , 2001 , 16, 37-45	10.9	1240
348	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, 13757-62	11.5	1104
347	GeoDis: a program for the cladistic nested analysis of the geographical distribution of genetic haplotypes. <i>Molecular Ecology</i> , 2000 , 9, 487-8	5.7	1094
346	PHYLOGENY ESTIMATION AND HYPOTHESIS TESTING USING MAXIMUM LIKELIHOOD. <i>Annual Review of Ecology, Evolution, and Systematics</i> , 1997 , 28, 437-466		710
345	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, 13486-91	11.5	696
344	Multiple and ancient origins of the domestic dog. <i>Science</i> , 1997 , 276, 1687-9	33.3	694
343	Empirical tests of some predictions from coalescent theory with applications to intraspecific phylogeny reconstruction. <i>Genetics</i> , 1993 , 134, 959-69	4	683
342	Selecting the Best-Fit Model of Nucleotide Substitution. <i>Systematic Biology</i> , 2001 , 50, 580-601	8.4	669
341	A modified bootscan algorithm for automated identification of recombinant sequences and recombination breakpoints. <i>AIDS Research and Human Retroviruses</i> , 2005 , 21, 98-102	1.6	615
340	Phylogeography: past, present, and future: 10 years after Avise, 2000. <i>Molecular Phylogenetics and Evolution</i> , 2010 , 54, 291-301	4.1	406
339	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, 12764-9	11.5	400
338	The impact of species concept on biodiversity studies. <i>Quarterly Review of Biology</i> , 2004 , 79, 161-79	5.4	381
337	The causes and consequences of HIV evolution. <i>Nature Reviews Genetics</i> , 2004 , 5, 52-61	30.1	372

336	The effect of recombination on the accuracy of phylogeny estimation. <i>Journal of Molecular Evolution</i> , 2002 , 54, 396-402	3.1	335
335	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	11.5	334
334	Crayfish Molecular Systematics: Using a Combination of Procedures to Estimate Phylogeny. <i>Systematic Biology</i> , 1996 , 45, 1-26	8.4	313
333	Beyond FST: Analysis of population genetic data for conservation. <i>Conservation Genetics</i> , 2004 , 5, 585-602	6.6	279
332	Mitochondrial DNA phylogeography and population history of the grey wolf <i>canis lupus</i> . <i>Molecular Ecology</i> , 1999 , 8, 2089-103	5.7	264
331	Selecting the Best-Fit Model of Nucleotide Substitution. <i>Systematic Biology</i> , 2001 , 50, 580-601	8.4	254
330	Recombination in evolutionary genomics. <i>Annual Review of Genetics</i> , 2002 , 36, 75-97	14.5	236
329	TreeSAAP: selection on amino acid properties using phylogenetic trees. <i>Bioinformatics</i> , 2003 , 19, 671-2	7.2	233
328	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, 284-91	8.3	222
327	Multiple interspecies transmissions of human and simian T-cell leukemia/lymphoma virus type I sequences. <i>Molecular Biology and Evolution</i> , 1996 , 13, 115-31	8.3	206
326	Beyond FST: Analysis of population genetic data for conservation. <i>Conservation Genetics</i> , 2004 , 5, 585-602	6.6	203
325	Model-based multi-locus estimation of decapod phylogeny and divergence times. <i>Molecular Phylogenetics and Evolution</i> , 2005 , 37, 355-69	4.1	194
324	Selecting the best-fit model of nucleotide substitution. <i>Systematic Biology</i> , 2001 , 50, 580-601	8.4	187
323	TCS: estimating gene genealogies 2002 ,		178
322	Global diversity of crayfish (Astacidae, Cambaridae, and Parastacidae Decapoda) in freshwater. <i>Hydrobiologia</i> , 2008 , 595, 295-301	2.4	169
321	Targeted amplicon sequencing (TAS): a scalable next-gen approach to multilocus, multitaxa phylogenetics. <i>Genome Biology and Evolution</i> , 2011 , 3, 1312-23	3.9	156
320	Genome-wide analysis of SARS-CoV-2 virus strains circulating worldwide implicates heterogeneity. <i>Scientific Reports</i> , 2020 , 10, 14004	4.9	156
319	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	5.8	155

318	Composition, taxonomy and functional diversity of the oropharynx microbiome in individuals with schizophrenia and controls. <i>PeerJ</i> , 2015 , 3, e1140	3.1	154
317	Lost along the way: the significance of evolution in reverse. <i>Trends in Ecology and Evolution</i> , 2003 , 18, 541-547	10.9	152
316	Testing Species Boundaries in Biodiversity Studies. <i>Conservation Biology</i> , 1997 , 11, 1289-1297	6	140
315	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, 372-82	8.3	136
314	Selecting models of nucleotide substitution: an application to human immunodeficiency virus 1 (HIV-1). <i>Molecular Biology and Evolution</i> , 2001 , 18, 897-906	8.3	127
313	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	126
312	PathoScope 2.0: a complete computational framework for strain identification in environmental or clinical sequencing samples. <i>Microbiome</i> , 2014 , 2, 33	16.6	124
311	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	7	121
310	Pathogen typing in the genomics era: MLST and the future of molecular epidemiology. <i>Infection, Genetics and Evolution</i> , 2013 , 16, 38-53	4.5	120
309	Population genetics of microbial pathogens estimated from multilocus sequence typing (MLST) data. <i>Infection, Genetics and Evolution</i> , 2006 , 6, 97-112	4.5	120
308	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, 1679-86	4.4	119
307	Characterization of the follicular dendritic cell reservoir of human immunodeficiency virus type 1. <i>Journal of Virology</i> , 2008 , 82, 5548-61	6.6	116
306	Intraspecific Cladogram Estimation: Accuracy at Higher Levels of Divergence. <i>Systematic Biology</i> , 1994 , 43, 222-235	8.4	112
305	The tempo and mode of barnacle evolution. <i>Molecular Phylogenetics and Evolution</i> , 2008 , 46, 328-46	4.1	109
304	Pathoscope: species identification and strain attribution with unassembled sequencing data. <i>Genome Research</i> , 2013 , 23, 1721-9	9.7	100
303	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, 244-64	8.4	99
302	Molecular systematics and biogeography of the southern South American freshwater "crabs" <i>Aegla</i> (Decapoda: Anomura: Aegliidae) using multiple heuristic tree search approaches. <i>Systematic Biology</i> , 2004 , 53, 767-80	8.4	99
301	Subterranean phylogeography of freshwater crayfishes shows extensive gene flow and surprisingly large population sizes. <i>Molecular Ecology</i> , 2005 , 14, 4259-73	5.7	93

300	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, 457-79	8.4	89
299	Independent evolution of HIV type 1 in different brain regions. <i>AIDS Research and Human Retroviruses</i> , 1999 , 15, 811-20	1.6	89
298	A comparison of phylogenetic network methods using computer simulation. <i>PLoS ONE</i> , 2008 , 3, e1913	3.7	87
297	Phylogenetic relationships among the Australian and New Zealand genera of freshwater crayfishes (Decapoda : Parastacidae). <i>Australian Journal of Zoology</i> , 1999 , 47, 199	0.5	85
296	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, 2667-79	5.7	84
295	A comprehensive and integrative reconstruction of evolutionary history for Anomura (Crustacea: Decapoda). <i>BMC Evolutionary Biology</i> , 2013 , 13, 128	3	80
294	The Cancer Microbiome: Distinguishing Direct and Indirect Effects Requires a Systemic View. <i>Trends in Cancer</i> , 2020 , 6, 192-204	12.5	79
293	Effective population sizes: missing measures and missing concepts. <i>Animal Conservation</i> , 1999 , 2, 317-319	2	78
292	2573. Impact of Anaerobic Antibacterial Spectrum on Cystic Fibrosis Lung Microbiome Diversity and Pulmonary Function. <i>Open Forum Infectious Diseases</i> , 2019 , 6, S894-S894	1	78
291	Molecular taxonomy in the dark: evolutionary history, phylogeography, and diversity of cave crayfish in the subgenus <i>Aviticambarus</i> , genus <i>Cambarus</i> . <i>Molecular Phylogenetics and Evolution</i> , 2007 , 42, 435-48	4.1	76
290	Pleistocene glaciation leaves deep signature on the freshwater crab <i>Aegla alacalufi</i> in Chilean Patagonia. <i>Molecular Ecology</i> , 2009 , 18, 904-18	5.7	74
289	Linear habitats and the nested clade analysis: an empirical evaluation of geographic versus river distances using an Ozark crayfish (Decapoda: Cambaridae). <i>Evolution; International Journal of Organic Evolution</i> , 2003 , 57, 2101-18	3.8	74
288	Evolutionary biology in biodiversity science, conservation, and policy: a call to action. <i>Evolution; International Journal of Organic Evolution</i> , 2010 , 64, 1517-28	3.8	73
287	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	70
286	Opsin phylogeny and evolution: a model for blue shifts in wavelength regulation. <i>Molecular Phylogenetics and Evolution</i> , 1995 , 4, 31-43	4.1	70
285	Dual Transcriptomic Profiling of Host and Microbiota during Health and Disease in Pediatric Asthma. <i>PLoS ONE</i> , 2015 , 10, e0131819	3.7	68
284	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	4.4	67
283	Comparing phylogenetic codivergence between polyomaviruses and their hosts. <i>Journal of Virology</i> , 2006 , 80, 5663-9	6.6	67

282	Evaluating the performance of likelihood methods for detecting population structure and migration. <i>Molecular Ecology</i> , 2004 , 13, 837-51	5.7	67
281	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. <i>Biology Letters</i> , 2007 , 3, 695-8	3.6	65
280	Cryptic species of <i>Clavelina</i> (Ascidiacea) in two different habitats: harbours and rocky littoral zones in the northwestern Mediterranean. <i>Marine Biology</i> , 2001 , 139, 455-462	2.5	64
279	Molecular characterization of crustacean visual pigments and the evolution of pancrustacean opsins. <i>Molecular Biology and Evolution</i> , 2007 , 24, 253-68	8.3	63
278	Biogeographic regionalization of Australia: assigning conservation priorities based on endemic freshwater crayfish phylogenetics. <i>Animal Conservation</i> , 2000 , 3, 155-163	3.2	63
277	The evolution of HIV: inferences using phylogenetics. <i>Molecular Phylogenetics and Evolution</i> , 2012 , 62, 777-92	4.1	61
276	Nested clade analysis statistics. <i>Molecular Ecology Notes</i> , 2006 , 6, 590-593		61
275	Epitope-based chimeric peptide vaccine design against S, M and E proteins of SARS-CoV-2, the etiologic agent of COVID-19 pandemic: an in silico approach. <i>PeerJ</i> , 2020 , 8, e9572	3.1	61
274	Phylogeography and speciation of colour morphs in the colonial ascidian <i>Pseudodistoma crucigaster</i> . <i>Molecular Ecology</i> , 2004 , 13, 3125-36	5.7	60
273	Baseline human gut microbiota profile in healthy people and standard reporting template. <i>PLoS ONE</i> , 2019 , 14, e0206484	3.7	59
272	Gondwanan radiation of the Southern Hemisphere crayfishes (Decapoda: Parastacidae): evidence from fossils and molecules. <i>Journal of Biogeography</i> , 2010 , 37, 2275-2290	4.1	59
271	Cocaine abuse and HIV-1 infection: epidemiology and neuropathogenesis. <i>Journal of Neuroimmunology</i> , 1998 , 83, 88-101	3.5	58
270	Metataxonomic and Metagenomic Approaches vs. Culture-Based Techniques for Clinical Pathology. <i>Frontiers in Microbiology</i> , 2016 , 7, 484	5.7	58
269	Incorporating gaps as phylogenetic characters across eight DNA regions: ramifications for North American Psoraleeae (Leguminosae). <i>Molecular Phylogenetics and Evolution</i> , 2008 , 46, 532-46	4.1	56
268	Evolution of Afrotropical freshwater crab lineages obscured by morphological convergence. <i>Molecular Phylogenetics and Evolution</i> , 2006 , 40, 227-35	4.1	56
267	Phylogenetic relationships between spiny, slipper and coral lobsters (Crustacea, Decapoda, Achelata). <i>Molecular Phylogenetics and Evolution</i> , 2009 , 50, 152-62	4.1	54
266	Rhodopsin evolution in the dark. <i>Nature</i> , 1997 , 387, 667-8	50.4	54
265	SYSTEMATICS OF THE EUROPEAN ENDANGERED CRAYFISH SPECIES AUSTROPOTAMOBIVS PALLIPES (DECAPODA: ASTACIDAE). <i>Journal of Crustacean Biology</i> , 2000 , 20, 522-529	0.8	54

264	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, 312-9	5.1	52
263	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	4.1	52
262	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, 249-63	4.1	50
261	Conservation phylogenetics of Chilean freshwater crabs <i>Aegla</i> (Anomura, Aeglidae): assigning priorities for aquatic habitat protection. <i>Biological Conservation</i> , 2002 , 105, 345-353	6.2	50
260	Global diversity of crabs (Aeglidae: Anomura: Decapoda) in freshwater. <i>Hydrobiologia</i> , 2008 , 595, 267-273.	4.4	49
259	Phylogenetic position, systematic status, and divergence time of the Procarididea (Crustacea: Decapoda). <i>Zoologica Scripta</i> , 2010 , 39, 198-212	2.5	48
258	THE ZOOGEOGRAPHY AND CENTERS OF ORIGIN OF THE CRAYFISH SUBGENUS PROCERICAMBARUS (DECAPODA: CAMBARIDAE). <i>Evolution; International Journal of Organic Evolution</i> , 1999 , 53, 123-134	3.8	48
257	Kisspeptin/GPR54 System: What Do We Know About Its Role in Human Reproduction?. <i>Cellular Physiology and Biochemistry</i> , 2018 , 49, 1259-1276	3.9	48
256	Gut microbiome differences between wild and captive black rhinoceros - implications for rhino health. <i>Scientific Reports</i> , 2019 , 9, 7570	4.9	47
255	Using phylogenetically-informed annotation (PIA) to search for light-interacting genes in transcriptomes from non-model organisms. <i>BMC Bioinformatics</i> , 2014 , 15, 350	3.6	47
254	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	1.7	47
253	Integrating microbial and host transcriptomics to characterize asthma-associated microbial communities. <i>BMC Medical Genomics</i> , 2015 , 8, 50	3.7	46
252	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	11.5	46
251	Life in extreme environments: microbial diversity in Great Salt Lake, Utah. <i>Extremophiles</i> , 2014 , 18, 525-35	3.5	46
250	Lost branches on the tree of life. <i>PLoS Biology</i> , 2013 , 11, e1001636	9.7	45
249	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 ⁶	6	45
248	Empirical tests for ecological exchangeability. <i>Animal Conservation</i> , 2005 , 8, 239-247	3.2	45
247	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, 3913-21	9.7	44

246	Clinical PathoScope: rapid alignment and filtration for accurate pathogen identification in clinical samples using unassembled sequencing data. <i>BMC Bioinformatics</i> , 2014 , 15, 262	3.6	43
245	Different models, different trees: the geographic origin of PTLV-I. <i>Molecular Phylogenetics and Evolution</i> , 1999 , 13, 336-47	4.1	42
244	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	5.8	41
243	DNA evidence for nonhybrid origins of parthenogenesis in natural populations of vertebrates. <i>Evolution; International Journal of Organic Evolution</i> , 2010 , 64, 1346-57	3.8	41
242	Metagenomic deep sequencing reveals association of microbiome signature with functional biases in bovine mastitis. <i>Scientific Reports</i> , 2019 , 9, 13536	4.9	39
241	Nasopharyngeal Microbiome Diversity Changes over Time in Children with Asthma. <i>PLoS ONE</i> , 2017 , 12, e0170543	3.7	39
240	Conservation phylogenetics of Ozark crayfishes: Assigning priorities for aquatic habitat protection. <i>Biological Conservation</i> , 1998 , 84, 107-117	6.2	37
239	Recombination favors the evolution of drug resistance in HIV-1 during antiretroviral therapy. <i>Infection, Genetics and Evolution</i> , 2007 , 7, 476-83	4.5	37
238	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	3.7	37
237	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, 1887-902	8.3	37
236	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	10.4	37
235	Gene flow estimates in Utah cougars imply management beyond Utah. <i>Animal Conservation</i> , 2001 , 4, 257-264	3.2	36
234	Recombination estimation under complex evolutionary models with the coalescent composite-likelihood method. <i>Molecular Biology and Evolution</i> , 2006 , 23, 817-27	8.3	35
233	Remarkable convergent evolution in specialized parasitic Thecostraca (Crustacea). <i>BMC Biology</i> , 2009 , 7, 15	7.3	34
232	Decapod Phylogenetics and Molecular Evolution. <i>Crustacean Issues</i> , 2009 , 15-29		34
231	The evolution of foot-and-mouth disease virus: impacts of recombination and selection. <i>Infection, Genetics and Evolution</i> , 2008 , 8, 786-98	4.5	34
230	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, 423-36	8.3	34
229	HIV-1 heterogeneity and cytokines. Neuropathogenesis. <i>Advances in Experimental Medicine and Biology</i> , 1995 , 373, 225-38	3.6	34

228	Telescope: Characterization of the retrotranscriptome by accurate estimation of transposable element expression. <i>PLoS Computational Biology</i> , 2019 , 15, e1006453	5	33
227	Population genomics and phylogeography of an Australian dairy factory derived lytic bacteriophage. <i>Genome Biology and Evolution</i> , 2012 , 4, 382-93	3.9	33
226	Systematics of the European Endangered Crayfish Species <i>Austropotamobius Pallipes</i> (Decapoda: Astacidae). <i>Journal of Crustacean Biology</i> , 2000 , 20, 522-529	0.8	33
225	Temporal trends in gonococcal population genetics in a high prevalence urban community. <i>Infection, Genetics and Evolution</i> , 2007 , 7, 271-8	4.5	32
224	Crayfish Molecular Systematics: Using a Combination of Procedures to Estimate Phylogeny		32
223	Fish-T1K (Transcriptomes of 1,000 Fishes) Project: large-scale transcriptome data for fish evolution studies. <i>GigaScience</i> , 2016 , 5, 18	7.6	31
222	Machine learning approaches to predict lupus disease activity from gene expression data. <i>Scientific Reports</i> , 2019 , 9, 9617	4.9	31
221	Molecular phylogeny, systematics and morphological evolution of the acorn barnacles (Thoracica: Sessilia: Balanomorpha). <i>Molecular Phylogenetics and Evolution</i> , 2014 , 81, 147-58	4.1	31
220	Phylodynamics of HIV-1 from a phase III AIDS vaccine trial in Bangkok, Thailand. <i>PLoS ONE</i> , 2011 , 6, e16907	9.7	31
219	A synthetic phylogeny of freshwater crayfish: insights for conservation. <i>Philosophical Transactions of the Royal Society B: Biological Sciences</i> , 2015 , 370, 20140009	5.8	30
218	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, 580-98	4.1	30
217	PHYLOGENETIC RELATIONSHIPS AMONG THE SPECIES OF <i>AEGLA</i> (ANOMURA: AEGLIDAE) FRESHWATER CRABS FROM CHILE. <i>Journal of Crustacean Biology</i> , 2002 , 22, 304-313	0.8	30
216	Intraspecific phylogenetics: support for dental transmission of human immunodeficiency virus. <i>Journal of Virology</i> , 1995 , 69, 2351-6	6.6	30
215	Phylogenetics links monster larva to deep-sea shrimp. <i>Ecology and Evolution</i> , 2012 , 2, 2367-73	2.8	29
214	Phylogenetic relationships and molecular adaptation dynamics of human rhinoviruses. <i>Molecular Biology and Evolution</i> , 2009 , 26, 969-81	8.3	29
213	The molecular evolution of visual pigments of freshwater crayfishes (Decapoda: Cambaridae). <i>Journal of Molecular Evolution</i> , 1997 , 45, 524-34	3.1	29
212	The ecology and conservation status of Madagascar's endemic freshwater crayfish (Parastacidae; Astacoides). <i>Freshwater Biology</i> , 2007 , 52, 1820-1833	3.1	29
211	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, 4455-81	5.7	29

210	Divergence and diversification in North American Psoraleeae (Fabaceae) due to climate change. <i>BMC Biology</i> , 2008 , 6, 55	7.3	29
209	Living with the genetic signature of Miocene induced change: evidence from the phylogeographic structure of the endemic angulate tortoise <i>Chersina angulata</i> . <i>Molecular Phylogenetics and Evolution</i> , 2007 , 45, 915-26	4.1	28
208	Environmental DNA survey captures patterns of fish and invertebrate diversity across a tropical seascape. <i>Scientific Reports</i> , 2020 , 10, 6729	4.9	27
207	ON THE PHYLOGENETIC POSITIONING OF THE SOUTH AMERICAN FRESHWATER CRAYFISH GENERA (DECAPODA: PARASTACIDAE). <i>Journal of Crustacean Biology</i> , 2000 , 20, 530-540	0.8	26
206	Squamate relationships based on C-mos nuclear DNA sequences: increased taxon sampling improves bootstrap support. <i>Amphibia - Reptilia</i> , 2001 , 22, 235-242	1.2	25
205	Phylogenetic relationships, character evolution, and taxonomic implications within the slipper lobsters (Crustacea: Decapoda: Scyllaridae). <i>Molecular Phylogenetics and Evolution</i> , 2012 , 62, 237-50	4.1	24
204	A new species of burrowing crayfish, <i>Virilastacus rucapihuelensis</i> (Crustacea: Decapoda: Parastacidae), from southern Chile. <i>Proceedings of the Biological Society of Washington</i> , 2005 , 118, 765-776	0.2	24
203	PHYLOGENY OF THE THORACICAN BARNACLES BASED ON 18S rDNA SEQUENCES. <i>Journal of Crustacean Biology</i> , 2000 , 20, 393-398	0.8	24
202	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	1.8	23
201	Three new species of <i>Aegla</i> (Anomura) freshwater crabs from the upper Uruguay River hydrographic basin in Brazil. <i>Journal of Crustacean Biology</i> , 2012 , 32, 529-540	0.8	23
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