

# Ward C Wheeler

## List of Publications by Year in descending order

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152  
papers

17,630  
citations

19608

61  
h-index

13727

129  
g-index

160  
all docs

160  
docs citations

160  
times ranked

9765  
citing authors

#	ARTICLE	IF	CITATIONS
1	Phylogenetic supergraphs. <i>Cladistics</i> , 2022, 38, 147-158.	1.5	1
2	Comprehensive Species Sampling and Sophisticated Algorithmic Approaches Refute the Monophyly of Arachnida. <i>Molecular Biology and Evolution</i> , 2022, 39, .	3.5	41
3	Evidence for reduced BRCA2 functional activity in <i>Homo sapiens</i> after divergence from the chimpanzee-human last common ancestor. <i>Cell Reports</i> , 2022, 39, 110771.	2.9	5
4	Phylogenetic relationships of the <i>Boana pulchella</i> Group (Anura: Hylidae). <i>Molecular Phylogenetics and Evolution</i> , 2021, 155, 106981.	1.2	15
5	Phylogenomic Resolution of Sea Spider Diversification through Integration of Multiple Data Classes. <i>Molecular Biology and Evolution</i> , 2021, 38, 686-701.	3.5	47
6	The phylogeny of <i>Dendropsophini</i> (Anura: Hylidae: Hylinae). <i>Cladistics</i> , 2021, 37, 73-105.	1.5	20
7	Evolution in the Genus <i>Rhinella</i> : A Total Evidence Phylogenetic Analysis of Neotropical True Toads (Anura: Bufonidae). <i>Bulletin of the American Museum of Natural History</i> , 2021, 447, .	1.2	31
8	Distance Wagner tree refinement as a heuristic approach to characterâ€based initial tree construction. <i>Cladistics</i> , 2021, 37, 829-837.	1.5	2
9	Statistical Modeling of Distribution Patterns: A Markov Random Field Implementation and Its Application on Areas of Endemism. <i>Systematic Biology</i> , 2020, 69, 76-90.	2.7	4
10	Efficient implied alignment. <i>BMC Bioinformatics</i> , 2020, 21, 296.	1.2	2
11	Comparing and displaying phylogenetic trees using edge union networks. <i>Cladistics</i> , 2019, 35, 688-694.	1.5	2
12	<sc>FASTC</sc>: a file format for multiâ€character sequence data. <i>Cladistics</i> , 2019, 35, 573-575.	1.5	1
13	Revising the Bantu tree. <i>Cladistics</i> , 2019, 35, 329-348.	1.5	9
14	Revisiting habitat and lifestyle transitions in Heteroptera (Insecta: Hemiptera): insights from a combined morphological and molecular phylogeny. <i>Cladistics</i> , 2019, 35, 67-105.	1.5	84
15	Myrmecicultoridae, a New Family of Myrmecophilic Spiders from the Chihuahuan Desert (Araneae: Tj ETQq1 1 0.784314 rgBT /Overlock	0.2	12
16	On the Monophyly and Relationships of Several Genera of Hylini (Anura: Hylidae: Hylinae), with Comments on Recent Taxonomic Changes in Hylids. <i>South American Journal of Herpetology</i> , 2018, 13, 1.	0.5	37
17	There is no evidence that Podoctidae carry eggs of their own species: Reply to Machado and Wolff (2017). <i>Molecular Phylogenetics and Evolution</i> , 2018, 129, 349-353.	1.2	1
18	Phylogeny of Map Tree Frogs, <i>Boana semilineata</i> Species Group, with a New Amazonian Species (Anura:) Tj ETQq0 0.0 rgBT /Overlock 18	0.5	18

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19	Taxon cycle predictions supported by model-based inference in Indo-Pacific trapjaw ants (Hymenoptera: Tj EJOq1 1 0.784314 rgBT /Overlock	2.0	28
20	Hennig's semaphoront concept and the use of ontogenetic stages in phylogenetic reconstruction. Cladistics, 2017, 33, 93-108.	1.5	21
21	Nomenclatural stability does not justify recognition of paraphyletic taxa: A response to Scherz et al. (2016). Molecular Phylogenetics and Evolution, 2017, 111, 56-64.	1.2	5
22	The spider tree of life: phylogeny of Araneae based on targeted gene analyses from an extensive taxon sampling. Cladistics, 2017, 33, 574-616.	1.5	341
23	First global molecular phylogeny and biogeographical analysis of two arachnid orders (Schizomida) Tj ETQq1 1 0.784314 rgBT /Overlock Biogeography, 2017, 44, 2660-2672.	1.4	37
24	Expression and function of spineless orthologs correlate with distal deutocerebral appendage morphology across Arthropoda. Developmental Biology, 2017, 430, 224-236.	0.9	18
25	A multilocus phylogeny of Podocetidae (Arachnida, Opiliones, Laniatores) and parametric shape analysis reveal the disutility of subfamilial nomenclature in armored harvestman systematics. Molecular Phylogenetics and Evolution, 2017, 106, 164-173.	1.2	24
26	Comparison of heuristic approaches to the generalized tree alignment problem. Cladistics, 2016, 32, 452-460.	1.5	10
27	Phylogeography of the harvestman genus Metasiro (Arthropoda, Arachnida, Opiliones) reveals a potential solution to the Pangean paradox. Organisms Diversity and Evolution, 2016, 16, 167-184.	0.7	16
28	The impact of anchored phylogenomics and taxon sampling on phylogenetic inference in narrow-mouthed frogs (Anura, Microhylidae). Cladistics, 2016, 32, 113-140.	1.5	90
29	A phylogeny of sand flies (<sc>D</sc>iptera: <sc>P</sc>ychodidae: <sc>P</sc>hlebotominae), using recent <sc>E</sc>thiopian collections and a broad selection of publicly available <sc>DNA</sc> sequence data. Systematic Entomology, 2015, 40, 733-744.	1.7	15
30	Phylogenetic network analysis as a parsimony optimization problem. BMC Bioinformatics, 2015, 16, 296.	1.2	41
31	Evidence of duplicated Hox genes in the most recent common ancestor of extant scorpions. Evolution & Development, 2015, 17, 347-355.	1.1	25
32	Forked Tongues Revisited: Molecular Apomorphies Support Morphological Hypotheses of Squamate Evolution. Copeia, 2015, 103, 525-529.	1.4	15
33	A conserved genetic mechanism specifies deutocerebral appendage identity in insects and arachnids. Proceedings of the Royal Society B: Biological Sciences, 2015, 282, 20150698.	1.2	29
34	Historical linguistics as a sequence optimization problem: the evolution and biogeography of <sc>U</sc>toâ€<sc>A</sc>ztecan languages. Cladistics, 2015, 31, 113-125.	1.5	22
35	<sc>POY</sc> version 5: phylogenetic analysis using dynamic homologies under multiple optimality criteria. Cladistics, 2015, 31, 189-196.	1.5	74
36	Molecular phylogeny of <sc>I</sc>ndoâ€<sc>P</sc>acific carpenter ants (<sc>H</sc>ymenoptera: Tj ETQq0 0 0 rgBT /Overlock from diverse source areas. Cladistics, 2015, 31, 424-437.	1.5	22

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37	Towards Improving Searches for Optimal Phylogenies. <i>Systematic Biology</i> , 2015, 64, 56-65.	2.7	3
38	Descriptions of two new, cryptic species of <i>Metasiro</i> (Arachnida: Opiliones: Cyphophthalmi: <i>Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50 707 T</i> ) <i>Zootaxa</i> , 2014, 3814, 177-201.	0.2	26
39	Exactly Computing the Parsimony Scores on Phylogenetic Networks Using Dynamic Programming. <i>Journal of Computational Biology</i> , 2014, 21, 303-319.	0.8	7
40	Maximum a posteriori probability assignment (<sc>MAP</sc>â€A): an optimality criterion for phylogenetic trees via weighting and dynamic programming. <i>Cladistics</i> , 2014, 30, 282-290.	1.5	1
41	Phyletic groups on networks. <i>Cladistics</i> , 2014, 30, 447-451.	1.5	3
42	Hox gene duplications correlate with posterior heteronomy in scorpions. <i>Proceedings of the Royal Society B: Biological Sciences</i> , 2014, 281, 20140661.	1.2	59
43	Phylogenomic Interrogation of Arachnida Reveals Systemic Conflicts in Phylogenetic Signal. <i>Molecular Biology and Evolution</i> , 2014, 31, 2963-2984.	3.5	261
44	Phylogeny, Taxonomic Revision, and Character Evolution of the Genera <i>Chiasmocleis</i> and <i>Syncope</i> (Anura, Microhylidae) in Amazonia, with Descriptions of Three New Species. <i>Bulletin of the American Museum of Natural History</i> , 2014, 386, 1-112.	1.2	38
45	Into the deep: A phylogenetic approach to the bivalve subclass Protobranchia. <i>Molecular Phylogenetics and Evolution</i> , 2013, 69, 188-204.	1.2	77
46	Revenant clades in historical biogeography: the geology of New Zealand predisposes endemic clades to root age shifts. <i>Journal of Biogeography</i> , 2013, 40, 1609-1618.	1.4	39
47	Local search for the generalized tree alignment problem. <i>BMC Bioinformatics</i> , 2013, 14, 66.	1.2	18
48	Phylogenetic relationships of a Patagonian frog radiation, the <i>Alsodesâ€f</i>+<i>â€fEupsophus</i> clade (Anura: Alsodidae), with comments on the supposed paraphyly of <i>Eupsophus</i>. <i>Cladistics</i> , 2013, 29, 113-131.	1.5	63
49	Elongation factor-1Î±, a putative single-copy nuclear gene, has divergent sets of paralogs in an arachnid. <i>Molecular Phylogenetics and Evolution</i> , 2013, 68, 471-481.	1.2	12
50	Systematics of spinyâ€backed treefrogs (<sc>H</sc>yliidae: <i><sc>O</sc>steocephalus</i>): an <sc>A</sc>mazonian puzzle. <i>Zoologica Scripta</i> , 2013, 42, 351-380.	0.7	75
51	Venation patterns of neotropical blueberries (Vaccinieae: Ericaceae) and their phylogenetic utility. <i>Phytotaxa</i> , 2013, 96, 1.	0.1	5
52	The tree alignment problem. <i>BMC Bioinformatics</i> , 2012, 13, 293.	1.2	27
53	Maximum Parsimony on Phylogenetic networks. <i>Algorithms for Molecular Biology</i> , 2012, 7, 9.	0.3	54
54	Phylogenetic relationships among superfamilies of Hymenoptera. <i>Cladistics</i> , 2012, 28, 80-112.	1.5	147

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55	Trivial minimization of extra steps under dynamic homology. <i>Cladistics</i> , 2012, 28, 188-189.	1.5	10
56	Analysis and visualization of H7 influenza using genomic, evolutionary and geographic information in a modular web service. <i>Cladistics</i> , 2012, 28, 483-488.	1.5	3
57	Indel information eliminates trivial sequence alignment in maximum likelihood phylogenetic analysis. <i>Cladistics</i> , 2012, 28, 514-528.	1.5	11
58	A phylogenetic analysis of <i>Pleurodema</i> (Anura: Leptodactylidae: Leiuperinae) based on mitochondrial and nuclear gene sequences, with comments on the evolution of anuran foam nests. <i>Cladistics</i> , 2012, 28, 460-482.	1.5	57
59	Evolution of the hymenopteran megaradiation. <i>Molecular Phylogenetics and Evolution</i> , 2011, 60, 73-88.	1.2	171
60	The Supramap project: linking pathogen genomes with geography to fight emergent infectious diseases. <i>Cladistics</i> , 2011, 27, 61-66.	1.5	20
61	The phylogenetic relationships of the charismatic poster frogs, Phyllomedusinae (Anura, Hylidae). <i>Cladistics</i> , 2010, 26, 227-261.	1.5	110
62	POY version 4: phylogenetic analysis using dynamic homologies. <i>Cladistics</i> , 2010, 26, 72-85.	1.5	186
63	Distinctions between optimal and expected support. <i>Cladistics</i> , 2010, 26, 657-663.	1.5	7
64	Mitochondrial Intergenic Spacer in Fairy Basslets (Serranidae: Anthiinae) and the Simultaneous Analysis of Nucleotide and Rearrangement Data. <i>American Museum Novitates</i> , 2009, 3652, 1-10.	0.2	8
65	Phylogenetic relationships within the Cimicomorpha (Hemiptera: Heteroptera): a total evidence analysis. <i>Systematic Entomology</i> , 2009, 34, 15-48.	1.7	164
66	Assessing the root of bilaterian animals with scalable phylogenomic methods. <i>Proceedings of the Royal Society B: Biological Sciences</i> , 2009, 276, 4261-4270.	1.2	645
67	Is The Amphibian Tree of Life really fatally flawed?. <i>Cladistics</i> , 2008, 24, 385-395.	1.5	23
68	Application note: on extension gap in POY version 3. <i>Cladistics</i> , 2008, 24, 1070-1070.	1.5	6
69	Phylogenetic relationships of family groups in Pentatomoidea based on morphology and DNA sequences (Insecta: Heteroptera). <i>Cladistics</i> , 2008, 24, 932-976.	1.5	122
70	Broad phylogenomic sampling improves resolution of the animal tree of life. <i>Nature</i> , 2008, 452, 745-749.	18.7	1,698
71	Topology-Bayes versus Clade-Bayes in Phylogenetic Analysis. <i>Molecular Biology and Evolution</i> , 2008, 25, 447-453.	3.5	22
72	Genomic Analysis and Geographic Visualization of the Spread of Avian Influenza (H5N1). <i>Systematic Biology</i> , 2007, 56, 321-329.	2.7	63

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73	Linking of Digital Images to Phylogenetic Data Matrices Using a Morphological Ontology. <i>Systematic Biology</i> , 2007, 56, 283-294.	2.7	84
74	The evolutionary transition from subsocial to eusocial behaviour in Dictyoptera: Phylogenetic evidence for modification of the "shift-in-dependent-care" hypothesis with a new subsocial cockroach. <i>Molecular Phylogenetics and Evolution</i> , 2007, 43, 616-626.	1.2	59
75	Chromosomal character optimization. <i>Molecular Phylogenetics and Evolution</i> , 2007, 44, 1130-1140.	1.2	6
76	Phylogeny of the sea spiders (Arthropoda, Pycnogonida) based on direct optimization of six loci and morphology. <i>Cladistics</i> , 2007, 23, 255-293.	1.5	110
77	The case for sensitivity: a response to Grant and Kluge. <i>Cladistics</i> , 2007, 23, 294-296.	1.5	18
78	Phylogeny of Branchiopoda (Crustacea) based on a combined analysis of morphological data and six molecular loci. <i>Cladistics</i> , 2007, 23, 301-336.	1.5	103
79	Taxonomic Impediment or Impediment to Taxonomy? A Commentary on Systematics and the Cybertaxonomic-Automation Paradigm. <i>Evolutionary Biology</i> , 2007, 34, 140-143.	0.5	179
80	PHYLOGENETIC SYSTEMATICS OF DART-POISON FROGS AND THEIR RELATIVES (AMPHIBIA: ATHESPHATANURA:). <i>Trends in Ecology &amp; Evolution</i> , 2007, 22, 438-445.	1.2	438
81	THE AMPHIBIAN TREE OF LIFE. <i>Bulletin of the American Museum of Natural History</i> , 2006, 297, 1-291.	1.2	1,555
82	Dynamic homology and the likelihood criterion. <i>Cladistics</i> , 2006, 22, 157-170.	1.5	37
83	Partition-free congruence analysis: implications for sensitivity analysis. <i>Cladistics</i> , 2006, 22, 256-263.	1.5	16
84	Venom Evolution Widespread in Fishes: A Phylogenetic Road Map for the Bioprospecting of Piscine Venoms. <i>Journal of Heredity</i> , 2006, 97, 206-217.	1.0	203
85	Pairwise alignment with rearrangements. <i>Genome Informatics</i> , 2006, 17, 141-51.	0.4	8
86	Poor taxon sampling, poor character sampling, and non-repeatable analyses of a contrived dataset do not provide a more credible estimate of insect phylogeny: a reply to Kjer. <i>Cladistics</i> , 2005, 21, 295-302.	1.5	20
87	Scorpion higher phylogeny and classification, taxonomic anarchy, and standards for peer review in online publishing. <i>Cladistics</i> , 2005, 21, 446-494.	1.5	171
88	Parsimony overcomes statistical inconsistency with the addition of more data from the same gene. <i>Cladistics</i> , 2005, 21, 438-445.	1.5	19
89	SYSTEMATIC REVIEW OF THE FROG FAMILY HYLIDAE, WITH SPECIAL REFERENCE TO HYLINAE: PHYLOGENETIC ANALYSIS AND TAXONOMIC REVISION. <i>Bulletin of the American Museum of Natural History</i> , 2005, 294, 1.	1.2	663
90	Comparative and phylogenetic analysis of developmental sequences. <i>Evolution &amp; Development</i> , 2004, 6, 50-57.	1.1	95

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91	Polyphyly of the mail-cheeked fishes (Teleostei: Scorpaeniformes): evidence from mitochondrial and nuclear sequence data. <i>Molecular Phylogenetics and Evolution</i> , 2004, 32, 627-646.	1.2	120
92	A molecular perspective on the phylogeny of the <i>Hyla pulchella</i> species group (Anura, Hylidae). <i>Molecular Phylogenetics and Evolution</i> , 2004, 32, 938-950.	1.2	77
93	Iterative pass optimization of sequence data. <i>Cladistics</i> , 2003, 19, 254-260.	1.5	96
94	Implied alignment: a synapomorphy-based multiple-sequence alignment method and its use in cladogram search. <i>Cladistics</i> , 2003, 19, 261-268.	1.5	155
95	Search-based optimization. <i>Cladistics</i> , 2003, 19, 348-355.	1.5	27
96	Systematics and biogeography of the family Scorpionidae (Chelicerata : Scorpiones), with a discussion on phylogenetic methods. <i>Invertebrate Systematics</i> , 2003, 17, 185.	0.5	81
97	Missing entry replacement data analysis: a replacement approach to dealing with missing data in paleontological and total evidence data sets. <i>Journal of Vertebrate Paleontology</i> , 2003, 23, 275-283.	0.4	31
98	Iterative pass optimization of sequence data. , 2003, 19, 254.		2
99	Implied alignment: a synapomorphy-based multiple-sequence alignment method and its use in cladogram search. <i>Cladistics</i> , 2003, 19, 261-268.	1.5	2
100	Search-based optimization. <i>Cladistics</i> , 2003, 19, 348-355.	1.5	1
101	Iterative pass optimization of sequence data. <i>Cladistics</i> , 2003, 19, 254-60.	1.5	14
102	Implied alignment: a synapomorphy-based multiple-sequence alignment method and its use in cladogram search. <i>Cladistics</i> , 2003, 19, 261-8.	1.5	19
103	Search-based optimization. <i>Cladistics</i> , 2003, 19, 348-55.	1.5	5
104	Phylogeny of Henicopidae (Chilopoda: Lithobiomorpha): a combined analysis of morphology and five molecular loci. <i>Systematic Entomology</i> , 2002, 27, 31-64.	1.7	90
105	Phylogeny and Systematic Position of Opiliones: A Combined Analysis of Chelicerate Relationships Using Morphological and Molecular Data1. <i>Cladistics</i> , 2002, 18, 5-70.	1.5	237
106	Simultaneous analysis of the basal lineages of Hymenoptera (Insecta) using sensitivity analysis. <i>Cladistics</i> , 2002, 18, 455-484.	1.5	124
107	On bivalve phylogeny: a high-level analysis of the Bivalvia (Mollusca) based on combined morphology and DNA sequence data. <i>Invertebrate Biology</i> , 2002, 121, 271-324.	0.3	239
108	DNA multiple sequence alignments. , 2002, , 107-114.		19

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109	Optimization Alignment:Down,Up,Error,and Improvements. , 2002, , 55-69.		21
110	Phylogeny and systematic position of Opiliones: a combined analysis of chelicerate relationships using morphological and molecular data. Cladistics, 2002, 18, 5-70.	1.5	178
111	Some Unusual Small-Subunit Ribosomal RNA Sequences of Metazoans. American Museum Novitates, 2001, 3337, 1-16.	0.2	56
112	Homology and the Optimization of DNA Sequence Data. Cladistics, 2001, 17, S3-S11.	1.5	95
113	Efficiency of Parallel Direct Optimization. Cladistics, 2001, 17, S71-S82.	1.5	17
114	The Phylogeny of the Extant Hexapod Orders. Cladistics, 2001, 17, 113-169.	1.5	417
115	Arthropod phylogeny based on eight molecular loci and morphology. Nature, 2001, 413, 157-161.	13.7	502
116	The Phylogeny of the Extant Hexapod Orders. Cladistics, 2001, 17, 113-169.	1.5	81
117	Homology and the Optimization of DNA Sequence Data. Cladistics, 2001, 17, S3-S11.	1.5	35
118	Efficiency of Parallel Direct Optimization. Cladistics, 2001, 17, S71-S82.	1.5	9
119	Homology and DNA Sequence Data. , 2001, , 303-317.		29
120	Multiple Sequence Alignment in Phylogenetic Analysis. Molecular Phylogenetics and Evolution, 2000, 16, 317-330.	1.2	216
121	Triploblastic Relationships with Emphasis on the Acoelomates and the Position of Gnathostomulida, Cycliophora, Plathelminthes, and Chaetognatha: A Combined Approach of 18S rDNA Sequences and Morphology. Systematic Biology, 2000, 49, 539-562.	2.7	381
122	Transformationalism, Taxism, and Developmental Biology in Systematics. Systematic Biology, 2000, 49, 19-27.	2.7	12
123	Measuring Topological Congruence by Extending Character Techniques. Cladistics, 1999, 15, 131-135.	1.5	34
124	Fixed Character States and the Optimization of Molecular Sequence Data. Cladistics, 1999, 15, 379-385.	1.5	88
125	On Gaps. Molecular Phylogenetics and Evolution, 1999, 13, 132-143.	1.2	266
126	The Position of Arthropods in the Animal Kingdom: Ecdysozoa, Islands, Trees, and the "Parsimony Ratchet". Molecular Phylogenetics and Evolution, 1999, 13, 619-623.	1.2	95



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127	Measuring Topological Congruence by Extending Character Techniques. <i>Cladistics</i> , 1999, 15, 131-135.	1.5	13
128	Fixed Character States and the Optimization of Molecular Sequence Data. <i>Cladistics</i> , 1999, 15, 379-385.	1.5	22
129	The Phylogeny of the Extant Chelicerate Orders. <i>Cladistics</i> , 1998, 14, 173-192.	1.5	287
130	The Phylogeny of the Extant Chelicerate Orders. <i>Cladistics</i> , 1998, 14, 173-192.	1.5	22
131	The Strepsiptera Problem: Phylogeny of the Holometabolous Insect Orders Inferred from 18S and 28S Ribosomal DNA Sequences and Morphology. <i>Systematic Biology</i> , 1997, 46, 1-68.	2.7	675
132	The Strepsiptera Problem: Phylogeny of the Holometabolous Insect Orders Inferred from 18S and 28S Ribosomal DNA Sequences and Morphology. <i>Systematic Biology</i> , 1997, 46, 1.	2.7	542
133	OPTIMIZATION ALIGNMENT: THE END OF MULTIPLE SEQUENCE ALIGNMENT IN PHYLOGENETICS?. <i>Cladistics</i> , 1996, 12, 1-9.	1.5	556
134	Molecular Evolution and Phylogenetic Utility of the Polyubiquitin Locus in Mammals and Higher Vertebrates. <i>Molecular Phylogenetics and Evolution</i> , 1996, 6, 259-269.	1.2	14
135	OPTIMIZATION ALIGNMENT: THE END OF MULTIPLE SEQUENCE ALIGNMENT IN PHYLOGENETICS?. <i>Cladistics</i> , 1996, 12, 1-9.	1.5	134
136	EXPLANATION. <i>Cladistics</i> , 1995, 11, 211-218.	1.5	45
137	Elision: A Method for Accommodating Multiple Molecular Sequence Alignments with Alignment-Ambiguous Sites. <i>Molecular Phylogenetics and Evolution</i> , 1995, 4, 1-9.	1.2	145
138	Sequence Alignment, Parameter Sensitivity, and the Phylogenetic Analysis of Molecular Data. <i>Systematic Biology</i> , 1995, 44, 321.	2.7	94
139	Sequence Alignment, Parameter Sensitivity, and the Phylogenetic Analysis of Molecular Data. <i>Systematic Biology</i> , 1995, 44, 321-331.	2.7	441
140	Higher Level Relationships of the Arctoid Carnivora Based on Sequence Data and "Total Evidence". <i>Molecular Phylogenetics and Evolution</i> , 1994, 3, 47-58.	1.2	123
141	Insect homeotic transformation. <i>Nature</i> , 1994, 368, 696-696.	13.7	72
142	A NOVEL METHOD FOR ECONOMICAL DIAGNOSIS OF CLADOGRAMS UNDER SANKOFF OPTIMIZATION. <i>Cladistics</i> , 1994, 10, 207-213.	1.5	8
143	A Novel Method for Economical Diagnosis of Cladograms under Sankoff Optimization. <i>Cladistics</i> , 1994, 10, 207-213.	1.5	4
144	Alignment-Ambiguous Nucleotide Sites and the Exclusion of Systematic Data. <i>Molecular Phylogenetics and Evolution</i> , 1993, 2, 152-157.	1.2	323

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145	ARTHROPOD PHYLOGENY: A COMBINED APPROACH. <i>Cladistics</i> , 1993, 9, 1-39.	1.5	293
146	Cladistic relationships among higher groups of Heteroptera: congruence between morphological and molecular data sets. <i>Insect Systematics and Evolution</i> , 1993, 24, 121-137.	0.2	151
147	[4] Collection and storage of invertebrate samples. <i>Methods in Enzymology</i> , 1993, 224, 51-65.	0.4	19
148	Arthropod Phylogeny: a Combined Approach. <i>Cladistics</i> , 1993, 9, 1-39.	1.5	48
149	INDIVIDUAL ORGANISMS AS TERMINAL ENTITIES: LAYING THE SPECIES PROBLEM TO REST. <i>Cladistics</i> , 1992, 8, 67-72.	1.5	84
150	QUO VADIS?. <i>Cladistics</i> , 1992, 8, 85-86.	1.5	7
151	COMBINATORIAL WEIGHTS IN PHYLOGENETIC ANALYSIS: A STATISTICAL PARSIMONY PROCEDURE. <i>Cladistics</i> , 1990, 6, 269-275.	1.5	104
152	NUCLEIC ACID SEQUENCE PHYLOGENY AND RANDOM OUTGROUPS. <i>Cladistics</i> , 1990, 6, 363-367.	1.5	233