

Andrew J Roger

List of Publications by Year in descending order

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174
papers

13,992
citations

19608

61
h-index

25716

108
g-index

192
all docs

192
docs citations

192
times ranked

10604
citing authors

#	ARTICLE	IF	CITATIONS
1	Evolution of amino acid propensities under stability-mediated epistasis. <i>Molecular Biology and Evolution</i> , 2022, , .	3.5	7
2	Site-and-branch-heterogeneous analyses of an expanded dataset favour mitochondria as sister to known Alphaproteobacteria. <i>Nature Ecology and Evolution</i> , 2022, 6, 253-262.	3.4	48
3	The <i>Mastigamoeba balamuthi</i> Genome and the Nature of the Free-Living Ancestor of <i>Entamoeba</i> . <i>Molecular Biology and Evolution</i> , 2021, 38, 2240-2259.	3.5	14
4	Evolution: Reconstructing the Timeline of Eukaryogenesis. <i>Current Biology</i> , 2021, 31, R193-R196.	1.8	12
5	Long Branch Attraction Biases in Phylogenetics. <i>Systematic Biology</i> , 2021, 70, 838-843.	2.7	26
6	Characterization and Comparative Analyses of Mitochondrial Genomes in Single-Celled Eukaryotes to Shed Light on the Diversity and Evolution of Linear Molecular Architecture. <i>International Journal of Molecular Sciences</i> , 2021, 22, 2546.	1.8	12
7	Shifts in amino acid preferences as proteins evolve: A synthesis of experimental and theoretical work. <i>Protein Science</i> , 2021, 30, 2009-2028.	3.1	5
8	Unexpected organellar locations of ESCRT machinery in <i>Giardia intestinalis</i> and complex evolutionary dynamics spanning the transition to parasitism in the lineage Fornicata. <i>BMC Biology</i> , 2021, 19, 167.	1.7	8
9	Thomas Cavalier-Smith (1942–2021). <i>Current Biology</i> , 2021, 31, R977-R981.	1.8	5
10	PhyloFisher: A phylogenomic package for resolving eukaryotic relationships. <i>PLoS Biology</i> , 2021, 19, e3001365.	2.6	51
11	Conditions under which distributions of edge length ratios on phylogenetic trees can be used to order evolutionary events. <i>Journal of Theoretical Biology</i> , 2021, 526, 110788.	0.8	6
12	Genomic analysis finds no evidence of canonical eukaryotic DNA processing complexes in a free-living protist. <i>Nature Communications</i> , 2021, 12, 6003.	5.8	17
13	Anaeramoebae are a divergent lineage of eukaryotes that shed light on the transition from anaerobic mitochondria to hydrogenosomes. <i>Current Biology</i> , 2021, 31, 5605-5612.e5.	1.8	29
14	The New Tree of Eukaryotes. <i>Trends in Ecology and Evolution</i> , 2020, 35, 43-55.	4.2	537
15	On the Use of Information Criteria for Model Selection in Phylogenetics. <i>Molecular Biology and Evolution</i> , 2020, 37, 549-562.	3.5	22
16	Lateral Gene Transfer Mechanisms and Pan-genomes in Eukaryotes. <i>Trends in Parasitology</i> , 2020, 36, 927-941.	1.5	41
17	The draft nuclear genome sequence and predicted mitochondrial proteome of <i>Andalucia godoyi</i> , a protist with the most gene-rich and bacteria-like mitochondrial genome. <i>BMC Biology</i> , 2020, 18, 22.	1.7	43
18	The Oxymonad Genome Displays Canonical Eukaryotic Complexity in the Absence of a Mitochondrion. <i>Molecular Biology and Evolution</i> , 2019, 36, 2292-2312.	3.5	49

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19	A natural toroidal microswimmer with a rotary eukaryotic flagellum. <i>Nature Microbiology</i> , 2019, 4, 1620-1626.	5.9	14
20	The Relative Importance of Modeling Site Pattern Heterogeneity Versus Partition-Wise Heterotachy in Phylogenomic Inference. <i>Systematic Biology</i> , 2019, 68, 1003-1019.	2.7	45
21	An updated phylogeny of the Alphaproteobacteria reveals that the parasitic Rickettsiales and Holosporales have independent origins. <i>ELife</i> , 2019, 8, .	2.8	91
22	Accelerated Estimation of Frequency Classes in Site-Heterogeneous Profile Mixture Models. <i>Molecular Biology and Evolution</i> , 2018, 35, 1266-1283.	3.5	22
23	Combined morphological and phylogenomic re-examination of malawimonads, a critical taxon for inferring the evolutionary history of eukaryotes. <i>Royal Society Open Science</i> , 2018, 5, 171707.	1.1	34
24	Phylogenomics Places Orphan Protistan Lineages in a Novel Eukaryotic Super-Group. <i>Genome Biology and Evolution</i> , 2018, 10, 427-433.	1.1	112
25	Demystifying Eukaryote Lateral Gene Transfer (Response to Martin 2017 DOI: 10.1002/bies.201700115). <i>BioEssays</i> , 2018, 40, e1700242.	1.2	64
26	Reply to 'Eukaryote lateral gene transfer is Lamarckian'. <i>Nature Ecology and Evolution</i> , 2018, 2, 755-755.	3.4	8
27	Modeling Site Heterogeneity with Posterior Mean Site Frequency Profiles Accelerates Accurate Phylogenomic Estimation. <i>Systematic Biology</i> , 2018, 67, 216-235.	2.7	328
28	Hemimastigophora is a novel supra-kingdom-level lineage of eukaryotes. <i>Nature</i> , 2018, 564, 410-414.	13.7	101
29	Nuclear genome sequence of the plastid-lacking cryptomonad <i>Goniomonas avonlea</i> provides insights into the evolution of secondary plastids. <i>BMC Biology</i> , 2018, 16, 137.	1.7	42
30	A Single Tim Translocase in the Mitosomes of <i>Giardia intestinalis</i> Illustrates Convergence of Protein Import Machines in Anaerobic Eukaryotes. <i>Genome Biology and Evolution</i> , 2018, 10, 2813-2822.	1.1	37
31	Molecular clocks provide little information to date methanogenic Archaea. <i>Nature Ecology and Evolution</i> , 2018, 2, 1676-1677.	3.4	9
32	Microbial eukaryotes have adapted to hypoxia by horizontal acquisitions of a gene involved in ridoquinone biosynthesis. <i>ELife</i> , 2018, 7, .	2.8	51
33	The origin of mitochondrial cristae from alphaproteobacteria. <i>Molecular Biology and Evolution</i> , 2017, 34, msw298.	3.5	71
34	Lateral Gene Transfer in the Adaptation of the Anaerobic Parasite <i>Blastocystis</i> to the Gut. <i>Current Biology</i> , 2017, 27, 807-820.	1.8	94
35	Between a Pod and a Hard Test: The Deep Evolution of Amoebae. <i>Molecular Biology and Evolution</i> , 2017, 34, 2258-2270.	3.5	161
36	Mitochondrial Genome Evolution and a Novel RNA Editing System in Deep-Branching Heteroloboseids. <i>Genome Biology and Evolution</i> , 2017, 9, 1161-1174.	1.1	19

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37	Microbial Eukaryotes that Lack Sterols. <i>Journal of Eukaryotic Microbiology</i> , 2017, 64, 897-900.	0.8	14
38	Organelles that illuminate the origins of <i>Trichomonas</i> hydrogenosomes and <i>Giardia</i> mitosomes. <i>Nature Ecology and Evolution</i> , 2017, 1, 0092.	3.4	90
39	The Origin and Diversification of Mitochondria. <i>Current Biology</i> , 2017, 27, R1177-R1192.	1.8	681
40	Adaptations to High Salt in a Halophilic Protist: Differential Expression and Gene Acquisitions through Duplications and Gene Transfers. <i>Frontiers in Microbiology</i> , 2017, 8, 944.	1.5	71
41	Extreme genome diversity in the hyper-prevalent parasitic eukaryote <i>Blastocystis</i> . <i>PLoS Biology</i> , 2017, 15, e2003769.	2.6	99
42	Arginine deiminase pathway enzymes: evolutionary history in metamonads and other eukaryotes. <i>BMC Evolutionary Biology</i> , 2016, 16, 197.	3.2	40
43	On the reversibility of parasitism: adaptation to a free-living lifestyle via gene acquisitions in the diplomonad <i>Trepomonas</i> sp. PC1. <i>BMC Biology</i> , 2016, 14, 62.	1.7	38
44	A Eukaryote without a Mitochondrial Organelle. <i>Current Biology</i> , 2016, 26, 1274-1284.	1.8	302
45	Minimal cytosolic iron-sulfur cluster assembly machinery of <i>Giardia intestinalis</i> is partially associated with mitosomes. <i>Molecular Microbiology</i> , 2016, 102, 701-714.	1.2	19
46	The changing view of eukaryogenesis – fossils, cells, lineages and how they all come together. <i>Journal of Cell Science</i> , 2016, 129, 3695-3703.	1.2	77
47	Split-specific bootstrap measures for quantifying phylogenetic stability and the influence of taxon selection. <i>Molecular Phylogenetics and Evolution</i> , 2016, 105, 114-125.	1.2	1
48	The Earliest Stages of Mitochondrial Adaptation to Low Oxygen Revealed in a Novel Rhizarian. <i>Current Biology</i> , 2016, 26, 2729-2738.	1.8	46
49	Osmoadaptative Strategy and Its Molecular Signature in Obligately Halophilic Heterotrophic Protists. <i>Genome Biology and Evolution</i> , 2016, 8, 2241-2258.	1.1	53
50	Environmental Breviatea harbour mutualistic <i>Arcobacter</i> epibionts. <i>Nature</i> , 2016, 534, 254-258.	13.7	68
51	Novel Hydrogenosomes in the Microaerophilic Jakobid <i>Stygiella incarcerata</i> . <i>Molecular Biology and Evolution</i> , 2016, 33, 2318-2336.	3.5	52
52	First multigene analysis of Archamoebae (Amoebozoa: Conosa) robustly reveals its phylogeny and shows that Entamoebidae represents a deep lineage of the group. <i>Molecular Phylogenetics and Evolution</i> , 2016, 98, 41-51.	1.2	23
53	Group II Intron-Mediated Trans-Splicing in the Gene-Rich Mitochondrial Genome of an Enigmatic Eukaryote, <i>Diphyllia rotans</i> . <i>Genome Biology and Evolution</i> , 2016, 8, 458-466.	1.1	28
54	Leaving negative ancestors behind. <i>ELife</i> , 2016, 5, .	2.8	2

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55	Lateral Gene Transfer and Gene Duplication Played a Key Role in the Evolution of <i>Mastigamoeba</i> <i>balamuthi</i> Hydrogenosomes. <i>Molecular Biology and Evolution</i> , 2015, 32, 1039-1055.	3.5	63
56	Gene fusion, fission, lateral transfer, and loss: Not-so-rare events in the evolution of eukaryotic ATP citrate lyase. <i>Molecular Phylogenetics and Evolution</i> , 2015, 91, 12-16.	1.2	13
57	An ancestral bacterial division system is widespread in eukaryotic mitochondria. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2015, 112, 10239-10246.	3.3	70
58	Phylogenomics Reveals Convergent Evolution of Lifestyles in Close Relatives of Animals and Fungi. <i>Current Biology</i> , 2015, 25, 2404-2410.	1.8	169
59	Diversity and origins of anaerobic metabolism in mitochondria and related organelles. <i>Philosophical Transactions of the Royal Society B: Biological Sciences</i> , 2015, 370, 20140326.	1.8	124
60	Timing the Origins of Multicellular Eukaryotes Through Phylogenomics and Relaxed Molecular Clock Analyses. <i>Advances in Marine Genomics</i> , 2015, , 3-29.	1.2	19
61	An Amino Acid Substitution-Selection Model Adjusts Residue Fitness to Improve Phylogenetic Estimation. <i>Molecular Biology and Evolution</i> , 2014, 31, 779-792.	3.5	22
62	Gene Content Evolution in Discobid Mitochondria Deduced from the Phylogenetic Position and Complete Mitochondrial Genome of <i>Tsukubamonas globosa</i> . <i>Genome Biology and Evolution</i> , 2014, 6, 306-315.	1.1	48
63	Evolution of the Cytosolic Iron-Sulfur Cluster Assembly Machinery in Blastocystis Species and Other Microbial Eukaryotes. <i>Eukaryotic Cell</i> , 2014, 13, 143-153.	3.4	47
64	On the Age of Eukaryotes: Evaluating Evidence from Fossils and Molecular Clocks. <i>Cold Spring Harbor Perspectives in Biology</i> , 2014, 6, a016139-a016139.	2.3	203
65	A SUF Fe-S Cluster Biogenesis System in the Mitochondrion-Related Organelles of the Anaerobic Protist <i>Pygmaia</i> . <i>Current Biology</i> , 2014, 24, 1176-1186.	1.8	94
66	A Large Number of Nuclear Genes in the Human Parasite Blastocystis Require mRNA Polyadenylation to Create Functional Termination Codons. <i>Genome Biology and Evolution</i> , 2014, 6, 1956-1961.	1.1	11
67	Parallel re-modeling of EF-1 β function: divergent EF-1 β genes co-occur with EFL genes in diverse distantly related eukaryotes. <i>BMC Evolutionary Biology</i> , 2013, 13, 131.	3.2	11
68	Phylogenomics demonstrates that breviate flagellates are related to opisthokonts and apusomonads. <i>Proceedings of the Royal Society B: Biological Sciences</i> , 2013, 280, 20131755.	1.2	119
69	Amoeba Stages in the Deepest Branching Heteroloboseans, Including <i>Pharyngomonas</i> : Evolutionary and Systematic Implications. <i>Protist</i> , 2013, 164, 272-286.	0.6	33
70	The other eukaryotes in light of evolutionary protistology. <i>Biology and Philosophy</i> , 2013, 28, 299-330.	0.7	20
71	The Site-Wise Log-Likelihood Score is a Good Predictor of Genes under Positive Selection. <i>Journal of Molecular Evolution</i> , 2013, 76, 280-294.	0.8	9
72	Problems With Estimation of Ancestral Frequencies Under Stationary Models. <i>Systematic Biology</i> , 2013, 62, 330-338.	2.7	10

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73	Evidence for a Hydrogenosomal-Type Anaerobic ATP Generation Pathway in <i>Acanthamoeba castellanii</i> . PLoS ONE, 2013, 8, e69532.	1.1	34
74	Functional Divergence and Convergent Evolution in the Plastid-Targeted Glyceraldehyde-3-Phosphate Dehydrogenases of Diverse Eukaryotic Algae. PLoS ONE, 2013, 8, e70396.	1.1	9
75	Fitting Nonstationary General-Time-Reversible Models to Obtain Edge-Lengths and Frequencies for the Barry-Hartigan Model. Systematic Biology, 2012, 61, 927-940.	2.7	21
76	Evolution of Fe/S cluster biogenesis in the anaerobic parasite <i>Blastocystis</i> . Proceedings of the National Academy of Sciences of the United States of America, 2012, 109, 10426-10431.	3.3	74
77	The Probability of Correctly Resolving a Split as an Experimental Design Criterion in Phylogenetics. Systematic Biology, 2012, 61, 811-821.	2.7	15
78	The Biochemical Adaptations of Mitochondrion-Related Organelles of Parasitic and Free-Living Microbial Eukaryotes to Low Oxygen Environments. Cellular Origin and Life in Extreme Habitats, 2012, , 51-81.	0.3	5
79	The interface of protein structure, protein biophysics, and molecular evolution. Protein Science, 2012, 21, 769-785.	3.1	188
80	Phylogenetic Relationships within the Opisthokonta Based on Phylogenomic Analyses of Conserved Single-Copy Protein Domains. Molecular Biology and Evolution, 2012, 29, 531-544.	3.5	166
81	Aggregative Multicellularity Evolved Independently in the Eukaryotic Supergroup Rhizaria. Current Biology, 2012, 22, 1123-1127.	1.8	103
82	Multigene Phylogenies of Diverse Carpediemonas-like Organisms Identify the Closest Relatives of <i>Amitochondriate</i> ™ Diplomonads and Retortamonads. Protist, 2012, 163, 344-355.	0.6	32
83	Lateral transfer of tetrahymanol-synthesizing genes has allowed multiple diverse eukaryote lineages to independently adapt to environments without oxygen. Biology Direct, 2012, 7, 5.	1.9	41
84	Splintrons in <i>Giardia intestinalis</i> . Communicative and Integrative Biology, 2011, 4, 454-456.	0.6	4
85	Stage-specific requirement for Isa1 and Isa2 proteins in the mitochondrion of <i>Trypanosoma brucei</i> and heterologous rescue by human and <i>Blastocystis</i> orthologues. Molecular Microbiology, 2011, 81, 1403-1418.	1.2	36
86	Split Introns in the Genome of <i>Giardia intestinalis</i> Are Excised by Spliceosome-Mediated trans-Splicing. Current Biology, 2011, 21, 311-315.	1.8	45
87	The tangled past of eukaryotic enzymes involved in anaerobic metabolism. Mobile Genetic Elements, 2011, 1, 71-74.	1.8	19
88	Fast Statistical Tests for Detecting Heterotachy in Protein Evolution. Molecular Biology and Evolution, 2011, 28, 2305-2315.	3.5	6
89	A Functional Tom70 in the Human Parasite <i>Blastocystis</i> sp.: Implications for the Evolution of the Mitochondrial Import Apparatus. Molecular Biology and Evolution, 2011, 28, 781-791.	3.5	25
90	Eukaryotic Pyruvate Formate Lyase and Its Activating Enzyme Were Acquired Laterally from a Firmicute. Molecular Biology and Evolution, 2011, 28, 2087-2099.	3.5	66

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91	The Parameters of the Barry and Hartigan General Markov Model Are Statistically Nonidentifiable. <i>Systematic Biology</i> , 2011, 60, 872-875.	2.7	13
92	A phylogenetic mixture model for the identification of functionally divergent protein residues. <i>Bioinformatics</i> , 2011, 27, 2655-2663.	1.8	27
93	Splintrons in <i>Giardia intestinalis</i> : Spliceosomal introns in a split form. <i>Communicative and Integrative Biology</i> , 2011, 4, 454-6.	0.6	3
94	Phylogenomic Evidence for Separate Acquisition of Plastids in Cryptophytes, Haptophytes, and Stramenopiles. <i>Molecular Biology and Evolution</i> , 2010, 27, 1698-1709.	3.5	248
95	A wide diversity of previously undetected free-living relatives of diplomonads isolated from marine/saline habitats. <i>Environmental Microbiology</i> , 2010, 12, 2700-2710.	1.8	44
96	<i>Sawyeria marylandensis</i> (Heterolobosea) Has a Hydrogenosome with Novel Metabolic Properties. <i>Eukaryotic Cell</i> , 2010, 9, 1913-1924.	3.4	40
97	Ancient origin of the integrin-mediated adhesion and signaling machinery. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2010, 107, 10142-10147.	3.3	225
98	Phylogenetic Distributions and Histories of Proteins Involved in Anaerobic Pyruvate Metabolism in Eukaryotes. <i>Molecular Biology and Evolution</i> , 2010, 27, 311-324.	3.5	81
99	Phylogenomic analyses support the monophyly of Excavata and resolve relationships among eukaryotic "supergroups". <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2009, 106, 3859-3864.	3.3	444
100	Chapter 2 Predicting Proteomes of Mitochondria and Related Organelles from Genomic and Expressed Sequence Tag Data. <i>Methods in Enzymology</i> , 2009, 457, 21-47.	0.4	26
101	PROCOV: maximum likelihood estimation of protein phylogeny under covarion models and site-specific covarion pattern analysis. <i>BMC Evolutionary Biology</i> , 2009, 9, 225.	3.2	17
102	Evolution: Revisiting the Root of the Eukaryote Tree. <i>Current Biology</i> , 2009, 19, R165-R167.	1.8	120
103	Expanded phylogenies of canonical and non-canonical types of methionine adenosyltransferase reveal a complex history of these gene families in eukaryotes. <i>Molecular Phylogenetics and Evolution</i> , 2009, 53, 565-570.	1.2	9
104	Topological Estimation Biases with Covarion Evolution. <i>Journal of Molecular Evolution</i> , 2008, 66, 50-60.	0.8	15
105	An independent heterotachy model and its implications for phylogeny and divergence time estimation. <i>Molecular Phylogenetics and Evolution</i> , 2008, 46, 801-806.	1.2	8
106	A New Divergent Type of Eukaryotic Methionine Adenosyltransferase is Present in Multiple Distantly Related Secondary Algal Lineages. <i>Journal of Eukaryotic Microbiology</i> , 2008, 55, 374-381.	0.8	10
107	Localization and nucleotide specificity of <i>Blastocystis</i> succinyl-CoA synthetase. <i>Molecular Microbiology</i> , 2008, 68, 1395-1405.	1.2	21
108	A class frequency mixture model that adjusts for site-specific amino acid frequencies and improves inference of protein phylogeny. <i>BMC Evolutionary Biology</i> , 2008, 8, 331.	3.2	94

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109	Organelles in Blastocystis that Blur the Distinction between Mitochondria and Hydrogenosomes. <i>Current Biology</i> , 2008, 18, 580-585.	1.8	167
110	A Phylogenomic Investigation into the Origin of Metazoa. <i>Molecular Biology and Evolution</i> , 2008, 25, 664-672.	3.5	259
111	Testing Congruence in Phylogenomic Analysis. <i>Systematic Biology</i> , 2008, 57, 104-115.	2.7	180
112	Genetic Evidence for a Mitochondriate Ancestry in the "Amitochondriate"™ Flagellate <i>Trimastix pyriformis</i> . <i>PLoS ONE</i> , 2008, 3, e1383.	1.1	56
113	On Reduced Amino Acid Alphabets for Phylogenetic Inference. <i>Molecular Biology and Evolution</i> , 2007, 24, 2139-2150.	3.5	157
114	Testing for Covarion-like Evolution in Protein Sequences. <i>Molecular Biology and Evolution</i> , 2007, 24, 294-305.	3.5	65
115	The Impact of Fossils and Taxon Sampling on Ancient Molecular Dating Analyses. <i>Molecular Biology and Evolution</i> , 2007, 24, 1889-1897.	3.5	137
116	The Diversity of Mitochondrion-Related Organelles Amongst Eukaryotic Microbes. , 2007, , 239-275.		17
117	Novel mitochondrion-related organelles in the anaerobic amoeba <i>Mastigamoeba balamuthi</i> . <i>Molecular Microbiology</i> , 2007, 66, 1306-1320.	1.2	73
118	Toward Resolving the Eukaryotic Tree: The Phylogenetic Positions of Jakobids and Cercozoans. <i>Current Biology</i> , 2007, 17, 1420-1425.	1.8	170
119	The origins of multicellularity: a multi-taxon genome initiative. <i>Trends in Genetics</i> , 2007, 23, 113-118.	2.9	201
120	Using Confidence Set Heuristics During Topology Search Improves the Robustness of Phylogenetic Inference. <i>Journal of Molecular Evolution</i> , 2007, 64, 80-89.	0.8	0
121	On the correlation between genomic G+C content and optimal growth temperature in prokaryotes: Data quality and confounding factors. <i>Biochemical and Biophysical Research Communications</i> , 2006, 342, 681-684.	1.0	74
122	Modelling Prokaryote Gene Content. <i>Evolutionary Bioinformatics</i> , 2006, 2, 117693430600200.	0.6	10
123	Insights into the Evolutionary Origin and Genome Architecture of the Unicellular Opisthokonts <i>Capsaspora owczarzaki</i> and <i>Sphaeroforma arctica</i> . <i>Journal of Eukaryotic Microbiology</i> , 2006, 53, 379-384.	0.8	61
124	Phylogenetic estimation under codon models can be biased by codon usage heterogeneity. <i>Molecular Phylogenetics and Evolution</i> , 2006, 40, 428-434.	1.2	28
125	The glycolytic pathway of <i>Trimastix pyriformis</i> is an evolutionary mosaic. <i>BMC Evolutionary Biology</i> , 2006, 6, 101.	3.2	32
126	Evolution of four gene families with patchy phylogenetic distributions: influx of genes into protist genomes. <i>BMC Evolutionary Biology</i> , 2006, 6, 27.	3.2	94

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127	Comprehensive Multigene Phylogenies of Excavate Protists Reveal the Evolutionary Positions of "Primitive" Eukaryotes. <i>Molecular Biology and Evolution</i> , 2006, 23, 615-625.	3.5	155
128	The origin and diversification of eukaryotes: problems with molecular phylogenetics and molecular clock estimation. <i>Philosophical Transactions of the Royal Society B: Biological Sciences</i> , 2006, 361, 1039-1054.	1.8	159
129	Recombination between elongation factor 1A genes from distantly related archaeal lineages. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2006, 103, 4528-4533.	3.3	33
130	Invasion and Persistence of a Selfish Gene in the Cnidaria. <i>PLoS ONE</i> , 2006, 1, e3.	1.1	54
131	The evolutionary relationships amongst excavates: a concatenated protein analysis. <i>Journal of Eukaryotic Microbiology</i> , 2005, 52, 7S-27S.	0.8	1
132	Biases in Phylogenetic Estimation Can Be Caused by Random Sequence Segments. <i>Journal of Molecular Evolution</i> , 2005, 61, 351-359.	0.8	25
133	Likelihood, Parsimony, and Heterogeneous Evolution. <i>Molecular Biology and Evolution</i> , 2005, 22, 1161-1164.	3.5	114
134	The tree of eukaryotes. <i>Trends in Ecology and Evolution</i> , 2005, 20, 670-676.	4.2	549
135	On Inconsistency of the Neighbor-Joining, Least Squares, and Minimum Evolution Estimation When Substitution Processes Are Incorrectly Modeled. <i>Molecular Biology and Evolution</i> , 2004, 21, 1629-1642.	3.5	43
136	Gene Transfers from Nanoarchaeota to an Ancestor of Diplomonads and Parabasalids. <i>Molecular Biology and Evolution</i> , 2004, 22, 85-90.	3.5	58
137	Covariation Shifts Cause a Long-Branch Attraction Artifact That Unites Microsporidia and Archaeobacteria in EF-1A Phylogenies. <i>Molecular Biology and Evolution</i> , 2004, 21, 1340-1349.	3.5	93
138	Phylogenetic Artifacts Can be Caused by Leucine, Serine, and Arginine Codon Usage Heterogeneity: Dinoflagellate Plastid Origins as a Case Study. <i>Systematic Biology</i> , 2004, 53, 582-593.	2.7	60
139	Ellobiopsids of the Genus <i>Thalassomyces</i> are Alveolates. <i>Journal of Eukaryotic Microbiology</i> , 2004, 51, 246-252.	0.8	28
140	Early Evolution within Kinetoplastids (Euglenozoa), and the Late Emergence of Trypanosomatids. <i>Protist</i> , 2004, 155, 407-422.	0.6	53
141	The real "kingdoms" of eukaryotes. <i>Current Biology</i> , 2004, 14, R693-R696.	1.8	285
142	<i>Capsaspora owczarzaki</i> is an independent opisthokont lineage. <i>Current Biology</i> , 2004, 14, R946-R947.	1.8	82
143	Protein phylogenies robustly resolve the deep-level relationships within Euglenozoa. <i>Molecular Phylogenetics and Evolution</i> , 2004, 30, 201-212.	1.2	72
144	Phylogenetic Analyses of Diplomonad Genes Reveal Frequent Lateral Gene Transfers Affecting Eukaryotes. <i>Current Biology</i> , 2003, 13, 94-104.	1.8	253

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145	Evolution of glutamate dehydrogenase genes: evidence for lateral gene transfer within and between prokaryotes and eukaryotes. <i>BMC Evolutionary Biology</i> , 2003, 3, 14.	3.2	53
146	Inferring functional constraints and divergence in protein families using 3D mapping of phylogenetic information. <i>Nucleic Acids Research</i> , 2003, 31, 790-797.	6.5	35
147	Assessing functional divergence in EF-1 \hat{A} and its paralogs in eukaryotes and archaeobacteria. <i>Nucleic Acids Research</i> , 2003, 31, 4227-4237.	6.5	33
148	Estimation of Rates-Across-Sites Distributions in Phylogenetic Substitution Models. <i>Systematic Biology</i> , 2003, 52, 594-603.	2.7	55
149	Convergence and constraint in eukaryotic release factor 1 (eRF1) domain 1: the evolution of stop codon specificity. <i>Nucleic Acids Research</i> , 2002, 30, 532-544.	6.5	58
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