Andrew J Roger

List of Publications by Year
in descending order

174 papers	13,992 citations	19657 61 h-index	25787 108 g-index
192 all docs	192 docs citations	192 times ranked	10604 citing authors

#	Article	IF	Citations
1	The Origin and Diversification of Mitochondria. Current Biology, 2017, 27, R1177-R1192.	3.9	681
2	Phylogeny of Dissimilatory Sulfite Reductases Supports an Early Origin of Sulfate Respiration. Journal of Bacteriology, 1998, 180, 2975-2982.	2.2	635
3	The tree of eukaryotes. Trends in Ecology and Evolution, 2005, 20, 670-676.	8.7	549
4	The New Tree of Eukaryotes. Trends in Ecology and Evolution, 2020, 35, 43-55.	8.7	537
5	Phylogenomic analyses support the monophyly of Excavata and resolve relationships among eukaryotic â€œsupergroupsâ€• Proceedings of the National Academy of Sciences of the United States of America, 2009, 106, 3859-3864.	7.1	444
6	Modeling Site Heterogeneity with Posterior Mean Site Frequency Profiles Accelerates Accurate Phylogenomic Estimation. Systematic Biology, 2018, 67, 216-235.	5.6	328
7	Multiple Lateral Transfers of Dissimilatory Sulfite Reductase Genes between Major Lineages of Sulfate-Reducing Prokaryotes. Journal of Bacteriology, 2001, 183, 6028-6035.	2.2	309
8	A Eukaryote without a Mitochondrial Organelle. Current Biology, 2016, 26, 1274-1284.	3.9	302
9	The real â€˜kingdomsâ€™ of eukaryotes. Current Biology, 2004, 14, R693-R696.	3.9	285
10	Reconstructing Early Events in Eukaryotic Evolution. American Naturalist, 1999, 154, S146-S163.	2.1	266
11	A Phylogenomic Investigation into the Origin of Metazoa. Molecular Biology and Evolution, 2008, 25, 664-672.	8.9	259
12	Phylogenetic Analyses of Diplomonad Genes Reveal Frequent Lateral Gene Transfers Affecting Eukaryotes. Current Biology, 2003, 13, 94-104.	3.9	253
13	Phylogenomic Evidence for Separate Acquisition of Plastids in Cryptophytes, Haptophytes, and Stramenopiles. Molecular Biology and Evolution, 2010, 27, 1698-1709.	8.9	248
14	Ancient origin of the integrin-mediated adhesion and signaling machinery. Proceedings of the National Academy of Sciences of the United States of America, 2010, 107, 10142-10147.	7.1	225
15	On the Age of Eukaryotes: Evaluating Evidence from Fossils and Molecular Clocks. Cold Spring Harbor Perspectives in Biology, 2014, 6, a016139-a016139.	5.5	203
16	The origins of multicellularity: a multi-taxon genome initiative. Trends in Genetics, 2007, 23, 113-118.	6.7	201
17	The interface of protein structure, protein biophysics, and molecular evolution. Protein Science, 2012, 21, 769-785.	7.6	188
18	Testing Congruence in Phylogenomic Analysis. Systematic Biology, 2008, 57, 104-115.	5.6	180

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19	Toward Resolving the Eukaryotic Tree: The Phylogenetic Positions of Jakobids and Cercozoans. Current Biology, 2007, 17, 1420-1425.	3.9	170
20	Phylogenomics Reveals Convergent Evolution of Lifestyles in Close Relatives of Animals and Fungi. Current Biology, 2015, 25, 2404-2410.	3.9	169
21	Organelles in Blastocystis that Blur the Distinction between Mitochondria and Hydrogenosomes. Current Biology, 2008, 18, 580-585.	3.9	167
22	Phylogenetic Relationships within the Opisthokonta Based on Phylogenomic Analyses of Conserved Single-Copy Protein Domains. Molecular Biology and Evolution, 2012, 29, 531-544.	8.9	166
23	Between a Pod and a Hard Test: The Deep Evolution of Amoebae. Molecular Biology and Evolution, 2017, 34, 2258-2270.	8.9	161
24	The origin and diversification of eukaryotes: problems with molecular phylogenetics and molecular clock estimation. Philosophical Transactions of the Royal Society B: Biological Sciences, 2006, 361, 1039-1054.	4.0	159
25	On Reduced Amino Acid Alphabets for Phylogenetic Inference. Molecular Biology and Evolution, 2007, 24, 2139-2150.	8.9	157
26	Comprehensive Multigene Phylogenies of Excavate Protists Reveal the Evolutionary Positions of â€œPrimitiveâ€•Eukaryotes. Molecular Biology and Evolution, 2006, 23, 615-625.	8.9	155
27	The First Sexual Lineage and the Relevance of Facultative Sex. Journal of Molecular Evolution, 1999, 48, 779-783.	1.8	143
28	The Impact of Fossils and Taxon Sampling on Ancient Molecular Dating Analyses. Molecular Biology and Evolution, 2007, 24, 1889-1897.	8.9	137
29	Diversity and origins of anaerobic metabolism in mitochondria and related organelles. Philosophical Transactions of the Royal Society B: Biological Sciences, 2015, 370, 20140326.	4.0	124
30	Evolution: Revisiting the Root of the Eukaryote Tree. Current Biology, 2009, 19, R165-R167.	3.9	120
31	Phylogenomics demonstrates that breviate flagellates are related to opisthokonts and apusomonads. Proceedings of the Royal Society B: Biological Sciences, 2013, 280, 20131755.	2.6	119
32	The Evolutionary History of Kinetoplastids and Their Kinetoplasts. Molecular Biology and Evolution, 2002, 19, 2071-2083.	8.9	116
33	Likelihood, Parsimony, and Heterogeneous Evolution. Molecular Biology and Evolution, 2005, 22, 1161-1164.	8.9	114
34	Phylogenomics Places Orphan Protistan Lineages in a Novel Eukaryotic Super-Group. Genome Biology and Evolution, 2018, 10, 427-433.	2.5	112
35	Aggregative Multicellularity Evolved Independently in the Eukaryotic Supergroup Rhizaria. Current Biology, 2012, 22, 1123-1127.	3.9	103
36	Hemimastigophora is a novel supra-kingdom-level lineage of eukaryotes. Nature, 2018, 564, 410-414.	27.8	101

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37	Extreme genome diversity in the hyper-prevalent parasitic eukaryote Blastocystis. PLoS Biology, 2017, 15, e2003769.	5.6	99
38	Evolution of four gene families with patchy phylogenetic distributions: influx of genes into protist genomes. BMC Evolutionary Biology, 2006, 6, 27.	3.2	94
39	A class frequency mixture model that adjusts for site-specific amino acid frequencies and improves inference of protein phylogeny. BMC Evolutionary Biology, 2008, 8, 331.	3.2	94
40	A SUF Fe-S Cluster Biogenesis System in the Mitochondrion-Related Organelles of the Anaerobic Protist Pygsuia. Current Biology, 2014, 24, 1176-1186.	3.9	94
41	Lateral Gene Transfer in the Adaptation of the Anaerobic Parasite Blastocystis to the Gut. Current Biology, 2017, 27, 807-820.	3.9	94
42	Covarion Shifts Cause a Long-Branch Attraction Artifact That Unites Microsporidia and Archaebacteria in EF-1Î± Phylogenies. Molecular Biology and Evolution, 2004, 21, 1340-1349.	8.9	93
43	An updated phylogeny of the Alphaproteobacteria reveals that the parasitic Rickettsiales and Holosporales have independent origins. ELife, 2019, 8, .	6.0	91
44	Evolutionary History of â€œEarly-Divergingâ€•Eukaryotes: The Excavate Taxon Carpediemonas is a Close Relative of Giardia1. Molecular Biology and Evolution, 2002, 19, 1782-1791.	8.9	90
45	Organelles that illuminate the origins of Trichomonas hydrogenosomes and Giardia mitosomes. Nature Ecology and Evolution, 2017, 1, 0092.	7.8	90
46	A Cyanobacterial Gene in Nonphotosynthetic Protistsâ€"An Early Chloroplast Acquisition in Eukaryotes?. Current Biology, 2002, 12, 115-119.	3.9	88
47	Capsaspora owczarzaki is an independent opisthokont lineage. Current Biology, 2004, 14, R946-R947.	3.9	82
48	Phylogenetic Distributions and Histories of Proteins Involved in Anaerobic Pyruvate Metabolism in Eukaryotes. Molecular Biology and Evolution, 2010, 27, 311-324.	8.9	81
49	The changing view of eukaryogenesis â€" fossils, cells, lineages and how they all come together. Journal of Cell Science, 2016, 129, 3695-3703.	2.0	77
50	On the correlation between genomic G+C content and optimal growth temperature in prokaryotes: Data quality and confounding factors. Biochemical and Biophysical Research Communications, 2006, 342, 681-684.	2.1	74
51	Evolution of Fe/S cluster biogenesis in the anaerobic parasite Blastocystis. Proceedings of the National Academy of Sciences of the United States of America, 2012, 109, 10426-10431.	7.1	74
52	Eukaryotic Evolution: Getting to the Root of the Problem. Current Biology, 2002, 12, R691-R693.	3.9	73
53	Novel mitochondrionâ€•related organelles in the anaerobic amoeba Mastigamoeba balamuthi. Molecular Microbiology, 2007, 66, 1306-1320.	2.5	73
54	Protein phylogenies robustly resolve the deep-level relationships within Euglenozoa. Molecular Phylogenetics and Evolution, 2004, 30, 201-212.	2.7	72

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55	The origin of mitochondrial cristae from alphaproteobacteria. Molecular Biology and Evolution, 2017, 34, msw298.	8.9	71
56	Adaptations to High Salt in a Halophilic Protist: Differential Expression and Gene Acquisitions through Duplications and Gene Transfers. Frontiers in Microbiology, 2017, 8, 944.	3.5	71
57	An ancestral bacterial division system is widespread in eukaryotic mitochondria. Proceedings of the National Academy of Sciences of the United States of America, 2015, 112, 10239-10246.	7.1	70
58	Environmental Breviatea harbour mutualistic Arcobacter epibionts. Nature, 2016, 534, 254-258.	27.8	68
59	Evolutionary Relationships Among â€œJakobidâ€•Flagellates as Indicated by Alpha- and Beta-Tubulin Phylogenies. Molecular Biology and Evolution, 2001, 18, 514-522.	8.9	67
60	Retortamonad Flagellates are Closely Related to Diplomonadsâ€"Implications for the History of Mitochondrial Function in Eukaryote Evolution. Molecular Biology and Evolution, 2002, 19, 777-786.	8.9	67
61	Eukaryotic Pyruvate Formate Lyase and Its Activating Enzyme Were Acquired Laterally from a Firmicute. Molecular Biology and Evolution, 2011, 28, 2087-2099.	8.9	66
62	Testing for Covarion-like Evolution in Protein Sequences. Molecular Biology and Evolution, 2007, 24, 294-305.	8.9	65
63	Demystifying Eukaryote Lateral Gene Transfer (Response to Martin 2017 DOI: 10.1002/bies.201700115). BioEssays, 2018, 40, e1700242.	2.5	64
64	Lateral Gene Transfer and Gene Duplication Played a Key Role in the Evolution of Mastigamoeba balamuthi Hydrogenosomes. Molecular Biology and Evolution, 2015, 32, 1039-1055.	8.9	63
65	Sequence Analysis of the Mitochondrial Genome of Sarcophyton glaucum: Conserved Gene Order Among Octocorals. Journal of Molecular Evolution, 1998, 47, 697-708.	1.8	62
66	Insights into the Evolutionary Origin and Genome Architecture of the Unicellular Opisthokonts Capsaspora owczarzaki and Sphaeroforma arctica. Journal of Eukaryotic Microbiology, 2006, 53, 379-384.	1.7	61
67	Phylogenetic Artifacts Can be Caused by Leucine, Serine, and Arginine Codon Usage Heterogeneity: Dinoflagellate Plastid Origins as a Case Study. Systematic Biology, 2004, 53, 582-593.	5.6	60
68	Convergence and constraint in eukaryotic release factor 1 (eRF1) domain 1: the evolution of stop codon specificity. Nucleic Acids Research, 2002, 30, 532-544.	14.5	58
69	Gene Transfers from Nanoarchaeota to an Ancestor of Diplomonads and Parabasalids. Molecular Biology and Evolution, 2004, 22, 85-90.	8.9	58
70	Genetic Evidence for a Mitochondriate Ancestry in the â€˜Amitochondriateâ€™ Flagellate Trimastix pyriformis. PLoS ONE, 2008, 3, e1383.	2.5	56
71	Early origin of canonical introns. Nature, 2002, 419, 270-270.	27.8	55
72	Estimation of Rates-Across-Sites Distributions in Phylogenetic Substitution Models. Systematic Biology, 2003, 52, 594-603.	5.6	55

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73	Invasion and Persistence of a Selfish Gene in the Cnidaria. PLoS ONE, 2006, 1, e3.	2.5	54
74	Evidence for the Heterolobosea from Phylogenetic Analysis of Genes Encoding Glyceraldehyde-3-Phosphate Dehydrogenase. Journal of Eukaryotic Microbiology, 1996, 43, 475-485.	1.7	53
75	Gene duplication and gene conversion shape the evolution of archaeal chaperonins. Journal of Molecular Biology, 2002, 316, 1041-1050.	4.2	53
76	Evolution of glutamate dehydrogenase genes: evidence for lateral gene transfer within and between prokaryotes and eukaryotes. BMC Evolutionary Biology, 2003, 3, 14.	3.2	53
77	Early Evolution within Kinetoplastids (Euglenozoa), and the Late Emergence of Trypanosomatids. Protist, 2004, 155, 407-422.	1.5	53
78	Osmoadaptative Strategy and Its Molecular Signature in Obligately Halophilic Heterotrophic Protists. Genome Biology and Evolution, 2016, 8, 2241-2258.	2.5	53
79	Novel Hydrogenosomes in the Microaerophilic JakobidStygiella incarcerata. Molecular Biology and Evolution, 2016, 33, 2318-2336.	8.9	52
80	Testing for Differences in Rates-Across-Sites Distributions in Phylogenetic Subtrees. Molecular Biology and Evolution, 2002, 19, 1514-1523.	8.9	51
81	PhyloFisher: A phylogenomic package for resolving eukaryotic relationships. PLoS Biology, 2021, 19, e3001365.	5.6	51
82	Microbial eukaryotes have adapted to hypoxia by horizontal acquisitions of a gene involved in rhodoquinone biosynthesis. ELife, 2018, 7, .	6.0	51
83	Giardia lamblia Expresses a Proteobacterial-like DnaK Homolog. Molecular Biology and Evolution, 2001, 18, 530-541.	8.9	49
84	The Oxymonad Genome Displays Canonical Eukaryotic Complexity in the Absence of a Mitochondrion. Molecular Biology and Evolution, 2019, 36, 2292-2312.	8.9	49
85	Gene Content Evolution in Discobid Mitochondria Deduced from the Phylogenetic Position and Complete Mitochondrial Genome of Tsukubamonas globosa. Genome Biology and Evolution, 2014, 6, 306-315.	2.5	48
86	Site-and-branch-heterogeneous analyses of an expanded dataset favour mitochondria as sister to known Alphaproteobacteria. Nature Ecology and Evolution, 2022, 6, 253-262.	7.8	48
87	Evolution of the Cytosolic Iron-Sulfur Cluster Assembly Machinery in Blastocystis Species and Other Microbial Eukaryotes. Eukaryotic Cell, 2014, 13, 143-153.	3.4	47
88	The Earliest Stages of Mitochondrial Adaptation to Low Oxygen Revealed in a Novel Rhizarian. Current Biology, 2016, 26, 2729-2738.	3.9	46
89	Evolutionary Analyses of the Small Subunit of Glutamate Synthase: Gene Order Conservation, Gene Fusions, and Prokaryote-to- Eukaryote Lateral Gene Transfers. Eukaryotic Cell, 2002, 1, 304-310.	3.4	45
90	Split Introns in the Genome of Giardia intestinalis Are Excised by Spliceosome-Mediated trans-Splicing. Current Biology, 2011, 21, 311-315.	3.9	45

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91	The Relative Importance of Modeling Site Pattern Heterogeneity Versus Partition-Wise Heterotachy in Phylogenomic Inference. Systematic Biology, 2019, 68, 1003-1019.	5.6	45
92	A wide diversity of previously undetected freeâ€living relatives of diplomonads isolated from marine/saline habitats. Environmental Microbiology, 2010, 12, 2700-2710.	3.8	44
93	On Inconsistency of the Neighbor-Joining, Least Squares, and Minimum Evolution Estimation When Substitution Processes Are Incorrectly Modeled. Molecular Biology and Evolution, 2004, 21, 1629-1642.	8.9	43
94	The draft nuclear genome sequence and predicted mitochondrial proteome of Andalucia godoyi, a protist with the most gene-rich and bacteria-like mitochondrial genome. BMC Biology, 2020, 18, 22.	3.8	43
95	Nuclear genome sequence of the plastid-lacking cryptomonad Goniomonas avonlea provides insights into the evolution of secondary plastids. BMC Biology, 2018, 16, 137.	3.8	42
96	Lateral transfer of tetrahymanol-synthesizing genes has allowed multiple diverse eukaryote lineages to independently adapt to environments without oxygen. Biology Direct, 2012, 7, 5.	4.6	41
97	Lateral Gene Transfer Mechanisms and Pan-genomes in Eukaryotes. Trends in Parasitology, 2020, 36, 927-941.	3.3	41
98	Why introns-in-pieces?. Nature, 1993, 364, 289-290.	27.8	40
99	Mitochondria in hiding. Nature, 2002, 418, 827-829.	27.8	40
100	Sawyeria marylandensis (Heterolobosea) Has a Hydrogenosome with Novel Metabolic Properties. Eukaryotic Cell, 2010, 9, 1913-1924.	3.4	40
101	Arginine deiminase pathway enzymes: evolutionary history in metamonads and other eukaryotes. BMC Evolutionary Biology, 2016, 16, 197.	3.2	40
102	On the reversibility of parasitism: adaptation to a free-living lifestyle via gene acquisitions in the diplomonad Trepomonas sp. PC1. BMC Biology, 2016, 14, 62.	3.8	38
103	A Single Tim Translocase in the Mitosomes of Giardia intestinalis Illustrates Convergence of Protein Import Machines in Anaerobic Eukaryotes. Genome Biology and Evolution, 2018, 10, 2813-2822.	2.5	37
104	Stageâ€specific requirement for Isa1 and Isa2 proteins in the mitochondrion of Trypanosoma brucei and heterologous rescue by human and Blastocystis orthologues. Molecular Microbiology, 2011, 81, 1403-1418.	2.5	36
105	Inferring functional constraints and divergence in protein families using 3D mapping of phylogenetic information. Nucleic Acids Research, 2003, 31, 790-797.	14.5	35
106	Evidence for a Hydrogenosomal-Type Anaerobic ATP Generation Pathway in Acanthamoeba castellanii. PLoS ONE, 2013, 8, e69532.	2.5	34
107	Combined morphological and phylogenomic re-examination of malawimonads, a critical taxon for inferring the evolutionary history of eukaryotes. Royal Society Open Science, 2018, 5, 171707.	2.4	34
108	Assessing functional divergence in EF-1Â and its paralogs in eukaryotes and archaebacteria. Nucleic Acids Research, 2003, 31, 4227-4237.	14.5	33

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109	Recombination between elongation factor 1Â genes from distantly related archaeal lineages. Proceedings of the National Academy of Sciences of the United States of America, 2006, 103, 4528-4533.	7.1	33
110	Amoeba Stages in the Deepest Branching Heteroloboseans, Including Pharyngomonas: Evolutionary and Systematic Implications. Protist, 2013, 164, 272-286.	1.5	33
111	Primary Structure and Phylogenetic Relationships of a Malate Dehydrogenase Gene from Giardia lamblia. Journal of Molecular Evolution, 1999, 48, 750-755.	1.8	32
112	The glycolytic pathway of Trimastix pyriformis is an evolutionary mosaic. BMC Evolutionary Biology, 2006, 6, 101.	3.2	32
113	Multigene Phylogenies of Diverse Carpediemonas-like Organisms Identify the Closest Relatives of â€˜Amitochondriateâ€™ Diplomonads and Retortamonads. Protist, 2012, 163, 344-355.	1.5	32
114	New Insights into the Phylogeny of Trichomonads Inferred from Small Subunit rRNA Sequences. Protist, 1998, 149, 359-366.	1.5	31
115	The selfish pursuit of sex. Nature, 1995, 375, 283-283.	27.8	30
116	Primary Structure and Phylogenetic Relationships of Glyceraldehyde-3-Phosphate Dehydrogenase Genes of Free-Living and Parasitic Diplomonad Flagellates. Journal of Eukaryotic Microbiology, 1996, 43, 330-340.	1.7	30
117	Gene Conversion and the Evolution of Euryarchaeal Chaperonins: A Maximum Likelihood-Based Method for Detecting Conflicting Phylogenetic Signals. Journal of Molecular Evolution, 2002, 55, 232-245.	1.8	30
118	Lateral Transfer of an EF-1Î± Gene. Current Biology, 2002, 12, 772-776.	3.9	29
119	Anaeramoebae are a divergent lineage of eukaryotes that shed light on the transition from anaerobic mitochondria to hydrogenosomes. Current Biology, 2021, 31, 5605-5612.e5.	3.9	29
120	Ellobiopsids of the Genus Thalassomyces are Alveolates. Journal of Eukaryotic Microbiology, 2004, 51, 246-252.	1.7	28
121	Phylogenetic estimation under codon models can be biased by codon usage heterogeneity. Molecular Phylogenetics and Evolution, 2006, 40, 428-434.	2.7	28
122	Group II Intron-MediatedTrans-Splicing in the Gene-Rich Mitochondrial Genome of an Enigmatic Eukaryote,Diphylleia rotans. Genome Biology and Evolution, 2016, 8, 458-466.	2.5	28
123	A phylogenetic mixture model for the identification of functionally divergent protein residues. Bioinformatics, 2011, 27, 2655-2663.	4.1	27
124	Chapter 2 Predicting Proteomes of Mitochondria and Related Organelles from Genomic and Expressed Sequence Tag Data. Methods in Enzymology, 2009, 457, 21-47.	1.0	26
125	Long Branch Attraction Biases in Phylogenetics. Systematic Biology, 2021, 70, 838-843.	5.6	26
126	Biases in Phylogenetic Estimation Can Be Caused by Random Sequence Segments. Journal of Molecular Evolution, 2005, 61, 351-359.	1.8	25

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127	A Functional Tom70 in the Human Parasite Blastocystis sp.: Implications for the Evolution of the Mitochondrial Import Apparatus. Molecular Biology and Evolution, 2011, 28, 781-791.	8.9	25
128	First multigene analysis of Archamoebae (Amoebozoa: Conosa) robustly reveals its phylogeny and shows that Entamoebidae represents a deep lineage of the group. Molecular Phylogenetics and Evolution, 2016, 98, 41-51.	2.7	23
129	An Amino Acid Substitution-Selection Model Adjusts Residue Fitness to Improve Phylogenetic Estimation. Molecular Biology and Evolution, 2014, 31, 779-792.	8.9	22
130	Accelerated Estimation of Frequency Classes in Site-Heterogeneous Profile Mixture Models. Molecular Biology and Evolution, 2018, 35, 1266-1283.	8.9	22
131	On the Use of Information Criteria for Model Selection in Phylogenetics. Molecular Biology and Evolution, 2020, 37, 549-562.	8.9	22
132	Localization and nucleotide specificity of Blastocystis succinylâ€CoA synthetase. Molecular Microbiology, 2008, 68, 1395-1405.	2.5	21
133	Fitting Nonstationary General-Time-Reversible Models to Obtain Edge-Lengths and Frequencies for the Barryâ€"Hartigan Model. Systematic Biology, 2012, 61, 927-940.	5.6	21
134	The other eukaryotes in light of evolutionary protistology. Biology and Philosophy, 2013, 28, 299-330.	1.4	20
135	The tangled past of eukaryotic enzymes involved in anaerobic metabolism. Mobile Genetic Elements, 2011, 1, 71-74.	1.8	19
136	Minimal cytosolic ironâ€sulfur cluster assembly machinery of Giardia intestinalis is partially associated with mitosomes. Molecular Microbiology, 2016, 102, 701-714.	2.5	19
137	Mitochondrial Genome Evolution and a Novel RNA Editing System in Deep-Branching Heteroloboseids. Genome Biology and Evolution, 2017, 9, 1161-1174.	2.5	19
138	Timing the Origins of Multicellular Eukaryotes Through Phylogenomics and Relaxed Molecular Clock Analyses. Advances in Marine Genomics, 2015, , 3-29.	1.2	19
139	The Diversity of Mitochondrion-Related Organelles Amongst Eukaryotic Microbes. , 2007, , 239-275.		17
140	PROCOV: maximum likelihood estimation of protein phylogeny under covarion models and site-specific covarion pattern analysis. BMC Evolutionary Biology, 2009, 9, 225.	3.2	17
141	Genomic analysis finds no evidence of canonical eukaryotic DNA processing complexes in a free-living protist. Nature Communications, 2021, 12, 6003.	12.8	17
142	Topological Estimation Biases with Covarion Evolution. Journal of Molecular Evolution, 2008, 66, 50-60.	1.8	15
143	The Probability of Correctly Resolving a Split as an Experimental Design Criterion in Phylogenetics. Systematic Biology, 2012, 61, 811-821.	5.6	15
144	Microbial Eukaryotes that Lack Sterols. Journal of Eukaryotic Microbiology, 2017, 64, 897-900.	1.7	14

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145	A natural toroidal microswimmer with a rotary eukaryotic flagellum. Nature Microbiology, 2019, 4, 1620-1626.	13.3	14
146	The Mastigamoeba balamuthi Genome and the Nature of the Free-Living Ancestor of Entamoeba. Molecular Biology and Evolution, 2021, 38, 2240-2259.	8.9	14
147	The Parameters of the Barry and Hartigan General Markov Model Are Statistically NonIdentifiable. Systematic Biology, 2011, 60, 872-875.	5.6	13
148	Gene fusion, fission, lateral transfer, and loss: Not-so-rare events in the evolution of eukaryotic ATP citrate lyase. Molecular Phylogenetics and Evolution, 2015, 91, 12-16.	2.7	13
149	Evolution: Reconstructing the Timeline ofÂEukaryogenesis. Current Biology, 2021, 31, R193-R196.	3.9	12
150	Characterization and Comparative Analyses of Mitochondrial Genomes in Single-Celled Eukaryotes to Shed Light on the Diversity and Evolution of Linear Molecular Architecture. International Journal of Molecular Sciences, 2021, 22, 2546.	4.1	12
151	Parallel re-modeling of EF-1Î± function: divergent EF-1Î± genes co-occur with EFL genes in diverse distantly related eukaryotes. BMC Evolutionary Biology, 2013, 13, 131.	3.2	11
152	A Large Number of Nuclear Genes in the Human Parasite Blastocystis Require mRNA Polyadenylation to Create Functional Termination Codons. Genome Biology and Evolution, 2014, 6, 1956-1961.	2.5	11
153	Modelling Prokaryote Gene Content. Evolutionary Bioinformatics, 2006, 2, 117693430600200.	1.2	10
154	A New Divergent Type of Eukaryotic Methionine Adenosyltransferase is Present in Multiple Distantly Related Secondary Algal Lineages. Journal of Eukaryotic Microbiology, 2008, 55, 374-381.	1.7	10
155	Problems With Estimation of Ancestral Frequencies Under Stationary Models. Systematic Biology, 2013, 62, 330-338.	5.6	10
156	Expanded phylogenies of canonical and non-canonical types of methionine adenosyltransferase reveal a complex history of these gene families in eukaryotes. Molecular Phylogenetics and Evolution, 2009, 53, 565-570.	2.7	9
157	The Site-Wise Log-Likelihood Score is a Good Predictor of Genes under Positive Selection. Journal of Molecular Evolution, 2013, 76, 280-294.	1.8	9
158	Molecular clocks provide little information to date methanogenic Archaea. Nature Ecology and Evolution, 2018, 2, 1676-1677.	7.8	9
159	Functional Divergence and Convergent Evolution in the Plastid-Targeted Glyceraldehyde-3-Phosphate Dehydrogenases of Diverse Eukaryotic Algae. PLoS ONE, 2013, 8, e70396.	2.5	9
160	An independent heterotachy model and its implications for phylogeny and divergence time estimation. Molecular Phylogenetics and Evolution, 2008, 46, 801-806.	2.7	8
161	Reply to 'Eukaryote lateral gene transfer is Lamarckian'. Nature Ecology and Evolution, 2018, 2, 755-755.	7.8	8
162	Unexpected organellar locations of ESCRT machinery in Giardia intestinalis and complex evolutionary dynamics spanning the transition to parasitism in the lineage Fornicata. BMC Biology, 2021, 19, 167.	3.8	8

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163	Evolution of amino acid propensities under stability-mediated epistasis. Molecular Biology and Evolution, 2022, , .	8.9	7
164	Fast Statistical Tests for Detecting Heterotachy in Protein Evolution. Molecular Biology and Evolution, 2011, 28, 2305-2315.	8.9	6
165	Conditions under which distributions of edge length ratios on phylogenetic trees can be used to order evolutionary events. Journal of Theoretical Biology, 2021, 526, 110788.	1.7	6
166	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
167	Shifts in amino acid preferences as proteins evolve: A synthesis of experimental and theoretical work. Protein Science, 2021, 30, 2009-2028.	7.6	5
168	Thomas Cavalier-Smith (1942â€“2021). Current Biology, 2021, 31, R977-R981.	3.9	5
169	Splintrons inGiardia intestinalis. Communicative and Integrative Biology, 2011, 4, 454-456.	1.4	4
170	Splintrons in Giardia intestinalis: Spliceosomal introns in a split form. Communicative and Integrative Biology, 2011, 4, 454-6.	1.4	3
171	Leaving negative ancestors behind. ELife, 2016, 5, .	6.0	2
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