#	Article	IF	Citations
1	Horizontal gene transfer in eukaryotic evolution. Nature Reviews Genetics, 2008, 9, 605-618.	16.3	1,122
2	The Marine Microbial Eukaryote Transcriptome Sequencing Project (MMETSP): Illuminating the Functional Diversity of Eukaryotic Life in the Oceans through Transcriptome Sequencing. PLoS Biology, 2014, 12, e1001889.	5.6	885
3	Nuclear-encoded proteins target to the plastid in Toxoplasma gondii and Plasmodium falciparum. Proceedings of the National Academy of Sciences of the United States of America, 1998, 95, 12352-12357.	7.1	691
4	Rethinking the marine carbon cycle: Factoring in the multifarious lifestyles of microbes. Science, 2015, 347, 1257594.	12.6	679
5	Macronuclear Genome Sequence of the Ciliate Tetrahymena thermophila, a Model Eukaryote. PLoS Biology, 2006, 4, e286.	5.6	657
6	The endosymbiotic origin, diversification and fate of plastids. Philosophical Transactions of the Royal Society B: Biological Sciences, 2010, 365, 729-748.	4.0	565
7	The tree of eukaryotes. Trends in Ecology and Evolution, 2005, 20, 670-676.	8.7	549
8	CBOL Protist Working Group: Barcoding Eukaryotic Richness beyond the Animal, Plant, and Fungal Kingdoms. PLoS Biology, 2012, 10, e1001419.	5.6	488
9	Microsporidia: Biology and Evolution of Highly Reduced Intracellular Parasites. Annual Review of Microbiology, 2002, 56, 93-116.	7.3	430
10	A common red algal origin of the apicomplexan, dinoflagellate, and heterokont plastids. Proceedings of the National Academy of Sciences of the United States of America, 2010, 107, 10949-10954.	7.1	406
11	Nuclear-Encoded, Plastid-Targeted Genes Suggest a Single Common Origin for Apicomplexan and Dinoflagellate Plastids. Molecular Biology and Evolution, 2001, 18, 418-426.	8.9	395
12	Algal genomes reveal evolutionary mosaicism and the fate of nucleomorphs. Nature, 2012, 492, 59-65.	27.8	377
13	The Number, Speed, and Impact of Plastid Endosymbioses in Eukaryotic Evolution. Annual Review of Plant Biology, 2013, 64, 583-607.	18.7	376
14	Diversity and evolutionary history of plastids and their hosts. American Journal of Botany, 2004, 91, 1481-1493.	1.7	344
15	Mitochondrial and plastid genome architecture: Reoccurring themes, but significant differences at the extremes. Proceedings of the National Academy of Sciences of the United States of America, 2015, 112, 10177-10184.	7.1	327
16	Dinoflagellate Nuclear SSU rRNA Phylogeny Suggests Multiple Plastid Losses and Replacements. Journal of Molecular Evolution, 2001, 53, 204-213.	1.8	313
17	Alpha-tubulin from early-diverging eukaryotic lineages and the evolution of the tubulin family. Molecular Biology and Evolution, 1996, 13, 1297-1305.	8.9	299
18	Evidence from Beta-Tubulin Phylogeny that Microsporidia Evolved from Within the Fungi. Molecular Biology and Evolution, 2000, 17, 23-31.	8.9	299

#	Article	IF	Citations
19	Microsporidia Evolved from Ancestral Sexual Fungi. Current Biology, 2008, 18, 1675-1679.	3.9	256
20	Lateral gene transfer and the evolution of plastid-targeted proteins in the secondary plastid-containing alga <i>Bigelowiella natans</i>. Proceedings of the National Academy of Sciences of the United States of America, 2003, 100, 7678-7683.	7.1	241
21	Untangling the early diversification of eukaryotes: a phylogenomic study of the evolutionary origins of Centrohelida, Haptophyta and Cryptista. Proceedings of the Royal Society B: Biological Sciences, 2016, 283, 20152802.	2.6	222
22	Microsporidia â€“ Emergent Pathogens in the Global Food Chain. Trends in Parasitology, 2016, 32, 336-348.	3.3	221
23	The evolutionary history of haptophytes and cryptophytes: phylogenomic evidence for separate origins. Proceedings of the Royal Society B: Biological Sciences, 2012, 279, 2246-2254.	2.6	218
24	Recycled plastids: a â€˜green movementâ€™ in eukaryotic evolution. Trends in Genetics, 2002, 18, 577-584.	6.7	212
25	Microbial diversity associated with four functional groups of benthic reef algae and the reefâ€building coral <i>Montastraea annularis</i>. Environmental Microbiology, 2011, 13, 1192-1204.	3.8	208
26	Irremediable Complexity?. Science, 2010, 330, 920-921.	12.6	204
27	Molecular data and the evolutionary history of dinoflagellates. European Journal of Protistology, 2004, 40, 85-111.	1.5	203
28	Factors mediating plastid dependency and the origins of parasitism in apicomplexans and their close relatives. Proceedings of the National Academy of Sciences of the United States of America, 2015, 112, 10200-10207.	7.1	203
29	The complete sequence of the smallest known nuclear genome from the microsporidian Encephalitozoon intestinalis. Nature Communications, 2010, 1, 77.	12.8	198
30	Chromerid genomes reveal the evolutionary path from photosynthetic algae to obligate intracellular parasites. ELife, 2015, 4, e06974.	6.0	198
31	Congruent evidence from Î±-tubulin and Î²-tubulin gene phylogenies for a zygomycete origin of microsporidia. Fungal Genetics and Biology, 2003, 38, 298-309.	2.1	195
32	Complete nucleotide sequence of the chlorarachniophyte nucleomorph: Nature's smallest nucleus. Proceedings of the National Academy of Sciences of the United States of America, 2006, 103, 9566-9571.	7.1	185
33	The Complete Chloroplast Genome of the Chlorarachniophyte Bigelowiella natans: Evidence for Independent Origins of Chlorarachniophyte and Euglenid Secondary Endosymbionts. Molecular Biology and Evolution, 2007, 24, 54-62.	8.9	185
34	Multiple protein phylogenies show that Oxyrrhis marina and Perkinsus marinus are early branches of the dinoflagellate lineage. International Journal of Systematic and Evolutionary Microbiology, 2003, 53, 355-365.	1.7	180
35	Nucleus-Encoded, Plastid-Targeted Glyceraldehyde-3-Phosphate Dehydrogenase (GAPDH) Indicates a Single Origin for Chromalveolate Plastids. Molecular Biology and Evolution, 2003, 20, 1730-1735.	8.9	179
36	Tracing the Evolution of the Light-Harvesting Antennae in Chlorophyll a/b-Containing Organisms. Plant Physiology, 2007, 143, 1802-1816.	4.8	179

#	Article	IF	Citations
37	Diverse, uncultivated bacteria and archaea underlying the cycling of dissolved protein in the ocean. ISME Journal, 2016, 10, 2158-2173.	9.8	177
38	The others: our biased perspective of eukaryotic genomes. Trends in Ecology and Evolution, 2014, 29, 252-259.	8.7	167
39	Chromalveolates and the Evolution of Plastids by Secondary Endosymbiosis¹. Journal of Eukaryotic Microbiology, 2009, 56, 1-8.	1.7	162
40	On the monophyly of chromalveolates using a six-protein phylogeny of eukaryotes. International Journal of Systematic and Evolutionary Microbiology, 2005, 55, 487-496.	1.7	161
41	How a neutral evolutionary ratchet can build cellular complexity. IUBMB Life, 2011, 63, 528-537.	3.4	160
42	Morphostasis in alveolate evolution. Trends in Ecology and Evolution, 2003, 18, 395-402.	8.7	148
43	Phylogeny of gregarines (Apicomplexa) as inferred from small-subunit rDNA and Î²-tubulin. International Journal of Systematic and Evolutionary Microbiology, 2003, 53, 345-354.	1.7	146
44	A Tertiary Plastid Uses Genes from Two Endosymbionts. Journal of Molecular Biology, 2006, 357, 1373-1382.	4.2	146
45	Complex Protein Targeting to Dinoflagellate Plastids. Journal of Molecular Biology, 2005, 348, 1015-1024.	4.2	143
46	Large-Scale Phylogenomic Analyses Reveal That Two Enigmatic Protist Lineages, Telonemia and Centroheliozoa, Are Related to Photosynthetic Chromalveolates. Genome Biology and Evolution, 2009, 1, 231-238.	2.5	143
47	Reâ€examining Alveolate Evolution Using Multiple Protein Molecular Phylogenies. Journal of Eukaryotic Microbiology, 2002, 49, 30-37.	1.7	139
48	Five Questions about Microsporidia. PLoS Pathogens, 2009, 5, e1000489.	4.7	137
49	Gene Replacement of Fructose-1,6-Bisphosphate Aldolase Supports the Hypothesis of a Single Photosynthetic Ancestor of Chromalveolates. Eukaryotic Cell, 2004, 3, 1169-1175.	3.4	132
50	Functional and ecological impacts of horizontal gene transfer in eukaryotes. Current Opinion in Genetics and Development, 2009, 19, 613-619.	3.3	130
51	Evolution of Rhizaria: new insights from phylogenomic analysis of uncultivated protists. BMC Evolutionary Biology, 2010, 10, 377.	3.2	130
52	Comparative genomics of parasitic silkworm microsporidia reveal an association between genome expansion and host adaptation. BMC Genomics, 2013, 14, 186.	2.8	127
53	A bacterial proteorhodopsin proton pump in marine eukaryotes. Nature Communications, 2011, 2, 183.	12.8	126
54	The complete plastid genome sequence of the parasitic green alga Helicosporidium sp. is highly reduced and structured. BMC Biology, 2006, 4, 12.	3.8	122

#	Article	IF	Citations
55	Microsporidian mitosomes retain elements of the general mitochondrial targeting system. Proceedings of the National Academy of Sciences of the United States of America, 2006, 103, 15916-15920.	7.1	121
56	A distinct lineage of giant viruses brings a rhodopsin photosystem to unicellular marine predators. Proceedings of the National Academy of Sciences of the United States of America, 2019, 116, 20574-20583.	7.1	120
57	Multiple Gene Phylogenies Support the Monophyly of Cryptomonad and Haptophyte Host Lineages. Current Biology, 2007, 17, 887-891.	3.9	119
58	Genomic Survey of the Non-Cultivatable Opportunistic Human Pathogen, Enterocytozoon bieneusi. PLoS Pathogens, 2009, 5, e1000261.	4.7	119
59	Microsporidia: a journey through radical taxonomical revisions. Fungal Biology Reviews, 2009, 23, 1-8.	4.7	118
60	Foraminifera and Cercozoa Are Related in Actin Phylogeny: Two Orphans Find a Home?. Molecular Biology and Evolution, 2001, 18, 1551-1557.	8.9	117
61	Evidence that eukaryotic triosephosphate isomerase is of alpha-proteobacterial origin. Proceedings of the National Academy of Sciences of the United States of America, 1997, 94, 1270-1275.	7.1	116
62	Origins of microsporidia. Trends in Microbiology, 1998, 6, 19-23.	7.7	115
63	Evidence That Plant-Like Genes in Chlamydia Species Reflect an Ancestral Relationship between Chlamydiaceae, Cyanobacteria, and the Chloroplast. Genome Research, 2002, 12, 1159-1167.	5.5	114
64	Environmental Barcoding Reveals Massive Dinoflagellate Diversity in Marine Environments. PLoS ONE, 2010, 5, e13991.	2.5	112
65	Evolution of Red Algal Plastid Genomes: Ancient Architectures, Introns, Horizontal Gene Transfer, and Taxonomic Utility of Plastid Markers. PLoS ONE, 2013, 8, e59001.	2.5	112
66	The Reduced Genome of the Parasitic Microsporidian Enterocytozoon bieneusi Lacks Genes for Core Carbon Metabolism. Genome Biology and Evolution, 2010, 2, 304-309.	2.5	110
67	A New Lineage of Eukaryotes Illuminates Early Mitochondrial Genome Reduction. Current Biology, 2017, 27, 3717-3724.e5.	3.9	109
68	Molecular Phylogeny and Description of the Novel Katablepharid Roombia truncata gen. et sp. nov., and Establishment of the Hacrobia Taxon nov. PLoS ONE, 2009, 4, e7080.	2.5	108
69	Marine Protists Are Not Just Big Bacteria. Current Biology, 2017, 27, R541-R549.	3.9	108
70	Non-photosynthetic predators are sister to red algae. Nature, 2019, 572, 240-243.	27.8	107
71	Genome Compaction and Stability in Microsporidian Intracellular Parasites. Current Biology, 2004, 14, 891-896.	3.9	104
72	A widespread coral-infecting apicomplexan with chlorophyll biosynthesis genes. Nature, 2019, 568, 103-107.	27.8	102

#	Article	IF	Citations
73	EukRef: Phylogenetic curation of ribosomal RNA to enhance understanding of eukaryotic diversity and distribution. PLoS Biology, 2018, 16, e2005849.	5.6	101
74	Archaea: narrowing the gap between prokaryotes and eukaryotes.. Proceedings of the National Academy of Sciences of the United States of America, 1995, 92, 5761-5764.	7.1	98
75	The Highly Reduced and Fragmented Mitochondrial Genome of the Early-branching Dinoflagellate Oxyrrhis marina Shares Characteristics with both Apicomplexan and Dinoflagellate Mitochondrial Genomes. Journal of Molecular Biology, 2007, 372, 356-368.	4.2	98
76	Progress towards the Tree of Eukaryotes. Current Biology, 2019, 29, R808-R817.	3.9	98
77	EARLY EVOLUTIONARY HISTORY OF DINOFLAGELLATES AND APICOMPLEXANS (ALVEOLATA) AS INFERRED FROM HSP90 AND ACTIN PHYLOGENIES1. Journal of Phycology, 2004, 40, 341-350.	2.3	97
78	Gain and loss of multiple functionally related, horizontally transferred genes in the reduced genomes of two microsporidian parasites. Proceedings of the National Academy of Sciences of the United States of America, 2012, 109, 12638-12643.	7.1	97
79	Genetic tool development in marine protists: emerging model organisms for experimental cell biology. Nature Methods, 2020, 17, 481-494.	19.0	97
80	A class of eukaryotic GTPase with a punctate distribution suggesting multiple functional replacements of translation elongation factor 1Â. Proceedings of the National Academy of Sciences of the United States of America, 2004, 101, 15380-15385.	7.1	96
81	COMMON EVOLUTIONARY ORIGIN OF STARCH BIOSYNTHETIC ENZYMES IN GREEN AND RED ALGAE1. Journal of Phycology, 2005, 41, 1131-1141.	2.3	96
82	Global analysis of plastid diversity reveals apicomplexan-related lineages in coral reefs. Current Biology, 2012, 22, R518-R519.	3.9	95
83	Rhizaria. Current Biology, 2014, 24, R103-R107.	3.9	95
84	Parabasalian flagellates are ancient eukaryotes. Nature, 2000, 405, 635-637.	27.8	93
85	Morphology and Ultrastructure of Multiple Life Cycle Stages of the Photosynthetic Relative of Apicomplexa, Chromera velia. Protist, 2011, 162, 115-130.	1.5	93
86	Evaluating the Ribosomal Internal Transcribed Spacer (ITS) as a Candidate Dinoflagellate Barcode Marker. PLoS ONE, 2012, 7, e42780.	2.5	92
87	Shikimate pathway in apicomplexan parasites. Nature, 1999, 397, 219-220.	27.8	91
88	A high frequency of overlapping gene expression in compacted eukaryotic genomes. Proceedings of the National Academy of Sciences of the United States of America, 2005, 102, 10936-10941.	7.1	90
89	The Complete Plastid Genomes of the Two â€˜Dinotomsâ€™ Durinskia baltica and Kryptoperidinium foliaceum. PLoS ONE, 2010, 5, e10711.	2.5	89
90	Lateral Gene Transfer and Metabolic Adaptation in the Human Parasite Trichomonas vaginalis. Molecular Biology and Evolution, 2000, 17, 1769-1773.	8.9	88

#	Article	IF	Citations
91	The Phylogeny of Colpodellids (Alveolata) Using Small Subunit rRNA Gene Sequences Suggests They are the Free-living Sister Group to Apicomplexans. Journal of Eukaryotic Microbiology, 2002, 49, 498-504.	1.7	87
92	A Novel Polyubiquitin Structure in Cercozoa and Foraminifera: Evidence for a New Eukaryotic Supergroup. Molecular Biology and Evolution, 2003, 20, 62-66.	8.9	87
93	The Role of Host Phylogeny Varies in Shaping Microbial Diversity in the Hindguts of Lower Termites. Applied and Environmental Microbiology, 2015, 81, 1059-1070.	3.1	87
94	Novel Predators Reshape Holozoan Phylogeny and Reveal the Presence of a Two-Component Signaling System in the Ancestor of Animals. Current Biology, 2017, 27, 2043-2050.e6.	3.9	87
95	Systematic evaluation of horizontal gene transfer between eukaryotes and viruses. Nature Microbiology, 2022, 7, 327-336.	13.3	87
96	Plastid-Derived Genes in the Nonphotosynthetic Alveolate Oxyrrhis marina. Molecular Biology and Evolution, 2008, 25, 1297-1306.	8.9	85
97	Multiple Independent Origins of Apicomplexan-Like Parasites. Current Biology, 2019, 29, 2936-2941.e5.	3.9	84
98	Cascades of convergent evolution: The corresponding evolutionary histories of euglenozoans and dinoflagellates. Proceedings of the National Academy of Sciences of the United States of America, 2009, 106, 9963-9970.	7.1	83
99	Morphological Identification and Single-Cell Genomics of Marine Diplonemids. Current Biology, 2016, 26, 3053-3059.	3.9	83
100	Endosymbiosis: The feeling is not mutual. Journal of Theoretical Biology, 2017, 434, 75-79.	1.7	83
101	Collodictyon--An Ancient Lineage in the Tree of Eukaryotes. Molecular Biology and Evolution, 2012, 29, 1557-1568.	8.9	82
102	Nucleus-to-Nucleus Gene Transfer and Protein Retargeting into a Remnant Cytoplasm of Cryptophytes and Diatoms. Molecular Biology and Evolution, 2006, 23, 2413-2422.	8.9	80
103	Divergent Mitochondrial Respiratory Chains in Phototrophic Relatives of Apicomplexan Parasites. Molecular Biology and Evolution, 2015, 32, 1115-1131.	8.9	79
104	Lateral transfer at the gene and subgenic levels in the evolution of eukaryotic enolase. Proceedings of the National Academy of Sciences of the United States of America, 2001, 98, 10745-10750.	7.1	78
105	Lateral Gene Transfer of a Multigene Region from Cyanobacteria to Dinoflagellates Resulting in a Novel Plastid-Targeted Fusion Protein. Molecular Biology and Evolution, 2006, 23, 1437-1443.	8.9	78
106	Evolution of the sex-Related Locus and Genomic Features Shared in Microsporidia and Fungi. PLoS ONE, 2010, 5, e10539.	2.5	77
107	Causes and effects of nuclear genome reduction. Current Opinion in Genetics and Development, 2005, 15, 601-608.	3.3	76
108	An aerobic eukaryotic parasite with functional mitochondria that likely lacks a mitochondrial genome. Science Advances, 2019, 5, eaav1110.	10.3	76

#	Article	IF	Citations
109	The Function and Evolution of Motile DNA Replication Systems in Ciliates. Current Biology, 2021, 31, 66-76.e6.	3.9	76
110	Eye-like ocelloids are built from different endosymbiotically acquired components. Nature, 2015, 523, 204-207.	27.8	74
111	Bacterial and archaeal symbioses with protists. Current Biology, 2021, 31, R862-R877.	3.9	74
112	Symbionts of the ciliate <i>Euplotes</i> : diversity, patterns and potential as models for bacteriaâ€“eukaryote endosymbioses. Proceedings of the Royal Society B: Biological Sciences, 2019, 286, 20190693.	2.6	73
113	The â€˜otherâ€™ coral symbiont: <i>Ostreobium</i> diversity and distribution. ISME Journal, 2017, 11, 296-299.	9.8	72
114	Phylogenomics of the Intracellular Parasite Mikrocytos mackini Reveals Evidence for a Mitosome in Rhizaria. Current Biology, 2013, 23, 1541-1547.	3.9	71
115	A non-canonical genetic code in an early diverging eukaryotic lineage.. EMBO Journal, 1996, 15, 2285-2290.	7.8	70
116	Tetrapyrrole Synthesis of Photosynthetic Chromerids Is Likely Homologous to the Unusual Pathway of Apicomplexan Parasites Â. Plant Cell, 2011, 23, 3454-3462.	6.6	70
117	Single-cell transcriptomics for microbial eukaryotes. Current Biology, 2014, 24, R1081-R1082.	3.9	70
118	Pyruvate-Phosphate Dikinase of Oxymonads and Parabasalia and the Evolution of Pyrophosphate-Dependent Glycolysis in Anaerobic Eukaryotes. Eukaryotic Cell, 2006, 5, 148-154.	3.4	69
119	Broad genomic and transcriptional analysis reveals a highly derived genome in dinoflagellate mitochondria. BMC Biology, 2007, 5, 41.	3.8	69
120	Widespread recycling of processed cDNAs in dinoflagellates. Current Biology, 2008, 18, R550-R552.	3.9	69
121	Comment on "A Green Algal Apicoplast Ancestor". Science, 2003, 301, 49a-49.	12.6	68
122	Cryptic Organelles in Parasitic Protists and Fungi. Advances in Parasitology, 2003, 54, 9-68.	3.2	67
123	MOLECULAR PHYLOGENY AND SURFACE MORPHOLOGY OF MARINE ASEPTATE GREGARINES (APICOMPLEXA): SELENIDIUM SPP. AND LECUDINA SPP. Journal of Parasitology, 2003, 89, 1191-1205.	0.7	67
124	Lateral Transfer and Recompartmentalization of Calvin Cycle Enzymes of Plants and Algae. Journal of Molecular Evolution, 2004, 58, 367-375.	1.8	67
125	Draft genome sequence of the Daphnia pathogen Octosporea bayeri: insights into the gene content of a large microsporidian genome and a model for host-parasite interactions. Genome Biology, 2009, 10, R106.	9.6	67
126	Molecular Phylogeny and Surface Morphology of Colpodella edax (Alveolata): Insights into the Phagotrophic Ancestry of Apicomplexans. Journal of Eukaryotic Microbiology, 2003, 50, 334-340.	1.7	65

#	Article	IF	Citations
127	Global distribution of a wild alga revealed by targeted metagenomics. Current Biology, 2012, 22, R675-R677.	3.9	65
128	Sympatric kelp species share a large portion of their surface bacterial communities. Environmental Microbiology, 2018, 20, 658-670.	3.8	65
129	Widespread and ancient distribution of a noncanonical genetic code in diplomonads. Molecular Biology and Evolution, 1997, 14, 895-901.	8.9	64
130	Re-evaluating the Green versus Red Signal in Eukaryotes with Secondary Plastid of Red Algal Origin. Genome Biology and Evolution, 2012, 4, 626-635.	2.5	64
131	Complete Nucleotide Sequence of theSulfolobus islandicusMulticopy Plasmid pRN1. Plasmid, 1996, 35, 141-144.	1.4	63
132	Characterisation of a Non-canonical Genetic Code in the Oxymonad Streblomastix strix. Journal of Molecular Biology, 2003, 326, 1337-1349.	4.2	63
133	The search for the missing link: A relic plastid in Perkinsus?. International Journal for Parasitology, 2011, 41, 1217-1229.	3.1	63
134	Actin and Ubiquitin Protein Sequences Support a Cercozoan/Foraminiferan Ancestry for the Plasmodiophorid Plant Pathogens. Journal of Eukaryotic Microbiology, 2004, 51, 113-118.	1.7	62
135	Parallel genome reduction in symbionts descended from closely related free-living bacteria. Nature Ecology and Evolution, 2017, 1, 1160-1167.	7.8	62
136	Phylogenetic Diversity of Parabasalian Symbionts from Termites, Including the Phylogenetic Position of Pseudotrypanosoma and Trichonympha. Journal of Eukaryotic Microbiology, 1998, 45, 643-650.	1.7	61
137	Molecular phylogenetic position of Trichomitopsis termopsidis (Parabasalia) and evidence for the Trichomitopsiinae. European Journal of Protistology, 2002, 38, 279-286.	1.5	61
138	Bacterial Catalase in the Microsporidian Nosema locustae : Implications for Microsporidian Metabolism and Genome Evolution. Eukaryotic Cell, 2003, 2, 1069-1075.	3.4	61
139	Simplicity and Complexity of Microsporidian Genomes. Eukaryotic Cell, 2004, 3, 1363-1369.	3.4	60
140	Organelle Evolution: What's in a Name?. Current Biology, 2008, 18, R345-R347.	3.9	60
141	A kingdom's progress: Archezoa and the origin of eukaryotes. BioEssays, 1998, 20, 87-95.	2.5	59
142	Split Photosystem Protein, Linear-Mapping Topology, and Growth of Structural Complexity in the Plastid Genome of Chromera velia. Molecular Biology and Evolution, 2013, 30, 2447-2462.	8.9	59
143	Chromulinavorax destructans, a pathogen of microzooplankton that provides a window into the enigmatic candidate phylum Dependentiae. PLoS Pathogens, 2019, 15, e1007801.	4.7	59
144	Transfer of Nosema locustae (Microsporidia) to Antonospora locustae n. comb. Based on Molecular and Ultrastructural Data1. Journal of Eukaryotic Microbiology, 2004, 51, 207-213.	1.7	58

#	Article	IF	Citations
145	Genome sequence surveys of Brachiola algerae and Edhazardia aedis reveal microsporidia with low gene densities. BMC Genomics, 2008, 9, 200.	2.8	58
146	Archaebacterial genomes: eubacterial form and eukaryotic content. Current Opinion in Genetics and Development, 1994, 4, 816-822.	3.3	57
147	First Complete Mitochondrial Genome Sequence from a Box Jellyfish Reveals a Highly Fragmented Linear Architecture and Insights into Telomere Evolution. Genome Biology and Evolution, 2012, 4, 52-58.	2.5	57
148	Complete Genome Sequences from Three Genetically Distinct Strains Reveal High Intraspecies Genetic Diversity in the Microsporidian Encephalitozoon cuniculi. Eukaryotic Cell, 2013, 12, 503-511.	3.4	57
149	A Lack of Parasitic Reduction in the Obligate Parasitic Green Alga Helicosporidium. PLoS Genetics, 2014, 10, e1004355.	3.5	57
150	Reduction and Compaction in the Genome of the Apicomplexan Parasite Cryptosporidium parvum. Developmental Cell, 2004, 6, 614-616.	7.0	56
151	A kleptoplastidic dinoflagellate and the tipping point between transient and fully integrated plastid endosymbiosis. Proceedings of the National Academy of Sciences of the United States of America, 2019, 116, 17934-17942.	7.1	56
152	The dinoflagellates Durinskia baltica and Kryptoperidinium foliaceum retain functionally overlapping mitochondria from two evolutionarily distinct lineages. BMC Evolutionary Biology, 2007, 7, 172.	3.2	55
153	A Broad Distribution of the Alternative Oxidase in Microsporidian Parasites. PLoS Pathogens, 2010, 6, e1000761.	4.7	54
154	Patterns that Define the Four Domains Conserved in Known and Novel Isoforms of the Protein Import Receptor Tom20. Journal of Molecular Biology, 2005, 347, 81-93.	4.2	53
155	Relative rates of evolution among the three genetic compartments of the red alga Porphyra differ from those of green plants and do not correlate with genome architecture. Molecular Phylogenetics and Evolution, 2012, 65, 339-344.	2.7	53
156	Environmental distribution of coral-associated relatives of apicomplexan parasites. ISME Journal, 2013, 7, 444-447.	9.8	53
157	The GC-Rich Mitochondrial and Plastid Genomes of the Green Alga Coccomyxa Give Insight into the Evolution of Organelle DNA Nucleotide Landscape. PLoS ONE, 2011, 6, e23624.	2.5	53
158	Foraminifera and Cercozoa share a common origin according to RNA polymerase II phylogenies. International Journal of Systematic and Evolutionary Microbiology, 2003, 53, 1735-1739.	1.7	52
159	Organelle Genome Complexity Scales Positively with Organism Size in Volvocine Green Algae. Molecular Biology and Evolution, 2013, 30, 793-797.	8.9	52
160	Endosymbiotic Gene Transfer in Tertiary Plastid-Containing Dinoflagellates. Eukaryotic Cell, 2014, 13, 246-255.	3.4	52
161	Alpha and beta subunits of pyruvate dehydrogenase E1 from the microsporidian Nosema locustae: mitochondrion-derived carbon metabolism in microsporidia. Molecular and Biochemical Parasitology, 2001, 117, 201-209.	1.1	51
162	Identifying protist consumers of photosynthetic picoeukaryotes in the surface ocean using stable isotope probing. Environmental Microbiology, 2018, 20, 815-827.	3.8	51

#	Article	IF	Citations
163	The secondary endosymbiont of the cryptomonad Guillardia theta contains alpha-, beta-, and gamma-tubulin genes. Molecular Biology and Evolution, 1999, 16, 1308-1313.	8.9	50
164	Description of Colponema vietnamica sp.n. and Acavomonas peruviana n. gen. n. sp., Two New Alveolate Phyla (Colponemidia nom. nov. and Acavomonidia nom. nov.) and Their Contributions to Reconstructing the Ancestral State of Alveolates and Eukaryotes. PLoS ONE, 2014, 9, e95467.	2.5	50
165	Global diversity and distribution of close relatives of apicomplexan parasites. Environmental Microbiology, 2018, 20, 2824-2833.	3.8	50
166	The Phylogenetic Position of Alpha- and Beta-Tubulins from the Chlorarachnion Host and Cercomonas (Cercozoa). Journal of Eukaryotic Microbiology, 1998, 45, 561-570.	1.7	49
167	Nuclear Genome Sequence Survey of the Dinoflagellate <i>Heterocapsa triquetra</i>. Journal of Eukaryotic Microbiology, 2008, 55, 530-535.	1.7	49
168	Patterns of Genome Evolution among the Microsporidian Parasites Encephalitozoon cuniculi, Antonospora locustae and Enterocytozoon bieneusi. PLoS ONE, 2007, 2, e1277.	2.5	49
169	Class II Photolyase in a Microsporidian Intracellular Parasite. Journal of Molecular Biology, 2004, 341, 713-721.	4.2	48
170	Identification of Plant-like Galactolipids in Chromera velia, a Photosynthetic Relative of Malaria Parasites. Journal of Biological Chemistry, 2011, 286, 29893-29903.	3.4	48
171	Evolution of metabolic capabilities and molecular features of diplonemids, kinetoplastids, and euglenids. BMC Biology, 2020, 18, 23.	3.8	48
172	The Inadequacy of Morphology for Species and Genus Delineation in Microbial Eukaryotes: An Example from the Parabasalian Termite Symbiont Coronympha. PLoS ONE, 2009, 4, e6577.	2.5	48
173	Tertiary Endosymbiosis in Two Dinotoms Has Generated Little Change in the Mitochondrial Genomes of Their Dinoflagellate Hosts and Diatom Endosymbionts. PLoS ONE, 2012, 7, e43763.	2.5	47
174	Evidence for the Retention of Two Evolutionary Distinct Plastids in Dinoflagellates with Diatom Endosymbionts. Genome Biology and Evolution, 2014, 6, 2321-2334.	2.5	47
175	Nucleus-Encoded Genes for Plastid-Targeted Proteins in Helicosporidium : Functional Diversity of a Cryptic Plastid in a Parasitic Alga. Eukaryotic Cell, 2004, 3, 1198-1205.	3.4	46
176	The 3D Structure of the Apical Complex and Association with the Flagellar Apparatus Revealed by Serial TEM Tomography in Psammosa pacifica, a Distant Relative of the Apicomplexa. PLoS ONE, 2014, 9, e84653.	2.5	46
177	A new case of kleptoplasty in animals: Marine flatworms steal functional plastids from diatoms. Science Advances, 2019, 5, eaaw4337.	10.3	46
178	The Mitochondrial Genome of the Entomoparasitic Green Alga Helicosporidium. PLoS ONE, 2010, 5, e8954.	2.5	46
179	A complex and punctate distribution of three eukaryotic genes derived by lateral gene transfer. BMC Evolutionary Biology, 2007, 7, 89.	3.2	45
180	Highâ€throughput environmental sequencing reveals high diversity of litter and moss associated protist communities along a gradient of drainage and tree productivity. Environmental Microbiology, 2018, 20, 1185-1203.	3.8	45

#	Article	IF	Citations
181	Sulfolobus islandicus plasmids pRN1 and pRN2 share distant but common evolutionary ancestry. Extremophiles, 1998, 2, 391-393.	2.3	44
182	Symbiotic Innovation in the Oxymonad Streblomastix strix. Journal of Eukaryotic Microbiology, 2004, 51, 291-300.	1.7	44
183	Molecular phylogenies of Parabasalia inferred from four protein genes and comparison with rRNA trees. Molecular Phylogenetics and Evolution, 2004, 31, 572-580.	2.7	44
184	Comparative profiling of overlapping transcription in the compacted genomes of microsporidia Antonospora locustae and Encephalitozoon cuniculi. Genomics, 2008, 91, 388-393.	2.9	44
185	Unexpected mitochondrial genome diversity revealed by targeted single-cell genomics of heterotrophic flagellated protists. Nature Microbiology, 2020, 5, 154-165.	13.3	44
186	Evolutionary Relationship Between Translation Initiation Factor eIF-2Î³ and Selenocysteine-Specific Elongation Factor SELB: Change of Function in Translation Factors. Journal of Molecular Evolution, 1998, 47, 649-655.	1.8	43
187	Colponemids Represent Multiple Ancient Alveolate Lineages. Current Biology, 2013, 23, 2546-2552.	3.9	43
188	Functional Relationship between a Dinoflagellate Host and Its Diatom Endosymbiont. Molecular Biology and Evolution, 2016, 33, 2376-2390.	8.9	43
189	Alveolate and chlorophycean mitochondrial cox2 genes split twice independently. Gene, 2006, 383, 33-37.	2.2	42
190	Genome Evolution and Nitrogen Fixation in Bacterial Ectosymbionts of a Protist Inhabiting Wood-Feeding Cockroaches. Applied and Environmental Microbiology, 2016, 82, 4682-4695.	3.1	41
191	Highly Reduced Genomes of Protist Endosymbionts Show Evolutionary Convergence. Current Biology, 2020, 30, 925-933.e3.	3.9	41
192	<i>Colpodella</i>spp.â€“like Parasite Infection in Woman, China. Emerging Infectious Diseases, 2012, 18, 125-127.	4.3	40
193	Arginine deiminase pathway enzymes: evolutionary history in metamonads and other eukaryotes. BMC Evolutionary Biology, 2016, 16, 197.	3.2	40
194	Reference Tree and Environmental Sequence Diversity of Labyrinthulomycetes. Journal of Eukaryotic Microbiology, 2017, 64, 88-96.	1.7	40
195	Single cell genomics of uncultured marine alveolates shows paraphyly of basal dinoflagellates. ISME Journal, 2018, 12, 304-308.	9.8	40
196	Revealing the metabolic capacity of <i>Streblomastix strix</i> and its bacterial symbionts using single-cell metagenomics. Proceedings of the National Academy of Sciences of the United States of America, 2019, 116, 19675-19684.	7.1	40
197	Single cell genomics reveals plastid-lacking Picozoa are close relatives of red algae. Nature Communications, 2021, 12, 6651.	12.8	40
198	Who is Oxyrrhis marina? Morphological and phylogenetic studies on an unusual dinoflagellate. Journal of Plankton Research, 2011, 33, 555-567.	1.8	39

#	Article	IF	Citations
199	Plastid-derived Type II fatty acid biosynthetic enzymes in chromists. Gene, 2003, 313, 139-148.	2.2	38
200	An introduction to the special issue: Oxyrrhis marina, a model organism?. Journal of Plankton Research, 2011, 33, 549-554.	1.8	38
201	Correlated SEM, FIB-SEM, TEM, and NanoSIMS Imaging of Microbes from the Hindgut of a Lower Termite: Methods for<i>In Situ</i>Functional and Ecological Studies of Uncultivable Microbes. Microscopy and Microanalysis, 2013, 19, 1490-1501.	0.4	38
202	Biogeography and Character Evolution of the Ciliate Genus Euplotes (Spirotrichea, Euplotia), with Description of Euplotes curdsi sp. nov.. PLoS ONE, 2016, 11, e0165442.	2.5	38
203	The fate of obligate endosymbionts: reduction, integration, or extinction. Current Opinion in Genetics and Development, 2019, 58-59, 1-8.	3.3	38
204	Description of Two Species of Early Branching Dinoflagellates, Psammosa pacifica n. g., n. sp. and P. atlantica n. sp. PLoS ONE, 2012, 7, e34900.	2.5	38
205	Pseudofinder: Detection of Pseudogenes in Prokaryotic Genomes. Molecular Biology and Evolution, 2022, 39, .	8.9	38
206	Seasonal and ecohydrological regulation of active microbial populations involved in DOC, CO2, and CH4 fluxes in temperate rainforest soil. ISME Journal, 2019, 13, 950-963.	9.8	37
207	The Phylogenetic Position of the Oxymonad Saccinobaculus Based on SSU rRNA. Protist, 2006, 157, 335-344.	1.5	36
208	The origins of malaria: there are more things in heaven and earth â€¦. Parasitology, 2015, 142, S16-S25.	1.5	36
209	The Ordospora colligata Genome: Evolution of Extreme Reduction in Microsporidia and Host-To-Parasite Horizontal Gene Transfer. MBio, 2015, 6, .	4.1	36
210	Microbial arms race: Ballistic â€œnematocystsâ€• in dinoflagellates represent a new extreme in organelle complexity. Science Advances, 2017, 3, e1602552.	10.3	36
211	Insights into the origin of metazoan multicellularity from predatory unicellular relatives of animals. BMC Biology, 2020, 18, 39.	3.8	36
212	Deep Questions in the Tree of Life. Science, 2007, 317, 1875-1876.	12.6	35
213	Shrink it or lose it: balancing loss of function with shrinking genomes in the microsporidia. Virulence, 2011, 2, 67-70.	4.4	35
214	Genomics: Evolution of the Genetic Code. Current Biology, 2016, 26, R851-R853.	3.9	35
215	An ADP/ATP-Specific Mitochondrial Carrier Protein in the Microsporidian Antonospora locustae. Journal of Molecular Biology, 2008, 375, 1249-1257.	4.2	34
216	Validation of a universal set of primers to study animalâ€associated microeukaryotic communities. Environmental Microbiology, 2019, 21, 3855-3861.	3.8	34

#	Article	IF	Citations
217	The eukaryome: Diversity and role of microeukaryotic organisms associated with animal hosts. Functional Ecology, 2020, 34, 2045-2054.	3.6	34
218	Plastid-Targeting Peptides from the Chlorarachniophyte Bigelowiella natans. Journal of Eukaryotic Microbiology, 2004, 51, 529-535.	1.7	33
219	HSP90, Tubulin and Actin are Retained in the Tertiary Endosymbiont Genome of Kryptoperidinium foliaceum. Journal of Eukaryotic Microbiology, 2004, 51, 651-659.	1.7	33
220	Phylogenetic history of plastid-targeted proteins in the peridinin-containing dinoflagellate Heterocapsa triquetra. International Journal of Systematic and Evolutionary Microbiology, 2006, 56, 1439-1447.	1.7	33
221	Genome-Based Reconstruction of the Protein Import Machinery in the Secondary Plastid of a Chlorarachniophyte Alga. Eukaryotic Cell, 2012, 11, 324-333.	3.4	33
222	Viral proteins as a potential driver of histone depletion in dinoflagellates. Nature Communications, 2018, 9, 1535.	12.8	33
223	Assessing the Diversity and Distribution of Apicomplexans in Host and Free-Living Environments Using High-Throughput Amplicon Data and a Phylogenetically Informed Reference Framework. Frontiers in Microbiology, 2019, 10, 2373.	3.5	33
224	Response to Comment on "A Green Algal Apicoplast Ancestor". Science, 2003, 301, 49b-49.	12.6	32
225	A high density of ancient spliceosomal introns in oxymonad excavates. BMC Evolutionary Biology, 2006, 6, 34.	3.2	32
226	Morphology and Phylogenetic Position of Eucomonympha imla (Parabasalia: Hypermastigida). Journal of Eukaryotic Microbiology, 2007, 54, 325-332.	1.7	32
227	Complex distribution of EFL and EF-1Î± proteins in the green algal lineage. BMC Evolutionary Biology, 2007, 7, 82.	3.2	32
228	Complex phylogenetic distribution of a non-canonical genetic code in green algae. BMC Evolutionary Biology, 2010, 10, 327.	3.2	32
229	Diplonemid Glyceraldehyde-3-PhosphateDehydrogenase (GAPDH) and Prokaryote-to-Eukaryote Lateral Gene Transfer. Protist, 2001, 152, 193-201.	1.5	31
230	A Brief History of Plastids and their Hosts. Protist, 2004, 155, 3-7.	1.5	31
231	Analysis of the ?-Tubulin Genes from Enterocytozoon bieneusi Isolates from a Human and Rhesus Macaque. Journal of Eukaryotic Microbiology, 2007, 54, 38-41.	1.7	31
232	Acquisition of an animal gene by microsporidian intracellular parasites. Current Biology, 2011, 21, R576-R577.	3.9	31
233	Evolution: Causality and the Origin of Parasitism. Current Biology, 2016, 26, R174-R177.	3.9	31
234	The selfish pursuit of sex. Nature, 1995, 375, 283-283.	27.8	30

#	Article	IF	Citations
235	Cthulhu Macrofasciculumque n. g., n. sp. and Cthylla Microfasciculumque n. g., n. sp., a Newly Identified Lineage of Parabasalian Termite Symbionts. PLoS ONE, 2013, 8, e58509.	2.5	30
236	Comparative genomics of microsporidia. Folia Parasitologica, 2005, 52, 8-14.	1.3	30
237	Distinct Localization Patterns of Two Putative Mitochondrial Proteins in the Microsporidian <i>Encephalitozoon cuniculi</i>. Journal of Eukaryotic Microbiology, 2008, 55, 131-133.	1.7	29
238	Morphology, Phylogeny, and Diversity of <i>Trichonympha</i> (Parabasalia: Hypermastigida) of the Woodâ€Feeding Cockroach <i>Cryptocercus punctulatus</i>. Journal of Eukaryotic Microbiology, 2009, 56, 305-313.	1.7	29
239	Endosymbiosis: Protein Targeting Further Erodes the Organelle/Symbiont Distinction. Current Biology, 2014, 24, R654-R655.	3.9	29
240	X-Cells Are Globally Distributed, Genetically Divergent Fish Parasites Related to Perkinsids and Dinoflagellates. Current Biology, 2017, 27, 1645-1651.e3.	3.9	29
241	Rhizarian â€˜Novel Clade 10â€™ Revealed as Abundant and Diverse Planktonic and Terrestrial Flagellates, including <i>Aquavolon</i> n. gen.. Journal of Eukaryotic Microbiology, 2018, 65, 828-842.	1.7	29
242	<i>LESSARDIA ELONGATA</i> GEN. ET SP. NOV. (DINOFLAGELLATA, PERIDINIALES, PODOLAMPACEAE) AND THE TAXONOMIC POSITION OF THE GENUS <i>ROSCOFFIA</i>¹. Journal of Phycology, 2003, 39, 368-378.	2.3	28
243	Novel Ubiquitin Fusion Proteins: Ribosomal Protein P1 and Actin. Journal of Molecular Biology, 2003, 328, 771-778.	4.2	28
244	Characterization of Periplastidal Compartmentâ€“Targeting Signals in Chlorarachniophytes. Molecular Biology and Evolution, 2010, 27, 1538-1545.	8.9	28
245	Comment on "The Evolution of Modern Eukaryotic Phytoplankton". Science, 2004, 306, 2191b-2191b.	12.6	27
246	Horizontal transfer of a eukaryotic plastid-targeted protein gene to cyanobacteria. BMC Biology, 2007, 5, 26.	3.8	27
247	Molecular and morphological analysis of the family Calonymphidae with a description of Calonympha chia sp. nov., Snyderella kirbyi sp. nov., Snyderella swezyae sp. nov. and Snyderella yamini sp. nov.. International Journal of Systematic and Evolutionary Microbiology, 2011, 61, 2547-2558.	1.7	27
248	Evidence for Transitional Stages in the Evolution of Euglenid Group II Introns and Twintrons in the Monomorphina aenigmatica Plastid Genome. PLoS ONE, 2012, 7, e53433.	2.5	27
249	EukRefâ€Ciliophora: a manually curated, phylogenyâ€based database of small subunit rRNA gene sequences of ciliates. Environmental Microbiology, 2018, 20, 2218-2230.	3.8	27
250	Symbiotic Origin of a Novel Actin Gene in the Cryptophyte Pyrenomonas helgolandii. Molecular Biology and Evolution, 2000, 17, 1731-1738.	8.9	26
251	EFL GTPase in Cryptomonads and the Distribution of EFL and EF-1Î± in Chromalveolates. Protist, 2006, 157, 435-444.	1.5	26
252	Analysis of EST data of the marine protist Oxyrrhis marina, an emerging model for alveolate biology and evolution. BMC Genomics, 2014, 15, 122.	2.8	26

#	Article	IF	Citations
253	The Morphology, Ultrastructure and SSU rRNA Gene Sequence of a New Freshwater Flagellate, <i>Neobodo borokensis</i> n. sp. (Kinetoplastea, Excavata). Journal of Eukaryotic Microbiology, 2016, 63, 220-232.	1.7	26
254	Parallel functional reduction in the mitochondria of apicomplexan parasites. Current Biology, 2021, 31, 2920-2928.e4.	3.9	26
255	Microbiomes of microscopic marine invertebrates do not reveal signatures of phylosymbiosis. Nature Microbiology, 2022, 7, 810-819.	13.3	26
256	Parasites go the full monty. Nature, 2001, 414, 401-402.	27.8	25
257	Lateral gene transfer and the complex distribution of insertions in eukaryotic enolase. Gene, 2004, 340, 227-235.	2.2	25
258	Evolution of Ultrasmall Spliceosomal Introns in Highly Reduced Nuclear Genomes. Molecular Biology and Evolution, 2009, 26, 1699-1705.	8.9	25
259	The RAB Family GTPase Rab1A from <i>Plasmodium falciparum</i> Defines a Unique Paralog Shared by Chromalveolates and Rhizaria. Journal of Eukaryotic Microbiology, 2009, 56, 348-356.	1.7	25
260	DNA BARCODING OF CHLORARACHNIOPHYTES USING NUCLEOMORPH ITS SEQUENCES1. Journal of Phycology, 2010, 46, 743-750.	2.3	25
261	Nucleusâ€•and nucleomorphâ€targeted histone proteins in a chlorarachniophyte alga. Molecular Microbiology, 2011, 80, 1439-1449.	2.5	25
262	Bridge over troublesome plastids. Nature, 2008, 451, 896-897.	27.8	24
263	Twentyâ€Fold Difference in Evolutionary Rates between the Mitochondrial and Plastid Genomes of Species with Secondary Red Plastids. Journal of Eukaryotic Microbiology, 2012, 59, 181-184.	1.7	24
264	New Lineage of Microbial Predators Adds Complexity to Reconstructing the Evolutionary Origin of Animals. Current Biology, 2020, 30, 4500-4509.e5.	3.9	24
265	Distribution and Phylogeny of EFL and EF-1Î± in Euglenozoa Suggest Ancestral Co-Occurrence Followed by Differential Loss. PLoS ONE, 2009, 4, e5162.	2.5	24
266	A non-canonical genetic code in an early diverging eukaryotic lineage. EMBO Journal, 1996, 15, 2285-90.	7.8	24
267	Contributions of Oxyrrhis marina to molecular biology, genomics and organelle evolution of dinoflagellates. Journal of Plankton Research, 2011, 33, 591-602.	1.8	23
268	Gene Conversion Shapes Linear Mitochondrial Genome Architecture. Genome Biology and Evolution, 2013, 5, 905-912.	2.5	23
269	Phylogenomics Identifies a New Major Subgroup of Apicomplexans, Marosporida <i>class nov.</i>, with Extreme Apicoplast Genome Reduction. Genome Biology and Evolution, 2021, 13, .	2.5	23
270	Surface morphology of the marine parasite Haplozoon axiothellae Siebert (Dinoflagellata). European Journal of Protistology, 2002, 38, 287-297.	1.5	22

#	Article	IF	Citations
271	Nucleus-Encoded Periplastid-Targeted EFL in Chlorarachniophytes. Molecular Biology and Evolution, 2008, 25, 1967-1977.	8.9	22
272	Mitochondrial Genome of a Tertiary Endosymbiont Retains Genes for Electron Transport Proteins. Journal of Eukaryotic Microbiology, 2007, 54, 146-153.	1.7	21
273	Ostreococcus tauri: seeing through the genes to the genome. Trends in Genetics, 2007, 23, 151-154.	6.7	21
274	The Distribution of Elongation Factorâ€1 Alpha (EFâ€1Î±), Elongation Factorâ€Like (EFL), and a Nonâ€Canonical Genetic Code in the Ulvophyceae: Discrete Genetic Characters Support a Consistent Phylogenetic Framework. Journal of Eukaryotic Microbiology, 2009, 56, 367-372.	1.7	21
275	The Impact of History on Our Perception of Evolutionary Events: Endosymbiosis and the Origin of Eukaryotic Complexity. Cold Spring Harbor Perspectives in Biology, 2014, 6, a016196-a016196.	5.5	21
276	Symbiont replacement between bacteria of different classes reveals additional layers of complexity in the evolution of symbiosis in the ciliate Euplotes. Protist, 2018, 169, 43-52.	1.5	21
277	Combining morphology, behaviour and genomics to understand the evolution and ecology of microbial eukaryotes. Philosophical Transactions of the Royal Society B: Biological Sciences, 2019, 374, 20190085.	4.0	21
278	Single-Cell DNA Barcoding Using Sequences from the Small Subunit rRNA and Internal Transcribed Spacer Region Identifies New Species of Trichonympha and Trichomitopsis from the Hindgut of the Termite Zootermopsis angusticollis. PLoS ONE, 2013, 8, e58728.	2.5	21
279	Concerted evolution in protists: Recent homogenization of a polyubiquitin gene in Trichomonas vaginalis. Journal of Molecular Evolution, 1995, 41, 556-62.	1.8	20
280	Phylogenetic Position and Morphology of Spirotrichosomidae (Parabasalia): New Evidence from Leptospironympha of Cryptocercus punctulatus. Protist, 2010, 161, 122-132.	1.5	20
281	Horizontal Gene Transfer and Redundancy of Tryptophan Biosynthetic Enzymes in Dinotoms. Genome Biology and Evolution, 2014, 6, 333-343.	2.5	20
282	Single-cell transcriptomics using spliced leader PCR: Evidence for multiple losses of photosynthesis in polykrikoid dinoflagellates. BMC Genomics, 2015, 16, 528.	2.8	20
283	Transformation of <i>Diplonema papillatum</i>, the type species of the highly diverse and abundant marine microeukaryotes Diplonemida (Euglenozoa). Environmental Microbiology, 2018, 20, 1030-1040.	3.8	20
284	Comparative rates of evolution in endosymbiotic nuclear genomes. BMC Evolutionary Biology, 2006, 6, 46.	3.2	19
285	Protein targeting in parasites with cryptic mitochondria. International Journal for Parasitology, 2007, 37, 265-272.	3.1	19
286	Splicing and Transcription Differ between Spore and Intracellular Life Stages in the Parasitic Microsporidia. Molecular Biology and Evolution, 2010, 27, 1579-1584.	8.9	19
287	Feâ€"S Cluster Assembly in Oxymonads and Related Protists. Molecular Biology and Evolution, 2018, 35, 2712-2718.	8.9	19
288	Controlled sampling of ribosomally active protistan diversity in sediment-surface layers identifies putative players in the marine carbon sink. ISME Journal, 2020, 14, 984-998.	9.8	19

#	Article	IF	Citations
289	Microsporidian Mitochondrial Proteins: Expression in <i>Antonospora locustae</i> Spores and Identification of Genes Coding for Two Further Proteins. Journal of Eukaryotic Microbiology, 2005, 52, 271-276.	1.7	18
290	Evidence from SSU rRNA Phylogeny that Octomitus is a Sister Lineage to Giardia. Protist, 2006, 157, 205-212.	1.5	18
291	Endosymbiosis: Bacteria Sharing the Load. Current Biology, 2011, 21, R623-R624.	3.9	18
292	Amalga-like virus infecting Antonospora locustae , a microsporidian pathogen of grasshoppers, plus related viruses associated with other arthropods. Virus Research, 2017, 233, 95-104.	2.2	18
293	Morphological complexity affects the diversity of marine microbiomes. ISME Journal, 2021, 15, 1372-1386.	9.8	18
294	Role of Horizontal Gene Transfer in the Evolution of Photosynthetic Eukaryotes and Their Plastids. Methods in Molecular Biology, 2009, 532, 501-515.	0.9	18
295	Environmental PCR survey to determine the distribution of a nonâ€canonical genetic code in uncultivable oxymonads. Environmental Microbiology, 2008, 10, 65-74.	3.8	17
296	(048â€"051) Proposals to exclude the phylum <i>Microsporidia</i> from the <i>Code</i>. Taxon, 2009, 58, 669-669.	0.7	17
297	Morphology and Molecular Phylogeny of <i>Pseudotrichonympha hertwigi</i> and <i>Pseudotrichonympha paulistana</i> (Trichonymphea, Parabasalia) from Neotropical Rhinotermitids. Journal of Eukaryotic Microbiology, 2011, 58, 487-496.	1.7	17
298	Dual targeting of aminoacyl-tRNA synthetases to the mitochondrion and complex plastid in chlorarachniophytes. Journal of Cell Science, 2012, 125, 6176-6184.	2.0	17
299	What Can Environmental Sequences Tell Us About the Distribution of Lowâ€Rank Taxa? The Case of <i>Euplotes</i> (Ciliophora, Spirotrichea), Including a Description of <i>Euplotes enigma</i> sp. nov.. Journal of Eukaryotic Microbiology, 2019, 66, 281-293.	1.7	17
300	A Revised Taxonomy of Diplonemids Including the Eupelagonemidae n. fam. and a Type Species, <i>Eupelagonema oceanica</i> n. gen. & sp.. Journal of Eukaryotic Microbiology, 2019, 66, 519-524.	1.7	17
301	Early eukaryotic origins and metazoan elaboration of MAPR family proteins. Molecular Phylogenetics and Evolution, 2020, 148, 106814.	2.7	17
302	How exaptations facilitated photosensory evolution: Seeing the light by accident. BioEssays, 2017, 39, 1600266.	2.5	16
303	Phylogenomics supports the monophyly of the Cercozoa. Molecular Phylogenetics and Evolution, 2019, 130, 416-423.	2.7	16
304	Predatory colponemids are the sister group to all other alveolates. Molecular Phylogenetics and Evolution, 2020, 149, 106839.	2.7	16
305	Surface Morphology of Saccinobaculus (Oxymonadida): Implications for Character Evolution and Function in Oxymonads. Protist, 2008, 159, 209-221.	1.5	15
306	Trichonympha burlesquei n. sp. from Reticulitermes virginicus and evidence against a cosmopolitan distribution of Trichonympha agilis in many termite hosts. International Journal of Systematic and Evolutionary Microbiology, 2013, 63, 3873-3876.	1.7	15

#	Article	IF	Citations
307	A Comparative Overview of the Flagellar Apparatus of Dinoflagellate, Perkinsids and Colpodellids. Microorganisms, 2014, 2, 73-91.	3.6	15
308	Multigene phylogenetics of euglenids based on single-cell transcriptomics of diverse phagotrophs. Molecular Phylogenetics and Evolution, 2021, 159, 107088.	2.7	15
309	Diplonemids â€“ A Review on "New" Flagellates on the Oceanic Block. Protist, 2022, 173, 125868.	1.5	15
310	Phylogenetic Analysis of Sulfate Assimilation and Cysteine Biosynthesis in Phototrophic Organisms. Advances in Photosynthesis and Respiration, 2008, , 31-58.	1.0	14
311	The â€œOtherâ€•<i>Rickettsiales</i> : an Overview of the Family â€œ <i>Candidatus</i> Midichloriaceaeâ€• Applied and Environmental Microbiology, 2022, 88, aem0243221.	3.1	14
312	Polymorphic Insertions and Deletions in Parabasalian Enolase Genes. Journal of Molecular Evolution, 2004, 58, 550-556.	1.8	13
313	A Transcriptional Fusion of Genes Encoding Glyceraldehyde-3-Phosphate Dehydrogenase (GAPDH) and Enolase in Dinoflagellates. Journal of Eukaryotic Microbiology, 2005, 52, 343-348.	1.7	13
314	Î±â€•and Î²â€•Tubulin Phylogenies Support a Close Relationship Between the Microsporidia <i>Brachiola algerae</i> and <i>Antonospora locustae</i>. Journal of Eukaryotic Microbiology, 2008, 55, 388-392.	1.7	13
315	Gene expression during bacterivorous growth of a widespread marine heterotrophic flagellate. ISME Journal, 2021, 15, 154-167.	9.8	13
316	First finding of free-living representatives of Prokinetoplastina and their nuclear and mitochondrial genomes. Scientific Reports, 2021, 11, 2946.	3.3	13
317	An Evaluation of Hsp90 as a Mediator of Cortical Patterning in Tetrahymena. Journal of Eukaryotic Microbiology, 2001, 48, 147-160.	1.7	12
318	Characterization of a Divergent Sec61Î² Gene in Microsporidia. Journal of Molecular Biology, 2006, 359, 1196-1202.	4.2	12
319	Symbiosis, Morphology, and Phylogeny of Hoplonymphidae (Parabasalia) of the Wood-Feeding Roach Cryptocercus punctulatus. Journal of Eukaryotic Microbiology, 2011, 58, 426-436.	1.7	12
320	Branching Network of Proteinaceous Filaments within the Parasitophorous Vacuole of Encephalitozoon cuniculi and Encephalitozoon hellem. Infection and Immunity, 2011, 79, 1374-1385.	2.2	12
321	Overexpression of Molecular Chaperone Genes in Nucleomorph Genomes. Molecular Biology and Evolution, 2014, 31, 1437-1443.	8.9	12
322	<i>Moramonas marocensis</i> gen. nov., sp. nov.: a jakobid flagellate isolated from desert soil with a bacteria-like, but bloated mitochondrial genome. Open Biology, 2016, 6, 150239.	3.6	12
323	New Species of <i>Spirotrichonympha</i> from <i>Reticulitermes</i> and the Relationships Among Genera in Spirotrichonymphea (Parabasalia). Journal of Eukaryotic Microbiology, 2018, 65, 159-169.	1.7	12
324	Dinoflagellate nucleus contains an extensive endomembrane network, the nuclear net. Scientific Reports, 2019, 9, 839.	3.3	12

#	Article	IF	Citations
325	Molecular characterization and phylogeny of four new species of the genus Trichonympha (Parabasalia, Trichonymphea) from lower termite hindguts. International Journal of Systematic and Evolutionary Microbiology, 2017, 67, 3570-3575.	1.7	12
326	Morphological Diversity between Culture Strains of a Chlorarachniophyte, Lotharella globosa. PLoS ONE, 2011, 6, e23193.	2.5	12
327	An Archaebacterial eIF-1A: new grist for the mill. Molecular Microbiology, 1995, 17, 399-400.	2.5	11
328	Expressed Sequence Tag (EST) Survey of the Highly Adapted Green Algal Parasite,. Protist, 2005, 156, 181-190.	1.5	11
329	Protists and the Wild, Wild West of Gene Expression: New Frontiers, Lawlessness, and Misfits. Annual Review of Microbiology, 2016, 70, 161-178.	7.3	11
330	Single-Cell Transcriptomics of Abedinium Reveals a New Early-Branching Dinoflagellate Lineage. Genome Biology and Evolution, 2020, 12, 2417-2428.	2.5	11
331	Three-Dimensional Molecular Cartography of the Caribbean Reef-Building Coral Orbicella faveolata. Frontiers in Marine Science, 2021, 8, .	2.5	11
332	Plant genomes: cyanobacterial genes revealed. Heredity, 2003, 90, 2-3.	2.6	10
333	mRNA processing in Antonospora locustae spores. Molecular Genetics and Genomics, 2008, 280, 565-574.	2.1	10
334	Comment on â€œDoes constructive neutral evolution play an important role in the origin of cellular complexity?â€•DOI 10.1002/bies.201100010. BioEssays, 2011, 33, 427-429.	2.5	10
335	Morphology and Molecular Phylogeny of <i>Staurojoenina mulleri</i> sp. nov. (Trichonymphida,) Tj ETQq1 1 0.784314 rgBT /Overlock 1 Microbiology, 2013, 60, 203-213.	1.7	10
336	The Phylogenetic Position of <i>Kofoidia loriculata</i> (Parabasalia) and its Implications for the Evolution of the Cristamonadea. Journal of Eukaryotic Microbiology, 2015, 62, 255-259.	1.7	10
337	High Prevalence and Endemism of Trypanosomatids on a Small Caribbean Island. Journal of Eukaryotic Microbiology, 2019, 66, 600-607.	1.7	10
338	Extensive molecular tinkering in the evolution of the membrane attachment mode of the Rheb GTPase. Scientific Reports, 2018, 8, 5239.	3.3	9
339	Taxonomy of the Apicomplexan Symbionts of Coral, including Corallicolida ord. nov., Reassignment of the Genus <i>Gemmocystis</i>, and Description of New Species <i>Corallicola</i><i>aquarius</i> gen. nov. sp. nov. and <i>Anthozoaphila</i><i>gnarlus</i> gen. nov. sp. nov.. Journal of Eukaryotic Microbiology, 2021, 68, e12852.	1.7	9
340	Single-cell Microbiomics Unveils Distribution and Patterns of Microbial Symbioses in the Natural Environment. Microbial Ecology, 2023, 85, 307-316.	2.8	9
341	Linked Genes for Calmodulin and E2 Ubiquitin-Conjugating Enzyme in Trichomonas vaginalis. Journal of Eukaryotic Microbiology, 1996, 43, 468-474.	1.7	8
342	Puromycin selection for stable transfectants of the oyster-infecting parasite Perkinsus marinus. Parasitology International, 2019, 69, 13-16.	1.3	8

#	Article	IF	Citations
343	Gene Transfer Agents in Bacterial Endosymbionts of Microbial Eukaryotes. Genome Biology and Evolution, 2022, 14, .	2.5	8
344	Highly divergentCaenorhabditis andSaccharomyces tubulins evolved recently from genes encoding Î³-tubulin. Trends in Cell Biology, 1996, 6, 375-375.	7.9	7
345	2 Microsporidia â€" Highly Reduced and Derived Relatives of Fungi. , 2011, , 25-36.		7
346	Termite Hindguts and the Ecology of Microbial Communities in the Sequencing Age. Journal of Eukaryotic Microbiology, 2013, 60, 421-428.	1.7	7
347	Molecular Characterization of Parabasalian Symbionts <i><scp>C</scp>oronympha clevelandii</i> and <i><scp>T</scp>richonympha subquasilla</i> from the <scp>H</scp>awaiian Lowland Tree Termite <i><scp>I</scp>ncisitermes immigrans</i>. Journal of Eukaryotic Microbiology, 2013, 60, 313-316.	1.7	7
348	A Complex Distribution of Elongation Family GTPases EF1A and EFL in Basal Alveolate Lineages. Genome Biology and Evolution, 2014, 6, 2361-2367.	2.5	7
349	Molecular Evidence for the Polyphyly of <i>Macrotrichomonas</i> (Parabasalia: Cristamonadea) and a Proposal for <i>Macrotrichomonoides</i> n. gen.. Journal of Eukaryotic Microbiology, 2015, 62, 494-504.	1.7	7
350	Monophyly of diverse Bigyromonadea and their impact on phylogenomic relationships within stramenopiles. Molecular Phylogenetics and Evolution, 2022, 171, 107468.	2.7	7
351	An infB-Homolog in Sulfolobus acidocaldarius. Systematic and Applied Microbiology, 1996, 19, 312-321.	2.8	6
352	Microbial communities in sandy beaches from the three domains of life differ by microhabitat and intertidal location. Molecular Ecology, 2022, 31, 3210-3227.	3.9	6
353	All essential endosymbionts of the ciliate Euplotes are cyclically replaced. Current Biology, 2022, 32, R826-R827.	3.9	6
354	Chlorarachniophytes. , 2017, , 765-781.		5
355	Pseudotrichonympha leei, Pseudotrichonympha lifesoni, and Pseudotrichonympha pearti, new species of parabasalian flagellates and the description of a rotating subcellular structure. Scientific Reports, 2017, 7, 16349.	3.3	5
356	High-efficiency transformation of the chlorarachniophyte Amorphochlora amoebiformis by electroporation. Algal Research, 2020, 48, 101903.	4.6	5
357	Heterotrophic flagellates and centrohelid heliozoans from marine waters of Curacao, the Netherlands Antilles. European Journal of Protistology, 2021, 77, 125758.	1.5	5
358	Corallicolids: The elusive coral-infecting apicomplexans. PLoS Pathogens, 2021, 17, e1009845.	4.7	5
359	Intragenomic Spread of Plastid-Targeting Presequences in the Coccolithophore Emiliania huxleyi. Molecular Biology and Evolution, 2012, 29, 2109-2112.	8.9	4
360	A new vesicular compartment in Encephalitozoon cuniculi. Microbes and Infection, 2012, 14, 324-328.	1.9	4

#	Article	IF	Citations
361	Extensive Reduction of the Nuclear Pore Complex in Nucleomorphs. Genome Biology and Evolution, 2019, 11, 678-687.	2.5	4
362	A kingdom's progress: Archezoa and the origin of eukaryotes. BioEssays, 1998, 20, 87-95.	2.5	4
363	Reply to Speijer: Does complexity necessarily arise from selective advantage?. Proceedings of the National Academy of Sciences of the United States of America, 2010, 107, .	7.1	3
364	Phylogeny, Evidence for a Cryptic Plastid, and Distribution of <i>Chytriodinium</i> Parasites (Dinophyceae) Infecting Copepods. Journal of Eukaryotic Microbiology, 2019, 66, 574-581.	1.7	2
365	Chlorarachniophytes. , 2016, , 1-17.		1
366	Fish Parasite Dinoflagellates <i>Haidadinium ichthyophilum</i> and <i>Piscinoodinium</i> Share a Recent Common Ancestor. Journal of Eukaryotic Microbiology, 2018, 65, 127-131.	1.7	1
367	The molecular phylogeny of Chionaster nivalis reveals a novel order of psychrophilic and globally distributed Tremellomycetes (Fungi, Basidiomycota). PLoS ONE, 2021, 16, e0247594.	2.5	1
368	64 Nucleus-encoded, plastid-targeted glyceraldehyde-3-phosphate dehydrogenase (GAPDH) indicates a single origin for chromalveolate plastids. Journal of Phycology, 2003, 39, 22-22.	2.3	0
369	Molecular evidence for a single common origin of chromalveolate plastids. Journal of Eukaryotic Microbiology, 2005, 52, 7S-27S.	1.7	0
370	Genome evolution in Microsporidia. Journal of Eukaryotic Microbiology, 2005, 52, 7S-27S.	1.7	0
371	Filling in the gaps: EST surveys of under-represented chromalveolates. Journal of Eukaryotic Microbiology, 2005, 52, 7S-27S.	1.7	0
372	THE KINGDOM PROTISTA: THE DAZZLING WORLD OF LIVING CELLS by Pickett-Heaps, Jeremy D. and Pickett-Heaps, Julianne. Journal of Phycology, 2006, 42, 1155-1156.	2.3	0
373	Patrick Keeling. Current Biology, 2017, 27, R85-R87.	3.9	0
374	A letter to Denis Lynn. Aquatic Ecosystem Health and Management, 2020, 23, 17-18.	0.6	0
375	Characterization of new cristamonad species from kalotermitid termites including a novel genus, Runanympha. Scientific Reports, 2021, 11, 7270.	3.3	0