

# David Moreira

## List of Publications by Year in descending order

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192  
papers

14,114  
citations

16451

64  
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24258

110  
g-index

202  
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202  
docs citations

202  
times ranked

11610  
citing authors

#	ARTICLE	IF	CITATIONS
1	Unexpected diversity of small eukaryotes in deep-sea Antarctic plankton. <i>Nature</i> , 2001, 409, 603-607.	27.8	838
2	The origin of red algae and the evolution of chloroplasts. <i>Nature</i> , 2000, 405, 69-72.	27.8	402
3	Autochthonous eukaryotic diversity in hydrothermal sediment and experimental microcolonizers at the Mid-Atlantic Ridge. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2003, 100, 697-702.	7.1	337
4	Ten reasons to exclude viruses from the tree of life. <i>Nature Reviews Microbiology</i> , 2009, 7, 306-311.	28.6	322
5	Symbiosis Between Methanogenic Archaea and Î-Proteobacteria as the Origin of Eukaryotes: The Syntrophic Hypothesis. <i>Journal of Molecular Evolution</i> , 1998, 47, 517-530.	1.8	282
6	The molecular ecology of microbial eukaryotes unveils a hidden world. <i>Trends in Microbiology</i> , 2002, 10, 31-38.	7.7	279
7	An Early-Branching Freshwater Cyanobacterium at the Origin of Plastids. <i>Current Biology</i> , 2017, 27, 386-391.	3.9	275
8	Origins and Early Evolution of the Mevalonate Pathway of Isoprenoid Biosynthesis in the Three Domains of Life. <i>Molecular Biology and Evolution</i> , 2011, 28, 87-99.	8.9	270
9	Ancestral lipid biosynthesis and early membrane evolution. <i>Trends in Biochemical Sciences</i> , 2004, 29, 469-477.	7.5	252
10	The early evolution of lipid membranes and the three domains of life. <i>Nature Reviews Microbiology</i> , 2012, 10, 507-515.	28.6	249
11	Earlyâ€“branching or fastâ€“evolving eukaryotes? An answer based on slowly evolving positions. <i>Proceedings of the Royal Society B: Biological Sciences</i> , 2000, 267, 1213-1221.	2.6	226
12	Giant viruses, giant chimeras: The multiple evolutionary histories of Mimivirus genes. <i>BMC Evolutionary Biology</i> , 2008, 8, 12.	3.2	223
13	Eubacterial phylogeny based on translational apparatus proteins. <i>Trends in Genetics</i> , 2002, 18, 1-5.	6.7	221
14	Intracellular Ca-carbonate biomineralization is widespread in cyanobacteria. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2014, 111, 10933-10938.	7.1	221
15	Bacterial diversity in hydrothermal sediment and epsilonproteobacterial dominance in experimental microcolonizers at the Mid-Atlantic Ridge. <i>Environmental Microbiology</i> , 2003, 5, 961-976.	3.8	218
16	Metabolic symbiosis at the origin of eukaryotes. <i>Trends in Biochemical Sciences</i> , 1999, 24, 88-93.	7.5	213
17	Metagenomics of the Deep Mediterranean, a Warm Bathypelagic Habitat. <i>PLoS ONE</i> , 2007, 2, e914.	2.5	213
18	Global Dispersal and Ancient Cryptic Species in the Smallest Marine Eukaryotes. <i>Molecular Biology and Evolution</i> , 2006, 23, 23-29.	8.9	210

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19	An Early-Branching Microbialite Cyanobacterium Forms Intracellular Carbonates. <i>Science</i> , 2012, 336, 459-462.	12.6	208
20	The extent of protist diversity: insights from molecular ecology of freshwater eukaryotes. <i>Proceedings of the Royal Society B: Biological Sciences</i> , 2005, 272, 2073-2081.	2.6	203
21	The Environmental Clade LKM11 and Rozella Form the Deepest Branching Clade of Fungi. <i>Protist</i> , 2010, 161, 116-121.	1.5	197
22	Global eukaryote phylogeny: Combined small- and large-subunit ribosomal DNA trees support monophyly of Rhizaria, Retaria and Excavata. <i>Molecular Phylogenetics and Evolution</i> , 2007, 44, 255-266.	2.7	166
23	Eukaryotic diversity associated with carbonates and fluid-seawater interface in Lost City hydrothermal field. <i>Environmental Microbiology</i> , 2007, 9, 546-554.	3.8	166
24	Marked seasonality and high spatial variability of protist communities in shallow freshwater systems. <i>ISME Journal</i> , 2015, 9, 1941-1953.	9.8	165
25	Accuracy of protist diversity assessments: morphology compared with cloning and direct pyrosequencing of 18S rRNA genes and ITS regions using the conspicuous tintinnid ciliates as a case study. <i>ISME Journal</i> , 2013, 7, 244-255.	9.8	159
26	Metabolic Symbiosis and the Birth of the Plant Kingdom. <i>Molecular Biology and Evolution</i> , 2008, 25, 536-548.	8.9	153
27	Comparative metagenomics of bathypelagic plankton and bottom sediment from the Sea of Marmara. <i>ISME Journal</i> , 2011, 5, 285-304.	9.8	140
28	Bacterial diversity and carbonate precipitation in the giant microbialites from the highly alkaline Lake Van, Turkey. <i>Extremophiles</i> , 2005, 9, 263-274.	2.3	137
29	An updated view of kinetoplastid phylogeny using environmental sequences and a closer outgroup: proposal for a new classification of the class Kinetoplastea. <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2004, 54, 1861-1875.	1.7	130
30	Selective forces for the origin of the eukaryotic nucleus. <i>BioEssays</i> , 2006, 28, 525-533.	2.5	129
31	Archaeal and bacterial community composition of sediment and plankton from a suboxic freshwater pond. <i>Research in Microbiology</i> , 2007, 158, 213-227.	2.1	128
32	A Phylogenomic Framework to Study the Diversity and Evolution of Stramenopiles (=Heterokonts). <i>Molecular Biology and Evolution</i> , 2016, 33, 2890-2898.	8.9	125
33	The evolutionary history of ribosomal protein RpS14. <i>Trends in Genetics</i> , 2000, 16, 529-533.	6.7	124
34	Rooting the Domain Archaea by Phylogenomic Analysis Supports the Foundation of the New Kingdom Proteoarchaeota. <i>Genome Biology and Evolution</i> , 2015, 7, 191-204.	2.5	124
35	Hindsight in the relative abundance, metabolic potential and genome dynamics of uncultivated marine archaea from comparative metagenomic analyses of bathypelagic plankton of different oceanic regions. <i>ISME Journal</i> , 2008, 2, 865-886.	9.8	113
36	Symbiosis in eukaryotic evolution. <i>Journal of Theoretical Biology</i> , 2017, 434, 20-33.	1.7	113

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37	Phytoplankton diversity and cyanobacterial dominance in a hypereutrophic shallow lake with biologically produced alkaline pH. <i>Extremophiles</i> , 2004, 8, 109-115.	2.3	111
38	Prokaryotic and Eukaryotic Community Structure in Field and Cultured Microbialites from the Alkaline Lake Alchichica (Mexico). <i>PLoS ONE</i> , 2011, 6, e28767.	2.5	111
39	Metagenome of the Mediterranean deep chlorophyll maximum studied by direct and fosmid library 454 pyrosequencing. <i>ISME Journal</i> , 2010, 4, 1154-1166.	9.8	109
40	Wide bacterial diversity associated with tubes of the vent worm <i>Riftia pachyptila</i> . <i>Environmental Microbiology</i> , 2002, 4, 204-215.	3.8	108
41	Open Questions on the Origin of Eukaryotes. <i>Trends in Ecology and Evolution</i> , 2015, 30, 697-708.	8.7	107
42	The new phylogeny of eukaryotes. <i>Current Opinion in Genetics and Development</i> , 2000, 10, 596-601.	3.3	106
43	The Syntrophy hypothesis for the origin of eukaryotes revisited. <i>Nature Microbiology</i> , 2020, 5, 655-667.	13.3	104
44	A metagenomic analysis of soil bacteria extends the diversity of quorum-sensing lactonases. <i>Environmental Microbiology</i> , 2008, 10, 560-570.	3.8	100
45	Reevaluating the Green Contribution to Diatom Genomes. <i>Genome Biology and Evolution</i> , 2012, 4, 683-688.	2.5	99
46	Diversity of functional genes of methanogens, methanotrophs and sulfate reducers in deep-sea hydrothermal environments. <i>Environmental Microbiology</i> , 2005, 7, 118-132.	3.8	95
47	Diversity and Vertical Distribution of Microbial Eukaryotes in the Snow, Sea Ice and Seawater Near the North Pole at the End of the Polar Night. <i>Frontiers in Microbiology</i> , 2011, 2, 106.	3.5	95
48	A new class of marine Euryarchaeota group II from the mediterranean deep chlorophyll maximum. <i>ISME Journal</i> , 2015, 9, 1619-1634.	9.8	95
49	Hydrochemistry and microbialites of the alkaline crater lake Alchichica, Mexico. <i>Facies</i> , 2011, 57, 543-570.	1.4	92
50	Pangenome Evidence for Extensive Interdomain Horizontal Transfer Affecting Lineage Core and Shell Genes in Uncultured Planktonic Thaumarchaeota and Euryarchaeota. <i>Genome Biology and Evolution</i> , 2014, 6, 1549-1563.	2.5	91
51	A novel haloarchaeal-related lineage is widely distributed in deep oceanic regions. <i>Environmental Microbiology</i> , 2001, 3, 72-78.	3.8	90
52	Bacterial gene import and mesophilic adaptation in archaea. <i>Nature Reviews Microbiology</i> , 2015, 13, 447-456.	28.6	90
53	Are hydrothermal vents oases for parasitic protists?. <i>Trends in Parasitology</i> , 2003, 19, 556-558.	3.3	86
54	Polyubiquitin Insertions and the Phylogeny of Cercozoa and Rhizaria. <i>Protist</i> , 2005, 156, 149-161.	1.5	86

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55	Tracking microbial biodiversity through molecular and genomic ecology. <i>Research in Microbiology</i> , 2008, 159, 67-73.	2.1	86
56	Comparative analysis of a genome fragment of an uncultivated mesopelagic crenarchaeote reveals multiple horizontal gene transfers. <i>Environmental Microbiology</i> , 2004, 6, 19-34.	3.8	84
57	Diversity of free-living prokaryotes from a deep-sea site at the Antarctic Polar Front. <i>FEMS Microbiology Ecology</i> , 2001, 36, 193-202.	2.7	82
58	Pan-oceanic distribution of new highly diverse clades of deep-sea diplomonads. <i>Environmental Microbiology</i> , 2009, 11, 47-55.	3.8	82
59	Complex communities of small protists and unexpected occurrence of typical marine lineages in shallow freshwater systems. <i>Environmental Microbiology</i> , 2015, 17, 3610-3627.	3.8	80
60	Specific carbonate-microbe interactions in the modern microbialites of Lake Alchichica (Mexico). <i>ISME Journal</i> , 2013, 7, 1997-2009.	9.8	75
61	Highly Diverse and Seasonally Dynamic Protist Community in a Pristine Peat Bog. <i>Protist</i> , 2011, 162, 14-32.	1.5	74
62	Evolution of viruses and cells: do we need a fourth domain of life to explain the origin of eukaryotes?. <i>Philosophical Transactions of the Royal Society B: Biological Sciences</i> , 2015, 370, 20140327.	4.0	72
63	New insights into marine group III Euryarchaeota, from dark to light. <i>ISME Journal</i> , 2017, 11, 1102-1117.	9.8	72
64	Description of <i>Gloeomargarita lithophora</i> gen. nov., sp. nov., a thylakoid-bearing, basal-branching cyanobacterium with intracellular carbonates, and proposal for <i>Gloeomargaritales</i> ord. nov.. <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2017, 67, 653-658.	1.7	72
65	Smr: a bacterial and eukaryotic homologue of the C-terminal region of the MutS2 family. <i>Trends in Biochemical Sciences</i> , 1999, 24, 298-300.	7.5	70
66	Phylogenomic Analysis of Kinetoplastids Supports That Trypanosomatids Arose from within Bodonids. <i>Molecular Biology and Evolution</i> , 2011, 28, 53-58.	8.9	68
67	Respiratory Chains in the Last Common Ancestor of Living Organisms. <i>Journal of Molecular Evolution</i> , 1999, 49, 453-460.	1.8	66
68	Eukaryotic diversity and phylogeny using small- and large-subunit ribosomal RNA genes from environmental samples. <i>Environmental Microbiology</i> , 2009, 11, 3179-3188.	3.8	64
69	Reductive evolution and unique predatory mode in the CPR bacterium <i>Vampirococcus lugosii</i> . <i>Nature Communications</i> , 2021, 12, 2454.	12.8	64
70	Evolutionary relationships of <i>Fusobacterium nucleatum</i> based on phylogenetic analysis and comparative genomics. <i>BMC Evolutionary Biology</i> , 2004, 4, 50.	3.2	63
71	Global transcriptome analysis of the aphelid <i>Paraphelidium tribonemae</i> supports the phagotrophic origin of fungi. <i>Communications Biology</i> , 2018, 1, 231.	4.4	63
72	Sunlight-Exposed Biofilm Microbial Communities Are Naturally Resistant to Chernobyl Ionizing-Radiation Levels. <i>PLoS ONE</i> , 2011, 6, e21764.	2.5	63

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73	Hyperdiverse archaea near life limits at the polyextreme geothermal Dallol area. <i>Nature Ecology and Evolution</i> , 2019, 3, 1552-1561.	7.8	62
74	Extending the Conserved Phylogenetic Core of Archaea Disentangles the Evolution of the Third Domain of Life. <i>Molecular Biology and Evolution</i> , 2015, 32, 1242-1254.	8.9	59
75	Polyclonality of Concurrent Natural Populations of <i>Alteromonas macleodii</i> . <i>Genome Biology and Evolution</i> , 2012, 4, 1360-1374.	2.5	57
76	Different biogeographic patterns of prokaryotes and microbial eukaryotes in epilithic biofilms. <i>Molecular Ecology</i> , 2012, 21, 3852-3868.	3.9	57
77	Formation of low-T hydrated silicates in modern microbialites from Mexico and implications for microbial fossilization. <i>Frontiers in Earth Science</i> , 2015, 3, .	1.8	57
78	Horizontal and endosymbiotic gene transfer in early plastid evolution. <i>New Phytologist</i> , 2019, 224, 618-624.	7.3	57
79	Rampant horizontal gene transfer and phospho-donor change in the evolution of the phosphofructokinase. <i>Gene</i> , 2003, 318, 185-191.	2.2	55
80	Complete-fosmid and fosmid-end sequences reveal frequent horizontal gene transfers in marine uncultured planktonic archaea. <i>ISME Journal</i> , 2011, 5, 1291-1302.	9.8	55
81	Molecular Phylogeny of Tintinnid Ciliates (Tintinnida, Ciliophora). <i>Protist</i> , 2012, 163, 873-887.	1.5	55
82	New haptophyte lineages and multiple independent colonizations of freshwater ecosystems. <i>Environmental Microbiology Reports</i> , 2013, 5, 322-332.	2.4	55
83	Multiple independent horizontal transfers of informational genes from bacteria to plasmids and phages: implications for the origin of bacterial replication machinery. <i>Molecular Microbiology</i> , 2000, 35, 1-5.	2.5	52
84	Response to Comment on "The 1.2-Megabase Genome Sequence of Mimivirus". <i>Science</i> , 2005, 308, 1114-1114.	12.6	52
85	Analysis of a genome fragment of a deep-sea uncultivated Group II euryarchaeote containing 16S rDNA, a spectinomycin-like operon and several energy metabolism genes. <i>Environmental Microbiology</i> , 2004, 6, 959-969.	3.8	51
86	Signal Conflicts in the Phylogeny of the Primary Photosynthetic Eukaryotes. <i>Molecular Biology and Evolution</i> , 2009, 26, 2745-2753.	8.9	50
87	<i>Neoceratium</i> gen. nov., a New Genus for All Marine Species Currently Assigned to <i>Ceratium</i> (Dinophyceae). <i>Protist</i> , 2010, 161, 35-54.	1.5	50
88	<i>Solenicola setigera</i> is the first characterized member of the abundant and cosmopolitan uncultured marine stramenopile group MAST. <i>Environmental Microbiology</i> , 2011, 13, 193-202.	3.8	50
89	Metagenome-based diversity analyses suggest a significant contribution of non-cyanobacterial lineages to carbonate precipitation in modern microbialites. <i>Frontiers in Microbiology</i> , 2015, 6, 797.	3.5	50
90	Phylogenetic Analysis of Eukaryotic Thiolases Suggests Multiple Proteobacterial Origins. <i>Journal of Molecular Evolution</i> , 2005, 61, 65-74.	1.8	48

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91	Comparative analysis of genome fragments of <i>Acidobacteria</i> from deep Mediterranean plankton. <i>Environmental Microbiology</i> , 2008, 10, 2704-2717.	3.8	48
92	Biom mineralization Patterns of Intracellular Carbonatogenesis in Cyanobacteria: Molecular Hypotheses. <i>Minerals</i> (Basel, Switzerland), 2016, 6, 10.	2.0	48
93	Phylogenomics of a new fungal phylum reveals multiple waves of reductive evolution across Holomycota. <i>Nature Communications</i> , 2021, 12, 4973.	12.8	48
94	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.	7.8	48
95	16S rDNA-based analysis reveals cosmopolitan occurrence but limited diversity of two cyanobacterial lineages with contrasted patterns of intracellular carbonate mineralization. <i>Frontiers in Microbiology</i> , 2014, 5, 331.	3.5	47
96	Involvement of microbial mats in early fossilization by decay delay and formation of impressions and replicas of vertebrates and invertebrates. <i>Scientific Reports</i> , 2016, 6, 25716.	3.3	45
97	Phylogenomic Investigation of Phospholipid Synthesis in Archaea. <i>Archaea</i> , 2012, 2012, 1-13.	2.3	44
98	Toward the Monophyly of Haeckel's Radiolaria: 18S rRNA Environmental Data Support the Sisterhood of Polycystinea and Acantharea. <i>Molecular Biology and Evolution</i> , 2002, 19, 118-121.	8.9	43
99	Early evolution of the biotin-dependent carboxylase family. <i>BMC Evolutionary Biology</i> , 2011, 11, 232.	3.2	43
100	Molecular Phylogeny and Ultrastructure of <i>Aphelidium</i> aff. <i>melosirae</i> (Aphelida, Opisthosporidia). <i>Protist</i> , 2014, 165, 512-526.	1.5	43
101	An ACP-Independent Fatty Acid Synthesis Pathway in Archaea: Implications for the Origin of Phospholipids. <i>Molecular Biology and Evolution</i> , 2012, 29, 3261-3265.	8.9	42
102	Functional shifts in microbial mats recapitulate early Earth metabolic transitions. <i>Nature Ecology and Evolution</i> , 2018, 2, 1700-1708.	7.8	40
103	Characterization of two new thermoacidophilic microalgae: Genome organization and comparison with <i>Galdieria sulphuraria</i> . <i>FEMS Microbiology Letters</i> , 1994, 122, 109-114.	1.8	37
104	Molecular Phylogeny of Noctiluroid Dinoflagellates (Noctilucales, Dinophyceae). <i>Protist</i> , 2010, 161, 466-478.	1.5	36
105	Microbial diversity on the Tatahouine meteorite. <i>Meteoritics and Planetary Science</i> , 2006, 41, 1249-1265.	1.6	35
106	Unveiling microbial interactions in stratified mat communities from a warm saline shallow pond. <i>Environmental Microbiology</i> , 2017, 19, 2405-2421.	3.8	35
107	Horizontal gene transfer of a chloroplast DnaJ-Fer protein to Thaumarchaeota and the evolutionary history of the DnaK chaperone system in Archaea. <i>BMC Evolutionary Biology</i> , 2012, 12, 226.	3.2	34
108	Evolutionary Genomics of <i>Metchnikovella incurvata</i> (Metchnikovellidae): An Early Branching Microsporidium. <i>Genome Biology and Evolution</i> , 2018, 10, 2736-2748.	2.5	34

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109	The phylogenomic analysis of the anaphase promoting complex and its targets points to complex and modern-like control of the cell cycle in the last common ancestor of eukaryotes. <i>BMC Evolutionary Biology</i> , 2011, 11, 265.	3.2	33
110	Sure facts and open questions about the origin and evolution of photosynthetic plastids. <i>Research in Microbiology</i> , 2001, 152, 771-780.	2.1	32
111	Horizontal gene transfer and archaeal origin of deoxyhypusine synthase homologous genes in bacteria. <i>Gene</i> , 2004, 330, 169-176.	2.2	32
112	Metagenomic analysis of mesopelagic Antarctic plankton reveals a novel deltaproteobacterial group. <i>Microbiology (United Kingdom)</i> , 2006, 152, 505-517.	1.8	32
113	Life cycle and molecular phylogeny of the dinoflagellates <i>Chytriodinium</i> and <i>Dissodinium</i> , ectoparasites of copepod eggs. <i>European Journal of Protistology</i> , 2009, 45, 260-270.	1.5	32
114	The rise and fall of Picobiliphytes: How assumed autotrophs turned out to be heterotrophs. <i>BioEssays</i> , 2014, 36, 468-474.	2.5	31
115	High-resolution imaging of sulfur oxidation states, trace elements, and organic molecules distribution in individual microfossils and contemporary microbial filaments 1 Associate editor: N. E. Ostrom. <i>Geochimica Et Cosmochimica Acta</i> , 2004, 68, 1561-1569.	3.9	30
116	Comparative metagenomics unveils functions and genome features of microbialite-associated communities along a depth gradient. <i>Environmental Microbiology</i> , 2016, 18, 4990-5004.	3.8	30
117	Molecular Phylogeny of the Ocelloid-bearing Dinoflagellates <i>Erythrospidinium</i> and <i>Warnowia</i> ( <i>Warnowiaceae</i> , <i>Dinophyceae</i> ). <i>Journal of Eukaryotic Microbiology</i> , 2009, 56, 440-445.	1.7	29
118	Evolution of Eukaryotic Translation Elongation and Termination Factors: Variations of Evolutionary Rate and Genetic Code Deviations. <i>Molecular Biology and Evolution</i> , 2002, 19, 189-200.	8.9	28
119	Integrative analysis of the mineralogical and chemical composition of modern microbialites from ten Mexican lakes: What do we learn about their formation?. <i>Geochimica Et Cosmochimica Acta</i> , 2021, 305, 148-184.	3.9	28
120	Geochemical Conditions Allowing the Formation of Modern Lacustrine Microbialites. <i>Procedia Earth and Planetary Science</i> , 2017, 17, 380-383.	0.6	27
121	Resilience of Freshwater Communities of Small Microbial Eukaryotes Undergoing Severe Drought Events. <i>Frontiers in Microbiology</i> , 2016, 7, 812.	3.5	26
122	Core microbial communities of lacustrine microbialites sampled along an alkalinity gradient. <i>Environmental Microbiology</i> , 2021, 23, 51-68.	3.8	26
123	Microbial diversity in the deep-subsurface hydrothermal aquifer feeding the giant gypsum crystal-bearing Naica Mine, Mexico. <i>Frontiers in Microbiology</i> , 2013, 4, 37.	3.5	25
124	Morphological and Genetic Diversity of Opisthosporidia: New Aphelid <i>Paraphelidium tribonemae</i> gen. et sp. nov.. <i>Journal of Eukaryotic Microbiology</i> , 2017, 64, 204-212.	1.7	25
125	Protist Interactions and Community Structure During Early Autumn in the Kerguelen Region (Southern Ocean). <i>Protist</i> , 2020, 171, 125709.	1.5	25
126	Horizontal transfers confuse the prokaryotic phylogeny based on the HSP70 protein family. <i>Molecular Microbiology</i> , 1999, 31, 1007-1009.	2.5	24



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127	Aurigamonas solis n. gen., n. sp., a Soil-Dwelling Predator with unusual Helioflagellate Organisation and Belonging to a Novel Clade within the Cercozoa. Protist, 2005, 156, 335-354.	1.5	24
128	MOLECULAR PHYLOGENY OF DINOPHYSOID DINOFLAGELLATES: THE SYSTEMATIC POSITION OF OXYPHYSIS OXYTOXOIDES AND THE DINOPHYYSIS HASTATA GROUP (DINOPHYSALES, DINOPHYCEAE)1. Journal of Phycology, 2011, 47, 393-406.	2.3	24
129	The Chytrid-like Parasites of Algae Amoeboradix gromovi gen. et sp. nov. and Sanchytrium tribonematis Belong to a New Fungal Lineage. Protist, 2018, 169, 122-140.	1.5	24
130	Combined cultivation and single-cell approaches to the phylogenomics of nuclearioid amoebae, close relatives of fungi. Philosophical Transactions of the Royal Society B: Biological Sciences, 2019, 374, 20190094.	4.0	24
131	Modern Subsurface Bacteria in Pristine 2.7 Ga-Old Fossil Stromatolite Drillcore Samples from the Fortescue Group, Western Australia. PLoS ONE, 2009, 4, e5298.	2.5	23
132	The crustacean parasites Ellobiopsis Caullery, 1910 and Thalassomyces Niezabitowski, 1913 form a monophyletic divergent clade within the Alveolata. Systematic Parasitology, 2009, 74, 65-74.	1.1	23
133	What Was the Real Contribution of Endosymbionts to the Eukaryotic Nucleus? Insights from Photosynthetic Eukaryotes. Cold Spring Harbor Perspectives in Biology, 2014, 6, a016014-a016014.	5.5	23
134	7. Ancient Fossil Record and Early Evolution (ca. 3.8 to 0.5 Ga). Earth, Moon and Planets, 2006, 98, 247-290.	0.6	22
135	Seasonal dynamics of free-living tintinnid ciliate communities revealed by environmental sequences from the North-West Mediterranean Sea. FEMS Microbiology Ecology, 2014, 87, 330-342.	2.7	22
136	Cultured Asgard Archaea Shed Light on Eukaryogenesis. Cell, 2020, 181, 232-235.	28.9	22
137	Environmental drivers of plankton protist communities along latitudinal and vertical gradients in the oldest and deepest freshwater lake. Environmental Microbiology, 2021, 23, 1436-1451.	3.8	22
138	Genomic organization analysis of acidophilic chemolithotrophic bacteria using pulsed field gel electrophoretic techniques. Biochimie, 1998, 80, 911-921.	2.6	21
139	Molecular Phylogeny of <i>Paraphelidium letcheri</i> sp. nov. (Aphelida, Opisthosporidia). Journal of Eukaryotic Microbiology, 2017, 64, 573-578.	1.7	21
140	<i>Parvularia atlantis</i> gen. et sp. nov., a Nuclearioid Filose Amoeba (Holomycota, Opisthokonta). Journal of Eukaryotic Microbiology, 2018, 65, 170-179.	1.7	21
141	A Complex Cell Division Machinery Was Present in the Last Common Ancestor of Eukaryotes. PLoS ONE, 2009, 4, e5021.	2.5	21
142	Palaeontological and molecular arguments for the origin of silica-secreting marine organisms. Comptes Rendus - Palevol, 2004, 3, 229-236.	0.2	18
143	Uncultured Archaea in a hydrothermal microbial assemblage: phylogenetic diversity and characterization of a genome fragment from a euryarchaeote. FEMS Microbiology Ecology, 2006, 57, 452-469.	2.7	18
144	Yet viruses cannot be included in the tree of life. Nature Reviews Microbiology, 2009, 7, 615-617.	28.6	18

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145	Phylogenetic and ecological diversity of apusomonads, a lineage of deep-branching eukaryotes. <i>Environmental Microbiology Reports</i> , 2017, 9, 113-119.	2.4	18
146	Secondary Plastids of Euglenids and Chlorarachniophytes Function with a Mix of Genes of Red and Green Algal Ancestry. <i>Molecular Biology and Evolution</i> , 2018, 35, 2198-2204.	8.9	17
147	Eukaryogenesis, a syntrophy affair. <i>Nature Microbiology</i> , 2019, 4, 1068-1070.	13.3	17
148	Origin and Evolution of the Halo-Volcanic Complex of Dallol: Proto-Volcanism in Northern Afar (Ethiopia). <i>Frontiers in Earth Science</i> , 2020, 7, .	1.8	17
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