Purificacion Lopez-Garcia

List of Publications by Year
in descending order

218 papers	13,453 citations	18482 62 h-index	28297 105 g-index
233 all docs	233 docs citations	233 times ranked	11012 citing authors

#	Article	IF	Citations
1	Unexpected diversity of small eukaryotes in deep-sea Antarctic plankton. Nature, 2001, 409, 603-607.	27.8	838
2	Autochthonous eukaryotic diversity in hydrothermal sediment and experimental microcolonizers at the Mid-Atlantic Ridge. Proceedings of the National Academy of Sciences of the United States of America, 2003, 100, 697-702.	7.1	337
3	Ten reasons to exclude viruses from the tree of life. Nature Reviews Microbiology, 2009, 7, 306-311.	28.6	322
4	Symbiosis Between Methanogenic Archaea and Î´-Proteobacteria as the Origin of Eukaryotes: The Syntrophic Hypothesis. Journal of Molecular Evolution, 1998, 47, 517-530.	1.8	282
5	The molecular ecology of microbial eukaryotes unveils a hidden world. Trends in Microbiology, 2002, 10, 31-38.	7.7	279
6	An Early-Branching Freshwater Cyanobacterium at the Origin of Plastids. Current Biology, 2017, 27, 386-391.	3.9	275
7	Ancestral lipid biosynthesis and early membrane evolution. Trends in Biochemical Sciences, 2004, 29, 469-477.	7.5	252
8	The early evolution of lipid membranes and the three domains of life. Nature Reviews Microbiology, 2012, 10, 507-515.	28.6	249
9	Major role of nitrite-oxidizing bacteria in dark ocean carbon fixation. Science, 2017, 358, 1046-1051.	12.6	229
10	Intracellular Ca-carbonate biomineralization is widespread in cyanobacteria. Proceedings of the National Academy of Sciences of the United States of America, 2014, 111, 10933-10938.	7.1	221
11	Bacterial Mode of Replication with Eukaryotic-Like Machinery in a Hyperthermophilic Archaeon. Science, 2000, 288, 2212-2215.	12.6	220
12	Bacterial diversity in hydrothermal sediment and epsilonproteobacterial dominance in experimental microcolonizers at the Mid-Atlantic Ridge. Environmental Microbiology, 2003, 5, 961-976.	3.8	218
13	Metabolic symbiosis at the origin of eukaryotes. Trends in Biochemical Sciences, 1999, 24, 88-93.	7.5	213
14	Metagenomics of the Deep Mediterranean, a Warm Bathypelagic Habitat. PLoS ONE, 2007, 2, e914.	2.5	213
15	Nanoscale detection of organic signatures in carbonate microbialites. Proceedings of the National Academy of Sciences of the United States of America, 2006, 103, 9440-9445.	7.1	212
16	Global Dispersal and Ancient Cryptic Species in the Smallest Marine Eukaryotes. Molecular Biology and Evolution, 2006, 23, 23-29.	8.9	210
17	An Early-Branching Microbialite Cyanobacterium Forms Intracellular Carbonates. Science, 2012, 336, 459-462.	12.6	208
18	The extent of protist diversity: insights from molecular ecology of freshwater eukaryotes. Proceedings of the Royal Society B: Biological Sciences, 2005, 272, 2073-2081.	2.6	203

#	Article	IF	Citations
19	The Environmental Clade LKM11 and Rozella Form the Deepest Branching Clade of Fungi. Protist, 2010, 161, 116-121.	1.5	197
20	Global eukaryote phylogeny: Combined small- and large-subunit ribosomal DNA trees support monophyly of Rhizaria, Retaria and Excavata. Molecular Phylogenetics and Evolution, 2007, 44, 255-266.	2.7	166
21	Eukaryotic diversity associated with carbonates and fluid?seawater interface in Lost City hydrothermal field. Environmental Microbiology, 2007, 9, 546-554.	3.8	166
22	Marked seasonality and high spatial variability of protist communities in shallow freshwater systems. ISME Journal, 2015, 9, 1941-1953.	9.8	165
23	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. ISME Journal, 2013, 7, 244-255.	9.8	159
24	Comparative metagenomics of bathypelagic plankton and bottom sediment from the Sea of Marmara. ISME Journal, 2011, 5, 285-304.	9.8	140
25	Bacterial diversity and carbonate precipitation in the giant microbialites from the highly alkaline Lake Van, Turkey. Extremophiles, 2005, 9, 263-274.	2.3	137
26	An updated view of kinetoplastid phylogeny using environmental sequences and a closer outgroup: proposal for a new classification of the class Kinetoplastea. International Journal of Systematic and Evolutionary Microbiology, 2004, 54, 1861-1875.	1.7	130
27	Selective forces for the origin of the eukaryotic nucleus. BioEssays, 2006, 28, 525-533.	2.5	129
28	Archaeal and bacterial community composition of sediment and plankton from a suboxic freshwater pond. Research in Microbiology, 2007, 158, 213-227.	2.1	128
29	A Phylogenomic Framework to Study the Diversity and Evolution of Stramenopiles (=Heterokonts). Molecular Biology and Evolution, 2016, 33, 2890-2898.	8.9	125
30	Diversity of free-living prokaryotes from a deep-sea site at the Antarctic Polar Front. , 2001, 36, 193-202.		124
31	Rooting the Domain Archaea by Phylogenomic Analysis Supports the Foundation of the New Kingdom Proteoarchaeota. Genome Biology and Evolution, 2015, 7, 191-204.	2.5	124
32	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. ISME Journal, 2008, 2, 865-886.	9.8	113
33	Symbiosis in eukaryotic evolution. Journal of Theoretical Biology, 2017, 434, 20-33.	1.7	113
34	â€œMissingâ€•protists: a molecular prospective. Biodiversity and Conservation, 2008, 17, 261-276.	2.6	112
35	Phytoplankton diversity and cyanobacterial dominance in a hypereutrophic shallow lake with biologically produced alkaline pH. Extremophiles, 2004, 8, 109-115.	2.3	111
36	Prokaryotic and Eukaryotic Community Structure in Field and Cultured Microbialites from the Alkaline Lake Alchichica (Mexico). PLoS ONE, 2011, 6, e28767.	2.5	111

#	Article	IF	Citations
37	Metagenome of the Mediterranean deep chlorophyll maximum studied by direct and fosmid library 454 pyrosequencing. ISME Journal, 2010, 4, 1154-1166.	9.8	109
38	Wide bacterial diversity associated with tubes of the vent worm Riftia pachyptila. Environmental Microbiology, 2002, 4, 204-215.	3.8	108
39	Open Questions on the Origin of Eukaryotes. Trends in Ecology and Evolution, 2015, 30, 697-708.	8.7	107
40	The Syntrophy hypothesis for the origin of eukaryotes revisited. Nature Microbiology, 2020, 5, 655-667.	13.3	104
41	The enigmatic SAR202 cluster up close: shedding light on a globally distributed dark ocean lineage involved in sulfur cycling. ISME Journal, 2018, 12, 655-668.	9.8	101
42	Genomes of Abundant and Widespread Viruses from the Deep Ocean. MBio, 2016, 7, .	4.1	99
43	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. Frontiers in Microbiology, 2011, 2, 106.	3.5	95
44	A new class of marine Euryarchaeota group II from the mediterranean deep chlorophyll maximum. ISME Journal, 2015, 9, 1619-1634.	9.8	95
45	Hydrochemistry and microbialites of the alkaline crater lake Alchichica, Mexico. Facies, 2011, 57, 543-570.	1.4	92
46	Pangenome Evidence for Extensive Interdomain Horizontal Transfer Affecting Lineage Core and Shell Genes in Uncultured Planktonic Thaumarchaeota and Euryarchaeota. Genome Biology and Evolution, 2014, 6, 1549-1563.	2.5	91
47	A novel haloarchaeal-related lineage is widely distributed in deep oceanic regions. Environmental Microbiology, 2001, 3, 72-78.	3.8	90
48	Bacterial gene import and mesophilic adaptation in archaea. Nature Reviews Microbiology, 2015, 13, 447-456.	28.6	90
49	Are hydrothermal vents oases for parasitic protists?. Trends in Parasitology, 2003, 19, 556-558.	3.3	86
50	Polyubiquitin Insertions and the Phylogeny of Cercozoa and Rhizaria. Protist, 2005, 156, 149-161.	1.5	86
51	Tracking microbial biodiversity through molecular and genomic ecology. Research in Microbiology, 2008, 159, 67-73.	2.1	86
52	DNA topology and the thermal stress response, a tale from mesophiles and hyperthermophiles. BioEssays, 2000, 22, 738-746.	2.5	85
53	Comparative analysis of a genome fragment of an uncultivated mesopelagic crenarchaeote reveals multiple horizontal gene transfers. Environmental Microbiology, 2004, 6, 19-34.	3.8	84
54	Panâ€oceanic distribution of new highly diverse clades of deepâ€sea diplonemids. Environmental Microbiology, 2009, 11, 47-55.	3.8	82

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55	DNA topology in hyperthermophilic archaea: reference states and their variation with growth phase, growth temperature, and temperature stresses. Molecular Microbiology, 1997, 23, 1267-1279.	2.5	80
56	Complex communities of small protists and unexpected occurrence of typical marine lineages in shallow freshwater systems. Environmental Microbiology, 2015, 17, 3610-3627.	3.8	80
57	The unique DNA topology and DNA topoisomerases of hyperthermophilic archaea. FEMS Microbiology Reviews, 1996, 18, 237-248.	8.6	76
58	Specific carbonateâ€“microbe interactions in the modern microbialites of Lake Alchichica (Mexico). ISME Journal, 2013, 7, 1997-2009.	9.8	75
59	Highly Diverse and Seasonally Dynamic Protist Community in a Pristine Peat Bog. Protist, 2011, 162, 14-32.	1.5	74
60	Evolution of viruses and cells: do we need a fourth domain of life to explain the origin of eukaryotes?. Philosophical Transactions of the Royal Society B: Biological Sciences, 2015, 370, 20140327.	4.0	72
61	New insights into marine group III Euryarchaeota, from dark to light. ISME Journal, 2017, 11, 1102-1117.	9.8	72
62	Description of Gloeomargarita lithophora gen. nov., sp. nov., a thylakoid-bearing, basal-branching cyanobacterium with intracellular carbonates, and proposal for Gloeomargaritales ord. nov.. International Journal of Systematic and Evolutionary Microbiology, 2017, 67, 653-658.	1.7	72
63	Phylogenomic Analysis of Kinetoplastids Supports That Trypanosomatids Arose from within Bodonids. Molecular Biology and Evolution, 2011, 28, 53-58.	8.9	68
64	Eukaryotic diversity and phylogeny using smallâ€•and largeâ€•subunit ribosomal RNA genes from environmental samples. Environmental Microbiology, 2009, 11, 3179-3188.	3.8	64
65	Reductive evolution and unique predatory mode in the CPR bacterium Vampirococcus lugosii. Nature Communications, 2021, 12, 2454.	12.8	64
66	Global transcriptome analysis of the aphelid Paraphelidium tribonemae supports the phagotrophic origin of fungi. Communications Biology, 2018, 1, 231.	4.4	63
67	Sunlight-Exposed Biofilm Microbial Communities Are Naturally Resistant to Chernobyl Ionizing-Radiation Levels. PLoS ONE, 2011, 6, e21764.	2.5	63
68	Hyperdiverse archaea near life limits at the polyextreme geothermal Dallol area. Nature Ecology and Evolution, 2019, 3, 1552-1561.	7.8	62
69	Extending the Conserved Phylogenetic Core of Archaea Disentangles the Evolution of the Third Domain of Life. Molecular Biology and Evolution, 2015, 32, 1242-1254.	8.9	59
70	Cyanobacterial calcification in modern microbialites at the submicrometer scale. Biogeosciences, 2013, 10, 5255-5266.	3.3	58
71	Polyclonality of Concurrent Natural Populations of Alteromonas macleodii. Genome Biology and Evolution, 2012, 4, 1360-1374.	2.5	57
72	Different biogeographic patterns of prokaryotes and microbial eukaryotes in epilithic biofilms. Molecular Ecology, 2012, 21, 3852-3868.	3.9	57

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73	Formation of low-T hydrated silicates in modern microbialites from Mexico and implications for microbial fossilization. Frontiers in Earth Science, 2015, 3, .	1.8	57
74	Horizontal and endosymbiotic gene transfer in early plastid evolution. New Phytologist, 2019, 224, 618-624.	7.3	57
75	Ectosymbiotic bacteria at the origin of magnetoreception in a marine protist. Nature Microbiology, 2019, 4, 1088-1095.	13.3	57
76	DNA Supercoiling and Temperature Adaptation: A Clue to Early Diversification of Life?. Journal of Molecular Evolution, 1999, 49, 439-452.	1.8	55
77	Complete-fosmid and fosmid-end sequences reveal frequent horizontal gene transfers in marine uncultured planktonic archaea. ISME Journal, 2011, 5, 1291-1302.	9.8	55
78	Molecular Phylogeny of Tintinnid Ciliates (Tintinnida, Ciliophora). Protist, 2012, 163, 873-887.	1.5	55
79	New haptophyte lineages and multiple independent colonizations of freshwater ecosystems. Environmental Microbiology Reports, 2013, 5, 322-332.	2.4	55
80	Morphological and phylogenetic diversity of thermophilic cyanobacteria in Algerian hot springs. Extremophiles, 2014, 18, 1035-1047.	2.3	53
81	Response to Comment on "The 1.2-Megabase Genome Sequence of Mimivirus". Science, 2005, 308, 1114-1114.	12.6	52
82	Analysis of a genome fragment of a deepâ€sea uncultivated Group II euryarchaeote containing 16S rDNA, a spectinomycinâ€like operon and several energy metabolism genes. Environmental Microbiology, 2004, 6, 959-969.	3.8	51
83	Neoceratium gen. nov., a New Genus for All Marine Species Currently Assigned to Ceratium (Dinophyceae). Protist, 2010, 161, 35-54.	1.5	50
84	Solenicola setigera is the first characterized member of the abundant and cosmopolitan uncultured marine stramenopile group MASTâ€3. Environmental Microbiology, 2011, 13, 193-202.	3.8	50
85	Metagenome-based diversity analyses suggest a significant contribution of non-cyanobacterial lineages to carbonate precipitation in modern microbialites. Frontiers in Microbiology, 2015, 6, 797.	3.5	50
86	Control of DNA topology during thermal stress in hyperthermophilic archaea: DNA topoisomerase levels, activities and induced thermotolerance during heat and cold shock in Sulfolobus. Molecular Microbiology, 1999, 33, 766-777.	2.5	48
87	Phylogenetic Analysis of Eukaryotic Thiolases Suggests Multiple Proteobacterial Origins. Journal of Molecular Evolution, 2005, 61, 65-74.	1.8	48
88	Comparative analysis of genome fragments of Acidobacteria from deep Mediterranean plankton. Environmental Microbiology, 2008, 10, 2704-2717.	3.8	48
89	Biomineralization Patterns of Intracellular Carbonatogenesis in Cyanobacteria: Molecular Hypotheses. Minerals (Basel, Switzerland), 2016, 6, 10.	2.0	48
90	Phylogenomics of a new fungal phylum reveals multiple waves of reductive evolution across Holomycota. Nature Communications, 2021, 12, 4973.	12.8	48

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91	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
92	16S rDNA-based analysis reveals cosmopolitan occurrence but limited diversity of two cyanobacterial lineages with contrasted patterns of intracellular carbonate mineralization. Frontiers in Microbiology, 2014, 5, 331.	3.5	47
93	In vitro DNA binding of the archaeal protein Sso7d induces negative supercoiling at temperatures typical for thermophilic growth. Nucleic Acids Research, 1998, 26, 2322-2328.	14.5	46
94	Biosignatures and Bacterial Diversity in Hydrothermal Deposits of Solfatara Crater, Italy. Geomicrobiology Journal, 2004, 21, 529-541.	2.0	44
95	Phylogenomic Investigation of Phospholipid Synthesis in Archaea. Archaea, 2012, 2012, 1-13.	2.3	44
96	Toward the Monophyly of Haeckel's Radiolaria: 18S rRNA Environmental Data Support the Sisterhood of Polycystinea and Acantharea. Molecular Biology and Evolution, 2002, 19, 118-121.	8.9	43
97	Molecular Phylogeny and Ultrastructure of Aphelidium aff. melosirae (Aphelida, Opisthosporidia). Protist, 2014, 165, 512-526.	1.5	43
98	An ACP-Independent Fatty Acid Synthesis Pathway in Archaea: Implications for the Origin of Phospholipids. Molecular Biology and Evolution, 2012, 29, 3261-3265.	8.9	42
99	Cyanobacterial formation of intracellular Caâ€carbonates in undersaturated solutions. Geobiology, 2018, 16, 49-61.	2.4	42
100	Genomic organization of the halophilic archaeonHaloferax mediterranei: physical map of the chromosome. Nucleic Acids Research, 1992, 20, 2459-2464.	14.5	41
101	Genomic stability in the archaeae Haloferax volcanii and Haloferax mediterranei. Journal of Bacteriology, 1995, 177, 1405-1408.	2.2	40
102	Biomarkers of Endolithic Communities within Gypsum Crusts (Southern Tunisia). Geomicrobiology Journal, 2010, 27, 101-110.	2.0	40
103	Functional shifts in microbial mats recapitulate early Earth metabolic transitions. Nature Ecology and Evolution, 2018, 2, 1700-1708.	7.8	40
104	Molecular Phylogeny of Noctilucoid Dinoflagellates (Noctilucales, Dinophyceae). Protist, 2010, 161, 466-478.	1.5	36
105	Microbial diversity on the Tatahouine meteorite. Meteoritics and Planetary Science, 2006, 41, 1249-1265.	1.6	35
106	Unveiling microbial interactions in stratified mat communities from a warm saline shallow pond. Environmental Microbiology, 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. BMC Evolutionary Biology, 2012, 12, 226.	3.2	34
108	Evolutionary Genomics of Metchnikovella incurvata (Metchnikovellidae): An Early Branching Microsporidium. Genome Biology and Evolution, 2018, 10, 2736-2748.	2.5	34

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109	Plasmid pGS5 from the Hyperthermophilic ArchaeonArchaeoglobus profundus Is Negatively Supercoiled. Journal of Bacteriology, 2000, 182, 4998-5000.	2.2	33
110	Early eukaryotes in Precambrian oceans. , 2011, , 414-449.		33
111	Horizontal gene transfer and archaeal origin of deoxyhypusine synthase homologous genes in bacteria. Gene, 2004, 330, 169-176.	2.2	32
112	Metagenomic analysis of mesopelagic Antarctic plankton reveals a novel deltaproteobacterial group. Microbiology (United Kingdom), 2006, 152, 505-517.	1.8	32
113	Life cycle and molecular phylogeny of the dinoflagellates Chytriodinium and Dissodinium, ectoparasites of copepod eggs. European Journal of Protistology, 2009, 45, 260-270.	1.5	32
114	The rise and fall of Picobiliphytes: How assumed autotrophs turned out to be heterotrophs. BioEssays, 2014, 36, 468-474.	2.5	31
115	New insights into the phylogenetic position of diplonemids: G+C content bias, differences of evolutionary rate and a new environmental sequence.. International Journal of Systematic and Evolutionary Microbiology, 2001, 51, 2211-2219.	1.7	30
116	High-resolution imaging of sulfur oxidation states, trace elements, and organic molecules distribution in individual microfossils and contempo rary microbial filaments 1 1Associate editor: N. E. Ostrom. Geochimica Et Cosmochimica Acta, 2004, 68, 1561-1569.	3.9	30
117	Comparative metagenomics unveils functions and genome features of microbialiteâ€associated communities along a depth gradient. Environmental Microbiology, 2016, 18, 4990-5004.	3.8	30
118	Fluorescence in situ hybridisation coupled to ultra small immunogold detection to identify prokaryotic cells using transmission and scanning electron microscopy. Journal of Microbiological Methods, 2005, 63, 20-28.	1.6	29
119	Molecular Phylogeny of the Ocelloidâ€Bearing Dinoflagellates Erythropsidinium and Warnowia (Warnowiaceae, Dinophyceae). Journal of Eukaryotic Microbiology, 2009, 56, 440-445.	1.7	29
120	Microbial methane turnover at <scp>M</scp>armara <scp>S</scp>ea cold seeps: a combined 16S <scp>rRNA</scp> and lipid biomarker investigation. Geobiology, 2013, 11, 55-71.	2.4	29
121	Physicochemical Conditions and Microbial Diversity Associated with the Evaporite Deposits in the Laguna de la Piedra (Salar de Atacama, Chile). Geomicrobiology Journal, 2011, 28, 83-95.	2.0	28
122	Integrative analysis of the mineralogical and chemical composition of modern microbialites from ten Mexican lakes: What do we learn about their formation?. Geochimica Et Cosmochimica Acta, 2021, 305, 148-184.	3.9	28
123	Resilience of Freshwater Communities of Small Microbial Eukaryotes Undergoing Severe Drought Events. Frontiers in Microbiology, 2016, 7, 812.	3.5	26
124	Core microbial communities of lacustrine microbialites sampled along an alkalinity gradient. Environmental Microbiology, 2021, 23, 51-68.	3.8	26
125	A phylogenetic and proteomic reconstruction of eukaryotic chromatin evolution. Nature Ecology and Evolution, 2022, 6, 1007-1023.	7.8	26
126	Archaeal and bacterial community composition of a pristine coastal aquifer in DoÃ±ana National Park, Spain. Aquatic Microbial Ecology, 2007, 47, 123-139.	1.8	25

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127	Microbial diversity in the deep-subsurface hydrothermal aquifer feeding the giant gypsum crystal-bearing Naica Mine, Mexico. Frontiers in Microbiology, 2013, 4, 37.	3.5	25
128	Ecological and evolutionary significance of novel protist lineages. European Journal of Protistology, 2016, 55, 4-11.	1.5	25
129	Morphological and Genetic Diversity of Opisthosporidia: New Aphelid Paraphelidium tribonemae gen. et sp. nov.. Journal of Eukaryotic Microbiology, 2017, 64, 204-212.	1.7	25
130	MOLECULAR PHYLOGENY OF DINOPHYSOID DINOFLAGELLATES: THE SYSTEMATIC POSITION OF OXYPHYSIS OXYTOXOIDES AND THE DINOPHYSIS HASTATA GROUP (DINOPHYSALES, DINOPHYCEAE)1. Journal of Phycology, 2011, 47, 393-406.	2.3	24
131	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
132	Combined cultivation and single-cell approaches to the phylogenomics of nucleariid amoebae, close relatives of fungi. Philosophical Transactions of the Royal Society B: Biological Sciences, 2019, 374, 20190094.	4.0	24
133	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
134	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
135	7. Ancient Fossil Record and Early Evolution (ca.Â3.8 to 0.5ÂGa). Earth, Moon and Planets, 2006, 98, 247-290.	0.6	22
136	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
137	Cultured Asgard Archaea Shed Light on Eukaryogenesis. Cell, 2020, 181, 232-235.	28.9	22
138	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
139	Molecular Phylogeny of Paraphelidium letcheri sp. nov. (Aphelida, Opisthosporidia). Journal of Eukaryotic Microbiology, 2017, 64, 573-578.	1.7	21
140	Parvularia atlantis gen. et sp. nov., a Nucleariid Filose Amoeba (Holomycota, Opisthokonta). Journal of Eukaryotic Microbiology, 2018, 65, 170-179.	1.7	21
141	Silicified Biota in High-Altitude, Geothermally Influenced Ignimbrites at El Tatio Geyser Field, Andean Cordillera (Chile). Geomicrobiology Journal, 2014, 31, 493-508.	2.0	20
142	The place of viruses in biology in light of the metabolism- versus-replication-first debate. History and Philosophy of the Life Sciences, 2012, 34, 391-406.	1.1	20
143	Isolation of new plasmids from hyperthermophilic Archaea of the order Thermococcales. Research in Microbiology, 1997, 148, 767-775.	2.1	19
144	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

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145	Yet viruses cannot be included in the tree of life. Nature Reviews Microbiology, 2009, 7, 615-617.	28.6	18
146	Phylogenetic and ecological diversity of apusomonads, a lineage of deepâ€branching eukaryotes. Environmental Microbiology Reports, 2017, 9, 113-119.	2.4	18
147	Secondary Plastids of Euglenids and Chlorarachniophytes Function with a Mix of Genes of Red and Green Algal Ancestry. Molecular Biology and Evolution, 2018, 35, 2198-2204.	8.9	17
148	Eukaryogenesis, a syntrophy affair. Nature Microbiology, 2019, 4, 1068-1070.	13.3	17
149	Origin and Evolution of the Halo-Volcanic Complex of Dallol: Proto-Volcanism in Northern Afar (Ethiopia). Frontiers in Earth Science, 2020, 7, .	1.8	17
150	Small freshwater ecosystems with dissimilar microbial communities exhibit similar temporal patterns. Molecular Ecology, 2021, 30, 2162-2177.	3.9	15
151	5. Prebiotic Chemistry â€“ Biochemistry â€“ Emergence of Life (4.4â€“2 Ga). Earth, Moon and Planets, 2006, 98, 153-203.	0.6	14
152	Young Sun, Early Earth and the Origins of Life. , 2012, , .		14
153	Balechina and the new genus Cucumeridinium gen. nov. (Dinophyceae), unarmored dinoflagellates with thick cell coverings. Journal of Phycology, 2015, 51, 1088-1105.	2.3	14
154	A New Gene Family Diagnostic for Intracellular Biomineralization of Amorphous Ca Carbonates by Cyanobacteria. Genome Biology and Evolution, 2022, 14, .	2.5	14
155	Halobacterial megaplasmids are negatively supercoiled. Molecular Microbiology, 1994, 11, 421-427.	2.5	12
156	The Ultrastructure of Sanchytrium tribonematis (Sanchytriaceae, Fungi incertae sedis) Confirms its Close Relationship to Amoeboradix. Journal of Eukaryotic Microbiology, 2019, 66, 892-898.	1.7	12
157	Time series are critical to understand microbial plankton diversity and ecology. Molecular Ecology, 2019, 28, 920-922.	3.9	12
158	Macrofilamentous microbial communities in the metal-rich and acidic River Tinto, Spain. FEMS Microbiology Letters, 2004, 235, 221-228.	1.8	11
159	Molecular phylogeny of the dinoflagellates Podolampas and Blepharocysta (Peridiniales,) Tj ETQq1 1 0.784314 rgBT /Ov	1.4	11
160	Sinophysis and Pseudophalacroma are Distantly Related to Typical Dinophysoid Dinoflagellates (Dinophysales, Dinophyceae). Journal of Eukaryotic Microbiology, 2012, 59, 188-190.	1.7	11
161	Protist Evolution: Stealing Genes to Gut It Out. Current Biology, 2017, 27, R223-R225.	3.9	11
162	Fe-bearing phases in modern lacustrine microbialites from Mexico. Geochimica Et Cosmochimica Acta, 2019, 253, 201-230.	3.9	11

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163	A Novel Microbialite-Associated Phototrophic Chloroflexi Lineage Exhibiting a Quasi-Clonal Pattern along Depth. Genome Biology and Evolution, 2020, 12, 1207-1216.	2.5	11
164	Present Status of the Molecular Ecology of Kathablepharids. Protist, 2006, 157, 7-11.	1.5	10
165	Thermophilic Lifestyle for an Uncultured Archaeon from Hydrothermal Vents: Evidence from Environmental Genomics. Applied and Environmental Microbiology, 2006, 72, 2268-2271.	3.1	10
166	Microbial eukaryotes in the suboxic chemosynthetic ecosystem of Movile Cave, Romania. Environmental Microbiology Reports, 2019, 11, 464-473.	2.4	9
167	Physical connections: prokaryotes parasitizing their kin. Environmental Microbiology Reports, 2021, 13, 54-61.	2.4	9
168	Sizing chromosomes and megaplasmids in haloarchaea. Microbiology (United Kingdom), 1996, 142, 1423-1428.	1.8	8
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