Frédéric Mahe

List of Articles by Year in descending order

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55 peer-reviewed articles	15,670 peer-reviewed citations	274857 26 peer-reviewed h-index	579727 3.64 score
59 documents	16473 doc citations	274557 28 h-index	34050 citing authors

#	Article	IF	Citations
1	NanoASV: a snakemake workflow for reproducible field-based Nanopore full-length 16S metabarcoding amplicon data analysis. Bioinformatics, 2025, 41, .	3.2	5
2	O short-branch Microsporidia, where art thou? Identifying diversity hotspots for future sampling. European Journal of Protistology, 2024, 96, 126119.	1.3	2
3	How marine are Marine Stramenopiles (MAST)? A cross-system evaluation. FEMS Microbiology Ecology, 2024, 100, .	2.2	14
4	Interpreting phylogenetic placements for taxonomic assignment of environmental DNA. Journal of Eukaryotic Microbiology, 2023, 70, .	1.7	7
5	pr2-primers: An 18S rRNA primer database for protists. Molecular Ecology Resources, 2022, 22, 168-179.	3.2	122
6	Fruit fly phylogeny imprints bacterial gut microbiota. Evolutionary Applications, 2022, 15, 1621-1638.	1.7	15
7	Seasonal dynamics of marine protist communities in tidally mixed coastal waters. Molecular Ecology, 2022, 31, 3761-3783.	2.2	52
8	The Windblown: Possible Explanations for Dinophyte DNA in Forest Soils. Journal of Eukaryotic Microbiology, 2021, 68, .	1.7	11
9	metaXplor: an interactive viral and microbial metagenomic data manager. GigaScience, 2021, 10, .	2.5	9
10	Temporal recovery of soil biological activity and diversity after 915-MHz microwave treatments. Biology and Fertility of Soils, 2021, 57, 603-616.	3.7	1
11	High and specific diversity of protists in the deep-sea basins dominated by diplonemids, kinetoplastids, ciliates and foraminiferans. Communications Biology, 2021, 4, .	3.1	57
12	Swarm v3: towards tera-scale amplicon clustering. Bioinformatics, 2021, 38, 267-269.	3.2	128
13	Genetic Variation in Host-Specific Competitiveness of the Symbiont Rhizobium leguminosarum Symbiovar viciae. Frontiers in Plant Science, 2021, 12, .	3.0	17
14	Periodontitis associates with species-specific gene expression of the oral microbiota. Npj Biofilms and Microbiomes, 2021, 7, .	6.0	56
15	Diversity and dynamics of relevant nanoplanktonic diatoms in the Western English Channel. ISME Journal, 2020, 14, 1966-1981.	5.9	28
16	Heterogeneity of the rice microbial community of the Chinese centuries-old Honghe Hani rice terraces system. Environmental Microbiology, 2020, 22, 3429-3445.	2.6	10
17	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.	5.9	27
18	The belowground bacterial and fungal communities differed in their significance as microbial indicator of Moroccan carob habitats. Ecological Indicators, 2020, 114, 106341.	5.4	11

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19	Global Trends in Marine Plankton Diversity across Kingdoms of Life. Cell, 2019, 179, 1084-1097.e21.	23.4	437
20	How deep can ectomycorrhizas go? A case study on Pisolithus down to 4 meters in a Brazilian eucalypt plantation. Mycorrhiza, 2019, 29, 637-648.	2.3	29
21	The rhizosphere microbiome: A key component of sustainable cork oak forests in trouble. Forest Ecology and Management, 2019, 434, 29-39.	2.6	29
22	Clarifying the Relationships between Microsporidia and Cryptomycota. Journal of Eukaryotic Microbiology, 2018, 65, 773-782.	1.7	124
23	Surface ocean metabarcoding confirms limited diversity in planktonic foraminifera but reveals unknown hyper-abundant lineages. Scientific Reports, 2018, 8, .	2.7	27
24	Consistent patterns of high alpha and low beta diversity in tropical parasitic and free-living protists. Molecular Ecology, 2018, 27, 2846-2857.	2.2	51
25	Transcriptome Profiles of Nod Factor-independent Symbiosis in the Tropical Legume Aeschynomene evenia. Scientific Reports, 2018, 8, .	2.7	35
26	UniEuk: Time to Speak a Common Language in Protistology!. Journal of Eukaryotic Microbiology, 2017, 64, 407-411.	1.7	90
27	Parasites dominate hyperdiverse soil protist communities in Neotropical rainforests. Nature Ecology and Evolution, 2017, 1, .	7.6	331
28	Meiotic Genes in Colpodean Ciliates Support Secretive Sexuality. Genome Biology and Evolution, 2017, 9, 1781-1787.	1.7	10
29	Habitat- and soil-related drivers of the root-associated fungal community of Quercus suber in the Northern Moroccan forest. PLoS ONE, 2017, 12, e0187758.	1.5	24
30	Global patterns of pelagic dinoflagellate diversity across protist size classes unveiled by metabarcoding. Environmental Microbiology, 2016, 18, 609-626.	2.6	123
31	Benthic protists: the under-charted majority. FEMS Microbiology Ecology, 2016, 92, fiw120.	2.2	115
32	Open-Source Sequence Clustering Methods Improve the State Of the Art. MSystems, 2016, 1, .	2.8	178
33	Marine protist diversity in E uropean coastal waters and sediments as revealed by high-throughput sequencing. Environmental Microbiology, 2015, 17, 4035-4049.	2.6	431
34	PFR2: a curated database of planktonic foraminifera 18S ribosomal DNA as a resource for studies of plankton ecology, biogeography and evolution. Molecular Ecology Resources, 2015, 15, 1472-1485.	3.2	67
35	Eukaryotic plankton diversity in the sunlit ocean. Science, 2015, 348, .	26.1	1,956
36	Comparing High-throughput Platforms for Sequencing the V4 Region of SSU-rDNA in Environmental Microbial Eukaryotic Diversity Surveys. Journal of Eukaryotic Microbiology, 2015, 62, 338-345.	1.7	58

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37	Intracellular Diversity of the V4 and V9 Regions of the 18S rRNA in Marine Protists (Radiolarians) Assessed by High-Throughput Sequencing. PLoS ONE, 2014, 9, e104297.	1.5	93
38	Meiosis Gene Inventory of Four Ciliates Reveals the Prevalence of a Synaptonemal Complex-Independent Crossover Pathway. Molecular Biology and Evolution, 2014, 31, 660-672.	3.1	34
39	Patterns of Rare and Abundant Marine Microbial Eukaryotes. Current Biology, 2014, 24, 813-821.	2.5	544
40	Placing Environmental Next-Generation Sequencing Amplicons from Microbial Eukaryotes into a Phylogenetic Context. Molecular Biology and Evolution, 2014, 31, 993-1009.	3.1	111
41	Ciliates and the Rare Biosphere: A Review. Journal of Eukaryotic Microbiology, 2014, 61, 404-409.	1.7	51
42	Deep sequencing uncovers protistan plankton diversity in the Portuguese Ria Formosa solar saltern ponds. Extremophiles, 2014, 19, 283-295.	1.4	50
43	Vampires in the oceans: predatory cercozoan amoebae in marine habitats. ISME Journal, 2013, 7, 2387-2399.	5.9	95
44	Diversity, Ecology and Biogeochemistry of Cyst-Forming Acantharia (Radiolaria) in the Oceans. PLoS ONE, 2013, 8, e53598.	1.5	84
45	The Protist Ribosomal Reference database (PR2): a catalog of unicellular eukaryote Small Sub-Unit rRNA sequences with curated taxonomy. Nucleic Acids Research, 2012, 41, D597-D604.	10.7	2,386
46	Molecular Phylogeny and Morphological Evolution of the Acantharia (Radiolaria). Protist, 2012, 163, 435-450.	1.1	79
47	Isolation, phylogeny and evolution of the SymRK gene in the legume genus Lupinus L.. Molecular Phylogenetics and Evolution, 2011, 60, 49-61.	2.1	13
48	Assignment of 3 Genetic Linkage Groups to 3 Chromosomes of Narrow-Leafed Lupin. Journal of Heredity, 2011, 102, 228-236.	1.3	29
49	Transcriptome divergence between the hexaploid salt-marsh sister species Spartina maritima and Spartina alterniflora (Poaceae). Molecular Ecology, 2010, 19, 2050-2063.	2.2	36
50	New data and phylogenetic placement of the enigmatic Old World lupin: Lupinus mariae-josephi H. Pascual. Genetic Resources and Crop Evolution, 2010, 58, 101-114.	1.0	23
51	Title is missing!. BMC Bioinformatics, 2006, 7, 477.	2.5	13
52	Swarm: robust and fast clustering method for amplicon-based studies. PeerJ, 0, 2, e593.	0.0	989
53	Swarm v2: highly-scalable and high-resolution amplicon clustering. PeerJ, 0, 3, e1420.	0.0	632
54	Comparison of three clustering approaches for detecting novel environmental microbial diversity. PeerJ, 0, 4, e1692.	0.0	30

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55	VSEARCH: a versatile open source tool for metagenomics. PeerJ, 0, 4, e2584.	0.0	10,764