

Frédéric Mahé

List of Publications by Year in descending order

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Version: 2024-02-01

56
papers

14,833
citations

172457

29
h-index

161849

54
g-index

76
all docs

76
docs citations

76
times ranked

17505
citing authors

#	ARTICLE	IF	CITATIONS
1	VSEARCH: a versatile open source tool for metagenomics. PeerJ, 2016, 4, e2584.	2.0	7,113
2	Eukaryotic plankton diversity in the sunlit ocean. Science, 2015, 348, 1261605.	12.6	1,551
3	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.	14.5	1,463
4	Swarm: robust and fast clustering method for amplicon-based studies. PeerJ, 2014, 2, e593.	2.0	828
5	Swarm v2: highly-scalable and high-resolution amplicon clustering. PeerJ, 2015, 3, e1420.	2.0	528
6	Patterns of Rare and Abundant Marine Microbial Eukaryotes. Current Biology, 2014, 24, 813-821.	3.9	450
7	Marine protist diversity in European coastal waters and sediments as revealed by high-throughput sequencing. Environmental Microbiology, 2015, 17, 4035-4049.	3.8	384
8	Global Trends in Marine Plankton Diversity across Kingdoms of Life. Cell, 2019, 179, 1084-1097.e21.	28.9	271
9	Parasites dominate hyperdiverse soil protist communities in Neotropical rainforests. Nature Ecology and Evolution, 2017, 1, 91.	7.8	262
10	Molecular diversity and distribution of marine fungi across 130 European environmental samples. Proceedings of the Royal Society B: Biological Sciences, 2015, 282, 20152243.	2.6	177
11	Open-Source Sequence Clustering Methods Improve the State Of the Art. MSystems, 2016, 1, .	3.8	155
12	Global patterns of pelagic dinoflagellate diversity across protist size classes unveiled by metabarcoding. Environmental Microbiology, 2016, 18, 609-626.	3.8	105
13	Clarifying the Relationships between Microsporidia and Cryptomycota. Journal of Eukaryotic Microbiology, 2018, 65, 773-782.	1.7	98
14	Placing Environmental Next-Generation Sequencing Amplicons from Microbial Eukaryotes into a Phylogenetic Context. Molecular Biology and Evolution, 2014, 31, 993-1009.	8.9	97
15	Benthic protists: the under-charted majority. FEMS Microbiology Ecology, 2016, 92, fiw120.	2.7	94
16	<i>UniEuk</i>: Time to Speak a Common Language in Protistology!. Journal of Eukaryotic Microbiology, 2017, 64, 407-411.	1.7	74
17	Vampires in the oceans: predatory cercozoan amoebae in marine habitats. ISME Journal, 2013, 7, 2387-2399.	9.8	73
18	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.	2.5	69

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19	Diversity, Ecology and Biogeochemistry of Cyst-Forming Acantharia (Radiolaria) in the Oceans. <i>PLoS ONE</i> , 2013, 8, e53598.	2.5	66
20	Molecular Phylogeny and Morphological Evolution of the Acantharia (Radiolaria). <i>Protist</i> , 2012, 163, 435-450.	1.5	62
21	PFGE: a curated database of planktonic foraminifera 18S ribosomal DNA as a resource for studies of plankton ecology, biogeography and evolution. <i>Molecular Ecology Resources</i> , 2015, 15, 1472-1485.	4.8	55
22	Comparing High-throughput Platforms for Sequencing the V4 Region of SSU rDNA in Environmental Microbial Eukaryotic Diversity Surveys. <i>Journal of Eukaryotic Microbiology</i> , 2015, 62, 338-345.	1.7	53
23	Worldwide Occurrence and Activity of the Reef-Building Coral Symbiont Symbiodinium in the Open Ocean. <i>Current Biology</i> , 2018, 28, 3625-3633.e3.	3.9	52
24	Ciliates and the Rare Biosphere: A Review. <i>Journal of Eukaryotic Microbiology</i> , 2014, 61, 404-409.	1.7	43
25	Deep sequencing uncovers protistan plankton diversity in the Portuguese Ria Formosa solar saltern ponds. <i>Extremophiles</i> , 2015, 19, 283-295.	2.3	43
26	Consistent patterns of high alpha and low beta diversity in tropical parasitic and free-living protists. <i>Molecular Ecology</i> , 2018, 27, 2846-2857.	3.9	43
27	Swarm v3: towards tera-scale amplicon clustering. <i>Bioinformatics</i> , 2021, 38, 267-269.	4.1	40
28	pr2primers: An 18S rRNA primer database for protists. <i>Molecular Ecology Resources</i> , 2022, 22, 168-179.	4.8	39
29	Transcriptome divergence between the hexaploid salt-marsh sister species <i>Spartina maritima</i> and <i>Spartina alterniflora</i> (Poaceae). <i>Molecular Ecology</i> , 2010, 19, 2050-2063.	3.9	34
30	Meiosis Gene Inventory of Four Ciliates Reveals the Prevalence of a Synaptonemal Complex-Independent Crossover Pathway. <i>Molecular Biology and Evolution</i> , 2014, 31, 660-672.	8.9	32
31	High and specific diversity of protists in the deep-sea basins dominated by diplomonads, kinetoplastids, ciliates and foraminiferans. <i>Communications Biology</i> , 2021, 4, 501.	4.4	30
32	Assignment of 3 Genetic Linkage Groups to 3 Chromosomes of Narrow-Leafed Lupin. <i>Journal of Heredity</i> , 2011, 102, 228-236.	2.4	29
33	Comparison of three clustering approaches for detecting novel environmental microbial diversity. <i>PeerJ</i> , 2016, 4, e1692.	2.0	26
34	Surface ocean metabarcoding confirms limited diversity in planktonic foraminifera but reveals unknown hyper-abundant lineages. <i>Scientific Reports</i> , 2018, 8, 2539.	3.3	23
35	Transcriptome Profiles of Nod Factor-independent Symbiosis in the Tropical Legume <i>Aeschynomene evenia</i> . <i>Scientific Reports</i> , 2018, 8, 10934.	3.3	23
36	The rhizosphere microbiome: A key component of sustainable cork oak forests in trouble. <i>Forest Ecology and Management</i> , 2019, 434, 29-39.	3.2	23

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37	New data and phylogenetic placement of the enigmatic Old World lupin: <i>Lupinus mariae-josephi</i> H. Pascual. <i>Genetic Resources and Crop Evolution</i> , 2011, 58, 101-114.	1.6	21
38	Habitat- and soil-related drivers of the root-associated fungal community of <i>Quercus suber</i> in the Northern Moroccan forest. <i>PLoS ONE</i> , 2017, 12, e0187758.	2.5	21
39	Diversity and dynamics of relevant nanoplanktonic diatoms in the Western English Channel. <i>ISME Journal</i> , 2020, 14, 1966-1981.	9.8	20
40	Controlled sampling of ribosomally active protistan diversity in sediment-surface layers identifies putative players in the marine carbon sink. <i>ISME Journal</i> , 2020, 14, 984-998.	9.8	19
41	Seasonal dynamics of marine protist communities in tidally mixed coastal waters. <i>Molecular Ecology</i> , 2022, 31, 3761-3783.	3.9	19
42	How deep can ectomycorrhizas go? A case study on <i>Pisolithus</i> down to 4 meters in a Brazilian eucalypt plantation. <i>Mycorrhiza</i> , 2019, 29, 637-648.	2.8	17
43	Yeasts dominate soil fungal communities in three lowland Neotropical rainforests. <i>Environmental Microbiology Reports</i> , 2017, 9, 668-675.	2.4	14
44	Browsing repeats in genomes: Pygram and an application to non-coding region analysis. <i>BMC Bioinformatics</i> , 2006, 7, 477.	2.6	13
45	Isolation, phylogeny and evolution of the <i>SymRK</i> gene in the legume genus <i>Lupinus</i> L.. <i>Molecular Phylogenetics and Evolution</i> , 2011, 60, 49-61.	2.7	13
46	The Windblown: Possible Explanations for Dinophyte DNA in Forest Soils. <i>Journal of Eukaryotic Microbiology</i> , 2021, 68, e12833.	1.7	9
47	Meiotic Genes in Colpodean Ciliates Support Secretive Sexuality. <i>Genome Biology and Evolution</i> , 2017, 9, 1781-1787.	2.5	8
48	Heterogeneity of the rice microbial community of the Chinese centuries-old Honghe Hani rice terraces system. <i>Environmental Microbiology</i> , 2020, 22, 3429-3445.	3.8	8
49	Fruit fly phylogeny imprints bacterial gut microbiota. <i>Evolutionary Applications</i> , 2022, 15, 1621-1638.	3.1	5
50	Identifying Potential Hosts of Short-Branch Microsporidia. <i>Microbial Ecology</i> , 2021, 82, 549-553.	2.8	4
51	metaXplor: an interactive viral and microbial metagenomic data manager. <i>GigaScience</i> , 2021, 10, .	6.4	4
52	Genetic Variation in Host-Specific Competitiveness of the Symbiont <i>Rhizobium leguminosarum</i> Symbiovar <i>viciae</i> . <i>Frontiers in Plant Science</i> , 2021, 12, 719987.	3.6	4
53	The belowground bacterial and fungal communities differed in their significance as microbial indicator of Moroccan carob habitats. <i>Ecological Indicators</i> , 2020, 114, 106341.	6.3	3
54	The Repetitive Content in Lupin Genomes. <i>Compendium of Plant Genomes</i> , 2020, , 161-186.	0.5	2

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55	Temporal recovery of soil biological activity and diversity after 915-MHz microwave treatments. <i>Biology and Fertility of Soils</i> , 2021, 57, 603-616.	4.3	0
56	OTU picking on large datasets: comparing methods on a diversity of situations. ARPHA Conference Abstracts, 0, 4, .	0.0	0