Frédéric Mahé

List of Publications by Year in descending order

Source: https://exaly.com/author-pdf/3740091/publications.pdf

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56 papers 14,833 citations

172457 29 h-index 54 g-index

76 all docs

76 docs citations

76 times ranked 17505 citing authors

#	Article	IF	Citations
1	pr2â€primers: An 18S rRNA primer database for protists. Molecular Ecology Resources, 2022, 22, 168-179.	4.8	39
2	Fruit fly phylogeny imprints bacterial gut microbiota. Evolutionary Applications, 2022, 15, 1621-1638.	3.1	5
3	Seasonal dynamics of marine protist communities in tidally mixed coastal waters. Molecular Ecology, 2022, 31, 3761-3783.	3.9	19
4	The Windblown: Possible Explanations for Dinophyte DNA in Forest Soils. Journal of Eukaryotic Microbiology, 2021, 68, e12833.	1.7	9
5	Identifying Potential Hosts of Short-Branch Microsporidia. Microbial Ecology, 2021, 82, 549-553.	2.8	4
6	metaXplor: an interactive viral and microbial metagenomic data manager. GigaScience, 2021, 10, .	6.4	4
7	Temporal recovery of soil biological activity and diversity after 915-MHz microwave treatments. Biology and Fertility of Soils, 2021, 57, 603-616.	4.3	O
8	High and specific diversity of protists in the deep-sea basins dominated by diplonemids, kinetoplastids, ciliates and foraminiferans. Communications Biology, 2021, 4, 501.	4.4	30
9	Swarm v3: towards tera-scale amplicon clustering. Bioinformatics, 2021, 38, 267-269.	4.1	40
10	Genetic Variation in Host-Specific Competitiveness of the Symbiont Rhizobium leguminosarum Symbiovar viciae. Frontiers in Plant Science, 2021, 12, 719987.	3.6	4
11	Diversity and dynamics of relevant nanoplanktonic diatoms in the Western English Channel. ISME Journal, 2020, 14, 1966-1981.	9.8	20
12	Heterogeneity of the rice microbial community of the Chinese centuriesâ€old Honghe Hani rice terraces system. Environmental Microbiology, 2020, 22, 3429-3445.	3.8	8
13	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
14	The belowground bacterial and fungal communities differed in their significance as microbial indicator of Moroccan carob habitats. Ecological Indicators, 2020, 114, 106341.	6.3	3
15	The Repetitive Content in Lupin Genomes. Compendium of Plant Genomes, 2020, , 161-186.	0.5	2
16	Global Trends in Marine Plankton Diversity across Kingdoms of Life. Cell, 2019, 179, 1084-1097.e21.	28.9	271
17	How deep can ectomycorrhizas go? A case study on Pisolithus down to 4 meters in a Brazilian eucalypt plantation. Mycorrhiza, 2019, 29, 637-648.	2.8	17
18	The rhizosphere microbiome: A key component of sustainable cork oak forests in trouble. Forest Ecology and Management, 2019, 434, 29-39.	3.2	23

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19	Clarifying the Relationships between Microsporidia and Cryptomycota. Journal of Eukaryotic Microbiology, 2018, 65, 773-782.	1.7	98
20	Surface ocean metabarcoding confirms limited diversity in planktonic foraminifera but reveals unknown hyper-abundant lineages. Scientific Reports, 2018, 8, 2539.	3.3	23
21	Worldwide Occurrence and Activity of the Reef-Building Coral Symbiont Symbiodinium in the Open Ocean. Current Biology, 2018, 28, 3625-3633.e3.	3.9	52
22	Consistent patterns of high alpha and low beta diversity in tropical parasitic and freeâ€living protists. Molecular Ecology, 2018, 27, 2846-2857.	3.9	43
23	Transcriptome Profiles of Nod Factor-independent Symbiosis in the Tropical Legume Aeschynomene evenia. Scientific Reports, 2018, 8, 10934.	3.3	23
24	<i>UniEuk</i> : Time to Speak a Common Language in Protistology!. Journal of Eukaryotic Microbiology, 2017, 64, 407-411.	1.7	74
25	Parasites dominate hyperdiverse soil protist communities in Neotropical rainforests. Nature Ecology and Evolution, 2017, 1, 91.	7.8	262
26	Yeasts dominate soil fungal communities in three lowland Neotropical rainforests. Environmental Microbiology Reports, 2017, 9, 668-675.	2.4	14
27	Meiotic Genes in Colpodean Ciliates Support Secretive Sexuality. Genome Biology and Evolution, 2017, 9, 1781-1787.	2.5	8
28	Habitat- and soil-related drivers of the root-associated fungal community of Quercus suber in the Northern Moroccan forest. PLoS ONE, 2017, 12, e0187758.	2.5	21
29	Global patterns of pelagic dinoflagellate diversity across protist size classes unveiled by metabarcoding. Environmental Microbiology, 2016, 18, 609-626.	3.8	105
30	Benthic protists: the under-charted majority. FEMS Microbiology Ecology, 2016, 92, fiw120.	2.7	94
31	Open-Source Sequence Clustering Methods Improve the State Of the Art. MSystems, 2016, 1, .	3.8	155
32	Comparison of three clustering approaches for detecting novel environmental microbial diversity. Peerl, 2016, 4, e1692.	2.0	26
33	VSEARCH: a versatile open source tool for metagenomics. PeerJ, 2016, 4, e2584.	2.0	7,113
34	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
35	Marine protist diversity in <scp>E</scp> uropean coastal waters and sediments as revealed by highâ€throughput sequencing. Environmental Microbiology, 2015, 17, 4035-4049.	3.8	384
36	PFR ² : a curated database of planktonic foraminifera 18S ribosomal <scp>DNA</scp> as a resource for studies of plankton ecology, biogeography and evolution. Molecular Ecology Resources, 2015, 15, 1472-1485.	4.8	55

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37	Swarm v2: highly-scalable and high-resolution amplicon clustering. PeerJ, 2015, 3, e1420.	2.0	528
38	Eukaryotic plankton diversity in the sunlit ocean. Science, 2015, 348, 1261605.	12.6	1,551
39	Deep sequencing uncovers protistan plankton diversity in the Portuguese Ria Formosa solar saltern ponds. Extremophiles, 2015, 19, 283-295.	2.3	43
40	Comparing Highâ€throughput Platforms for Sequencing the V4 Region of SSUâ€r <scp>DNA</scp> in Environmental Microbial Eukaryotic Diversity Surveys. Journal of Eukaryotic Microbiology, 2015, 62, 338-345.	1.7	53
41	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
42	Swarm: robust and fast clustering method for amplicon-based studies. PeerJ, 2014, 2, e593.	2.0	828
43	Meiosis Gene Inventory of Four Ciliates Reveals the Prevalence of a Synaptonemal Complex-Independent Crossover Pathway. Molecular Biology and Evolution, 2014, 31, 660-672.	8.9	32
44	Patterns of Rare and Abundant Marine Microbial Eukaryotes. Current Biology, 2014, 24, 813-821.	3.9	450
45	Placing Environmental Next-Generation Sequencing Amplicons from Microbial Eukaryotes into a Phylogenetic Context. Molecular Biology and Evolution, 2014, 31, 993-1009.	8.9	97
46	Ciliates and the Rare Biosphere: A Review. Journal of Eukaryotic Microbiology, 2014, 61, 404-409.	1.7	43
47	Vampires in the oceans: predatory cercozoan amoebae in marine habitats. ISME Journal, 2013, 7, 2387-2399.	9.8	73
48	Diversity, Ecology and Biogeochemistry of Cyst-Forming Acantharia (Radiolaria) in the Oceans. PLoS ONE, 2013, 8, e53598.	2.5	66
49	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
50	Molecular Phylogeny and Morphological Evolution of the Acantharia (Radiolaria). Protist, 2012, 163, 435-450.	1.5	62
51	Isolation, phylogeny and evolution of the SymRK gene in the legume genus Lupinus L Molecular Phylogenetics and Evolution, 2011, 60, 49-61.	2.7	13
52	New data and phylogenetic placement of the enigmatic Old World lupin: Lupinus mariae-josephi H. Pascual. Genetic Resources and Crop Evolution, 2011, 58, 101-114.	1.6	21
53	Assignment of 3 Genetic Linkage Groups to 3 Chromosomes of Narrow-Leafed Lupin. Journal of Heredity, 2011, 102, 228-236.	2.4	29
54	Transcriptome divergence between the hexaploid salt-marsh sister species Spartina maritima and Spartina alterniflora (Poaceae). Molecular Ecology, 2010, 19, 2050-2063.	3.9	34

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55	Browsing repeats in genomes: Pygram and an application to non-coding region analysis. BMC Bioinformatics, 2006, 7, 477.	2.6	13
56	OTU picking on large datasets: comparing methods on a diversity of situations. ARPHA Conference Abstracts, 0, 4, .	0.0	0