

Ramiro Logares

List of Publications by Year in descending order

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Version: 2024-02-01

91
papers

9,625
citations

71102

41
h-index

48315

88
g-index

121
all docs

121
docs citations

121
times ranked

8106
citing authors

#	ARTICLE	IF	CITATIONS
1	Seasonal niche differentiation among closely related marine bacteria. ISME Journal, 2022, 16, 178-189.	9.8	36
2	Microbial population genomes from the Amazon River reveal possible modulation of the organic matter degradation process in tropical freshwaters. Molecular Ecology, 2022, 31, 206-219.	3.9	2
3	Phylogenetically and functionally diverse microorganisms reside under the Ross Ice Shelf. Nature Communications, 2022, 13, 117.	12.8	17
4	Long-term patterns of an interconnected core marine microbiota. Environmental Microbiomes, 2022, 17, 22.	5.0	13
5	Bacterioplankton dynamics driven by interannual and spatial variation in diatom and dinoflagellate spring bloom communities in the Baltic Sea. Limnology and Oceanography, 2021, 66, 255-271.	3.1	13
6	Comparative genomics reveals new functional insights in uncultured MAST species. ISME Journal, 2021, 15, 1767-1781.	9.8	18
7	Deep ocean metagenomes provide insight into the metabolic architecture of bathypelagic microbial communities. Communications Biology, 2021, 4, 604.	4.4	107
8	A global overview of the trophic structure within microbiomes across ecosystems. Environment International, 2021, 151, 106438.	10.0	48
9	Low shifts in salinity determined assembly processes and network stability of microeukaryotic plankton communities in a subtropical urban reservoir. Microbiome, 2021, 9, 128.	11.1	191
10	Niche adaptation promoted the evolutionary diversification of tiny ocean predators. Proceedings of the National Academy of Sciences of the United States of America, 2021, 118, .	7.1	12
11	Microbial eukaryote assemblages and potential novel diversity in four tropical East African Great Lakes. FEMS Microbiology Ecology, 2021, 97, .	2.7	7
12	Recent advances in environmental DNA-based biodiversity assessment and conservation. Diversity and Distributions, 2021, 27, 1876-1879.	4.1	13
13	Disentangling environmental effects in microbial association networks. Microbiome, 2021, 9, 232.	11.1	21
14	Marked changes in diversity and relative activity of picoeukaryotes with depth in the world ocean. ISME Journal, 2020, 14, 437-449.	9.8	80
15	Response of pico-nano-eukaryotes to inorganic and organic nutrient additions. Estuarine, Coastal and Shelf Science, 2020, 235, 106565.	2.1	7
16	The planktonic protist interactome: where do we stand after a century of research?. ISME Journal, 2020, 14, 544-559.	9.8	111
17	Single Cell Genomics Reveals Viruses Consumed by Marine Protists. Frontiers in Microbiology, 2020, 11, 524828.	3.5	26
18	Uncovering the genomic potential of the Amazon River microbiome to degrade rainforest organic matter. Microbiome, 2020, 8, 151.	11.1	18

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19	Perspectives from Ten Years of Protist Studies by High-Throughput Metabarcoding. <i>Journal of Eukaryotic Microbiology</i> , 2020, 67, 612-622.	1.7	72
20	Tracing the Origin of Planktonic Protists in an Ancient Lake. <i>Microorganisms</i> , 2020, 8, 543.	3.6	28
21	Disentangling the mechanisms shaping the surface ocean microbiota. <i>Microbiome</i> , 2020, 8, 55.	11.1	154
22	Diversity patterns of planktonic microeukaryote communities in tropical floodplain lakes based on 18S rDNA gene sequences. <i>Journal of Plankton Research</i> , 2019, 41, 241-256.	1.8	13
23	Important contribution of macroalgae to oceanic carbon sequestration. <i>Nature Geoscience</i> , 2019, 12, 748-754.	12.9	141
24	Assessing the viral content of uncultured picoeukaryotes in the global ocean by single cell genomics. <i>Molecular Ecology</i> , 2019, 28, 4272-4289.	3.9	25
25	Higher contribution of globally rare bacterial taxa reflects environmental transitions across the surface ocean. <i>Molecular Ecology</i> , 2019, 28, 1930-1945.	3.9	41
26	Summer comes to the Southern Ocean: how phytoplankton shape bacterioplankton communities far into the deep dark sea. <i>Ecosphere</i> , 2019, 10, e02641.	2.2	20
27	Single cell genomics yields a wide diversity of small planktonic protists across major ocean ecosystems. <i>Scientific Reports</i> , 2019, 9, 6025.	3.3	35
28	Impact of grazing, resource availability and light on prokaryotic growth and diversity in the oligotrophic surface global ocean. <i>Environmental Microbiology</i> , 2019, 21, 1482-1496.	3.8	24
29	Quantifying long-term recurrence in planktonic microbial eukaryotes. <i>Molecular Ecology</i> , 2019, 28, 923-935.	3.9	79
30	Protist Diversity and Seasonal Dynamics in Skagerrak Plankton Communities as Revealed by Metabarcoding and Microscopy. <i>Journal of Eukaryotic Microbiology</i> , 2019, 66, 494-513.	1.7	60
31	Microzooplankton distribution in the Amundsen Sea Polynya (Antarctica) during an extensive <i>Phaeocystis antarctica</i> bloom. <i>Progress in Oceanography</i> , 2019, 170, 1-10.	3.2	15
32	Ecology of Rare Microorganisms. , 2019, , 90-90.		0
33	Primer Design for an Accurate View of Picocyanobacterial Community Structure by Using High-Throughput Sequencing. <i>Applied and Environmental Microbiology</i> , 2019, 85, .	3.1	9
34	Delineating closely related dinoflagellate lineages using phylotranscriptomics. <i>Journal of Phycology</i> , 2018, 54, 571-576.	2.3	5
35	Single-cell genomics of multiple uncultured stramenopiles reveals underestimated functional diversity across oceans. <i>Nature Communications</i> , 2018, 9, 310.	12.8	101
36	Large-scale ocean connectivity and planktonic body size. <i>Nature Communications</i> , 2018, 9, 142.	12.8	102

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37	Diatom diversity through HTS-metabarcoding in coastal European seas. <i>Scientific Reports</i> , 2018, 8, 18059.	3.3	48
38	Seasonal succession of small planktonic eukaryotes inhabiting surface waters of a coastal upwelling system. <i>Environmental Microbiology</i> , 2018, 20, 2955-2973.	3.8	44
39	Sinking particles promote vertical connectivity in the ocean microbiome. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2018, 115, E6799-E6807.	7.1	185
40	Contrasting prevalence of selection and drift in the community structuring of bacteria and microbial eukaryotes. <i>Environmental Microbiology</i> , 2018, 20, 2231-2240.	3.8	153
41	Planktonic protistan communities in lakes along a large-scale environmental gradient. <i>FEMS Microbiology Ecology</i> , 2017, 93, fiw231.	2.7	28
42	Seasonal patterns in Arctic prasinophytes and inferred ecology of <i>Bathycoccus</i> unveiled in an Arctic winter metagenome. <i>ISME Journal</i> , 2017, 11, 1372-1385.	9.8	54
43	Mixing of water masses caused by a drifting iceberg affects bacterial activity, community composition and substrate utilization capability in the Southern Ocean. <i>Environmental Microbiology</i> , 2017, 19, 2453-2467.	3.8	21
44	The roles of geographic distance and socioeconomic factors on international collaboration among ecologists. <i>Scientometrics</i> , 2017, 113, 1539-1550.	3.0	36
45	Viral to metazoan marine plankton nucleotide sequences from the Tara Oceans expedition. <i>Scientific Data</i> , 2017, 4, 170093.	5.3	147
46	Accessing the genomic information of unculturable oceanic picoeukaryotes by combining multiple single cells. <i>Scientific Reports</i> , 2017, 7, 41498.	3.3	47
47	Abundant and rare picoeukaryotic subcommunities present contrasting patterns in the epipelagic waters of marginal seas in the northwestern Pacific Ocean. <i>Environmental Microbiology</i> , 2017, 19, 287-300.	3.8	183
48	Exploring the oceanic microeukaryotic interactome with metaomics approaches. <i>Aquatic Microbial Ecology</i> , 2017, 79, 1-12.	1.8	46
49	Restructuring of the sponge microbiome favors tolerance to ocean acidification. <i>Environmental Microbiology Reports</i> , 2016, 8, 536-544.	2.4	60
50	Benthic protists: the under-charted majority. <i>FEMS Microbiology Ecology</i> , 2016, 92, fiw120.	2.7	94
51	Environmental Sequencing Provides Reasonable Estimates of the Relative Abundance of Specific Picoeukaryotes. <i>Applied and Environmental Microbiology</i> , 2016, 82, 4757-4766.	3.1	118
52	Ecological and evolutionary significance of novel protist lineages. <i>European Journal of Protistology</i> , 2016, 55, 4-11.	1.5	25
53	Large variability of bathypelagic microbial eukaryotic communities across the world's oceans. <i>ISME Journal</i> , 2016, 10, 945-958.	9.8	171
54	Probing the Rare Biosphere of the North-West Mediterranean Sea: An Experiment with High Sequencing Effort. <i>PLoS ONE</i> , 2016, 11, e0159195.	2.5	17

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55	Marine protist diversity in European coastal waters and sediments as revealed by high-throughput sequencing. <i>Environmental Microbiology</i> , 2015, 17, 4035-4049.	3.8	384
56	Weak Coherence in Abundance Patterns Between Bacterial Classes and Their Constituent OTUs Along a Regulated River. <i>Frontiers in Microbiology</i> , 2015, 6, 1293.	3.5	14
57	Eukaryotic plankton diversity in the sunlit ocean. <i>Science</i> , 2015, 348, 1261605.	12.6	1,551
58	Rarity in aquatic microbes: placing protists on the map. <i>Research in Microbiology</i> , 2015, 166, 831-841.	2.1	69
59	Evidence of concurrent local adaptation and high phenotypic plasticity in a polar microeukaryote. <i>Environmental Microbiology</i> , 2015, 17, 1510-1519.	3.8	41
60	The influence of light and water mass on bacterial population dynamics in the Amundsen Sea Polynya. <i>Elementa</i> , 2015, 3, .	3.2	9
61	Metagenomic 16S rDNA Illumina tags are a powerful alternative to amplicon sequencing to explore diversity and structure of microbial communities. <i>Environmental Microbiology</i> , 2014, 16, 2659-2671.	3.8	291
62	Patterns of Rare and Abundant Marine Microbial Eukaryotes. <i>Current Biology</i> , 2014, 24, 813-821.	3.9	450
63	Exploring the uncultured microeukaryote majority in the oceans: reevaluation of ribogroups within stramenopiles. <i>ISME Journal</i> , 2014, 8, 854-866.	9.8	157
64	Eukaryotic versus prokaryotic marine picoplankton ecology. <i>Environmental Microbiology</i> , 2013, 15, 1254-1261.	3.8	92
65	Biogeography of bacterial communities exposed to progressive long-term environmental change. <i>ISME Journal</i> , 2013, 7, 937-948.	9.8	330
66	Different bacterial communities in ectomycorrhizae and surrounding soil. <i>Scientific Reports</i> , 2013, 3, 3471.	3.3	77
67	General Patterns of Diversity in Major Marine Microeukaryote Lineages. <i>PLoS ONE</i> , 2013, 8, e57170.	2.5	54
68	The Protist Ribosomal Reference database (PR2): a catalog of unicellular eukaryote Small Sub-Unit rRNA sequences with curated taxonomy. <i>Nucleic Acids Research</i> , 2012, 41, D597-D604.	14.5	1,463
69	Diversity patterns and activity of uncultured marine heterotrophic flagellates unveiled with pyrosequencing. <i>ISME Journal</i> , 2012, 6, 1823-1833.	9.8	114
70	Low Evolutionary Diversification in a Widespread and Abundant Uncultured Protist (MAST-4). <i>Molecular Biology and Evolution</i> , 2012, 29, 1393-1406.	8.9	42
71	Environmental microbiology through the lens of high-throughput DNA sequencing: Synopsis of current platforms and bioinformatics approaches. <i>Journal of Microbiological Methods</i> , 2012, 91, 106-113.	1.6	115
72	Polar lakes may act as ecological islands to aquatic protists. <i>Molecular Ecology</i> , 2012, 21, 3200-3209.	3.9	33

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73	Black Swans in ecology and evolution: The importance of improbable but highly influential events. <i>Ideas in Ecology and Evolution</i> , 2012, , .	0.1	3
74	Draft genome sequence of strain HIMB100, a cultured representative of the SAR116 clade of marine Alphaproteobacteria. <i>Standards in Genomic Sciences</i> , 2011, 5, 269-278.	1.5	27
75	Population genetics: the next stop for microbial ecologists?. <i>Open Life Sciences</i> , 2011, 6, 887-892.	1.4	3
76	A data mining approach to dinoflagellate clustering according to sterol composition: correlations with evolutionary history. <i>International Journal of Data Mining and Bioinformatics</i> , 2010, 4, 431.	0.1	26
77	Freshwater Perkinsea and marine-freshwater colonizations revealed by pyrosequencing and phylogeny of environmental rDNA. <i>ISME Journal</i> , 2010, 4, 1144-1153.	9.8	208
78	Infrequent Transitions between Saline and Fresh Waters in One of the Most Abundant Microbial Lineages (SAR11). <i>Molecular Biology and Evolution</i> , 2010, 27, 347-357.	8.9	66
79	Thermal Tolerances in Tadpoles of Three Species of Patagonian Anurans. <i>South American Journal of Herpetology</i> , 2010, 5, 89-96.	0.5	17
80	Composition and dynamics of microeukaryote communities in the River Danube.. <i>Fottea</i> , 2010, 10, 99-113.	0.9	4
81	Genetic Diversity Patterns in Five Protist Species Occurring in Lakes. <i>Protist</i> , 2009, 160, 301-317.	1.5	55
82	Infrequent marineâ€œfreshwater transitions in the microbial world. <i>Trends in Microbiology</i> , 2009, 17, 414-422.	7.7	311
83	MARINEâ€œDERIVED DINOFLAGELLATES IN ANTARCTIC SALINE LAKES: COMMUNITY COMPOSITION AND ANNUAL DYNAMICS¹*[link]. <i>Journal of Phycology</i> , 2008, 44, 592-604.	2.3	23
84	Recent evolutionary diversification of a protist lineage. <i>Environmental Microbiology</i> , 2008, 10, 1231-1243.	3.8	31
85	Diversification of unicellular eukaryotes: cryptomonad colonizations of marine and fresh waters inferred from revised 18S rRNA phylogeny. <i>Environmental Microbiology</i> , 2008, 10, 2635-2644.	3.8	79
86	Applying Clustering and Phylogeny Analysis to Study Dinoflagellates Based on Sterol Composition. , 2008, , .		1
87	Extensive dinoflagellate phylogenies indicate infrequent marineâ€œfreshwater transitions. <i>Molecular Phylogenetics and Evolution</i> , 2007, 45, 887-903.	2.7	101
88	Phenotypically Different Microalgal Morphospecies with Identical Ribosomal DNA: A Case of Rapid Adaptive Evolution?. <i>Microbial Ecology</i> , 2007, 53, 549-561.	2.8	110
89	Fatty acid and sterol composition of two evolutionarily closely related dinoflagellate morphospecies from cold Scandinavian brackish and freshwaters. <i>European Journal of Phycology</i> , 2006, 41, 303-311.	2.0	29
90	First insights into the overwintering biology of <i>Alsodes gargola</i> frogs and tadpoles inhabiting harsh Andean-Patagonian alpine environments. <i>Amphibia - Reptilia</i> , 2006, 27, 263-267.	0.5	6

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91	Lifting the Lid: Nitrifying Archaea Sustain Diverse Microbial Communities Below the Ross Ice Shelf. SSRN Electronic Journal, 0, , .	0.4	3