

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	Eukaryotic plankton diversity in the sunlit ocean. <i>Science</i> , 2015, 348, 1261605.	12.6	1,551
2	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
3	Patterns of Rare and Abundant Marine Microbial Eukaryotes. <i>Current Biology</i> , 2014, 24, 813-821.	3.9	450
4	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
5	Biogeography of bacterial communities exposed to progressive long-term environmental change. <i>ISME Journal</i> , 2013, 7, 937-948.	9.8	330
6	Infrequent marine-freshwater transitions in the microbial world. <i>Trends in Microbiology</i> , 2009, 17, 414-422.	7.7	311
7	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
8	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
9	Low shifts in salinity determined assembly processes and network stability of microeukaryotic plankton communities in a subtropical urban reservoir. <i>Microbiome</i> , 2021, 9, 128.	11.1	191
10	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
11	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
12	Large variability of bathypelagic microbial eukaryotic communities across the world's oceans. <i>ISME Journal</i> , 2016, 10, 945-958.	9.8	171
13	Exploring the uncultured microeukaryote majority in the oceans: reevaluation of ribogroups within stramenopiles. <i>ISME Journal</i> , 2014, 8, 854-866.	9.8	157
14	Disentangling the mechanisms shaping the surface ocean microbiota. <i>Microbiome</i> , 2020, 8, 55.	11.1	154
15	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
16	Viral to metazoan marine plankton nucleotide sequences from the Tara Oceans expedition. <i>Scientific Data</i> , 2017, 4, 170093.	5.3	147
17	Important contribution of macroalgae to oceanic carbon sequestration. <i>Nature Geoscience</i> , 2019, 12, 748-754.	12.9	141
18	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

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19	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
20	Diversity patterns and activity of uncultured marine heterotrophic flagellates unveiled with pyrosequencing. <i>ISME Journal</i> , 2012, 6, 1823-1833.	9.8	114
21	The planktonic protist interactome: where do we stand after a century of research?. <i>ISME Journal</i> , 2020, 14, 544-559.	9.8	111
22	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
23	Deep ocean metagenomes provide insight into the metabolic architecture of bathypelagic microbial communities. <i>Communications Biology</i> , 2021, 4, 604.	4.4	107
24	Large-scale ocean connectivity and planktonic body size. <i>Nature Communications</i> , 2018, 9, 142.	12.8	102
25	Extensive dinoflagellate phylogenies indicate infrequent marine-freshwater transitions. <i>Molecular Phylogenetics and Evolution</i> , 2007, 45, 887-903.	2.7	101
26	Single-cell genomics of multiple uncultured stramenopiles reveals underestimated functional diversity across oceans. <i>Nature Communications</i> , 2018, 9, 310.	12.8	101
27	Benthic protists: the under-charted majority. <i>FEMS Microbiology Ecology</i> , 2016, 92, fiw120.	2.7	94
28	Eukaryotic versus prokaryotic marine picoplankton ecology. <i>Environmental Microbiology</i> , 2013, 15, 1254-1261.	3.8	92
29	Marked changes in diversity and relative activity of picoeukaryotes with depth in the world ocean. <i>ISME Journal</i> , 2020, 14, 437-449.	9.8	80
30	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
31	Quantifying long-term recurrence in planktonic microbial eukaryotes. <i>Molecular Ecology</i> , 2019, 28, 923-935.	3.9	79
32	Different bacterial communities in ectomycorrhizae and surrounding soil. <i>Scientific Reports</i> , 2013, 3, 3471.	3.3	77
33	Perspectives from Ten Years of Protist Studies by High-Throughput Metabarcoding. <i>Journal of Eukaryotic Microbiology</i> , 2020, 67, 612-622.	1.7	72
34	Rarity in aquatic microbes: placing protists on the map. <i>Research in Microbiology</i> , 2015, 166, 831-841.	2.1	69
35	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
36	Restructuring of the sponge microbiome favors tolerance to ocean acidification. <i>Environmental Microbiology Reports</i> , 2016, 8, 536-544.	2.4	60

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37	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
38	Genetic Diversity Patterns in Five Protist Species Occurring in Lakes. <i>Protist</i> , 2009, 160, 301-317.	1.5	55
39	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
40	General Patterns of Diversity in Major Marine Microeukaryote Lineages. <i>PLoS ONE</i> , 2013, 8, e57170.	2.5	54
41	Diatom diversity through HTS-metabarcoding in coastal European seas. <i>Scientific Reports</i> , 2018, 8, 18059.	3.3	48
42	A global overview of the trophic structure within microbiomes across ecosystems. <i>Environment International</i> , 2021, 151, 106438.	10.0	48
43	Accessing the genomic information of unculturable oceanic picoeukaryotes by combining multiple single cells. <i>Scientific Reports</i> , 2017, 7, 41498.	3.3	47
44	Exploring the oceanic microeukaryotic interactome with metaomics approaches. <i>Aquatic Microbial Ecology</i> , 2017, 79, 1-12.	1.8	46
45	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
46	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
47	Evidence of concurrent local adaptation and high phenotypic plasticity in a polar microeukaryote. <i>Environmental Microbiology</i> , 2015, 17, 1510-1519.	3.8	41
48	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
49	The roles of geographic distance and socioeconomic factors on international collaboration among ecologists. <i>Scientometrics</i> , 2017, 113, 1539-1550.	3.0	36
50	Seasonal niche differentiation among closely related marine bacteria. <i>ISME Journal</i> , 2022, 16, 178-189.	9.8	36
51	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
52	Polar lakes may act as ecological islands to aquatic protists. <i>Molecular Ecology</i> , 2012, 21, 3200-3209.	3.9	33
53	Recent evolutionary diversification of a protist lineage. <i>Environmental Microbiology</i> , 2008, 10, 1231-1243.	3.8	31
54	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

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55	Planktonic protistan communities in lakes along a large-scale environmental gradient. <i>FEMS Microbiology Ecology</i> , 2017, 93, fiw231.	2.7	28
56	Tracing the Origin of Planktonic Protists in an Ancient Lake. <i>Microorganisms</i> , 2020, 8, 543.	3.6	28
57	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
58	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
59	Single Cell Genomics Reveals Viruses Consumed by Marine Protists. <i>Frontiers in Microbiology</i> , 2020, 11, 524828.	3.5	26
60	Ecological and evolutionary significance of novel protist lineages. <i>European Journal of Protistology</i> , 2016, 55, 4-11.	1.5	25
61	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
62	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
63	MARINE-DERIVED DINOFLAGELLATES IN ANTARCTIC SALINE LAKES: COMMUNITY COMPOSITION AND ANNUAL DYNAMICS ¹ [link]. <i>Journal of Phycology</i> , 2008, 44, 592-604.	2.3	23
64	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
65	Disentangling environmental effects in microbial association networks. <i>Microbiome</i> , 2021, 9, 232.	11.1	21
66	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
67	Uncovering the genomic potential of the Amazon River microbiome to degrade rainforest organic matter. <i>Microbiome</i> , 2020, 8, 151.	11.1	18
68	Comparative genomics reveals new functional insights in uncultured MAST species. <i>ISME Journal</i> , 2021, 15, 1767-1781.	9.8	18
69	Thermal Tolerances in Tadpoles of Three Species of Patagonian Anurans. <i>South American Journal of Herpetology</i> , 2010, 5, 89-96.	0.5	17
70	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
71	Phylogenetically and functionally diverse microorganisms reside under the Ross Ice Shelf. <i>Nature Communications</i> , 2022, 13, 117.	12.8	17
72	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

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73	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
74	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
75	Bacterioplankton dynamics driven by interannual and spatial variation in diatom and dinoflagellate spring bloom communities in the Baltic Sea. <i>Limnology and Oceanography</i> , 2021, 66, 255-271.	3.1	13
76	Recent advances in environmental DNA-based biodiversity assessment and conservation. <i>Diversity and Distributions</i> , 2021, 27, 1876-1879.	4.1	13
77	Long-term patterns of an interconnected core marine microbiota. <i>Environmental Microbiomes</i> , 2022, 17, 22.	5.0	13
78	Niche adaptation promoted the evolutionary diversification of tiny ocean predators. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2021, 118, .	7.1	12
79	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
80	The influence of light and water mass on bacterial population dynamics in the Amundsen Sea Polynya. <i>Elementa</i> , 2015, 3, .	3.2	9
81	Response of pico-nano-eukaryotes to inorganic and organic nutrient additions. <i>Estuarine, Coastal and Shelf Science</i> , 2020, 235, 106565.	2.1	7
82	Microbial eukaryote assemblages and potential novel diversity in four tropical East African Great Lakes. <i>FEMS Microbiology Ecology</i> , 2021, 97, .	2.7	7
83	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
84	Delineating closely related dinoflagellate lineages using phylotranscriptomics. <i>Journal of Phycology</i> , 2018, 54, 571-576.	2.3	5
85	Composition and dynamics of microeukaryote communities in the River Danube.. <i>Fottea</i> , 2010, 10, 99-113.	0.9	4
86	Population genetics: the next stop for microbial ecologists?. <i>Open Life Sciences</i> , 2011, 6, 887-892.	1.4	3
87	Lifting the Lid: Nitrifying Archaea Sustain Diverse Microbial Communities Below the Ross Ice Shelf. <i>SSRN Electronic Journal</i> , 0, , .	0.4	3
88	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
89	Microbial population genomes from the Amazon River reveal possible modulation of the organic matter degradation process in tropical freshwaters. <i>Molecular Ecology</i> , 2022, 31, 206-219.	3.9	2
90	Applying Clustering and Phylogeny Analysis to Study Dinoflagellates Based on Sterol Composition. , 2008, , .		1

#	ARTICLE	IF	CITATIONS
91	Ecology of Rare Microorganisms. , 2019, , 90-90.		0