

# Emilio O Casamayor

## List of Publications by Year in descending order

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Version: 2024-02-01

138  
papers

12,307  
citations

30070

54  
h-index

27406

106  
g-index

143  
all docs

143  
docs citations

143  
times ranked

12577  
citing authors

#	ARTICLE	IF	CITATIONS
1	A long-term atmospheric baseline for intercontinental exchange of airborne pathogens. <i>Environment International</i> , 2022, 158, 106916.	10.0	9
2	Global dispersal and potential sources of antibiotic resistance genes in atmospheric remote depositions. <i>Environment International</i> , 2022, 160, 107077.	10.0	8
3	Microbial ecology of the atmosphere. <i>FEMS Microbiology Reviews</i> , 2022, 46, .	8.6	44
4	Unifying the known and unknown microbial coding sequence space. <i>ELife</i> , 2022, 11, .	6.0	41
5	Biological Microbial Interactions from Cooccurrence Networks in a High Mountain Lacustrine District. <i>MSphere</i> , 2022, 7, .	2.9	1
6	Microbial metabolic routes in metagenome assembled genomes are mirrored by the mass balance of polycyclic aromatic hydrocarbons in a high altitude lake. <i>Environmental Pollution</i> , 2022, 308, 119592.	7.5	0
7	The characteristic time of ecological communities. <i>Ecology</i> , 2021, 102, e03247.	3.2	11
8	Ecological and Metabolic Thresholds in the Bacterial, Protist, and Fungal Microbiome of Ephemeral Saline Lakes (Monegros Desert, Spain). <i>Microbial Ecology</i> , 2021, 82, 885-896.	2.8	18
9	Individual fate and gut microbiome composition in the European wild rabbit ( <i>Oryctolagus cuniculus</i> ). <i>Scientific Reports</i> , 2021, 11, 766.	3.3	12
10	General decline in the diversity of the airborne microbiota under future climatic scenarios. <i>Scientific Reports</i> , 2021, 11, 20223.	3.3	8
11	Partitioning between atmospheric deposition and canopy microbial nitrification into throughfall nitrate fluxes in a Mediterranean forest. <i>Journal of Ecology</i> , 2020, 108, 626-640.	4.0	20
12	Regional community assembly drivers and microbial environmental sources shaping bacterioplankton in an alpine lacustrine district (Pyrenees, Spain). <i>Environmental Microbiology</i> , 2020, 22, 297-309.	3.8	22
13	Temperature drives local contributions to beta diversity in mountain streams: Stochastic and deterministic processes. <i>Global Ecology and Biogeography</i> , 2020, 29, 420-432.	5.8	30
14	Taxonomy and functional interactions in upper and bottom waters of an oligotrophic high-mountain deep lake (Redon, Pyrenees) unveiled by microbial metagenomics. <i>Science of the Total Environment</i> , 2020, 707, 135929.	8.0	19
15	Climate mediates continental scale patterns of stream microbial functional diversity. <i>Microbiome</i> , 2020, 8, 92.	11.1	28
16	Dynamics and ecological distributions of the Archaea microbiome from inland saline lakes (Monegros) Tj ETQq0 0 0,rgBT /Overlock 10 T	2.7	11
17	The DNRA-Denitrification Dichotomy Differentiates Nitrogen Transformation Pathways in Mountain Lake Benthic Habitats. <i>Frontiers in Microbiology</i> , 2019, 10, 1229.	3.5	44
18	High similarity in bacterial bioaerosol compositions between the free troposphere and atmospheric depositions collected at high-elevation mountains. <i>Atmospheric Environment</i> , 2019, 203, 79-86.	4.1	28

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19	A Randomized Trait Community Clustering approach to unveil consistent environmental thresholds in community assembly. <i>ISME Journal</i> , 2019, 13, 2681-2689.	9.8	17
20	Microbial Community Structure and Functionality in the Deep Sea Floor: Evaluating the Causes of Spatial Heterogeneity in a Submarine Canyon System (NW Mediterranean, Spain). <i>Frontiers in Marine Science</i> , 2019, 6, .	2.5	17
21	Colonization and extinction rates estimated from temporal dynamics of ecological communities: The island r package. <i>Methods in Ecology and Evolution</i> , 2019, 10, 1108-1117.	5.2	12
22	Sponges and Their Microbiomes Show Similar Community Metrics Across Impacted and Well-Preserved Reefs. <i>Frontiers in Microbiology</i> , 2019, 10, 1961.	3.5	49
23	Microbial composition, potential functional roles and genetic novelty in gypsum-rich and hypersaline soils of Monegros and Gallocanta (Spain). <i>Science of the Total Environment</i> , 2019, 650, 343-353.	8.0	18
24	Consistent changes in the taxonomic structure and functional attributes of bacterial communities during primary succession. <i>ISME Journal</i> , 2018, 12, 1658-1667.	9.8	113
25	High planktonic diversity in mountain lakes contains similar contributions of autotrophic, heterotrophic and parasitic eukaryotic life forms. <i>Scientific Reports</i> , 2018, 8, 4457.	3.3	51
26	A long-term survey unveils strong seasonal patterns in the airborne microbiome coupled to general and regional atmospheric circulations. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2018, 115, 12229-12234.	7.1	161
27	Showcasing the role of seawater in bacteria recruitment and microbiome stability in sponges. <i>Scientific Reports</i> , 2018, 8, 15201.	3.3	82
28	Development of a 16S rRNA-targeted fluorescence in situ hybridization probe for quantification of the ammonia-oxidizer <i>Nitrosotalea devanaterrea</i> and its relatives. <i>Systematic and Applied Microbiology</i> , 2018, 41, 408-413.	2.8	3
29	Regional and global elevational patterns of microbial species richness and evenness. <i>Ecography</i> , 2017, 40, 393-402.	4.5	79
30	Speciation and ecological success in dimly lit waters: horizontal gene transfer in a green sulfur bacteria bloom unveiled by metagenomic assembly. <i>ISME Journal</i> , 2017, 11, 201-211.	9.8	40
31	Degradation of sulfonamides as a microbial resistance mechanism. <i>Water Research</i> , 2017, 115, 309-317.	11.3	81
32	Dayâ€“night ammonium oxidation in an urban stream: the influence of irradiance on ammonia oxidizers. <i>Freshwater Science</i> , 2017, 36, 272-283.	1.8	4
33	Photoinhibition on natural ammonia oxidizers biofilm populations and implications for nitrogen uptake in stream biofilms. <i>Limnology and Oceanography</i> , 2017, 62, 364-375.	3.1	21
34	Bioaerosols in the Barcelona subway system. <i>Indoor Air</i> , 2017, 27, 564-575.	4.3	45
35	Towards a Microbial Conservation Perspective in High Mountain Lakes. <i>Advances in Global Change Research</i> , 2017, , 157-180.	1.6	10
36	Stream drying drives microbial ammonia oxidation and firstâ€“flush nitrate export. <i>Ecology</i> , 2016, 97, 2192-2198.	3.2	35

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37	The dominant detritus-feeding invertebrate in Arctic peat soils derives its essential amino acids from gut symbionts. <i>Journal of Animal Ecology</i> , 2016, 85, 1275-1285.	2.8	40
38	High occurrence of <i>Pacearchaeota</i> and <i>Woesearchaeota</i> ( <i>A</i> ) Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50 707 <i>Environmental Microbiology Reports</i> , 2016, 8, 210-217.	2.4	112
39	Macrophyte landscape modulates lake ecosystem-level nitrogen losses through tightly coupled plant-microbe interactions. <i>Limnology and Oceanography</i> , 2016, 61, 78-88.	3.1	71
40	High Bacterial Diversity and Phylogenetic Novelty in Dark Euxinic Freshwaters Analyzed by 16S Tag Community Profiling. <i>Microbial Ecology</i> , 2016, 71, 566-574.	2.8	18
41	Insights in the ecology and evolutionary history of the <i>Miscellaneous Crenarchaeotic Group</i> lineage. <i>ISME Journal</i> , 2016, 10, 665-677.	9.8	100
42	High protists diversity in the plankton of sulfurous lakes and lagoons examined by 18s <i>rRNA</i> gene sequence analyses. <i>Environmental Microbiology Reports</i> , 2015, 7, 908-917.	2.4	12
43	Microbial food web components, bulk metabolism, and single-cell physiology of piconeuston in surface microlayers of high-altitude lakes. <i>Frontiers in Microbiology</i> , 2015, 6, 361.	3.5	29
44	Connecting biodiversity and potential functional role in modern euxinic environments by microbial metagenomics. <i>ISME Journal</i> , 2015, 9, 1648-1661.	9.8	123
45	Wastewater Treatment Plant Effluents Change Abundance and Composition of Ammonia-Oxidizing Microorganisms in Mediterranean Urban Stream Biofilms. <i>Microbial Ecology</i> , 2015, 69, 66-74.	2.8	44
46	Vertically aligned carbon nanotubes coated with manganese dioxide as cathode material for microbial fuel cells. <i>Journal of Materials Science</i> , 2015, 50, 1214-1220.	3.7	25
47	Comparison of <i>Artemia</i> bacteria associations in brines, laboratory cultures and the gut environment: a study based on Chilean hypersaline environments. <i>Extremophiles</i> , 2015, 19, 135-147.	2.3	17
48	Influence of Edaphic, Climatic, and Agronomic Factors on the Composition and Abundance of Nitrifying Microorganisms in the Rhizosphere of Commercial Olive Crops. <i>PLoS ONE</i> , 2015, 10, e0125787.	2.5	44
49	A phylogenetic perspective on species diversity, $\beta$ -diversity and biogeography for the microbial world. <i>Molecular Ecology</i> , 2014, 23, 5868-5876.	3.9	20
50	The microbial contribution to macroecology. <i>Frontiers in Microbiology</i> , 2014, 5, 203.	3.5	106
51	Targeting spatiotemporal dynamics of planktonic <i>SAGMGC</i> and segregation of ammonia-oxidizing thaumarchaeota ecotypes by newly designed primers and quantitative polymerase chain reaction. <i>Environmental Microbiology</i> , 2014, 16, 689-700.	3.8	25
52	Environmental controls and composition of anoxygenic photoheterotrophs in ultraoligotrophic high-altitude lakes ( <i>C</i> entral <i>P</i> yrenees). <i>Environmental Microbiology Reports</i> , 2014, 6, 145-151.	2.4	33
53	The phylogenetic and ecological context of cultured and whole genome-sequenced planktonic bacteria from the coastal NW Mediterranean Sea. <i>Systematic and Applied Microbiology</i> , 2014, 37, 216-228.	2.8	22
54	Environmental Heterogeneity and Microbial Inheritance Influence Sponge-Associated Bacterial Composition of Spongia lamella. <i>Microbial Ecology</i> , 2014, 68, 611-620.	2.8	5

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55	Nitrogen-Cycling Genes in Epilithic Biofilms of Oligotrophic High-Altitude Lakes (Central Pyrenees,) Tj ETQq1 1 0.784314 rgBT <sub>35</sub> /Overlook	2.8	35
56	Dynamics of bacterial community succession in a salt marsh chronosequence: evidences for temporal niche partitioning. ISME Journal, 2014, 8, 1989-2001.	9.8	221
57	Structure, inter-annual recurrence, and global-scale connectivity of airborne microbial communities. Science of the Total Environment, 2014, 487, 187-195.	8.0	89
58	Partitioning of <i>Thaumarchaeota</i> populations along environmental gradients in high mountain lakes. FEMS Microbiology Ecology, 2013, 84, 154-164.	2.7	71
59	Environmental distribution of two widespread uncultured freshwater <i>Euryarchaeota</i> clades unveiled by specific primers and quantitative PCR. Environmental Microbiology Reports, 2013, 5, 861-867.	2.4	10
60	Microbial biodiversity in saline shallow lakes of the Monegros Desert, Spain. FEMS Microbiology Ecology, 2013, 85, 503-518.	2.7	72
61	High genetic diversity and novelty in planktonic protists inhabiting inland and coastal high salinity water bodies. FEMS Microbiology Ecology, 2013, 85, 27-36.	2.7	36
62	Distribution of Microbial Arsenic Reduction, Oxidation and Extrusion Genes along a Wide Range of Environmental Arsenic Concentrations. PLoS ONE, 2013, 8, e78890.	2.5	97
63	Bacterial and archaeal community structure in the surface microlayer of high mountain lakes examined under two atmospheric aerosol loading scenarios. FEMS Microbiology Ecology, 2013, 84, 387-397.	2.7	36
64	Diel gene expression profiles of a phosphorus limited mountain lake using metatranscriptomics. Environmental Microbiology, 2013, 15, 1190-1203.	3.8	41
65	Heterogeneous vertical structure of the bacterioplankton community in a non-stratified Antarctic lake. Antarctic Science, 2013, 25, 229-238.	0.9	18
66	Stream Hydrological Fragmentation Drives Bacterioplankton Community Composition. PLoS ONE, 2013, 8, e64109.	2.5	58
67	Contrasting activity patterns determined by BrdU incorporation in bacterial ribotypes from the Arctic Ocean in winter. Frontiers in Microbiology, 2013, 4, 118.	3.5	14
68	Vertical segregation and phylogenetic characterization of ammonia-oxidizing Archaea in a deep oligotrophic lake. ISME Journal, 2012, 6, 1786-1797.	9.8	105
69	High Bacterial Diversity in Epilithic Biofilms of Oligotrophic Mountain Lakes. Microbial Ecology, 2012, 64, 860-869.	2.8	41
70	Using network analysis to explore co-occurrence patterns in soil microbial communities. ISME Journal, 2012, 6, 343-351.	9.8	2,051
71	Patterns and architecture of genomic islands in marine bacteria. BMC Genomics, 2012, 13, 347.	2.8	84
72	Differential photoinhibition of bacterial and archaeal ammonia oxidation. FEMS Microbiology Letters, 2012, 327, 41-46.	1.8	245

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73	Winter to spring changes in the slush bacterial community composition of a high mountain lake (Lake Tj ETQq1 1 0.784314 rgBT / Ov	2.4	15
74	ENDOSYMBIOTIC CALCIFYING BACTERIA: A NEW CUE TO THE ORIGIN OF CALCIFICATION IN METAZOA? Evolution; International Journal of Organic Evolution, 2012, 66, 2993-2999.	2.3	45
75	Exploration of community traits as ecological markers in microbial metagenomes. Molecular Ecology, 2012, 21, 1909-1917.	3.9	84
76	Genetic diversity of planktonic eukaryotes in high mountain lakes (Central Pyrenees, Spain). Environmental Microbiology, 2012, 14, 2445-2456.	3.8	81
77	Contribution of deep dark fixation processes to overall CO2 incorporation and large vertical changes of microbial populations in stratified karstic lakes. Aquatic Sciences, 2012, 74, 61-75.	1.5	40
78	Habitat-Associated Phylogenetic Community Patterns of Microbial Ammonia Oxidizers. PLoS ONE, 2012, 7, e47330.	2.5	55
79	Biofilm recovery in a wastewater treatment plant influenced stream and spatial segregation of ammonia oxidizing microbial populations. Limnology and Oceanography, 2011, 56, 1054-1064.	3.1	32
80	A close relationship between primary nucleotides sequence structure and the composition of functional genes in the genome of prokaryotes. Molecular Phylogenetics and Evolution, 2011, 61, 650-658.	2.7	22
81	Phylogenetic ecology of widespread uncultured clades of the Kingdom Euryarchaeota. Molecular Ecology, 2011, 20, 1988-1996.	3.9	36
82	Active bacteria and archaea cells fixing bicarbonate in the dark along the water column of a stratified eutrophic lagoon. FEMS Microbiology Ecology, 2011, 77, 370-384.	2.7	31
83	Maintenance of previously uncultured freshwater archaea from anoxic waters under laboratory conditions. Antonie Van Leeuwenhoek, 2011, 99, 403-408.	1.7	6
84	Sodium Dodecyl Sulfate-Polyacrylamide Gel Protein Electrophoresis of Freshwater Photosynthetic Sulfur Bacteria. Current Microbiology, 2011, 62, 111-116.	2.2	2
85	Euxinic Freshwater Hypolimnia Promote Bacterial Endemicity in Continental Areas. Microbial Ecology, 2011, 61, 465-472.	2.8	46
86	Seasonal Changes of Freshwater Ammonia-Oxidizing Archaeal Assemblages and Nitrogen Species in Oligotrophic Alpine Lakes. Applied and Environmental Microbiology, 2011, 77, 1937-1945.	3.1	98
87	Exploring the Links between Natural Products and Bacterial Assemblages in the Sponge <i>Aplysina aerophoba</i> . Applied and Environmental Microbiology, 2011, 77, 862-870.	3.1	54
88	Inter-annual recurrence of archaeal assemblages in the coastal NW Mediterranean Sea (Blanes Bay) Tj ETQq0 0 0 rgBT / Overlock 10 Tf	3.1	131
89	T-RFPred: a nucleotide sequence size prediction tool for microbial community description based on terminal-restriction fragment length polymorphism chromatograms. BMC Microbiology, 2010, 10, 262.	3.3	8
90	Global ecological patterns in uncultured Archaea. ISME Journal, 2010, 4, 182-190.	9.8	406

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91	Hydrography shapes bacterial biogeography of the deep Arctic Ocean. ISME Journal, 2010, 4, 564-576.	9.8	179
92	High bicarbonate assimilation in the dark by Arctic bacteria. ISME Journal, 2010, 4, 1581-1590.	9.8	131
93	Global phylogenetic community structure and $\beta$ -diversity patterns in surface bacterioplankton metacommunities. Aquatic Microbial Ecology, 2010, 59, 1-10.	1.8	195
94	Vertical Distribution of Ammonia-Oxidizing Crenarchaeota and Methanogens in the Epipelagic Waters of Lake Kivu (Rwanda-Democratic Republic of the Congo). Applied and Environmental Microbiology, 2010, 76, 6853-6863.	3.1	81
95	A close link between bacterial community composition and environmental heterogeneity in maritime Antarctic lakes. International Microbiology, 2010, 13, 67-77.	2.4	32
96	Vertical distribution of planktonic autotrophic thiobacilli and dark CO <sub>2</sub> fixation rates in lakes with oxygen-sulfide interfaces. Aquatic Microbial Ecology, 2010, 59, 217-228.	1.8	18
97	Potential Effect of Freshwater Virus on the Structure and Activity of Bacterial Communities in the Marennes-Oléron Bay (France). Microbial Ecology, 2009, 57, 295-306.	2.8	24
98	Bacterial "cosmopolitanism" and importance of local environmental factors for community composition in remote high-altitude lakes. Freshwater Biology, 2009, 54, 994-1005.	2.4	88
99	Unique archaeal assemblages in the Arctic Ocean unveiled by massively parallel tag sequencing. ISME Journal, 2009, 3, 860-869.	9.8	163
100	Spatial comparison of total vs. active bacterial populations by coupling genetic fingerprinting and clone library analyses in the NW Mediterranean Sea. FEMS Microbiology Ecology, 2009, 67, 30-42.	2.7	27
101	High similarity between bacterioneuston and airborne bacterial community compositions in a high mountain lake area. FEMS Microbiology Ecology, 2009, 67, 219-228.	2.7	75
102	Viability and potential for immigration of airborne bacteria from Africa that reach high mountain lakes in Europe. Environmental Microbiology, 2009, 11, 1612-1623.	3.8	141
103	Ecology of the rare microbial biosphere of the Arctic Ocean. Proceedings of the National Academy of Sciences of the United States of America, 2009, 106, 22427-22432.	7.1	488
104	Effect of Saharan dust inputs on bacterial activity and community composition in Mediterranean lakes and reservoirs. Limnology and Oceanography, 2009, 54, 869-879.	3.1	111
105	Novelty and spatio-temporal heterogeneity in the bacterial diversity of hypersaline Lake Tebenquiche (Salar de Atacama). Extremophiles, 2008, 12, 491-504.	2.3	118
106	High archaeal richness in the water column of a freshwater sulfurous karstic lake along an interannual study. FEMS Microbiology Ecology, 2008, 66, 331-342.	2.7	81
107	A hotspot for cold crenarchaeota in the neuston of high mountain lakes. Environmental Microbiology, 2008, 10, 1080-1086.	3.8	97
108	Fingerprinting the genetic diversity of the biotin carboxylase gene ( <i>accC</i> ) in aquatic ecosystems as a potential marker for studies of carbon dioxide assimilation in the dark. Environmental Microbiology, 2008, 10, 2527-2536.	3.8	31



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109	Ecophysiological significance of scale-dependent patterns in prokaryotic genomes unveiled by a combination of statistic and genometric analyses. <i>Genomics</i> , 2008, 91, 538-543.	2.9	9
110	Carbon dioxide fixation in the dark by photosynthetic bacteria in sulfide-rich stratified lakes with oxic-anoxic interfaces. <i>Limnology and Oceanography</i> , 2008, 53, 1193-1203.	3.1	57
111	Flow cytometric identification and enumeration of photosynthetic sulfur bacteria and potential for ecophysiological studies at the single-cell level. <i>Environmental Microbiology</i> , 2007, 9, 1969-1985.	3.8	38
112	DOES ECOSYSTEM SIZE DETERMINE AQUATIC BACTERIA RICHNESS? REPLY. <i>Ecology</i> , 2007, 88, 253-255.	3.2	8
113	Experimental test of bacteria-phytoplankton coupling in the Southern Ocean. <i>Limnology and Oceanography</i> , 2005, 50, 1844-1854.	3.1	85
114	Molecular characterization of microbial populations in a low-grade copper ore bioleaching test heap. <i>Hydrometallurgy</i> , 2005, 80, 241-253.	4.3	134
115	A survey on bacteria inhabiting the sea surface microlayer of coastal ecosystems. <i>FEMS Microbiology Ecology</i> , 2005, 54, 269-280.	2.7	133
116	Different Marine Heterotrophic Nanoflagellates Affect Differentially the Composition of Enriched Bacterial Communities. <i>Microbial Ecology</i> , 2005, 49, 474-485.	2.8	19
117	Partitioning of CO <sub>2</sub> Incorporation Among Planktonic Microbial Guilds and Estimation of In Situ Specific Growth Rates. <i>Microbial Ecology</i> , 2005, 50, 230-241.	2.8	32
118	Catalyzed Reported Deposition-Fluorescence In Situ Hybridization Protocol To Evaluate Phagotrophy in Mixotrophic Protists. <i>Applied and Environmental Microbiology</i> , 2005, 71, 7321-7326.	3.1	25
119	DOES ECOSYSTEM SIZE DETERMINE AQUATIC BACTERIAL RICHNESS?. <i>Ecology</i> , 2005, 86, 1715-1722.	3.2	238
120	Distribution of prokaryotic genetic diversity in athalassohaline lakes of the Atacama Desert, Northern Chile. <i>FEMS Microbiology Ecology</i> , 2004, 48, 57-69.	2.7	163
121	High-diversity biofilm for the oxidation of sulfide-containing effluents. <i>Applied Microbiology and Biotechnology</i> , 2004, 64, 726-734.	3.6	45
122	Diversity of planktonic photoautotrophic microorganisms along a salinity gradient as depicted by microscopy, flow cytometry, pigment analysis and DNA-based methods. <i>FEMS Microbiology Ecology</i> , 2004, 49, 281-293.	2.7	98
123	Comparison of samplers for the biological characterization of the sea surface microlayer. <i>Limnology and Oceanography: Methods</i> , 2004, 2, 213-225.	2.0	101
124	Microbial Ecology of an Extreme Acidic Environment, the Tinto River. <i>Applied and Environmental Microbiology</i> , 2003, 69, 4853-4865.	3.1	403
125	Microheterogeneity in 16S Ribosomal DNA-Defined Bacterial Populations from a Stratified Planktonic Environment Is Related to Temporal Changes and to Ecological Adaptations. <i>Applied and Environmental Microbiology</i> , 2002, 68, 1706-1714.	3.1	124
126	A transplant experiment to identify the factors controlling bacterial abundance, activity, production, and community composition in a eutrophic canyon-shaped reservoir. <i>Limnology and Oceanography</i> , 2002, 47, 62-77.	3.1	104



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127	Changes in archaeal, bacterial and eukaryal assemblages along a salinity gradient by comparison of genetic fingerprinting methods in a multipond solar saltern. <i>Environmental Microbiology</i> , 2002, 4, 338-348.	3.8	433
128	Prokaryotic genetic diversity throughout the salinity gradient of a coastal solar saltern. <i>Environmental Microbiology</i> , 2002, 4, 349-360.	3.8	287
129	Changes in marine bacterioplankton phylogenetic composition during incubations designed to measure biogeochemically significant parameters. <i>Limnology and Oceanography</i> , 2001, 46, 1181-1188.	3.1	162
130	In Situ Assessment on the Physiological State of Purple and Green Sulfur Bacteria through the Analyses of Pigment and 5S rRNA Content. <i>Microbial Ecology</i> , 2001, 42, 427-437.	2.8	13
131	Primary production in estuarine oxic/anoxic interfaces: contribution of microbial dark CO <sub>2</sub> fixation in the Ebro River Salt Wedge Estuary. <i>Marine Ecology - Progress Series</i> , 2001, 215, 49-56.	1.9	31
132	Comparison of pure cultures and natural assemblages of planktonic photosynthetic sulfur bacteria by low molecular mass RNA fingerprinting. <i>FEMS Microbiology Ecology</i> , 2000, 32, 25-34.	2.7	17
133	5S rRNA fingerprints of marine bacteria, halophilic archaea and natural prokaryotic assemblages along a salinity gradient. <i>FEMS Microbiology Ecology</i> , 2000, 34, 113-119.	2.7	39
134	Identification of and Spatio-Temporal Differences between Microbial Assemblages from Two Neighboring Sulfurous Lakes: Comparison by Microscopy and Denaturing Gradient Gel Electrophoresis. <i>Applied and Environmental Microbiology</i> , 2000, 66, 499-508.	3.1	392
135	Bacterial Community Structure Associated with a Dimethylsulfoniopropionate-Producing North Atlantic Algal Bloom. <i>Applied and Environmental Microbiology</i> , 2000, 66, 4237-4246.	3.1	402
136	5S rRNA fingerprints of marine bacteria, halophilic archaea and natural prokaryotic assemblages along a salinity gradient. <i>FEMS Microbiology Ecology</i> , 2000, 34, 113-119.	2.7	3
137	Comparison of pure cultures and natural assemblages of planktonic photosynthetic sulfur bacteria by low molecular mass RNA fingerprinting. <i>FEMS Microbiology Ecology</i> , 2000, 32, 25-34.	2.7	0
138	Identification of phototrophic sulfur bacteria through the analysis of lmwRNA band patterns. <i>Archives of Microbiology</i> , 1998, 170, 269-278.	2.2	13