

# Master recyclers: features and functions of bacteria associated with phytoplankton blooms

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Citation Report

#	ARTICLE	IF	CITATIONS
1	Draft Genome Sequence of <i>Sulfitobacter</i> sp. CB2047, a Member of the <i>Roseobacter</i> Clade of Marine Bacteria, Isolated from an <i>Emiliania huxleyi</i> Bloom. <i>Genome Announcements</i> , 2014, 2, .	0.8	12
2	Spatial and temporal variations in environmental variables in relation to phytoplankton composition and biomass in coral reef areas around Unguja, Zanzibar, Tanzania. <i>SpringerPlus</i> , 2015, 4, 646.	1.2	16
3	Hidden biosphere in an oxygen-deficient Atlantic open-ocean eddy: future implications of ocean deoxygenation on primary production in the eastern tropical North Atlantic. <i>Biogeosciences</i> , 2015, 12, 7467-7482.	3.3	29
4	In Silico Analysis of the Metabolic Potential and Niche Specialization of Candidate Phylum "Latescibacteria" (WS3). <i>PLoS ONE</i> , 2015, 10, e0127499.	2.5	102
5	Non-Selective Evolution of Growing Populations. <i>PLoS ONE</i> , 2015, 10, e0134300.	2.5	17
6	<i>Phaeobacter</i> sp. Strain Y4I Utilizes Two Separate Cell-to-Cell Communication Systems To Regulate Production of the Antimicrobial Indigoidine. <i>Applied and Environmental Microbiology</i> , 2015, 81, 1417-1425.	3.1	19
7	How do divergent ecological strategies emerge among marine bacterioplankton lineages?. <i>Trends in Microbiology</i> , 2015, 23, 577-584.	7.7	65
8	Marine microbial community dynamics and their ecological interpretation. <i>Nature Reviews Microbiology</i> , 2015, 13, 133-146.	28.6	681
9	Variation in the Presence of Anti-Batrachochytrium dendrobatidis Bacteria of Amphibians Across Life Stages and Elevations in Ecuador. <i>EcoHealth</i> , 2015, 12, 310-319.	2.0	42
10	Potential DMSP-degrading <i>Roseobacter</i> clade dominates endosymbiotic microflora of <i>Pyrodinium bahamense</i> var. <i>compressum</i> (Dinophyceae) in vitro. <i>Archives of Microbiology</i> , 2015, 197, 965-971.	2.2	15
11	Prokaryotic assemblages and metagenomes in pelagic zones of the South China Sea. <i>BMC Genomics</i> , 2015, 16, 219.	2.8	33
12	Changes in the <i>Synechococcus</i> Assemblage Composition at the Surface of the East China Sea Due to Flooding of the Changjiang River. <i>Microbial Ecology</i> , 2015, 70, 677-688.	2.8	17
13	Exploring mutualistic interactions between microalgae and bacteria in the omics age. <i>Current Opinion in Plant Biology</i> , 2015, 26, 147-153.	7.1	179
14	Annual dynamics of North Sea bacterioplankton: seasonal variability superimposes short-term variation. <i>FEMS Microbiology Ecology</i> , 2015, 91, fiv099.	2.7	45
15	Roles of diatom nutrient stress and species identity in determining the short- and long-term bioavailability of diatom exudates to bacterioplankton. <i>Marine Chemistry</i> , 2015, 177, 335-348.	2.3	28
16	Succession within the prokaryotic communities during the VAHINE mesocosms experiment in the New Caledonia lagoon. <i>Biogeosciences</i> , 2016, 13, 2319-2337.	3.3	16
17	<i>Marinobacter</i> Dominates the Bacterial Community of the <i>Ostreococcus tauri</i> Phycosphere in Culture. <i>Frontiers in Microbiology</i> , 2016, 7, 1414.	3.5	43
18	Recurring patterns in bacterioplankton dynamics during coastal spring algae blooms. <i>ELife</i> , 2016, 5, e11888.	6.0	414

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19	Autochthonous Dissolved Organic Matter Drives Bacterial Community Composition during a Bloom of Filamentous Cyanobacteria. <i>Frontiers in Marine Science</i> , 2016, 3, .	2.5	14
20	Coupled Response of Bacterial Production to a Wind-Induced Fall Phytoplankton Bloom and Sediment Resuspension in the Chukchi Sea Shelf, Western Arctic Ocean. <i>Frontiers in Marine Science</i> , 2016, 3, .	2.5	24
21	Short-Term Dynamics of North Sea Bacterioplankton-Dissolved Organic Matter Coherence on Molecular Level. <i>Frontiers in Microbiology</i> , 2016, 7, 321.	3.5	48
22	Spatio-Temporal Interdependence of Bacteria and Phytoplankton during a Baltic Sea Spring Bloom. <i>Frontiers in Microbiology</i> , 2016, 7, 517.	3.5	90
23	Bacterioplankton Biogeography of the Atlantic Ocean: A Case Study of the Distance-Decay Relationship. <i>Frontiers in Microbiology</i> , 2016, 7, 590.	3.5	45
24	Co-occurrence Analysis of Microbial Taxa in the Atlantic Ocean Reveals High Connectivity in the Free-Living Bacterioplankton. <i>Frontiers in Microbiology</i> , 2016, 7, 649.	3.5	152
25	Identification of Free-Living and Particle-Associated Microbial Communities Present in Hadal Regions of the Mariana Trench. <i>Frontiers in Microbiology</i> , 2016, 7, 665.	3.5	99
26	Gene Flow Across Genus Barriers – Conjugation of <i>Dinoroseobacter shibae</i> ’s 191-kb Killer Plasmid into <i>Phaeobacter inhibens</i> and AHL-mediated Expression of Type IV Secretion Systems. <i>Frontiers in Microbiology</i> , 2016, 7, 742.	3.5	24
27	Genetic Manipulation of Competition for Nitrate between Heterotrophic Bacteria and Diatoms. <i>Frontiers in Microbiology</i> , 2016, 7, 880.	3.5	55
28	A Metaproteomic Analysis of the Response of a Freshwater Microbial Community under Nutrient Enrichment. <i>Frontiers in Microbiology</i> , 2016, 7, 1172.	3.5	28
29	Phytoplankton-Associated Bacterial Community Composition and Succession during Toxic Diatom Bloom and Non-Bloom Events. <i>Frontiers in Microbiology</i> , 2016, 7, 1433.	3.5	60
30	Bacterial Communities Associated with Four Cyanobacterial Genera Display Structural and Functional Differences: Evidence from an Experimental Approach. <i>Frontiers in Microbiology</i> , 2016, 7, 1662.	3.5	57
31	Seasonal Succession of Free-Living Bacterial Communities in Coastal Waters of the Western Antarctic Peninsula. <i>Frontiers in Microbiology</i> , 2016, 7, 1731.	3.5	53
32	Complete genome sequence of bacteriophage P2559Y, a marine phage that infects <i>Croceibacter atlanticus</i> HTCC2559. <i>Marine Genomics</i> , 2016, 29, 35-38.	1.1	20
33	Biological hot spots and the accumulation of marine dissolved organic matter in a highly productive ocean margin. <i>Limnology and Oceanography</i> , 2016, 61, 1287-1300.	3.1	40
34	Viral infection of the marine alga <i>Emiliania huxleyi</i> triggers lipidome remodeling and induces the production of highly saturated triacylglycerol. <i>New Phytologist</i> , 2016, 210, 88-96.	7.3	98
35	Trace Metal Acquisition by Marine Heterotrophic Bacterioplankton with Contrasting Trophic Strategies. <i>Applied and Environmental Microbiology</i> , 2016, 82, 1613-1624.	3.1	51
36	Copiotrophic marine bacteria are associated with strong iron-binding ligand production during phytoplankton blooms. <i>Limnology and Oceanography Letters</i> , 2016, 1, 36-43.	3.9	25

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37	Spatiotemporal variation of the bacterioplankton community in the German Bight: from estuarine to offshore regions. <i>Helgoland Marine Research</i> , 2016, 70, .	1.3	17
38	Selective growth promotion of bloom-forming raphidophyte <i>Heterosigma akashiwo</i> by a marine bacterial strain. <i>Harmful Algae</i> , 2016, 60, 150-156.	4.8	8
39	Bacterial and protist community changes during a phytoplankton bloom. <i>Limnology and Oceanography</i> , 2016, 61, 198-213.	3.1	22
40	Regrowth in ship's ballast water tanks: Think again!. <i>Marine Pollution Bulletin</i> , 2016, 109, 46-48.	5.0	28
41	Oceanic fronts: transition zones for bacterioplankton community composition. <i>Environmental Microbiology Reports</i> , 2016, 8, 132-138.	2.4	65
42	Ultrastructural and Single-Cell-Level Characterization Reveals Metabolic Versatility in a Microbial Eukaryote Community from an Ice-Covered Antarctic Lake. <i>Applied and Environmental Microbiology</i> , 2016, 82, 3659-3670.	3.1	36
43	Contribution of airborne microbes to bacterial production and N <sub>2</sub> fixation in seawater upon aerosol deposition. <i>Geophysical Research Letters</i> , 2016, 43, 719-727.	4.0	32
44	Biological pretreatments of microalgal biomass for gaseous biofuel production and the potential use of rumen microorganisms: A review. <i>Algal Research</i> , 2016, 18, 341-351.	4.6	57
46	Quorum Sensing and Quorum Quenching in the Phycosphere of Phytoplankton: a Case of Chemical Interactions in Ecology. <i>Journal of Chemical Ecology</i> , 2016, 42, 1201-1211.	1.8	70
47	Habitat and taxon as driving forces of carbohydrate catabolism in marine heterotrophic bacteria: example of the model algae-associated bacterium <i>Zobellia galactanivorans</i> Dsij <sup>T</sup> . <i>Environmental Microbiology</i> , 2016, 18, 4610-4627.	3.8	131
48	Genomic, physiologic, and proteomic insights into metabolic versatility in <i>Roseobacter</i> clade bacteria isolated from deep-sea water. <i>Scientific Reports</i> , 2016, 6, 35528.	3.3	22
49	Pronounced daily succession of phytoplankton, archaea and bacteria following a spring bloom. <i>Nature Microbiology</i> , 2016, 1, 16005.	13.3	384
50	Biogeography and environmental genomics of the <i>Roseobacter</i> -affiliated pelagic CHAB-I-5 lineage. <i>Nature Microbiology</i> , 2016, 1, 16063.	13.3	36
51	A comprehensive insight into functional profiles of free-living microbial community responses to a toxic <i>Akashiwo sanguinea</i> bloom. <i>Scientific Reports</i> , 2016, 6, 34645.	3.3	25
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54	Response of marine bacterioplankton pH homeostasis gene expression to elevated CO <sub>2</sub> . <i>Nature Climate Change</i> , 2016, 6, 483-487.	18.8	68
55	Maltooligosaccharides in the northwestern Adriatic Sea. <i>Chemistry and Ecology</i> , 2016, 32, 88-102.	1.6	2

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56	Deciphering associations between dissolved organic molecules and bacterial communities in a pelagic marine system. ISME Journal, 2016, 10, 1717-1730.	9.8	155
57	Effects of biochar and compost amendments on soil physico-chemical properties and the total community within a temperate agricultural soil. Applied Soil Ecology, 2016, 98, 243-253.	4.3	199
58	Algae–bacteria interactions: Evolution, ecology and emerging applications. Biotechnology Advances, 2016, 34, 14-29.	11.7	937
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60	The Thermodynamics of Marine Biogeochemical Cycles: Lotka Revisited. Annual Review of Marine Science, 2016, 8, 333-356.	11.6	28
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62	Marine bacterial community structure resilience to changes in protist predation under phytoplankton bloom conditions. ISME Journal, 2016, 10, 568-581.	9.8	65
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66	Deep-sequencing of the bacterial microbiota in commercial-scale recirculating and semi-closed aquaculture systems for Atlantic salmon post-smolt production. Aquacultural Engineering, 2017, 78, 50-62.	3.1	83
67	Phylogenomics of <i>Rhodobacteraceae</i> reveals evolutionary adaptation to marine and non-marine habitats. ISME Journal, 2017, 11, 1483-1499.	9.8	283
68	Relationship between dissolved organic carbon and bacterial community in the coastal waters of Incheon, Korea. Oceanological and Hydrobiological Studies, 2017, 46, 50-61.	0.7	7
69	<i>Prochlorococcus</i> in the lab and in silico: The importance of representing exudation. Limnology and Oceanography, 2017, 62, 818-835.	3.1	26
70	Soda pans of the Pannonian steppe harbor unique bacterial communities adapted to multiple extreme conditions. Extremophiles, 2017, 21, 639-649.	2.3	44
71	The environmental and host-associated bacterial microbiota of Arctic seawater-farmed Atlantic salmon with ulcerative disorders. Journal of Fish Diseases, 2017, 40, 1645-1663.	1.9	74
72	Cascading influence of inorganic nitrogen sources on DOM production, composition, lability and microbial community structure in the open ocean. Environmental Microbiology, 2017, 19, 3450-3464.	3.8	34
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75	Zooming in on the phycosphere: the ecological interface for phytoplankton-bacteria relationships. <i>Nature Microbiology</i> , 2017, 2, 17065.	13.3	727
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77	Isolation of a bacterial strain, <i>Acinetobacter</i> sp. from centrate wastewater and study of its cooperation with algae in nutrients removal. <i>Bioresource Technology</i> , 2017, 235, 59-69.	9.6	69
78	Leucine, starch and bicarbonate utilization by specific bacterial groups in surface shelf waters off <sc>G</sc>alicia (<sc>NW</sc><sc>S</sc>pain). <i>Environmental Microbiology</i> , 2017, 19, 2379-2390.	3.8	7
79	Electricity and biomass production in a bacteria- <i>Chlorella</i> based microbial fuel cell treating wastewater. <i>Journal of Power Sources</i> , 2017, 356, 299-309.	7.8	66
80	Microbial players and processes involved in phytoplankton bloom utilization in the water column of a fast-flowing, river-dominated estuary. <i>MicrobiologyOpen</i> , 2017, 6, e00467.	3.0	18
81	Elevated temperature increases carbon and nitrogen fluxes between phytoplankton and heterotrophic bacteria through physical attachment. <i>ISME Journal</i> , 2017, 11, 641-650.	9.8	60
82	A unique large-scale undergraduate research experience in molecular systems biology for non-mathematics majors. <i>Biochemistry and Molecular Biology Education</i> , 2017, 45, 235-248.	1.2	10
83	Patterns of bacterial diversity in the marine planktonic particulate matter continuum. <i>ISME Journal</i> , 2017, 11, 999-1010.	9.8	128
84	Genomic and physiological analyses of <i>Reinekea forsetii</i> ™ reveal a versatile opportunistic lifestyle during spring algae blooms. <i>Environmental Microbiology</i> , 2017, 19, 1209-1221.	3.8	13
85	Coastal bacterioplankton community response to diatom-derived polysaccharide microgels. <i>Environmental Microbiology Reports</i> , 2017, 9, 151-157.	2.4	52
86	Algal polysaccharide utilisation by saprotrophic planktonic marine fungi. <i>Fungal Ecology</i> , 2017, 30, 135-138.	1.6	55
87	Fungal community dynamics during a marine dinoflagellate ( <i>Noctiluca scintillans</i> ) bloom. <i>Marine Environmental Research</i> , 2017, 131, 183-194.	2.5	46
88	Marine microbiology: Roommates in space and time. <i>Nature Microbiology</i> , 2017, 2, 17122.	13.3	1
89	Strategies and ecological roles of algicidal bacteria. <i>FEMS Microbiology Reviews</i> , 2017, 41, 880-899.	8.6	153
90	Testing the metabolic theory of ecology with marine bacteria: different temperature sensitivity of major phylogenetic groups during the spring phytoplankton bloom. <i>Environmental Microbiology</i> , 2017, 19, 4493-4505.	3.8	39
91	Phylogenetically conserved resource partitioning in the coastal microbial loop. <i>ISME Journal</i> , 2017, 11, 2781-2792.	9.8	82

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94	Identification of unique microbiomes associated with harmful algal blooms caused by <i>Alexandrium fundyense</i> and <i>Dinophysis acuminata</i> . <i>Harmful Algae</i> , 2017, 68, 17-30.	4.8	48
95	Bioprospecting North Atlantic microalgae with fast growth and high polyunsaturated fatty acid (PUFA) content for microalgae-based technologies. <i>Algal Research</i> , 2017, 26, 392-401.	4.6	70
96	Photosynthetic carbon uptake induces autoflocculation of the marine microalga <i>Nannochloropsis oculata</i> . <i>Algal Research</i> , 2017, 26, 302-311.	4.6	42
97	Spatial variability of marine bacterial and archaeal communities along the particulate matter continuum. <i>Molecular Ecology</i> , 2017, 26, 6827-6840.	3.9	42
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99	Effect of Macondo Prospect 252 Oil on Microbiota Associated with Pelagic Sargassum in the Northern Gulf of Mexico. <i>Microbial Ecology</i> , 2017, 73, 91-100.	2.8	19
100	Spatio-Temporal Monitoring and Ecological Significance of Retrievable Pelagic Heterotrophic Bacteria in Kongsfjorden, an Arctic Fjord. <i>Indian Journal of Microbiology</i> , 2017, 57, 116-120.	2.7	10
101	Pyrosequencing reveals specific associations of bacterial clades <i>Roseobacter</i> and <i>Flavobacterium</i> with the harmful dinoflagellate <i>Cochlodinium polykrikoides</i> growing in culture. <i>Marine Ecology</i> , 2017, 38, e12474.	1.1	17
102	Direct Heme Uptake by Phytoplankton-Associated <i>Roseobacter</i> Bacteria. <i>MSystems</i> , 2017, 2, .	3.8	29
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106	Characterization of Potential Polysaccharide Utilization Systems in the Marine Bacteroidetes <i>Gramella flava</i> JLT2011 Using a Multi-Omics Approach. <i>Frontiers in Microbiology</i> , 2017, 8, 220.	3.5	57
107	Bacterial Community Composition and Potential Driving Factors in Different Reef Habitats of the Spermonde Archipelago, Indonesia. <i>Frontiers in Microbiology</i> , 2017, 8, 662.	3.5	22
108	Bacterial Biogeography across the Amazon River-Ocean Continuum. <i>Frontiers in Microbiology</i> , 2017, 8, 882.	3.5	75
109	Exploring Microdiversity in Novel <i>Kordia</i> sp. (Bacteroidetes) with Proteorhodopsin from the Tropical Indian Ocean via Single Amplified Genomes. <i>Frontiers in Microbiology</i> , 2017, 8, 1317.	3.5	7



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110	Composition of Total and Cell-Proliferating Bacterioplankton Community in Early Summer in the North Sea – Roseobacters Are the Most Active Component. <i>Frontiers in Microbiology</i> , 2017, 8, 1771.	3.5	30
111	Gene Expression Analysis of <i>Zobellia galactanivorans</i> during the Degradation of Algal Polysaccharides Reveals both Substrate-Specific and Shared Transcriptome-Wide Responses. <i>Frontiers in Microbiology</i> , 2017, 8, 1808.	3.5	58
112	Insights into Microalga and Bacteria Interactions of Selected Phycosphere Biofilms Using Metagenomic, Transcriptomic, and Proteomic Approaches. <i>Frontiers in Microbiology</i> , 2017, 8, 1941.	3.5	97
113	Seasonal Shifts in Bacterial Community Responses to Phytoplankton-Derived Dissolved Organic Matter in the Western Antarctic Peninsula. <i>Frontiers in Microbiology</i> , 2017, 8, 2117.	3.5	35
114	Glyphosate Shapes a Dinoflagellate-Associated Bacterial Community While Supporting Algal Growth as Sole Phosphorus Source. <i>Frontiers in Microbiology</i> , 2017, 8, 2530.	3.5	42
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117	Spatiotemporal analysis of microbial community dynamics during seasonal stratification events in a freshwater lake (Grand Lake, OK, USA). <i>PLoS ONE</i> , 2017, 12, e0177488.	2.5	47
118	Seasonal variations of the sea surface microlayer at the Boknis Eck Times Series Station (Baltic Sea). <i>Journal of Plankton Research</i> , 2017, 39, 943-961.	1.8	12
119	Non-Redfield, nutrient synergy and flexible internal elemental stoichiometry in a marine bacterium. <i>FEMS Microbiology Ecology</i> , 2017, 93, .	2.7	8
120	Spatio-seasonal variability of chromophoric dissolved organic matter absorption and responses to photobleaching in a large shallow temperate lake. <i>Biogeosciences</i> , 2017, 14, 1215-1233.	3.3	18
121	Microbial dynamics during harmful dinoflagellate <i>Ostreopsis</i> cf. <i>ovata</i> growth: Bacterial succession and viral abundance pattern. <i>MicrobiologyOpen</i> , 2018, 7, e00584.	3.0	27
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123	Organic matter bioavailability in tropical coastal waters: The Great Barrier Reef. <i>Limnology and Oceanography</i> , 2018, 63, 1015-1035.	3.1	40
124	A multi-step approach for testing non-toxic amphiphilic antifouling coatings against marine microfouling at different levels of biological complexity. <i>Journal of Microbiological Methods</i> , 2018, 146, 104-114.	1.6	12
125	Combined diet of yeast, fermented soybean meal, and microparticulate as larval feed in extensive rearing systems for seed production of the oriental river prawn <i>Macrobrachium nipponense</i> . <i>Aquaculture International</i> , 2018, 26, 757-772.	2.2	1
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127	Spatiotemporal patterns of phytoplankton composition and abundance in the Maryland Coastal Bays: The influence of freshwater discharge and anthropogenic activities. <i>Estuarine, Coastal and Shelf Science</i> , 2018, 207, 119-131.	2.1	18



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129	Elucidation of the bacterial communities associated with the harmful microalgae <i>Alexandrium tamarense</i> and <i>Cochlodinium polykrikoides</i> using nanopore sequencing. Scientific Reports, 2018, 8, 5323.	3.3	43
130	Solar-panel and parasol strategies shape the proteorhodopsin distribution pattern in marine Flavobacteria. ISME Journal, 2018, 12, 1329-1343.	9.8	18
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132	Impact of nutrient enrichment on productivity of coastal water along the SE Mediterranean shore of Israel - A bioassay approach. Marine Pollution Bulletin, 2018, 127, 559-567.	5.0	39
133	Recurrent patterns of microdiversity in a temperate coastal marine environment. ISME Journal, 2018, 12, 237-252.	9.8	135
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137	Photoreactivity of riverine and phytoplanktonic dissolved organic matter and its effects on the dynamics of a bacterial community from the coastal Mediterranean Sea. Progress in Oceanography, 2018, 163, 82-93.	3.2	5
138	Drivers of coastal bacterioplankton community diversity and structure along a nutrient gradient in the East China Sea. Journal of Oceanology and Limnology, 2018, 36, 329-340.	1.3	3
139	Fast-growing algicidal <i>Streptomyces</i> sp. U3 and its potential in harmful algal bloom controls. Journal of Hazardous Materials, 2018, 341, 138-149.	12.4	37
140	The Ecology of One Cosmopolitan, One Newly Introduced and One Occasionally Advection Species from the Genus <i>Skeletonema</i> in a Highly Structured Ecosystem, the Northern Adriatic. Microbial Ecology, 2018, 75, 674-687.	2.8	18
141	The role of groundwater discharge fluxes on Si:P ratios in a major tributary to Lake Erie. Science of the Total Environment, 2018, 622-623, 814-824.	8.0	5
142	100 Days of marine <i>Synechococcus</i> " <i>Ruegeria pomeroyi</i> interaction: A detailed analysis of the exoproteome. Environmental Microbiology, 2018, 20, 785-799.	3.8	19
143	Metabolic versatility of a novel N <sub>2</sub> -fixing Alphaproteobacterium isolated from a marine oxygen minimum zone. Environmental Microbiology, 2018, 20, 755-768.	3.8	29
144	Dynamics of Heterotrophic Bacterial Assemblages within <i>Synechococcus</i> Cultures. Applied and Environmental Microbiology, 2018, 84, .	3.1	52
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