

Bacterial diversity, community structure and potential salinity gradient

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Citation Report

#	ARTICLE	IF	CITATIONS
1	Stability of Bacterial Composition and Activity in Different Salinity Waters in the Dynamic Patos Lagoon Estuary: Evidence from a Lagrangian-Like Approach. <i>Microbial Ecology</i> , 2013, 66, 551-562.	2.8	13
2	Growth and distribution patterns of <i>Roseobacter/Rhodobacter</i> , SAR11, and <i>Bacteroidetes</i> lineages in the Southern Ocean. <i>Polar Biology</i> , 2013, 36, 691-704.	1.2	18
3	Freshwater prokaryote and virus communities can adapt to a controlled increase in salinity through changes in their structure and interactions. <i>Estuarine, Coastal and Shelf Science</i> , 2013, 133, 58-66.	2.1	19
4	Detection of Fecal Bacteria and Source Tracking Identifiers in Environmental Waters Using rRNA-Based RT-qPCR and rDNA-Based qPCR Assays. <i>Environmental Science & Technology</i> , 2013, 47, 13611-13620.	10.0	58
5	Future-Generation Sequencing and Clinical Microbiology. <i>Clinics in Laboratory Medicine</i> , 2013, 33, 685-704.	1.4	3
6	Evaluating rRNA as an indicator of microbial activity in environmental communities: limitations and uses. <i>ISME Journal</i> , 2013, 7, 2061-2068.	9.8	661
7	Structure of the rare archaeal biosphere and seasonal dynamics of active ecotypes in surface coastal waters. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2013, 110, 6004-6009.	7.1	234
8	Spatial variability of particle-attached and free-living bacterial diversity in surface waters from the Mackenzie River to the Beaufort Sea (Canadian Arctic). <i>Biogeosciences</i> , 2013, 10, 2747-2759.	3.3	110
9	Functional gene pyrosequencing and network analysis: an approach to examine the response of denitrifying bacteria to increased nitrogen supply in salt marsh sediments. <i>Frontiers in Microbiology</i> , 2013, 4, 342.	3.5	52
10	Functional Tradeoffs Underpin Salinity-Driven Divergence in Microbial Community Composition. <i>PLoS ONE</i> , 2014, 9, e89549.	2.5	184
11	Network topology reveals high connectance levels and few key microbial genera within soils. <i>Frontiers in Environmental Science</i> , 2014, 2, .	3.3	226
13	Diversity and abundance of "Pelagibacterales" (SAR11) in the Baltic Sea salinity gradient. <i>Systematic and Applied Microbiology</i> , 2014, 37, 601-604.	2.8	58
14	Connecting the dots: linking nitrogen cycle gene expression to nitrogen fluxes in marine sediment mesocosms. <i>Frontiers in Microbiology</i> , 2014, 5, 429.	3.5	44
15	Late winter under ice pelagic microbial communities in the high Arctic Ocean and the impact of short-term exposure to elevated CO ₂ levels. <i>Frontiers in Microbiology</i> , 2014, 5, 490.	3.5	21
16	Diversity and geochemical structuring of bacterial communities along a salinity gradient in a carbonate aquifer subject to seawater intrusion. <i>FEMS Microbiology Ecology</i> , 2014, 90, 922-934.	2.7	38
17	Rare but active taxa contribute to community dynamics of benthic biofilms in glacier-fed streams. <i>Environmental Microbiology</i> , 2014, 16, 2514-2524.	3.8	101
18	Molecular characterization of the planktonic microorganisms in water of two mountain brackish lakes. <i>Journal of Basic Microbiology</i> , 2014, 54, 509-520.	3.3	12
19	<i>Nitrospina</i> -like bacteria are the main drivers of nitrite oxidation in the seasonal upwelling area of the eastern South Pacific (Central Chile 36°S). <i>Environmental Microbiology Reports</i> , 2014, 6, 565-573.	2.4	54

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20	Diurnal expression of SAR11 proteorhodopsin and 16S rRNA genes in coastal North Atlantic waters. <i>Aquatic Microbial Ecology</i> , 2014, 73, 185-194.	1.8	10
21	Impact of freshwater inflow on bacterial abundance and activity in the estuarine system Ria de Aveiro. <i>Estuarine, Coastal and Shelf Science</i> , 2014, 138, 107-120.	2.1	20
22	Effects of allylthiourea, salinity, and pH on ammonia/ammonium-oxidizing prokaryotes in mangrove sediment incubated in laboratory microcosms. <i>Applied Microbiology and Biotechnology</i> , 2014, 98, 3257-3274.	3.6	82
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24	Changes in free-living bacterial community diversity reflect the magnitude of environmental variability. <i>FEMS Microbiology Ecology</i> , 2014, 87, 291-301.	2.7	40
25	Biofouling and Microbial Communities in Membrane Distillation and Reverse Osmosis. <i>Environmental Science & Technology</i> , 2014, 48, 13155-13164.	10.0	75
26	Drivers shaping the diversity and biogeography of total and active bacterial communities in the South China Sea. <i>Molecular Ecology</i> , 2014, 23, 2260-2274.	3.9	194
27	Master recyclers: features and functions of bacteria associated with phytoplankton blooms. <i>Nature Reviews Microbiology</i> , 2014, 12, 686-698.	28.6	947
28	Rare taxa have potential to make metabolic contributions in enhanced biological phosphorus removal ecosystems. <i>Environmental Microbiology</i> , 2015, 17, 4979-4993.	3.8	68
29	MICCA: a complete and accurate software for taxonomic profiling of metagenomic data. <i>Scientific Reports</i> , 2015, 5, 9743.	3.3	228
30	The green impact: bacterioplankton response toward a phytoplankton spring bloom in the southern North Sea assessed by comparative metagenomic and metatranscriptomic approaches. <i>Frontiers in Microbiology</i> , 2015, 6, 805.	3.5	82
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34	Initial community and environment determine the response of bacterial communities to dispersant and oil contamination. <i>Marine Pollution Bulletin</i> , 2015, 90, 106-114.	5.0	22
35	Marine Sponges – <i>Molecular Biology and Biotechnology</i> , 2015, , 219-254.		5
36	Influence of freshwater discharge on the microbial degradation processes of dissolved organic nitrogen in a subtropical estuary. <i>Antonie Van Leeuwenhoek</i> , 2015, 107, 613-632.	1.7	15
37	Seasonal dynamics of active SAR11 ecotypes in the oligotrophic Northwest Mediterranean Sea. <i>ISME Journal</i> , 2015, 9, 347-360.	9.8	93

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38	Bacterial Community Composition and Physiological Shifts Associated with the El Niño Southern Oscillation (ENSO) in the Patos Lagoon Estuary. <i>Microbial Ecology</i> , 2015, 69, 525-534.	2.8	4
39	Distribution and diversity of bacterioplankton communities in subtropical seawater around Xiamen Island, China. <i>Microbiological Research</i> , 2015, 175, 16-23.	5.3	20
40	Microbial rRNA:rDNA gene ratios may be unexpectedly low due to extracellular DNA preservation in soils. <i>Journal of Microbiological Methods</i> , 2015, 115, 112-120.	1.6	55
41	16S rRNA-based bacterial community structure is a sensitive indicator of soil respiration activity. <i>Journal of Soils and Sediments</i> , 2015, 15, 1987-1990.	3.0	16
42	Microbial metagenomics in the Baltic Sea: Recent advancements and prospects for environmental monitoring. <i>Ambio</i> , 2015, 44, 439-450.	5.5	33
43	Phylogenetic shifts of bacterioplankton community composition along the Pearl Estuary: the potential impact of hypoxia and nutrients. <i>Frontiers in Microbiology</i> , 2015, 6, 64.	3.5	135
44	Bacterial community structure across environmental gradients in permafrost thaw ponds: methanotroph-rich ecosystems. <i>Frontiers in Microbiology</i> , 2015, 6, 192.	3.5	88
45	Vertical Distribution of Functional Potential and Active Microbial Communities in Meromictic Lake Kivu. <i>Microbial Ecology</i> , 2015, 70, 596-611.	2.8	52
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47	Permeable Reactive Barriers Designed To Mitigate Eutrophication Alter Bacterial Community Composition and Aquifer Redox Conditions. <i>Applied and Environmental Microbiology</i> , 2015, 81, 7114-7124.	3.1	21
48	Annual dynamics of North Sea bacterioplankton: seasonal variability superimposes short-term variation. <i>FEMS Microbiology Ecology</i> , 2015, 91, fiv099.	2.7	45
49	Comparing extracellular enzymatic hydrolysis between plain peptides and their corresponding analogs in the northern Gulf of Mexico Mississippi River plume. <i>Marine Chemistry</i> , 2015, 177, 398-407.	2.3	16
50	Salt effects on the soil microbial decomposer community and their role in organic carbon cycling: A review. <i>Soil Biology and Biochemistry</i> , 2015, 81, 108-123.	8.8	383
51	Effects of salinization and crude oil contamination on soil bacterial community structure in the Yellow River Delta region, China. <i>Applied Soil Ecology</i> , 2015, 86, 165-173.	4.3	95
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54	Spatial-Temporal Changes of Bacterioplankton Community along an Exorheic River. <i>Frontiers in Microbiology</i> , 2016, 7, 250.	3.5	32
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57	Bacterial Dormancy Is More Prevalent in Freshwater than Hypersaline Lakes. <i>Frontiers in Microbiology</i> , 2016, 7, 853.	3.5	39
58	Physical Factors Correlate to Microbial Community Structure and Nitrogen Cycling Gene Abundance in a Nitrate Fed Eutrophic Lagoon. <i>Frontiers in Microbiology</i> , 2016, 7, 1691.	3.5	17
59	Bacterial Active Community Cycling in Response to Solar Radiation and Their Influence on Nutrient Changes in a High-Altitude Wetland. <i>Frontiers in Microbiology</i> , 2016, 7, 1823.	3.5	43
60	Distinct interacting core taxa in co-occurrence networks enable discrimination of polymicrobial oral diseases with similar symptoms. <i>Scientific Reports</i> , 2016, 6, 30997.	3.3	70
61	Comparison and Interpretation of Taxonomical Structure of Bacterial Communities in Two Types of Lakes on Yun-Gui plateau of China. <i>Scientific Reports</i> , 2016, 6, 30616.	3.3	45
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63	Analysis of the Appendicularia class (subphylum Urochordata) as a possible tool for biomonitoring four estuaries of the tropical region. <i>Environmental Monitoring and Assessment</i> , 2016, 188, 606.	2.7	6
64	Monitoring and managing microbes in aquaculture – Towards a sustainable industry. <i>Microbial Biotechnology</i> , 2016, 9, 576-584.	4.2	169
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66	Distinct distribution patterns of prokaryotes between sediment and water in the Yellow River estuary. <i>Applied Microbiology and Biotechnology</i> , 2016, 100, 9683-9697.	3.6	61
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68	Evaluating digestion efficiency in full-scale anaerobic digesters by identifying active microbial populations through the lens of microbial activity. <i>Scientific Reports</i> , 2016, 6, 34090.	3.3	87
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71	Stability of full-scale engineered ecosystem under disturbance: Response of an activated sludge biological nutrient removal reactor to high flow rate condition. <i>International Biodeterioration and Biodegradation</i> , 2016, 109, 88-95.	3.9	6
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73	Genome Reconstruction from Metagenomic Data Sets Reveals Novel Microbes in the Brackish Waters of the Caspian Sea. <i>Applied and Environmental Microbiology</i> , 2016, 82, 1599-1612.	3.1	59

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75	Growth Rates of Microbes in the Oceans. <i>Annual Review of Marine Science</i> , 2016, 8, 285-309.	11.6	218
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77	Bacterial community structure in intertidal sediments of Fildes Peninsula, maritime Antarctica. <i>Polar Biology</i> , 2017, 40, 339-349.	1.2	28
78	Relationship between dissolved organic carbon and bacterial community in the coastal waters of Incheon, Korea. <i>Oceanological and Hydrobiological Studies</i> , 2017, 46, 50-61.	0.7	7
79	Shifts in soil microbial metabolic activities and community structures along a salinity gradient of irrigation water in a typical arid region of China. <i>Science of the Total Environment</i> , 2017, 598, 64-70.	8.0	81
80	Salinity fluctuation influencing biological adaptation: growth dynamics and Na ⁺ /K ⁺ -ATPase activity in a euryhaline bacterium. <i>Journal of Basic Microbiology</i> , 2017, 57, 617-624.	3.3	4
81	Challenges to Managing Microbial Fecal Pollution in Coastal Environments: Extra-Enteric Ecology and Microbial Exchange Among Water, Sediment, and Air. <i>Current Pollution Reports</i> , 2017, 3, 1-16.	6.6	27
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84	Sediment depth and habitat as predictors of the diversity and composition of sediment bacterial communities in an intertidal estuarine environment. <i>Marine Ecology</i> , 2017, 38, e12411.	1.1	25
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93	Total and active microbial communities in a full-scale system treating wastewater from soy sauce production. <i>International Biodeterioration and Biodegradation</i> , 2017, 123, 206-215.	3.9	19
94	Effect of inoculation of <i>Burkholderia</i> sp. strain SJ98 on bacterial community dynamics and para-nitrophenol, 3-methyl-4-nitrophenol, and 2-chloro-4-nitrophenol degradation in soil. <i>Scientific Reports</i> , 2017, 7, 5983.	3.3	32
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97	The development of permafrost bacterial communities under submarine conditions. <i>Journal of Geophysical Research G: Biogeosciences</i> , 2017, 122, 1689-1704.	3.0	21
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99	Source tracking using microbial community fingerprints: Method comparison with hydrodynamic modelling. <i>Water Research</i> , 2017, 109, 253-265.	11.3	56
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101	Effects of saline water irrigation and fertilization regimes on soil microbial metabolic activity. <i>Journal of Soils and Sediments</i> , 2017, 17, 376-383.	3.0	28
102	Linking Compositional and Functional Predictions to Decipher the Biogeochemical Significance in DFAA Turnover of Abundant Bacterioplankton Lineages in the North Sea. <i>Microorganisms</i> , 2017, 5, 68.	3.6	36
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106	Bacterial Biogeography across the Amazon River-Ocean Continuum. <i>Frontiers in Microbiology</i> , 2017, 8, 882.	3.5	75
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109	Evaluation of the Relationship Between the 18S <i>rRNA</i> / <i>rDNA</i> Ratio and Population Growth in the Marine Diatom <i>Skeletonema tropicum</i> via the Application of an Exogenous Nucleic Acid Standard. <i>Journal of Eukaryotic Microbiology</i> , 2018, 65, 792-803.	1.7	3

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111	Influence of environmental variation on the bacterioplankton community and its loss to viral lysis in the Curonian Lagoon. Estuarine, Coastal and Shelf Science, 2018, 204, 76-85.	2.1	2
112	A missing link in the estuarine nitrogen cycle?: Coupled nitrification-denitrification mediated by suspended particulate matter. Scientific Reports, 2018, 8, 2282.	3.3	30
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116	Microeukaryotic biogeography in the typical subtropical coastal waters with multiple environmental gradients. Science of the Total Environment, 2018, 635, 618-628.	8.0	37
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121	Metagenomic Analysis of Subtidal Sediments from Polar and Subpolar Coastal Environments Highlights the Relevance of Anaerobic Hydrocarbon Degradation Processes. Microbial Ecology, 2018, 75, 123-139.	2.8	30
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123	Overall bacterial community composition and abundance of nitrifiers and denitrifiers in a typical macrotidal estuary. Marine Pollution Bulletin, 2018, 126, 540-548.	5.0	8
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129	Dynamics of Sediment Microbial Functional Capacity and Community Interaction Networks in an Urbanized Coastal Estuary. <i>Frontiers in Microbiology</i> , 2018, 9, 2731.	3.5	22
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133	Role of Sediment Resuspension on Estuarine Suspended Particulate Mercury Dynamics. <i>Environmental Science & Technology</i> , 2018, 52, 7736-7744.	10.0	34
134	Membrane Distillation Biofouling: Impact of Feedwater Temperature on Biofilm Characteristics and Membrane Performance. <i>Environmental Science & Technology</i> , 2018, 52, 10019-10029.	10.0	57
135	Quantitative stable isotope probing with H ₂ ¹⁸ O reveals that most bacterial taxa in soil synthesize new ribosomal RNA. <i>ISME Journal</i> , 2018, 12, 3043-3045.	9.8	34
136	Linking Seasonal Reduction of Microbial Diversity to Increase in Winter Temperature of Waters of a Chilean Patagonia Fjord. <i>Frontiers in Marine Science</i> , 2018, 5, .	2.5	14
137	Impacts of Salinity and Oxygen on Particle-Associated Microbial Communities in the Broadkill River, Lewes DE. <i>Frontiers in Marine Science</i> , 2018, 5, .	2.5	12
138	Distribution of Archaeal Communities along the Coast of the Gulf of Finland and Their Response to Oil Contamination. <i>Frontiers in Microbiology</i> , 2018, 9, 15.	3.5	34
139	A year of monitoring 20 mesophilic full-scale bioreactors reveals the existence of stable but different core microbiomes in bio-waste and wastewater anaerobic digestion systems. <i>Biotechnology for Biofuels</i> , 2018, 11, 196.	6.2	138
140	Microbial ecological associations in the surface sediments of Bohai Strait. <i>Journal of Oceanology and Limnology</i> , 2018, 36, 795-804.	1.3	4
141	Organic carbon source and salinity shape sediment bacterial composition in two China marginal seas and their major tributaries. <i>Science of the Total Environment</i> , 2018, 633, 1510-1517.	8.0	15
142	Bacterial Biomarkers of Marcellus Shale Activity in Pennsylvania. <i>Frontiers in Microbiology</i> , 2018, 9, 1697.	3.5	11
143	Bacterial bioclusters relate to hydrochemistry in New Zealand groundwater. <i>FEMS Microbiology Ecology</i> , 2018, 94, .	2.7	10
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