

The Black Queen Hypothesis: Evolution of Dependence

MBio

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Citation Report

#	ARTICLE	IF	CITATIONS
1	Draft Genome Sequence of <i>Methanobacterium formicicum</i> DSM 3637, an Archaeobacterium Isolated from the Methane Producer <i>Amoeba Pelomyxa palustris</i> . <i>Journal of Bacteriology</i> , 2012, 194, 6967-6968.	1.0	14
2	The Tsetse Fly Obligate Mutualist <i>Wigglesworthia morsitans</i> Alters Gene Expression and Population Density via Exogenous Nutrient Provisioning. <i>Applied and Environmental Microbiology</i> , 2012, 78, 7792-7797.	1.4	30
3	From Metabolism to Ecology: Cross-Feeding Interactions Shape the Balance between Polymicrobial Conflict and Mutualism. <i>American Naturalist</i> , 2012, 180, 566-576.	1.0	71
4	Antibiotic-Mediated Selection of Quorum-Sensing-Negative <i>Staphylococcus aureus</i> . <i>MBio</i> , 2012, 3, e00459-12.	1.8	85
5	Intraguild predation provides a selection mechanism for bacterial antagonistic compounds. <i>Proceedings of the Royal Society B: Biological Sciences</i> , 2012, 279, 4513-4521.	1.2	14
6	Contrasting Life Strategies of Viruses that Infect Photo- and Heterotrophic Bacteria, as Revealed by Viral Tagging. <i>MBio</i> , 2012, 3, .	1.8	86
7	Vitamins in the sea. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2012, 109, 13888-13889.	3.3	38
8	The Origins of Cooperative Bacterial Communities. <i>MBio</i> , 2012, 3, .	1.8	104
9	Exoproteomics: exploring the world around biological systems. <i>Expert Review of Proteomics</i> , 2012, 9, 561-575.	1.3	80
10	Public good dynamics drive evolution of iron acquisition strategies in natural bacterioplankton populations. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2012, 109, 20059-20064.	3.3	294
11	Competition, Not Cooperation, Dominates Interactions among Culturable Microbial Species. <i>Current Biology</i> , 2012, 22, 1845-1850.	1.8	572
12	Nous Sommes Tous des Bacteries: Implications for medicine, pharmacology and public health. <i>Biochemical Pharmacology</i> , 2012, 84, 1543-1550.	2.0	13
13	Measured, modeled, and causal conceptions of fitness. <i>Frontiers in Genetics</i> , 2012, 3, 196.	1.1	21
14	The Mercury Resistance Operon: From an Origin in a Geothermal Environment to an Efficient Detoxification Machine. <i>Frontiers in Microbiology</i> , 2012, 3, 349.	1.5	209
15	Growing Unculturable Bacteria. <i>Journal of Bacteriology</i> , 2012, 194, 4151-4160.	1.0	893
16	Ecological interactions drive evolutionary loss of traits. <i>Ecology Letters</i> , 2012, 15, 1071-1082.	3.0	104
17	Probiotic treatment by indigenous bacteria decreases mortality without disturbing the natural microbiota of <i>Salvelinus fontinalis</i> . <i>Canadian Journal of Microbiology</i> , 2013, 59, 662-670.	0.8	53
18	<i>Polynucleobacter necessarius</i> , a model for genome reduction in both free-living and symbiotic bacteria. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2013, 110, 18590-18595.	3.3	80

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19	The Genotypic View of Social Interactions in Microbial Communities. <i>Annual Review of Genetics</i> , 2013, 47, 247-273.	3.2	257
20	Horizontal gene transfer in osmotrophs: playing with public goods. <i>Nature Reviews Microbiology</i> , 2013, 11, 720-727.	13.6	85
21	It Takes a Village: Ecological and Fitness Impacts of Multipartite Mutualism. <i>Annual Review of Microbiology</i> , 2013, 67, 161-178.	2.9	73
22	Spatiotemporal distributions of rare bacterioplankton populations indicate adaptive strategies in the oligotrophic ocean. <i>Aquatic Microbial Ecology</i> , 2013, 71, 1-13.	0.9	90
23	Blessings in disguise: biological benefits of prion-like mechanisms. <i>Trends in Cell Biology</i> , 2013, 23, 251-259.	3.6	130
24	Bacterial genome evolution within a clonal population: from <i>in vitro</i> investigations to <i>in vivo</i> observations. <i>Future Microbiology</i> , 2013, 8, 661-674.	1.0	4
25	The unique metabolism of SAR11 aquatic bacteria. <i>Journal of Microbiology</i> , 2013, 51, 147-153.	1.3	46
26	Diversity and Abundance of the Bacterial Community of the Red Macroalga <i>Porphyra umbilicalis</i> : Did Bacterial Farmers Produce Macroalgae?. <i>PLoS ONE</i> , 2013, 8, e58269.	1.1	122
27	Sequential extraction of denitrifying organisms from soils; strongly attached cells produce less N ₂ O than loosely attached cells. <i>Soil Biology and Biochemistry</i> , 2013, 67, 62-69.	4.2	10
28	Microbial Genomes That Drive Earth's Biogeochemical Cycles. , 2013, , 1-8.		4
29	Combining Quantitative Genetic Footprinting and Trait Enrichment Analysis to Identify Fitness Determinants of a Bacterial Pathogen. <i>PLoS Genetics</i> , 2013, 9, e1003716.	1.5	39
30	Interactions of photosynthesis with genome size and function. <i>Philosophical Transactions of the Royal Society B: Biological Sciences</i> , 2013, 368, 20120264.	1.8	48
31	Evolution of Divergent Life History Strategies in Marine Alphaproteobacteria. <i>MBio</i> , 2013, 4, .	1.8	103
32	Genome reduction as the dominant mode of evolution. <i>BioEssays</i> , 2013, 35, 829-837.	1.2	267
33	Copy-number changes in evolution: rates, fitness effects and adaptive significance. <i>Frontiers in Genetics</i> , 2013, 4, 273.	1.1	126
34	Starvation Induces Phenotypic Diversification and Convergent Evolution in <i>Vibrio vulnificus</i> . <i>PLoS ONE</i> , 2014, 9, e88658.	1.1	15
35	The origins of microbial adaptations: how introgressive descent, egalitarian evolutionary transitions and expanded kin selection shape the network of life. <i>Frontiers in Microbiology</i> , 2014, 5, 83.	1.5	11
36	Evolutionary Ecology of the Marine Roseobacter Clade. <i>Microbiology and Molecular Biology Reviews</i> , 2014, 78, 573-587.	2.9	279

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37	Evolution of microbial markets. Proceedings of the National Academy of Sciences of the United States of America, 2014, 111, 1237-1244.	3.3	180
38	Bacteria dialog with Santa Rosalia: Are aggregations of cosmopolitan bacteria mainly explained by habitat filtering or by ecological interactions?. BMC Microbiology, 2014, 14, 284.	1.3	27
39	Pernicious Pathogens or Expedient Elements of Inheritance: The Significance of Yeast Prions. PLoS Pathogens, 2014, 10, e1003992.	2.1	22
40	Illuminating Microbial Dark Matter in Meromictic Sakinaw Lake. Applied and Environmental Microbiology, 2014, 80, 6807-6818.	1.4	109
41	Different Levels of Catabolite Repression Optimize Growth in Stable and Variable Environments. PLoS Biology, 2014, 12, e1001764.	2.6	185
42	Social evolution of toxic metal bioremediation in <i>Pseudomonas aeruginosa</i> . Proceedings of the Royal Society B: Biological Sciences, 2014, 281, 20140858.	1.2	52
43	Evolutionary limits to cooperation in microbial communities. Proceedings of the National Academy of Sciences of the United States of America, 2014, 111, 17941-17946.	3.3	178
44	The biogeomorphological life cycle of poplars during the fluvial biogeomorphological succession: a special focus on <i>Populus nigra</i> L.. Earth Surface Processes and Landforms, 2014, 39, 546-563.	1.2	96
45	Reprint of Design of synthetic microbial communities for biotechnological production processes. Journal of Biotechnology, 2014, 192, 293-301.	1.9	26
46	Carl Woese's vision of cellular evolution and the domains of life. RNA Biology, 2014, 11, 197-204.	1.5	29
47	A Mechanistic Explanation Linking Adaptive Mutation, Niche Change, and Fitness Advantage for the Wrinkly Spreader. International Journal of Evolutionary Biology, 2014, 2014, 1-10.	1.0	25
48	Comparative Genomics Suggests That the Human Pathogenic Fungus <i>Pneumocystis jirovecii</i> Acquired Obligate Biotrophy through Gene Loss. Genome Biology and Evolution, 2014, 6, 1938-1948.	1.1	49
49	Tracing the primordial Chlamydiae: extinct parasites of plants?. Trends in Plant Science, 2014, 19, 36-43.	4.3	36
50	Interactions in the microbiome: communities of organisms and communities of genes. FEMS Microbiology Reviews, 2014, 38, 90-118.	3.9	174
51	Interactions in multispecies biofilms: do they actually matter?. Trends in Microbiology, 2014, 22, 84-91.	3.5	417
52	Community Interactions of Oral Streptococci. Advances in Applied Microbiology, 2014, 87, 43-110.	1.3	84
53	Explaining microbial genomic diversity in light of evolutionary ecology. Nature Reviews Microbiology, 2014, 12, 263-273.	13.6	310
54	Implications of streamlining theory for microbial ecology. ISME Journal, 2014, 8, 1553-1565.	4.4	664

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55	Bacterial Vesicles in the Ocean. <i>Science</i> , 2014, 343, 143-144.	6.0	17
56	Distinct microbial communities associated with buried soils in the Siberian tundra. <i>ISME Journal</i> , 2014, 8, 841-853.	4.4	137
57	Reductive genome evolution at both ends of the bacterial population size spectrum. <i>Nature Reviews Microbiology</i> , 2014, 12, 841-850.	13.6	158
58	Games of life and death: antibiotic resistance and production through the lens of evolutionary game theory. <i>Current Opinion in Microbiology</i> , 2014, 21, 35-44.	2.3	36
59	Niche engineering demonstrates a latent capacity for fungal-algal mutualism. <i>Science</i> , 2014, 345, 94-98.	6.0	192
60	Taking the pulse of ocean microbes. <i>Science</i> , 2014, 345, 134-135.	6.0	6
61	Metabolic pathways for the whole community. <i>BMC Genomics</i> , 2014, 15, 619.	1.2	50
62	What does the nr5S DNA multigene family tell us about the genomic relationship between <i>Dasypyrum breviaristatum</i> and <i>D. villosum</i> (Triticeae: Poaceae)?. <i>Molecular Genetics and Genomics</i> , 2014, 289, 553-565.	1.0	11
63	Comparative Functional Genomics of <i>Lactobacillus</i> spp. Reveals Possible Mechanisms for Specialization of Vaginal Lactobacilli to Their Environment. <i>Journal of Bacteriology</i> , 2014, 196, 1458-1470.	1.0	141
64	Evolutionary analysis of a streamlined lineage of surface ocean Roseobacters. <i>ISME Journal</i> , 2014, 8, 1428-1439.	4.4	55
65	An experimental test of whether cheating is context dependent. <i>Journal of Evolutionary Biology</i> , 2014, 27, 551-556.	0.8	60
66	An Ecological Network of Polysaccharide Utilization among Human Intestinal Symbionts. <i>Current Biology</i> , 2014, 24, 40-49.	1.8	336
67	Discovery of a SAR11 growth requirement for thiaminâ€™s pyrimidine precursor and its distribution in the Sargasso Sea. <i>ISME Journal</i> , 2014, 8, 1727-1738.	4.4	128
68	LESS IS MORE: SELECTIVE ADVANTAGES CAN EXPLAIN THE PREVALENT LOSS OF BIOSYNTHETIC GENES IN BACTERIA. <i>Evolution; International Journal of Organic Evolution</i> , 2014, 68, 2559-2570.	1.1	197
69	Design of synthetic microbial communities for biotechnological production processes. <i>Journal of Biotechnology</i> , 2014, 184, 209-218.	1.9	61
71	Modeling and quantifying frequency-dependent fitness in microbial populations with cross-feeding interactions. <i>Evolution; International Journal of Organic Evolution</i> , 2015, 69, 1313-1320.	1.1	37
72	Auxotrophy and intrapopulation complementarity in the â€™interactomeâ€™™ of a cultivated freshwater model community. <i>Molecular Ecology</i> , 2015, 24, 4449-4459.	2.0	97
73	Ecosystem productivity is associated with bacterial phylogenetic distance in surface marine waters. <i>Molecular Ecology</i> , 2015, 24, 5785-5795.	2.0	25

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74	Small genomes and the difficulty to define minimal translation and metabolic machineries. <i>Frontiers in Ecology and Evolution</i> , 2015, 3, .	1.1	9
75	Enrichment experiment changes microbial interactions in an ultra-oligotrophic environment. <i>Frontiers in Microbiology</i> , 2015, 6, 246.	1.5	57
76	The pan-genome as a shared genomic resource: mutual cheating, cooperation and the black queen hypothesis. <i>Frontiers in Microbiology</i> , 2015, 6, 728.	1.5	41
77	A network-based approach to disturbance transmission through microbial interactions. <i>Frontiers in Microbiology</i> , 2015, 6, 1182.	1.5	81
78	Species-Specific Dynamic Responses of Gut Bacteria to a Mammalian Glycan. <i>Journal of Bacteriology</i> , 2015, 197, 1538-1548.	1.0	34
79	How do divergent ecological strategies emerge among marine bacterioplankton lineages?. <i>Trends in Microbiology</i> , 2015, 23, 577-584.	3.5	65
80	Social dynamics within decomposer communities lead to nitrogen retention and organic matter build-up in soils. <i>Nature Communications</i> , 2015, 6, 8960.	5.8	80
81	Buried Treasure: Evolutionary Perspectives on Microbial Iron Piracy. <i>Trends in Genetics</i> , 2015, 31, 627-636.	2.9	111
82	The importance of the microbiome of the plant holobiont. <i>New Phytologist</i> , 2015, 206, 1196-1206.	3.5	1,509
83	Host-microbe and microbe-microbe interactions in the evolution of obligate plant parasitism. <i>New Phytologist</i> , 2015, 206, 1207-1228.	3.5	54
84	Marine microbial community dynamics and their ecological interpretation. <i>Nature Reviews Microbiology</i> , 2015, 13, 133-146.	13.6	681
85	Genomic and proteomic characterization of <i>Candidatus Nitrosopelagicus brevis</i> : An ammonia-oxidizing archaeon from the open ocean. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2015, 112, 1173-1178.	3.3	278
86	The physiology and ecological implications of efficient growth. <i>ISME Journal</i> , 2015, 9, 1481-1487.	4.4	155
87	How microbes adapt to a diversity of food niches. <i>Current Opinion in Food Science</i> , 2015, 2, 29-35.	4.1	52
88	Aquatic metagenomes implicate <i>Thaumarchaeota</i> in global cobalamin production. <i>ISME Journal</i> , 2015, 9, 461-471.	4.4	152
89	Health Effects of Toxic Cyanobacteria in U.S. Drinking and Recreational Waters: Our Current Understanding and Proposed Direction. <i>Current Environmental Health Reports</i> , 2015, 2, 75-84.	3.2	75
90	Evolution of small prokaryotic genomes. <i>Frontiers in Microbiology</i> , 2014, 5, 742.	1.5	83
91	Backbones of evolutionary history test biodiversity theory for microbes. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2015, 112, 8356-8361.	3.3	44

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92	Quorum Sensing Protects <i>Pseudomonas aeruginosa</i> against Cheating by Other Species in a Laboratory Coculture Model. <i>Journal of Bacteriology</i> , 2015, 197, 3154-3159.	1.0	58
93	Horizontal gene transfer: building the web of life. <i>Nature Reviews Genetics</i> , 2015, 16, 472-482.	7.7	1,018
94	Black Queen evolution: the role of leakiness in structuring microbial communities. <i>Trends in Genetics</i> , 2015, 31, 475-482.	2.9	171
95	Average genome size estimation improves comparative metagenomics and sheds light on the functional ecology of the human microbiome. <i>Genome Biology</i> , 2015, 16, 51.	3.8	241
96	Response of <i>Prochlorococcus</i> to varying CO ₂ :O ₂ ratios. <i>ISME Journal</i> , 2015, 9, 2232-2245.	4.4	22
97	Polymicrobial synergy and dysbiosis in inflammatory disease. <i>Trends in Molecular Medicine</i> , 2015, 21, 172-183.	3.5	397
98	<i>Trichodesmium</i> genome maintains abundant, widespread noncoding DNA in situ, despite oligotrophic lifestyle. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2015, 112, 4251-4256.	3.3	45
99	Microbial community transcriptional networks are conserved in three domains at ocean basin scales. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2015, 112, 5443-5448.	3.3	225
100	Plasticity and epistasis strongly affect bacterial fitness after losing multiple metabolic genes. <i>Evolution; International Journal of Organic Evolution</i> , 2015, 69, 1244-1254.	1.1	24
101	Ecology and exploration of the rare biosphere. <i>Nature Reviews Microbiology</i> , 2015, 13, 217-229.	13.6	926
102	Engineering Microbiomes to Improve Plant and Animal Health. <i>Trends in Microbiology</i> , 2015, 23, 606-617.	3.5	486
103	The rapidly expanding universe of giant viruses: Mimivirus, Pandoravirus, Pithovirus and Mollivirus. <i>FEMS Microbiology Reviews</i> , 2015, 39, 779-796.	3.9	219
104	Adaptation in Natural Microbial Populations. <i>Annual Review of Ecology, Evolution, and Systematics</i> , 2015, 46, 503-522.	3.8	47
105	Microbes don't play solitaire: how cooperation trumps isolation in the microbial world. <i>Environmental Microbiology Reports</i> , 2015, 7, 26-28.	1.0	78
106	OPINION PAPER Evolutionary Constraint-Based Formulation Requires New Bi-level Solving Techniques. <i>Lecture Notes in Computer Science</i> , 2015, , 279-281.	1.0	0
107	Multi-species biofilms in ecology, medicine, and biotechnology. <i>Microbiology</i> , 2015, 84, 731-750.	0.5	54
108	<i>Prochlorococcus</i> : the structure and function of collective diversity. <i>Nature Reviews Microbiology</i> , 2015, 13, 13-27.	13.6	435
109	Metabolic engineering to enhance the value of plants as green factories. <i>Metabolic Engineering</i> , 2015, 27, 83-91.	3.6	65

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110	High prevalence of biofilm synergy among bacterial soil isolates in cocultures indicates bacterial interspecific cooperation. <i>ISME Journal</i> , 2015, 9, 81-89.	4.4	261
111	Biotic Interactions in Microbial Communities as Modulators of Biogeochemical Processes: Methanotrophy as a Model System. <i>Frontiers in Microbiology</i> , 2016, 7, 1285.	1.5	95
112	Ammonia Oxidation in the Ocean Can Be Inhibited by Nanomolar Concentrations of Hydrogen Peroxide. <i>Frontiers in Marine Science</i> , 2016, 3, .	1.2	63
113	Uptake of Leucine, Chitin, and Iron by Prokaryotic Groups during Spring Phytoplankton Blooms Induced by Natural Iron Fertilization off Kerguelen Island (Southern Ocean). <i>Frontiers in Marine Science</i> , 2016, 3, .	1.2	12
114	Microevolution Analysis of <i>Bacillus coahuilensis</i> Unveils Differences in Phosphorus Acquisition Strategies and Their Regulation. <i>Frontiers in Microbiology</i> , 2016, 7, 58.	1.5	17
115	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.	1.5	152
116	Global Emergence and Dissemination of Enterococci as Nosocomial Pathogens: Attack of the Clones?. <i>Frontiers in Microbiology</i> , 2016, 7, 788.	1.5	248
117	Gene Loss and Horizontal Gene Transfer Contributed to the Genome Evolution of the Extreme Acidophile <i>Ferroplasma</i> . <i>Frontiers in Microbiology</i> , 2016, 7, 797.	1.5	42
118	Bacterial Communities: Interactions to Scale. <i>Frontiers in Microbiology</i> , 2016, 7, 1234.	1.5	465
119	Beyond 16S rRNA Community Profiling: Intra-Species Diversity in the Gut Microbiota. <i>Frontiers in Microbiology</i> , 2016, 7, 1475.	1.5	117
120	Metabolic Complementation in Bacterial Communities: Necessary Conditions and Optimality. <i>Frontiers in Microbiology</i> , 2016, 7, 1553.	1.5	17
121	Pervasive Selection for Cooperative Cross-Feeding in Bacterial Communities. <i>PLoS Computational Biology</i> , 2016, 12, e1004986.	1.5	81
122	Experimental Evolution of Metabolic Dependency in Bacteria. <i>PLoS Genetics</i> , 2016, 12, e1006364.	1.5	119
123	High-Throughput Parallel Sequencing to Measure Fitness of <i>Leptospira interrogans</i> Transposon Insertion Mutants during Acute Infection. <i>PLoS Neglected Tropical Diseases</i> , 2016, 10, e0005117.	1.3	19
124	Genome Analysis of the Biotechnologically Relevant Acidophilic Iron Oxidising Strain JA12 Indicates Phylogenetic and Metabolic Diversity within the Novel Genus <i>Ferroplasma</i> . <i>PLoS ONE</i> , 2016, 11, e0146832.	1.1	48
125	How mutualisms arise in phytoplankton communities: building eco-evolutionary principles for aquatic microbes. <i>Ecology Letters</i> , 2016, 19, 810-822.	3.0	75
126	Survival of <i>Prochlorococcus</i> in extended darkness. <i>Limnology and Oceanography</i> , 2016, 61, 1375-1388.	1.6	61
127	Effects of African dust deposition on phytoplankton in the western tropical Atlantic Ocean off Barbados. <i>Global Biogeochemical Cycles</i> , 2016, 30, 716-734.	1.9	85

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128	Private benefits and metabolic conflicts shape the emergence of microbial interdependencies. <i>Environmental Microbiology</i> , 2016, 18, 1415-1427.	1.8	66
129	Variable but persistent coexistence of <i>Prochlorococcus</i> ecotypes along temperature gradients in the ocean's surface mixed layer. <i>Environmental Microbiology Reports</i> , 2016, 8, 272-284.	1.0	24
130	The interconnected rhizosphere: High network complexity dominates rhizosphere assemblages. <i>Ecology Letters</i> , 2016, 19, 926-936.	3.0	803
131	Swimming performance of <i>Bradyrhizobium diazoefficiens</i> is an emergent property of its two flagellar systems. <i>Scientific Reports</i> , 2016, 6, 23841.	1.6	33
133	Enzymatic Antioxidant Systems in Early Anaerobes: Theoretical Considerations. <i>Astrobiology</i> , 2016, 16, 348-358.	1.5	48
134	Nondegenerative Evolution in Ancient Heritable Bacterial Endosymbionts of Fungi. <i>Molecular Biology and Evolution</i> , 2016, 33, 2216-2231.	3.5	14
135	The global regulator CodY is required for the fitness of <i>Bacillus cereus</i> in various laboratory media and certain beverages. <i>FEMS Microbiology Letters</i> , 2016, 363, fnw126.	0.7	4
136	Losing Complexity: The Role of Simplification in Macroevolution. <i>Trends in Ecology and Evolution</i> , 2016, 31, 608-621.	4.2	55
137	Establishment of stable synthetic mutualism without co-evolution between microalgae and bacteria demonstrated by mutual transfer of metabolites (NanoSIMS isotopic imaging) and persistent physical association (Fluorescent in situ hybridization). <i>Algal Research</i> , 2016, 15, 179-186.	2.4	59
138	Evidence for quorum sensing and differential metabolite production by a marine bacterium in response to DMSP. <i>ISME Journal</i> , 2016, 10, 2304-2316.	4.4	112
139	Deciphering ocean carbon in a changing world. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2016, 113, 3143-3151.	3.3	253
140	Holes in the Hologenome: Why Host-Microbe Symbioses Are Not Holobionts. <i>MBio</i> , 2016, 7, e02099.	1.8	260
141	Transitions in individuality through symbiosis. <i>Current Opinion in Microbiology</i> , 2016, 31, 191-198.	2.3	43
142	Transcriptional response of <i>Prochlorococcus</i> to co-culture with a marine <i>Alteromonas</i> : differences between strains and the involvement of putative infochemicals. <i>ISME Journal</i> , 2016, 10, 2892-2906.	4.4	71
143	Lack of Overt Genome Reduction in the Bryostatin-Producing Bryozoan Symbiont <i>Candidatus Endobugula sertula</i> . <i>Applied and Environmental Microbiology</i> , 2016, 82, 6573-6583.	1.4	41
144	The Genus <i>Dehalococcoides</i> . , 2016, , 107-136.		26
145	Genomic Comparisons of <i>Lactobacillus crispatus</i> and <i>Lactobacillus iners</i> Reveal Potential Ecological Drivers of Community Composition in the Vagina. <i>Applied and Environmental Microbiology</i> , 2016, 82, 7063-7073.	1.4	114
146	The Ecology and Evolution of Microbial Competition. <i>Trends in Microbiology</i> , 2016, 24, 833-845.	3.5	553

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148	Synthetic microbial ecology and the dynamic interplay between microbial genotypes. FEMS Microbiology Reviews, 2016, 40, 961-979.	3.9	70
149	Decoupling function and taxonomy in the global ocean microbiome. Science, 2016, 353, 1272-1277.	6.0	2,001
150	Spatial structure, cooperation and competition in biofilms. Nature Reviews Microbiology, 2016, 14, 589-600.	13.6	757
151	The Modern Synthesis in the Light of Microbial Genomics. Annual Review of Microbiology, 2016, 70, 279-297.	2.9	58
152	Exploiting rRNA operon copy number to investigate bacterial reproductive strategies. Nature Microbiology, 2016, 1, 16160.	5.9	371
153	Bacterial evolution: Genomics of metabolic trade-offs. Nature Microbiology, 2016, 1, 16181.	5.9	45
154	Cooperation and Public Goods, Bacterial. , 2016, , 374-380.		0
155	Holobionts and the ecology of organisms: Multi-species communities or integrated individuals?. Biology and Philosophy, 2016, 31, 875-892.	0.7	107
156	Molecular archeological evidence in support of the repeated loss of a papillomavirus gene. Scientific Reports, 2016, 6, 33028.	1.6	36
157	Microbial Communities Are Well Adapted to Disturbances in Energy Input. MSystems, 2016, 1, .	1.7	28
158	Defying Muller's Ratchet: Ancient Heritable Endobacteria Escape Extinction through Retention of Recombination and Genome Plasticity. MBio, 2016, 7, .	1.8	39
159	Presence of a loner strain maintains cooperation and diversity in well-mixed bacterial communities. Proceedings of the Royal Society B: Biological Sciences, 2016, 283, 20152682.	1.2	47
160	Diel regulation of hydrogen peroxide defenses by open ocean microbial communities. Journal of Plankton Research, 2016, 38, 1103-1114.	0.8	35
161	Torn apart and reunited: impact of a heterotroph on the transcriptome of <i>Prochlorococcus</i> . ISME Journal, 2016, 10, 2831-2843.	4.4	53
162	Grandeur Alliances: Symbiont Metabolic Integration and Obligate Arthropod Hematophagy. Trends in Parasitology, 2016, 32, 739-749.	1.5	95
163	Microbial interactions and community assembly at microscales. Current Opinion in Microbiology, 2016, 31, 227-234.	2.3	308
164	Pangenome Evolution in the Marine Bacterium <i>Alteromonas</i> . Genome Biology and Evolution, 2016, 8, 1556-1570.	1.1	73
165	Three Trends in the History of Life: An Evolutionary Syndrome. Evolutionary Biology, 2016, 43, 531-542.	0.5	19

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166	Indispensability of Horizontally Transferred Genes and Its Impact on Bacterial Genome Streamlining. <i>Molecular Biology and Evolution</i> , 2016, 33, 1257-1269.	3.5	80
167	Levels of selection in biofilms: multispecies biofilms are not evolutionary individuals. <i>Biology and Philosophy</i> , 2016, 31, 191-212.	0.7	52
168	Beyond the Black Queen Hypothesis. <i>ISME Journal</i> , 2016, 10, 2085-2091.	4.4	105
169	Synthetic Ecology of Microbes: Mathematical Models and Applications. <i>Journal of Molecular Biology</i> , 2016, 428, 837-861.	2.0	198
170	Towards Engineering Biological Systems in a Broader Context. <i>Journal of Molecular Biology</i> , 2016, 428, 928-944.	2.0	30
171	Co-occurring <i>Synechococcus</i> ecotypes occupy four major oceanic regimes defined by temperature, macronutrients and iron. <i>ISME Journal</i> , 2016, 10, 333-345.	4.4	169
172	Towards long-read metagenomics: complete assembly of three novel genomes from bacteria dependent on a diazotrophic cyanobacterium in a freshwater lake co-culture. <i>Standards in Genomic Sciences</i> , 2017, 12, 9.	1.5	53
173	Microdiversity shapes the traits, niche space, and biogeography of microbial taxa. <i>Environmental Microbiology Reports</i> , 2017, 9, 55-70.	1.0	120
174	Marine Ecosystems as Complex Adaptive Systems: Emergent Patterns, Critical Transitions, and Public Goods. <i>Ecosystems</i> , 2017, 20, 458-476.	1.6	33
175	The <i>Trichodesmium</i> consortium: conserved heterotrophic co-occurrence and genomic signatures of potential interactions. <i>ISME Journal</i> , 2017, 11, 1813-1824.	4.4	66
176	Microbial mutualism dynamics governed by dose-dependent toxicity of cross-fed nutrients. <i>ISME Journal</i> , 2017, 11, 337-348.	4.4	72
177	Communal Metabolism of Methane and the Rare Earth Element Switch. <i>Journal of Bacteriology</i> , 2017, 199, e00328-17.	1.0	46
178	Ecological Insights into the Dynamics of Plant Biomass-Degrading Microbial Consortia. <i>Trends in Microbiology</i> , 2017, 25, 788-796.	3.5	59
179	Zooming in on the phycosphere: the ecological interface for phytoplankton-bacteria relationships. <i>Nature Microbiology</i> , 2017, 2, 17065.	5.9	727
180	Ubiquity and quantitative significance of bacterioplankton lineages inhabiting the oxygenated hypolimnion of deep freshwater lakes. <i>ISME Journal</i> , 2017, 11, 2279-2293.	4.4	75
181	Excess of non-conservative amino acid changes in marine bacterioplankton lineages with reduced genomes. <i>Nature Microbiology</i> , 2017, 2, 17091.	5.9	41
182	Bacterial Unculturability and the Formation of Intercellular Metabolic Networks. <i>Trends in Microbiology</i> , 2017, 25, 349-361.	3.5	188
183	Metabolic evolution and the self-organization of ecosystems. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2017, 114, E3091-E3100.	3.3	139

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184	Spontaneous mutations of a model heterotrophic marine bacterium. <i>ISME Journal</i> , 2017, 11, 1713-1718.	4.4	22
185	Ecological systems biology: The dynamics of interacting populations. <i>Current Opinion in Systems Biology</i> , 2017, 1, 114-121.	1.3	66
186	Making the Most of Clade Selection. <i>Philosophy of Science</i> , 2017, 84, 275-295.	0.5	32
187	Junk DNA Contribution to Evolutionary Capacitance Can Drive Species Dynamics. <i>Evolutionary Biology</i> , 2017, 44, 190-205.	0.5	8
188	Archaeal Biocommunication in Hot Springs Revealed by Metagenomics. , 2017, , 85-101.		0
189	The microbiome beyond the horizon of ecological and evolutionary theory. <i>Nature Ecology and Evolution</i> , 2017, 1, 1606-1615.	3.4	216
190	Candidatus <i>Dactylopiibacterium carminicum</i> , a Nitrogen-Fixing Symbiont of <i>Dactylopius</i> Cochineal Insects (Hemiptera: Coccoidea: Dactylopiidae). <i>Genome Biology and Evolution</i> , 2017, 9, 2237-2250.	1.1	19
191	Maintenance of Microbial Cooperation Mediated by Public Goods in Single- and Multiple-Trait Scenarios. <i>Journal of Bacteriology</i> , 2017, 199, .	1.0	61
192	Environmental drivers of a microbial genomic transition zone in the ocean's interior. <i>Nature Microbiology</i> , 2017, 2, 1367-1373.	5.9	177
193	Nutrient limitation determines the fitness of cheaters in bacterial siderophore cooperation. <i>Nature Communications</i> , 2017, 8, 230.	5.8	69
194	Temperature Impacts on Soil Microbial Communities and Potential Implications for the Biodegradation of Turfgrass Pesticides. <i>Journal of Environmental Quality</i> , 2017, 46, 490-497.	1.0	16
195	Distinct Trajectories of Massive Recent Gene Gains and Losses in Populations of a Microbial Eukaryotic Pathogen. <i>Molecular Biology and Evolution</i> , 2017, 34, 2808-2822.	3.5	87
196	Recipient-Biased Competition for an Intracellularly Generated Cross-Fed Nutrient Is Required for Coexistence of Microbial Mutualists. <i>MBio</i> , 2017, 8, .	1.8	22
197	Ocean biogeochemistry modeled with emergent trait-based genomics. <i>Science</i> , 2017, 358, 1149-1154.	6.0	122
198	Genome-driven evolutionary game theory helps understand the rise of metabolic interdependencies in microbial communities. <i>Nature Communications</i> , 2017, 8, 1563.	5.8	130
199	Methanogenesis in oxygenated soils is a substantial fraction of wetland methane emissions. <i>Nature Communications</i> , 2017, 8, 1567.	5.8	195
200	Vitamin and Amino Acid Auxotrophy in Anaerobic Consortia Operating under Methanogenic Conditions. <i>MSystems</i> , 2017, 2, .	1.7	28
201	Paradoxes in leaky microbial trade. <i>Nature Communications</i> , 2017, 8, 1361.	5.8	27

#	ARTICLE	IF	CITATIONS
202	Nutrient recycling facilitates long-term stability of marine microbial phototroph-heterotroph interactions. <i>Nature Microbiology</i> , 2017, 2, 17100.	5.9	181
203	Co-niche construction between hosts and symbionts: ideas and evidence. <i>Journal of Genetics</i> , 2017, 96, 483-489.	0.4	26
204	Coordinated Changes in Mutation and Growth Rates Induced by Genome Reduction. <i>MBio</i> , 2017, 8, .	1.8	34
205	Emergence of microbial diversity due to cross-feeding interactions in a spatial model of gut microbial metabolism. <i>BMC Systems Biology</i> , 2017, 11, 56.	3.0	83
206	The drivers underlying biogeographical patterns of bacterial communities in soils under sugarcane cultivation. <i>Applied Soil Ecology</i> , 2017, 110, 12-20.	2.1	32
207	Survey of (Meta)genomic Approaches for Understanding Microbial Community Dynamics. <i>Indian Journal of Microbiology</i> , 2017, 57, 23-38.	1.5	21
208	Genome reduction in an abundant and ubiquitous soil bacterium - <i>Candidatus Udaeobacter copiosus</i> -™. <i>Nature Microbiology</i> , 2017, 2, 16198.	5.9	168
209	Life's utilization of B vitamins on early Earth. <i>Geobiology</i> , 2017, 15, 3-18.	1.1	58
210	Global occurrence and heterogeneity of the <i>Roseobacter</i> -clade species <i>Ruegeria mobilis</i> . <i>ISME Journal</i> , 2017, 11, 569-583.	4.4	75
211	SAR11 Bacteria: The Most Abundant Plankton in the Oceans. <i>Annual Review of Marine Science</i> , 2017, 9, 231-255.	5.1	417
212	Life history and eco-evolutionary dynamics in light of the gut microbiota. <i>Oikos</i> , 2017, 126, 508-531.	1.2	139
213	Phenotypic Microdiversity and Phylogenetic Signal Analysis of Traits Related to Social Interaction in <i>Bacillus</i> spp. from Sediment Communities. <i>Frontiers in Microbiology</i> , 2017, 8, 29.	1.5	21
214	Why Quorum Sensing Controls Private Goods. <i>Frontiers in Microbiology</i> , 2017, 8, 885.	1.5	33
215	Comparative Genomics Reveals High Genomic Diversity in the Genus <i>Photobacterium</i> . <i>Frontiers in Microbiology</i> , 2017, 8, 1204.	1.5	31
216	The Exometabolome of Two Model Strains of the <i>Roseobacter</i> Group: A Marketplace of Microbial Metabolites. <i>Frontiers in Microbiology</i> , 2017, 8, 1985.	1.5	96
217	Natural Selection in Synthetic Communities Highlights the Roles of <i>Methylococcaceae</i> and <i>Methylophilaceae</i> and Suggests Differential Roles for Alternative Methanol Dehydrogenases in Methane Consumption. <i>Frontiers in Microbiology</i> , 2017, 8, 2392.	1.5	51
218	Drivers of genetic diversity in secondary metabolic gene clusters within a fungal species. <i>PLoS Biology</i> , 2017, 15, e2003583.	2.6	187
219	Q&A: Friends (but sometimes foes) within: the complex evolutionary ecology of symbioses between host and microbes. <i>BMC Biology</i> , 2017, 15, 126.	1.7	9

#	ARTICLE	IF	CITATIONS
220	Quinones are growth factors for the human gut microbiota. <i>Microbiome</i> , 2017, 5, 161.	4.9	73
221	Cooperation-based branching as a mechanism of evolutionary speciation. <i>Journal of Theoretical Biology</i> , 2018, 445, 166-186.	0.8	7
222	How spatial structure and neighbor uncertainty promote mutualists and weaken black queen effects. <i>Journal of Theoretical Biology</i> , 2018, 446, 33-60.	0.8	18
223	Neutral Theory, Microbial Practice: Challenges in Bacterial Population Genetics. <i>Molecular Biology and Evolution</i> , 2018, 35, 1338-1347.	3.5	93
224	Function and functional redundancy in microbial systems. <i>Nature Ecology and Evolution</i> , 2018, 2, 936-943.	3.4	912
225	No effect of intraspecific relatedness on public goods cooperation in a complex community. <i>Evolution; International Journal of Organic Evolution</i> , 2018, 72, 1165-1173.	1.1	17
226	Impact of spatial organization on a novel auxotrophic interaction among soil microbes. <i>ISME Journal</i> , 2018, 12, 1443-1456.	4.4	51
227	Microbial Dark Matter Investigations: How Microbial Studies Transform Biological Knowledge and Empirically Sketch a Logic of Scientific Discovery. <i>Genome Biology and Evolution</i> , 2018, 10, 707-715.	1.1	82
228	Relative stability of ploidy in a marine <i>Synechococcus</i> across various growth conditions. <i>Environmental Microbiology Reports</i> , 2018, 10, 428-432.	1.0	4
229	Cross-protection from hydrogen peroxide by helper microbes: the impacts on the cyanobacterium <i>Prochlorococcus</i> and other beneficiaries in marine communities. <i>Environmental Microbiology Reports</i> , 2018, 10, 399-411.	1.0	30
230	Ultrarare marine microbes contribute to key sulphur-related ecosystem functions. <i>Molecular Ecology</i> , 2018, 27, 1494-1504.	2.0	14
231	Black Queen markets: commensalism, dependency, and the evolution of cooperative specialization in human society. <i>Journal of Bioeconomics</i> , 2018, 20, 69-105.	1.5	11
232	Chimeric Synergy in Natural Social Groups of a Cooperative Microbe. <i>Current Biology</i> , 2018, 28, 262-267.e3.	1.8	11
233	Exploiting rhizosphere microbial cooperation for developing sustainable agriculture strategies. <i>Environmental Science and Pollution Research</i> , 2018, 25, 29953-29970.	2.7	56
234	Genetic Competence Drives Genome Diversity in <i>Bacillus subtilis</i> . <i>Genome Biology and Evolution</i> , 2018, 10, 108-124.	1.1	67
235	Studying microbial functionality within the gut ecosystem by systems biology. <i>Genes and Nutrition</i> , 2018, 13, 5.	1.2	31
236	Processes and patterns of interaction as units of selection: An introduction to ITSNTS thinking. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2018, 115, 4006-4014.	3.3	95
237	The generality of Constructive Neutral Evolution. <i>Biology and Philosophy</i> , 2018, 33, 1.	0.7	20

#	ARTICLE	IF	CITATIONS
238	Integrated network analysis reveals the importance of microbial interactions for maize growth. <i>Applied Microbiology and Biotechnology</i> , 2018, 102, 3805-3818.	1.7	94
239	The multi-omics promise in context: from sequence to microbial isolate. <i>Critical Reviews in Microbiology</i> , 2018, 44, 212-229.	2.7	158
240	Transcriptional Activities of the Microbial Consortium Living with the Marine Nitrogen-Fixing Cyanobacterium <i>Trichodesmium</i> Reveal Potential Roles in Community-Level Nitrogen Cycling. <i>Applied and Environmental Microbiology</i> , 2018, 84, .	1.4	18
241	Degradation of hydrogen peroxide at the ocean's surface: the influence of the microbial community on the realized thermal niche of <i>Prochlorococcus</i> . <i>ISME Journal</i> , 2018, 12, 473-484.	4.4	45
242	The impact of elevated CO ₂ on <i>Prochlorococcus</i> and microbial interactions with "helper" bacterium <i>Alteromonas</i> . <i>ISME Journal</i> , 2018, 12, 520-531.	4.4	36
243	Why We Should Care About Universal Biology. <i>Biological Theory</i> , 2018, 13, 121-130.	0.8	6
244	Microdiversification in genome-streamlined ubiquitous freshwater Actinobacteria. <i>ISME Journal</i> , 2018, 12, 185-198.	4.4	227
245	Evolution on the bright side of life: microorganisms and the evolution of mutualism. <i>Annals of the New York Academy of Sciences</i> , 2018, 1422, 88-103.	1.8	22
246	Ecological selection of siderophore-producing microbial taxa in response to heavy metal contamination. <i>Ecology Letters</i> , 2018, 21, 117-127.	3.0	97
247	100 Days of marine <i>Synechococcus</i> " <i>Ruegeria pomeroyi</i> interaction: A detailed analysis of the exoproteome. <i>Environmental Microbiology</i> , 2018, 20, 785-799.	1.8	19
248	Design Principles of Microbial Communities: From Understanding to Engineering. <i>Current Genomics</i> , 2018, 19, 699-700.	0.7	6
249	The Cost of Metabolic Interactions in Symbioses between Insects and Bacteria with Reduced Genomes. <i>MBio</i> , 2018, 9, .	1.8	51
250	What is the hologenome concept of evolution?. <i>F1000Research</i> , 2018, 7, 1664.	0.8	48
251	Insights on <i>Mycobacterium leprae</i> Efflux Pumps and Their Implications in Drug Resistance and Virulence. <i>Frontiers in Microbiology</i> , 2018, 9, 3072.	1.5	27
252	Modeling the Role of the Microbiome in Evolution. <i>Frontiers in Physiology</i> , 2018, 9, 1836.	1.3	39
253	Metatranscriptomic and comparative genomic insights into resuscitation mechanisms during enrichment culturing. <i>Microbiome</i> , 2018, 6, 230.	4.9	113
254	Summer shifts of bacterial communities associated with the invasive brown seaweed <i>Sargassum muticum</i> are location and tissue dependent. <i>PLoS ONE</i> , 2018, 13, e0206734.	1.1	57
255	Collapse of genetic division of labour and evolution of autonomy in pellicle biofilms. <i>Nature Microbiology</i> , 2018, 3, 1451-1460.	5.9	51

#	ARTICLE	IF	CITATIONS
256	How Divergent Is the Cuatro Ciénegas Oasis? Genomic Studies of Microbial Populations and Niche Differentiation. Cuatro Ciénegas Basin: an Endangered Hyperdiverse Oasis, 2018, , 57-71.	0.4	2
257	The oral microbiota: dynamic communities and host interactions. Nature Reviews Microbiology, 2018, 16, 745-759.	13.6	1,143
258	Understanding the Mechanisms Behind the Response to Environmental Perturbation in Microbial Mats: A Metagenomic-Network Based Approach. Frontiers in Microbiology, 2018, 9, 2606.	1.5	41
259	Hidden in plain sight—highly abundant and diverse planktonic freshwater Chloroflexi. Microbiome, 2018, 6, 176.	4.9	130
260	Black Queen Evolution and Trophic Interactions Determine Plasmid Survival after the Disruption of the Conjugation Network. MSystems, 2018, 3, .	1.7	18
261	Mayr Versus Woese: Akaryotes and Eukaryotes. Grand Challenges in Biology and Biotechnology, 2018, , 13-54.	2.4	0
262	Metabolic adaptations underlying genome flexibility in prokaryotes. PLoS Genetics, 2018, 14, e1007763.	1.5	31
263	Model Microbial Consortia as Tools for Understanding Complex Microbial Communities. Current Genomics, 2018, 19, 723-733.	0.7	22
264	Osmotrophy. Current Biology, 2018, 28, R1179-R1180.	1.8	29
265	The evolution of fungal substrate specificity in a widespread group of crustose lichens. Proceedings of the Royal Society B: Biological Sciences, 2018, 285, 20180640.	1.2	19
266	Holobionts and their hologenomes: Evolution with mixed modes of inheritance. Genetics and Molecular Biology, 2018, 41, 189-197.	0.6	17
267	The birth, evolution and death of metabolic gene clusters in fungi. Nature Reviews Microbiology, 2018, 16, 731-744.	13.6	155
268	Heterotroph Interactions Alter <i>Prochlorococcus</i> Transcriptome Dynamics during Extended Periods of Darkness. MSystems, 2018, 3, .	1.7	38
269	Deforestation decreases spatial turnover and alters the network interactions in soil bacterial communities. Soil Biology and Biochemistry, 2018, 123, 80-86.	4.2	73
270	Selection for Gaia across Multiple Scales. Trends in Ecology and Evolution, 2018, 33, 633-645.	4.2	62
271	Ecology and evolution of seafloor and subseafloor microbial communities. Nature Reviews Microbiology, 2018, 16, 671-683.	13.6	128
272	Towards a Dynamic Interaction Network of Life to unify and expand the evolutionary theory. BMC Biology, 2018, 16, 56.	1.7	27
273	Experimental Design, Population Dynamics, and Diversity in Microbial Experimental Evolution. Microbiology and Molecular Biology Reviews, 2018, 82, .	2.9	132

#	ARTICLE	IF	CITATIONS
274	Pan-Genome Analysis Links the Hereditary Variation of <i>Leptospirillum ferriphilum</i> With Its Evolutionary Adaptation. <i>Frontiers in Microbiology</i> , 2018, 9, 577.	1.5	18
275	Population Dynamics of <i>Lactobacillus helveticus</i> in Swiss Gruyère-Type Cheese Manufactured With Natural Whey Cultures. <i>Frontiers in Microbiology</i> , 2018, 9, 637.	1.5	41
276	Concepts and Methods to Access Novel Antibiotics from Actinomycetes. <i>Antibiotics</i> , 2018, 7, 44.	1.5	119
277	Model Communities Hint at Promiscuous Metabolic Linkages between Ubiquitous Free-Living Freshwater Bacteria. <i>MSphere</i> , 2018, 3, .	1.3	20
278	Meanings, measurements, and musings on the significance of patterns in human microbiome variation. <i>Current Opinion in Genetics and Development</i> , 2018, 53, 43-52.	1.5	5
279	Cetacea are natural knockouts for IL20. <i>Immunogenetics</i> , 2018, 70, 681-687.	1.2	19
280	The evolution of three siderophore biosynthetic clusters in environmental and host-associating strains of <i>Pantoea</i> . <i>Molecular Genetics and Genomics</i> , 2018, 293, 1453-1467.	1.0	17
281	Genome Variation in the Model Halophilic Bacterium <i>Salinibacter ruber</i> . <i>Frontiers in Microbiology</i> , 2018, 9, 1499.	1.5	12
282	Nitrogen Fixation in Cereals. <i>Frontiers in Microbiology</i> , 2018, 9, 1794.	1.5	180
283	Division of Labor during Biofilm Matrix Production. <i>Current Biology</i> , 2018, 28, 1903-1913.e5.	1.8	203
284	Filling gaps in bacterial amino acid biosynthesis pathways with high-throughput genetics. <i>PLoS Genetics</i> , 2018, 14, e1007147.	1.5	90
285	Communities of Niche-Optimized Strains: Small-Genome Organism Consortia in Bioproduction. <i>Trends in Biotechnology</i> , 2019, 37, 126-139.	4.9	20
286	In the beginning was the word: How terminology drives our understanding of endosymbiotic organelles. <i>Microbial Cell</i> , 2019, 6, 134-141.	1.4	10
287	Substrate cross-feeding affects the speed and trajectory of molecular evolution within a synthetic microbial assemblage. <i>BMC Evolutionary Biology</i> , 2019, 19, 129.	3.2	21
288	Characterizing symbiont inheritance during host-microbiota evolution: Application to the great apes gut microbiota. <i>Molecular Ecology Resources</i> , 2019, 19, 1659-1671.	2.2	17
289	An evolutionary quantitative genetics model for phenotypic (co)variances under limited dispersal, with an application to socially synergistic traits. <i>Evolution; International Journal of Organic Evolution</i> , 2019, 73, 1695-1728.	1.1	22
290	Ammonia-oxidizing archaea release a suite of organic compounds potentially fueling prokaryotic heterotrophy in the ocean. <i>Environmental Microbiology</i> , 2019, 21, 4062-4075.	1.8	71
291	B-Vitamin Sharing Promotes Stability of Gut Microbial Communities. <i>Frontiers in Microbiology</i> , 2019, 10, 1485.	1.5	86

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292	Essential Biomolecules in Food Webs. <i>Frontiers in Ecology and Evolution</i> , 2019, 7, .	1.1	76
293	Syntrophy emerges spontaneously in complex metabolic systems. <i>PLoS Computational Biology</i> , 2019, 15, e1007169.	1.5	31
294	Genome evolution and host-microbiome shifts correspond with intraspecific niche divergence within harmful algal bloom-forming <i>Microcystis aeruginosa</i> . <i>Molecular Ecology</i> , 2019, 28, 3994-4011.	2.0	29
295	Defining Division of Labor in Microbial Communities. <i>Journal of Molecular Biology</i> , 2019, 431, 4712-4731.	2.0	50
296	The water depth-dependent co-occurrence patterns of marine bacteria in shallow and dynamic Southern Coast, Korea. <i>Scientific Reports</i> , 2019, 9, 9176.	1.6	33
297	Fresh Ideas Bloom in Gut Healthcare to Cross-Fertilize Lake Management. <i>Environmental Science & Technology</i> , 2019, 53, 14099-14112.	4.6	2
298	Complex Evolutionary Origins of Specialized Metabolite Gene Cluster Diversity among the Plant Pathogenic Fungi of the <i>Fusarium graminearum</i> Species Complex. <i>Genome Biology and Evolution</i> , 2019, 11, 3106-3122.	1.1	24
299	A conceptual framework for the phylogenetically constrained assembly of microbial communities. <i>Microbiome</i> , 2019, 7, 142.	4.9	28
300	Global Trends in Marine Plankton Diversity across Kingdoms of Life. <i>Cell</i> , 2019, 179, 1084-1097.e21.	13.5	271
301	Host specificity in diatom-bacteria interactions alleviates antagonistic effects. <i>FEMS Microbiology Ecology</i> , 2019, 95, .	1.3	33
302	Incorporating phylogenetic metrics to microbial co-occurrence networks based on amplicon sequences to discern community assembly processes. <i>Molecular Ecology Resources</i> , 2019, 19, 1552-1564.	2.2	41
303	<i>Janthinobacterium</i> CG23_2: Comparative Genome Analysis Reveals Enhanced Environmental Sensing and Transcriptional Regulation for Adaptation to Life in an Antarctic Supraglacial Stream. <i>Microorganisms</i> , 2019, 7, 454.	1.6	7
304	New <i>Halonotius</i> Species Provide Genomics-Based Insights Into Cobalamin Synthesis in Haloarchaea. <i>Frontiers in Microbiology</i> , 2019, 10, 1928.	1.5	34
305	Less Is More: Genome Reduction and the Emergence of Cooperation—Implications into the Coevolution of Microbial Communities. <i>International Journal of Genomics</i> , 2019, 2019, 1-5.	0.8	5
306	Metatranscriptomic Analyses of Diel Metabolic Functions During a <i>Microcystis</i> Bloom in Western Lake Erie (United States). <i>Frontiers in Microbiology</i> , 2019, 10, 2081.	1.5	22
307	Occurrence of auxotrophic variants among bacteria of <i>Enterobacteriaceae</i> family isolated from water objects of the north-west of the Murmansk region. <i>IOP Conference Series: Earth and Environmental Science</i> , 0, 263, 012036.	0.2	1
308	Genome-wide identification of <i>Pseudomonas syringae</i> genes required for fitness during colonization of the leaf surface and apoplast. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2019, 116, 18900-18910.	3.3	77
309	Exploring the effects of operational mode and microbial interactions on bacterial community assembly in a one-stage partial-nitrification anammox reactor using integrated multi-omics. <i>Microbiome</i> , 2019, 7, 122.	4.9	65

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310	The Pathobiome in Animal and Plant Diseases. <i>Trends in Ecology and Evolution</i> , 2019, 34, 996-1008.	4.2	208
311	Environmental stimuli drive a transition from cooperation to competition in synthetic phototrophic communities. <i>Nature Microbiology</i> , 2019, 4, 2184-2191.	5.9	54
312	Population Genomics Insights into Adaptive Evolution and Ecological Differentiation in <i>Streptomyces</i> . <i>Applied and Environmental Microbiology</i> , 2019, 85, .	1.4	16
313	Selfish, sharing and scavenging bacteria in the Atlantic Ocean: a biogeographical study of bacterial substrate utilisation. <i>ISME Journal</i> , 2019, 13, 1119-1132.	4.4	103
314	<i>Bifidobacterium bifidum</i> ATCC 15696 and <i>Bifidobacterium breve</i> 24b Metabolic Interaction Based on 2- <i>O</i> -Fucosyl-Lactose Studied in Steady-State Cultures in a Freter-Style Chemostat. <i>Applied and Environmental Microbiology</i> , 2019, 85, .	1.4	32
315	The Dynamic of a River Model Bacterial Community in Two Different Media Reveals a Divergent Succession and an Enhanced Growth of Most Strains Compared to Monocultures. <i>Microbial Ecology</i> , 2019, 78, 313-323.	1.4	3
316	Nanotube-mediated cross-feeding couples the metabolism of interacting bacterial cells. <i>Environmental Microbiology</i> , 2019, 21, 1306-1320.	1.8	29
317	The Classification and Evolution of Bacterial Cross-Feeding. <i>Frontiers in Ecology and Evolution</i> , 2019, 7, .	1.1	100
318	Determining Microbial Roles in Ecosystem Function: Redefining Microbial Food Webs and Transcending Kingdom Barriers. <i>MSystems</i> , 2019, 4, .	1.7	11
319	Proteomic Response of Three Marine Ammonia-Oxidizing Archaea to Hydrogen Peroxide and Their Metabolic Interactions with a Heterotrophic Alphaproteobacterium. <i>MSystems</i> , 2019, 4, .	1.7	57
320	Public goods and cheating in microbes. <i>Current Biology</i> , 2019, 29, R442-R447.	1.8	135
321	Understanding microbial community dynamics to improve optimal microbiome selection. <i>Microbiome</i> , 2019, 7, 85.	4.9	233
322	Influence of Light on Particulate Organic Matter Utilization by Attached and Free-Living Marine Bacteria. <i>Frontiers in Microbiology</i> , 2019, 10, 1204.	1.5	24
323	Phylogeny, Divergent Evolution, and Speciation of Sulfur-Oxidizing <i>Acidithiobacillus</i> Populations. <i>BMC Genomics</i> , 2019, 20, 438.	1.2	21
324	Culturing the ubiquitous freshwater actinobacterial <i>acl</i> lineage by supplying a biochemical "helper" catalase. <i>ISME Journal</i> , 2019, 13, 2252-2263.	4.4	37
325	Cycles of external dependency drive evolution of avian carotenoid networks. <i>Nature Communications</i> , 2019, 10, 1596.	5.8	5
326	Designing Metabolic Division of Labor in Microbial Communities. <i>MSystems</i> , 2019, 4, .	1.7	88
327	Spatial heterogeneity promotes antagonistic evolutionary scenarios in microbial community explained by ecological stratification: a simulation study. <i>Ecological Modelling</i> , 2019, 399, 66-76.	1.2	1

#	ARTICLE	IF	CITATIONS
328	Carbon Fixation by Marine Ultrasmall Prokaryotes. <i>Genome Biology and Evolution</i> , 2019, 11, 1166-1177.	1.1	24
329	A Developing Symbiosis: Enabling Cross-Talk Between Ecologists and Microbiome Scientists. <i>Frontiers in Microbiology</i> , 2019, 10, 292.	1.5	50
330	Carbon Cycle Implications of Soil Microbial Interactions. <i>Advances in Environmental Microbiology</i> , 2019, , 1-29.	0.1	0
331	Metagenomic Insights Into a Cellulose-Rich Niche Reveal Microbial Cooperation in Cellulose Degradation. <i>Frontiers in Microbiology</i> , 2019, 10, 618.	1.5	34
332	Evolution of CCL16 in Glires (Rodentia and Lagomorpha) shows an unusual random pseudogenization pattern. <i>BMC Evolutionary Biology</i> , 2019, 19, 59.	3.2	4
333	Bottom-Up Approaches to Synthetic Cooperation in Microbial Communities. <i>Life</i> , 2019, 9, 22.	1.1	54
334	Stable isotope probing and metagenomics highlight the effect of plants on uncultured phenanthrene-degrading bacterial consortium in polluted soil. <i>ISME Journal</i> , 2019, 13, 1814-1830.	4.4	72
335	New insights from uncultivated genomes of the global human gut microbiome. <i>Nature</i> , 2019, 568, 505-510.	13.7	505
336	Co-culture and biogeography of <i>Prochlorococcus</i> and SAR11. <i>ISME Journal</i> , 2019, 13, 1506-1519.	4.4	80
337	Does the Chemodiversity of Bacterial Exometabolomes Sustain the Chemodiversity of Marine Dissolved Organic Matter?. <i>Frontiers in Microbiology</i> , 2019, 10, 215.	1.5	50
338	Role of resource allocation and transport in emergence of cross-feeding in microbial consortia. <i>Journal of Theoretical Biology</i> , 2019, 467, 150-163.	0.8	8
339	Genomics insights into ecotype formation of ammonia-oxidizing archaea in the deep ocean. <i>Environmental Microbiology</i> , 2019, 21, 716-729.	1.8	39
340	Mass Spectrometry Uncovers the Role of Surfactin as an Interspecies Recruitment Factor. <i>ACS Chemical Biology</i> , 2019, 14, 459-467.	1.6	21
342	Trojan Horses and Black Queens: "causal core"™ explanations in microbiome research. <i>Biology and Philosophy</i> , 2019, 34, 1.	0.7	4
343	Labour sharing promotes coexistence in atrazine degrading bacterial communities. <i>Scientific Reports</i> , 2019, 9, 18363.	1.6	25
344	The Interactive Construction of Biological Individuality Through Biotic Entrenchment. <i>Frontiers in Psychology</i> , 2019, 10, 2578.	1.1	3
345	Bringing Community Ecology to Bear on the Issue of Antimicrobial Resistance. <i>Frontiers in Microbiology</i> , 2019, 10, 2626.	1.5	11
346	Can communities cause?. <i>Biology and Philosophy</i> , 2019, 34, 1.	0.7	4

#	ARTICLE	IF	CITATIONS
347	Dynamic genomic architecture of mutualistic cooperation in a wild population of <i>Mesorhizobium</i> . ISME Journal, 2019, 13, 301-315.	4.4	34
348	Cross-exchange of B-vitamins underpins a mutualistic interaction between <i>Ostreococcus tauri</i> and <i>Dinoroseobacter shibae</i> . ISME Journal, 2019, 13, 334-345.	4.4	83
349	Bowel Biofilms: Tipping Points between a Healthy and Compromised Gut?. Trends in Microbiology, 2019, 27, 17-25.	3.5	97
350	Genomic variation and strain-specific functional adaptation in the human gut microbiome during early life. Nature Microbiology, 2019, 4, 470-479.	5.9	164
351	Effects of elevated ground-level ozone on paddy soil bacterial community and assembly mechanisms across four years. Science of the Total Environment, 2019, 654, 505-513.	3.9	25
352	Uneven distribution of cobamide biosynthesis and dependence in bacteria predicted by comparative genomics. ISME Journal, 2019, 13, 789-804.	4.4	162
353	Concept of microbial gatekeepers: Positive guys?. Applied Microbiology and Biotechnology, 2019, 103, 633-641.	1.7	20
354	Costless metabolic secretions as drivers of interspecies interactions in microbial ecosystems. Nature Communications, 2019, 10, 103.	5.8	214
355	Interrogating metabolism as an electron flow system. Current Opinion in Systems Biology, 2019, 13, 59-67.	1.3	15
356	Analysis of a phenol-adapted microbial community: degradation capacity, taxonomy and metabolic description. Journal of Applied Microbiology, 2019, 126, 771-779.	1.4	5
357	Progress and promise of omics for predicting the impacts of climate change on harmful algal blooms. Harmful Algae, 2020, 91, 101587.	2.2	45
358	Metagenomic and chemical characterization of soil cobalamin production. ISME Journal, 2020, 14, 53-66.	4.4	59
359	Time-series metatranscriptomes reveal conserved patterns between phototrophic and heterotrophic microbes in diverse freshwater systems. Limnology and Oceanography, 2020, 65, S101.	1.6	18
360	Interactions of PAH-degradation and nitrate-/sulfate-reducing assemblages in anaerobic sediment microbial community. Journal of Hazardous Materials, 2020, 388, 122068.	6.5	37
361	Functional role of bloom-forming cyanobacterium Planktothrix in ecologically shaping aquatic environments. Science of the Total Environment, 2020, 710, 136314.	3.9	15
362	Networks Consolidate the Core Concepts of Evolution by Natural Selection. Trends in Microbiology, 2020, 28, 254-265.	3.5	17
363	Large-sized planktonic bioaggregates possess high biofilm formation potentials: Bacterial succession and assembly in the biofilm metacommunity. Water Research, 2020, 170, 115307.	5.3	31
364	Bacterial siderophores in community and host interactions. Nature Reviews Microbiology, 2020, 18, 152-163.	13.6	495

#	ARTICLE	IF	CITATIONS
365	Biosynthetic gene clusters and the evolution of fungal chemodiversity. <i>Natural Product Reports</i> , 2020, 37, 868-878.	5.2	93
366	Genomic mosaicism underlies the adaptation of marine <i>Synechococcus</i> ecotypes to distinct oceanic iron niches. <i>Environmental Microbiology</i> , 2020, 22, 1801-1815.	1.8	32
367	The global <i>Microcystis</i> interactome. <i>Limnology and Oceanography</i> , 2020, 65, S194-S207.	1.6	63
368	Seasonal Variability of Conditionally Rare Taxa in the Water Column Bacterioplankton Community of Subtropical Reservoirs in China. <i>Microbial Ecology</i> , 2020, 80, 14-26.	1.4	54
369	Spatial structure in the "Plastisphere": Molecular resources for imaging microscopic communities on plastic marine debris. <i>Molecular Ecology Resources</i> , 2020, 20, 620-634.	2.2	66
370	A succession of marine bacterial communities in batch reactor experiments during the degradation of five different petroleum types. <i>Marine Pollution Bulletin</i> , 2020, 150, 110775.	2.3	17
371	Genomic repertoire of <i>Mameliella alba</i> Ep20 associated with Symbiodinium from the endemic coral <i>Mussismilia braziliensis</i> . <i>Symbiosis</i> , 2020, 80, 53-60.	1.2	10
372	Horizontal persistence and the complexity hypothesis. <i>Biology and Philosophy</i> , 2020, 35, 1.	0.7	17
373	Positive linkage between bacterial social traits reveals that homogeneous rather than specialised behavioral repertoires prevail in natural <i>Pseudomonas</i> communities. <i>FEMS Microbiology Ecology</i> , 2020, 96, .	1.3	9
374	Environmental and Microbial Interactions Shape Methane-Oxidizing Bacterial Communities in a Stratified Lake. <i>Frontiers in Microbiology</i> , 2020, 11, 579427.	1.5	18
375	Coculture with <i>Synechococcus</i> facilitates growth of <i>Prochlorococcus</i> under ocean acidification conditions. <i>Environmental Microbiology</i> , 2020, 22, 4876-4889.	1.8	8
376	Metagenomic studies of SAR202 bacteria at the full-ocean depth in the Mariana Trench. <i>Deep-Sea Research Part I: Oceanographic Research Papers</i> , 2020, 165, 103396.	0.6	14
377	Evolution of specialized microbial cooperation in dynamic fluids. <i>Journal of Evolutionary Biology</i> , 2020, 33, 256-269.	0.8	5
378	Genome analyses provide insights into the evolution and adaptation of the eukaryotic Picophytoplankton <i>Mychonastes homosphaera</i> . <i>BMC Genomics</i> , 2020, 21, 477.	1.2	8
379	Synergism between the Black Queen effect and the proteomic constraint on genome size reduction in the photosynthetic picoeukaryotes. <i>Scientific Reports</i> , 2020, 10, 8918.	1.6	2
380	A Landscape of Opportunities for Microbial Ecology Research. <i>Frontiers in Microbiology</i> , 2020, 11, 561427.	1.5	34
381	<i>Portiera</i> Gets Wild: Genome Instability Provides Insights into the Evolution of Both Whiteflies and Their Endosymbionts. <i>Genome Biology and Evolution</i> , 2020, 12, 2107-2124.	1.1	14
382	From Microbial Communities to Distributed Computing Systems. <i>Frontiers in Bioengineering and Biotechnology</i> , 2020, 8, 834.	2.0	19

#	ARTICLE	IF	CITATIONS
383	Contingent evolution of alternative metabolic network topologies determines whether cross-feeding evolves. <i>Communications Biology</i> , 2020, 3, 401.	2.0	10
384	Globally Abundant <i>Candidatus</i> <i>Udaeobacter</i> Benefits from Release of Antibiotics in Soil and Potentially Performs Trace Gas Scavenging. <i>MSphere</i> , 2020, 5, .	1.3	32
385	Emergence of Metabolite Provisioning as a By-Product of Evolved Biological Functions. <i>MSystems</i> , 2020, 5, .	1.7	15
386	Microbial Strategies for Survival in the Glass Sponge <i>Vazella pourtalesii</i> . <i>MSystems</i> , 2020, 5, .	1.7	23
387	Streamlined and Abundant Bacterioplankton Thrive in Functional Cohorts. <i>MSystems</i> , 2020, 5, .	1.7	8
388	High-throughput cultivation based on dilution-to-extinction with catalase supplementation and a case study of cultivating acl bacteria from Lake Soyang. <i>Journal of Microbiology</i> , 2020, 58, 893-905.	1.3	14
389	Functional redundancy in natural pico-phytoplankton communities depends on temperature and biogeography. <i>Biology Letters</i> , 2020, 16, 20200330.	1.0	9
390	Bradymonabacteria, a novel bacterial predator group with versatile survival strategies in saline environments. <i>Microbiome</i> , 2020, 8, 126.	4.9	37
391	Understanding the Mechanisms of Positive Microbial Interactions That Benefit Lactic Acid Bacteria Co-cultures. <i>Frontiers in Microbiology</i> , 2020, 11, 2088.	1.5	67
392	Metabolic excretion associated with nutrient growth dysregulation promotes the rapid evolution of an overt metabolic defect. <i>PLoS Biology</i> , 2020, 18, e3000757.	2.6	17
393	<i>Prochlorococcus</i> Cells Rely on Microbial Interactions Rather than on Chlorotic Resting Stages To Survive Long-Term Nutrient Starvation. <i>MBio</i> , 2020, 11, .	1.8	39
394	Strain Structure and Dynamics Revealed by Targeted Deep Sequencing of the Honey Bee Gut Microbiome. <i>MSphere</i> , 2020, 5, .	1.3	19
395	Microbial Mutualism: Will You Still Need Me, Will You Still Feed Me?. <i>Current Biology</i> , 2020, 30, R1041-R1043.	1.8	3
396	The Evolution of Mutualistic Dependence. <i>Annual Review of Ecology, Evolution, and Systematics</i> , 2020, 51, 409-432.	3.8	78
397	Metagenome assembled genomes reveal similar functional profiles of <i>CPR</i> /Patescibacteria phyla in soils. <i>Environmental Microbiology Reports</i> , 2020, 12, 651-655.	1.0	27
398	Regularized S-Map Reveals Varying Bacterial Interactions. <i>Applied and Environmental Microbiology</i> , 2020, 86, .	1.4	8
399	Functional Integration and Individuality in Prokaryotic Collective Organisations. <i>Acta Biotheoretica</i> , 2021, 69, 391-415.	0.7	3
400	Thiamine-Mediated Cooperation Between Auxotrophic <i>Rhodococcus ruber</i> ZM07 and <i>Escherichia coli</i> K12 Drives Efficient Tetrahydrofuran Degradation. <i>Frontiers in Microbiology</i> , 2020, 11, 594052.	1.5	4

#	ARTICLE	IF	CITATIONS
401	Reflections on the Predictability of Evolution: Toward a Conceptual Framework. <i>IScience</i> , 2020, 23, 101736.	1.9	9
402	Genes and genomes and unnecessary complexity in precision medicine. <i>Npj Genomic Medicine</i> , 2020, 5, 21.	1.7	12
403	Methanogens and Methanotrophs Show Nutrient-Dependent Community Assemblage Patterns Across Tropical Peatlands of the Pastaza-Marañón Basin, Peruvian Amazonia. <i>Frontiers in Microbiology</i> , 2020, 11, 746.	1.5	29
404	Defining Cyanobacterial Species: Diversity and Description Through Genomics. <i>Critical Reviews in Plant Sciences</i> , 2020, 39, 101-124.	2.7	41
405	Dynamics and functional diversity of the smallest phytoplankton on the Northeast US Shelf. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2020, 117, 12215-12221.	3.3	16
406	Predictive biology: modelling, understanding and harnessing microbial complexity. <i>Nature Reviews Microbiology</i> , 2020, 18, 507-520.	13.6	80
407	New Methods, New Concepts: What Can Be Applied to Freshwater Periphyton?. <i>Frontiers in Microbiology</i> , 2020, 11, 1275.	1.5	20
408	Deciphering the succession dynamics of dominant and rare genera in biofilm development process. <i>Science of the Total Environment</i> , 2020, 739, 139961.	3.9	11
409	Iterative subtractive binning of freshwater chronoserries metagenomes identifies over 400 novel species and their ecologic preferences. <i>Environmental Microbiology</i> , 2020, 22, 3394-3412.	1.8	69
410	Earth microbial co-occurrence network reveals interconnection pattern across microbiomes. <i>Microbiome</i> , 2020, 8, 82.	4.9	239
411	Size Matters: Ultra-small and Filterable Microorganisms in the Environment. <i>Microbes and Environments</i> , 2020, 35, n/a.	0.7	45
412	Auxotrophic interactions: a stabilizing attribute of aquatic microbial communities?. <i>FEMS Microbiology Ecology</i> , 2020, 96, .	1.3	31
413	Synthetic Symbiosis under Environmental Disturbances. <i>MSystems</i> , 2020, 5, .	1.7	1
414	Members of <i>Prevotella</i> Genus Distinctively Modulate Innate Immune and Barrier Functions in a Human Three-Dimensional Endometrial Epithelial Cell Model. <i>Journal of Infectious Diseases</i> , 2020, 222, 2082-2092.	1.9	21
415	Sediment Microbial Communities and Their Potential Role as Environmental Pollution Indicators in Xuande Atoll, South China Sea. <i>Frontiers in Microbiology</i> , 2020, 11, 1011.	1.5	17
416	Complete Genome of <i>Lactobacillus iners</i> KY Using Flongle Provides Insight Into the Genetic Background of Optimal Adaption to Vaginal Ecniche. <i>Frontiers in Microbiology</i> , 2020, 11, 1048.	1.5	16
417	Experiment design and bacterial abundance control extracellular H ₂ O ₂ concentrations during four series of mesocosm experiments. <i>Biogeosciences</i> , 2020, 17, 1309-1326.	1.3	6
418	Horizontal Gene Transfer as a Source of Conflict and Cooperation in Prokaryotes. <i>Frontiers in Microbiology</i> , 2020, 11, 1569.	1.5	46

#	ARTICLE	IF	CITATIONS
419	Challenges of unculturable bacteria: environmental perspectives. <i>Reviews in Environmental Science and Biotechnology</i> , 2020, 19, 1-22.	3.9	193
420	Linking regional shifts in microbial genome adaptation with surface ocean biogeochemistry. <i>Philosophical Transactions of the Royal Society B: Biological Sciences</i> , 2020, 375, 20190254.	1.8	33
421	Metabolically cohesive microbial consortia and ecosystem functioning. <i>Philosophical Transactions of the Royal Society B: Biological Sciences</i> , 2020, 375, 20190245.	1.8	37
422	The microbial exometabolome: ecological resource and architect of microbial communities. <i>Philosophical Transactions of the Royal Society B: Biological Sciences</i> , 2020, 375, 20190250.	1.8	57
423	Marine Sediments Illuminate Chlamydiae Diversity and Evolution. <i>Current Biology</i> , 2020, 30, 1032-1048.e7.	1.8	52
424	Development of an S-layer gene-based PCR-DGGE assay for monitoring dominant <i>Lactobacillus helveticus</i> strains in natural whey starters of Grana Padano cheese. <i>Food Microbiology</i> , 2020, 89, 103457.	2.1	6
425	Dynamics of Insect-Microbiome Interaction Influence Host and Microbial Symbiont. <i>Frontiers in Microbiology</i> , 2020, 11, 1357.	1.5	98
426	Population genomics of Vibrionaceae isolated from an endangered oasis reveals local adaptation after an environmental perturbation. <i>BMC Genomics</i> , 2020, 21, 418.	1.2	6
427	The Trait Repertoire Enabling Cyanobacteria to Bloom Assessed through Comparative Genomic Complexity and Metatranscriptomics. <i>MBio</i> , 2020, 11, .	1.8	13
428	Species dynamics and interactions via metabolically informed consumer-resource models. <i>Theoretical Ecology</i> , 2020, 13, 503-518.	0.4	10
429	Understanding the evolution of interspecies interactions in microbial communities. <i>Philosophical Transactions of the Royal Society B: Biological Sciences</i> , 2020, 375, 20190256.	1.8	68
430	Mixotrophy in marine picocyanobacteria: use of organic compounds by <i>Prochlorococcus</i> and <i>Synechococcus</i> . <i>ISME Journal</i> , 2020, 14, 1065-1073.	4.4	63
431	Genome mining of biosynthetic and chemotherapeutic gene clusters in <i>Streptomyces</i> bacteria. <i>Scientific Reports</i> , 2020, 10, 2003.	1.6	117
432	Emerging Priorities for Microbiome Research. <i>Frontiers in Microbiology</i> , 2020, 11, 136.	1.5	113
433	Functional traits of the gut microbiome correlated with host lipid content in a natural population of <i>Drosophila melanogaster</i> . <i>Biology Letters</i> , 2020, 16, 20190803.	1.0	8
434	Community diversity and habitat structure shape the repertoire of extracellular proteins in bacteria. <i>Nature Communications</i> , 2020, 11, 758.	5.8	26
435	Insights into ecological roles and potential evolution of Mlr-dependent microcystin-degrading bacteria. <i>Science of the Total Environment</i> , 2020, 710, 136401.	3.9	20
436	Ecological insights into the underlying evolutionary patterns of biofilm formation from biological wastewater treatment systems: Red or Black Queen Hypothesis?. <i>Biotechnology and Bioengineering</i> , 2020, 117, 1270-1280.	1.7	4

#	ARTICLE	IF	CITATIONS
437	Advantage of Leakage of Essential Metabolites for Cells. <i>Physical Review Letters</i> , 2020, 124, 048101.	2.9	11
438	Subsistence and complexity of antimicrobial resistance on a community-wide level. <i>Environmental Microbiology</i> , 2020, 22, 2463-2468.	1.8	11
439	Toward a dynamical understanding of microbial communities. <i>Philosophical Transactions of the Royal Society B: Biological Sciences</i> , 2020, 375, 20190248.	1.8	21
440	Effects of Spatial Variability and Relic DNA Removal on the Detection of Temporal Dynamics in Soil Microbial Communities. <i>MBio</i> , 2020, 11, .	1.8	70
441	Small and mighty: adaptation of superphylum Patescibacteria to groundwater environment drives their genome simplicity. <i>Microbiome</i> , 2020, 8, 51.	4.9	205
442	Metabolic Modeling and Omics Data Integration: A Systems Biology Approach to Food Science. , 2021, , 396-417.		0
443	Strategies for culturing active/dormant marine microbes. <i>Marine Life Science and Technology</i> , 2021, 3, 121-131.	1.8	31
444	Probiotics and competitive exclusion of pathogens in shrimp aquaculture. <i>Reviews in Aquaculture</i> , 2021, 13, 324-352.	4.6	74
445	Characterization of a novel <i>Pantoea</i> symbiont allows inference of a pattern of convergent genome reduction in bacteria associated with Pentatomidae. <i>Environmental Microbiology</i> , 2021, 23, 36-50.	1.8	12
446	Unique genomic traits for cold adaptation in <i>Naganishia vishniacii</i> , a polyextremophile yeast isolated from Antarctica. <i>FEMS Yeast Research</i> , 2021, 21, .	1.1	14
447	Programmed cell death as a black queen in microbial communities. <i>Molecular Ecology</i> , 2021, 30, 1110-1119.	2.0	11
448	Community lifespan, niche expansion and the evolution of interspecific cooperation. <i>Journal of Evolutionary Biology</i> , 2021, 34, 352-363.	0.8	0
449	Selfishness driving reductive evolution shapes interdependent patterns in spatially structured microbial communities. <i>ISME Journal</i> , 2021, 15, 1387-1401.	4.4	30
450	From ecophysiology to cultivation methodology: filling the knowledge gap between uncultured and cultured microbes. <i>Marine Life Science and Technology</i> , 2021, 3, 132-147.	1.8	15
451	Frequency of mispackaging of <i>Prochlorococcus</i> DNA by cyanophage. <i>ISME Journal</i> , 2021, 15, 129-140.	4.4	8
452	The coevolutionary history of the microbial planet. <i>Environmental Microbiology Reports</i> , 2021, 13, 12-14.	1.0	0
454	Niche dimensions of a marine bacterium are identified using invasion studies in coastal seawater. <i>Nature Microbiology</i> , 2021, 6, 524-532.	5.9	18
455	Environmentally relevant concentrations of titanium dioxide nanoparticles pose negligible risk to marine microbes. <i>Environmental Science: Nano</i> , 2021, 8, 1236-1255.	2.2	29

#	ARTICLE	IF	CITATIONS
456	Molecular trafficking between bacteria determines the shape of gut microbial community. <i>Gut Microbes</i> , 2021, 13, 1959841.	4.3	20
457	Competitive Exclusion and Metabolic Dependency among Microorganisms Structure the Cellulose Economy of an Agricultural Soil. <i>MBio</i> , 2021, 12, .	1.8	23
458	Evolutionary Rescue of an Environmental <i>Pseudomonas otitidis</i> in Response to Anthropogenic Perturbation. <i>Frontiers in Microbiology</i> , 2020, 11, 563885.	1.5	5
459	An overview of theoretical and experimental approach to study environmental microflora. , 2021, , 119-139.		0
460	Polarization of microbial communities between competitive and cooperative metabolism. <i>Nature Ecology and Evolution</i> , 2021, 5, 195-203.	3.4	131
461	Microbiome establishment, adaptation, and contributions to anaerobic stress tolerance and nutrient acquisition in rice. , 2021, , 369-379.		0
462	Microbial diversity of co-occurring heterotrophs in cultures of marine picocyanobacteria. <i>Environmental Microbiomes</i> , 2021, 16, 1.	2.2	28
464	Cooperative Equilibrium in Biosphere Evolution: Reconciling Competition and Cooperation in Evolutionary Ecology. <i>Acta Biotheoretica</i> , 2021, 69, 629-641.	0.7	5
465	Positive interactions within and between populations decrease the likelihood of evolutionary rescue. <i>PLoS Computational Biology</i> , 2021, 17, e1008732.	1.5	4
466	Synergistic epistasis enhances the co-operativity of mutualistic interspecies interactions. <i>ISME Journal</i> , 2021, 15, 2233-2247.	4.4	6
467	Extracellular Metabolism Sets the Table for Microbial Cross-Feeding. <i>Microbiology and Molecular Biology Reviews</i> , 2021, 85, .	2.9	58
468	Dynamic Allocation of Carbon Storage and Nutrient-Dependent Exudation in a Revised Genome-Scale Model of <i>Prochlorococcus</i> . <i>Frontiers in Genetics</i> , 2021, 12, 586293.	1.1	15
470	Interspecific protection against oxidative stress: green algae protect harmful cyanobacteria against hydrogen peroxide. <i>Environmental Microbiology</i> , 2021, 23, 2404-2419.	1.8	33
472	Polymicrobial communities in periodontal disease: Their quasi-organismal nature and dialogue with the host. <i>Periodontology 2000</i> , 2021, 86, 210-230.	6.3	126
473	Biotechnological basis of microbial consortia for the removal of pesticides from the environment. <i>Critical Reviews in Biotechnology</i> , 2021, 41, 317-338.	5.1	107
474	Rapid transcriptional and metabolic adaptation of intestinal microbes to host immune activation. <i>Cell Host and Microbe</i> , 2021, 29, 378-393.e5.	5.1	52
476	Dysfunction of <i>CYC2g</i> is responsible for the evolutionary shift from radiate to disciform flowerheads in the <i>Chrysanthemum</i> group (Asteraceae: Anthemideae). <i>Plant Journal</i> , 2021, 106, 1024-1038.	2.8	24
477	Microbial and Genetic Resources for Cobalamin (Vitamin B12) Biosynthesis: From Ecosystems to Industrial Biotechnology. <i>International Journal of Molecular Sciences</i> , 2021, 22, 4522.	1.8	43

#	ARTICLE	IF	CITATIONS
478	Non-additive microbial community responses to environmental complexity. <i>Nature Communications</i> , 2021, 12, 2365.	5.8	34
479	Survival of the Systems. <i>Trends in Ecology and Evolution</i> , 2021, 36, 333-344.	4.2	25
480	Genomic and molecular evolutionary dynamics of transcriptional response regulator genes in bacterial species of the Harveyi clade of <i>Vibrio</i> . <i>Gene</i> , 2021, 783, 145577.	1.0	2
481	Genome Reduction and Secondary Metabolism of the Marine Sponge-Associated Cyanobacterium <i>Leptothoe</i> . <i>Marine Drugs</i> , 2021, 19, 298.	2.2	4
483	Engineering Cooperation in an Anaerobic Coculture. <i>Applied and Environmental Microbiology</i> , 2021, 87, .	1.4	4
484	Coping with darkness: The adaptive response of marine picocyanobacteria to repeated light energy deprivation. <i>Limnology and Oceanography</i> , 2021, 66, 3300-3312.	1.6	9
485	Seed dispersers shape the pulp nutrients of fleshy-fruited plants. <i>Proceedings of the Royal Society B: Biological Sciences</i> , 2021, 288, 20210817.	1.2	12
488	Adaptation of metabolite leakiness leads to symbiotic chemical exchange and to a resilient microbial ecosystem. <i>PLoS Computational Biology</i> , 2021, 17, e1009143.	1.5	10
489	Synergistic interactions prevail in multispecies biofilms formed by the human gut microbiota on mucin. <i>FEMS Microbiology Ecology</i> , 2021, 97, .	1.3	13
490	Mechanisms That Shape Microbial Pangenomes. <i>Trends in Microbiology</i> , 2021, 29, 493-503.	3.5	34
491	Iron transport in cyanobacteria – from molecules to communities. <i>Trends in Microbiology</i> , 2022, 30, 229-240.	3.5	19
492	The genetic and ecophysiological diversity of <i>Microcystis</i> . <i>Environmental Microbiology</i> , 2021, 23, 7278-7313.	1.8	56
493	Lichens and microbial syntrophies offer models for an interdependent route to multicellularity. <i>Lichenologist</i> , 2021, 53, 283-290.	0.5	6
495	Stress causes interspecific facilitation within a compost community. <i>Ecology Letters</i> , 2021, 24, 2169-2177.	3.0	22
496	Stoichiometric Modeling of Artificial String Chemistries Reveals Constraints on Metabolic Network Structure. <i>Journal of Molecular Evolution</i> , 2021, 89, 472-483.	0.8	2
497	Vertical Niche Partitioning of Archaea and Bacteria Linked to Shifts in Dissolved Organic Matter Quality and Hydrography in North Atlantic Waters. <i>Frontiers in Marine Science</i> , 2021, 8, .	1.2	6
498	Cell Growth Model with Stochastic Gene Expression Helps Understand the Growth Advantage of Metabolic Exchange and Auxotrophy. <i>MSystems</i> , 2021, 6, e0044821.	1.7	2
499	Metagenomic Insight into Lignocellulose Degradation of the Thermophilic Microbial Consortium TMC7. <i>Journal of Microbiology and Biotechnology</i> , 2021, 31, 1123-1133.	0.9	3

#	ARTICLE	IF	CITATIONS
500	Genetic innovations in animalâ€™microbe symbioses. <i>Nature Reviews Genetics</i> , 2022, 23, 23-39.	7.7	60
502	Seasonal succession of microbes in different size-fractions and their modular structures determined by both macro- and micro-environmental filtering in dynamic coastal waters. <i>Science of the Total Environment</i> , 2021, 784, 147046.	3.9	18
503	The Ecology and Evolution of Model Microbial Mutualisms. <i>Annual Review of Ecology, Evolution, and Systematics</i> , 2021, 52, 363-384.	3.8	6
505	Genome-resolved metagenome and metatranscriptome analyses of thermophilic composting reveal key bacterial players and their metabolic interactions. <i>BMC Genomics</i> , 2021, 22, 652.	1.2	16
506	Single-colony sequencing reveals microbe-by-microbiome phyllosymbiosis between the cyanobacterium <i>Microcystis</i> and its associated bacteria. <i>Microbiome</i> , 2021, 9, 194.	4.9	27
507	Market forces determine the distribution of a leaky function in a simple microbial community. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2021, 118, .	3.3	4
508	Contribution of single-cell omics to microbial ecology. <i>Trends in Ecology and Evolution</i> , 2022, 37, 67-78.	4.2	8
509	Structure and Long-Term Stability of the Microbiome in Diverse Diatom Cultures. <i>Microbiology Spectrum</i> , 2021, 9, e0026921.	1.2	8
510	Transferring concepts from plant to microbial ecology: A framework proposal to identify relevant bacterial functional traits. <i>Soil Biology and Biochemistry</i> , 2021, 162, 108415.	4.2	19
511	Genomic knockout of hsp23 both decreases and increases fitness under opposing thermal extremes in <i>Drosophila melanogaster</i> . <i>Insect Biochemistry and Molecular Biology</i> , 2021, 139, 103652.	1.2	4
512	Ecological selection of bacterial taxa with larger genome sizes in response to polycyclic aromatic hydrocarbons stress. <i>Journal of Environmental Sciences</i> , 2022, 112, 82-93.	3.2	12
513	Limitation by a shared mutualist promotes coexistence of multiple competing partners. <i>Nature Communications</i> , 2021, 12, 619.	5.8	16
515	Bacterial Opportunistic Pathogens of Fish. <i>Advances in Environmental Microbiology</i> , 2016, , 81-108.	0.1	38
516	The Genus <i>Prochlorococcus</i> , Phylum Cyanobacteria. , 2014, , 829-845.		10
517	Endosymbiosis before eukaryotes: mitochondrial establishment in protoeukaryotes. <i>Cellular and Molecular Life Sciences</i> , 2020, 77, 3503-3523.	2.4	34
518	Invasions of Host-Associated Microbiome Networks. <i>Advances in Ecological Research</i> , 2017, , 201-281.	1.4	19
519	Silent rain: does the atmosphere-mediated connectivity between microbiomes influence bacterial evolutionary rates?. <i>FEMS Microbiology Ecology</i> , 2020, 96, .	1.3	8
520	Absence of genome reduction in diverse, facultative endohyphal bacteria. <i>Microbial Genomics</i> , 2017, 3, e000101.	1.0	30

#	ARTICLE	IF	CITATIONS
544	Determination of the molecular basis for coprogen import by Gram-negative bacteria. <i>IUCrj</i> , 2019, 6, 401-411.	1.0	19
545	Horizontal Gene Transfer to a Defensive Symbiont with a Reduced Genome in a Multipartite Beetle Microbiome. <i>MBio</i> , 2020, 11, .	1.8	52
546	Is the pan-genome also a pan-selectome?. <i>F1000Research</i> , 2012, 1, 16.	0.8	33
547	Sharing the sandbox: Evolutionary mechanisms that maintain bacterial cooperation. <i>F1000Research</i> , 2015, 4, 1504.	0.8	34
548	What Is the Tree of Life?. <i>PLoS Genetics</i> , 2016, 12, e1005912.	1.5	35
549	Strong Genome-Wide Selection Early in the Evolution of <i>Prochlorococcus</i> Resulted in a Reduced Genome through the Loss of a Large Number of Small Effect Genes. <i>PLoS ONE</i> , 2014, 9, e88837.	1.1	58
550	Adaptation of a Cyanobacterium to a Biochemically Rich Environment in Experimental Evolution as an Initial Step toward a Chloroplast-Like State. <i>PLoS ONE</i> , 2014, 9, e98337.	1.1	10
551	Adaptive Evolution of Synthetic Cooperating Communities Improves Growth Performance. <i>PLoS ONE</i> , 2014, 9, e108297.	1.1	47
552	An Economic Framework of Microbial Trade. <i>PLoS ONE</i> , 2015, 10, e0132907.	1.1	46
553	Tracing the active genetic diversity of <i>Microcystis</i> and <i>Microcystis</i> phage through a temporal survey of Taihu. <i>PLoS ONE</i> , 2020, 15, e0244482.	1.1	9
554	NOVEL INSIGHT INTO EVOLUTIONARY PROCESS FROM AVERAGE GENOME SIZE IN MARINE BACTERIOPLANKTONIC BIOTA. <i>Applied Ecology and Environmental Research</i> , 2016, 14, 65-75.	0.2	8
555	Mixed cultures as model communities: hunting for ubiquitous microorganisms, their partners, and interactions. <i>Aquatic Microbial Ecology</i> , 2016, 77, 79-85.	0.9	34
556	The Effects of Ocean Acidity and Elevated Temperature on Bacterioplankton Community Structure and Metabolism. <i>Open Journal of Ecology</i> , 2014, 04, 434-455.	0.4	12
557	The lost world of Cuatro Ci�negas Basin, a relictual bacterial niche in a desert oasis. <i>ELife</i> , 2018, 7, .	2.8	51
558	Reconstructing the functions of endosymbiotic Mollicutes in fungus-growing ants. <i>ELife</i> , 2018, 7, .	2.8	39
559	Disentangling strictly self-serving mutations from win-win mutations in a mutualistic microbial community. <i>ELife</i> , 2019, 8, .	2.8	13
560	Genomic adaptations in information processing underpin trophic strategy in a whole-ecosystem nutrient enrichment experiment. <i>ELife</i> , 2020, 9, .	2.8	21
561	Emergence and diversification of a host-parasite RNA ecosystem through Darwinian evolution. <i>ELife</i> , 2020, 9, .	2.8	30

#	ARTICLE	IF	CITATIONS
562	Slightly beneficial genes are retained by bacteria evolving DNA uptake despite selfish elements. <i>ELife</i> , 2020, 9, .	2.8	29
563	Does diversity beget diversity in microbiomes?. <i>ELife</i> , 2020, 9, .	2.8	33
564	Energy Availability Determines Strategy of Microbial Amino Acid Synthesis in Volatile Fatty Acidâ€Fed Anaerobic Methanogenic Chemostats. <i>Frontiers in Microbiology</i> , 2021, 12, 744834.	1.5	3
565	Genome Streamlining, Plasticity, and Metabolic Versatility Distinguish Co-occurring Toxic and Nontoxic Cyanobacterial Strains of <i>Microcoleus</i> . <i>MBio</i> , 2021, 12, e0223521.	1.8	11
566	Molecular signatures of <i>Janthinobacterium lividum</i> from Trinidad support high potential for crude oil metabolism. <i>BMC Microbiology</i> , 2021, 21, 287.	1.3	2
567	A cellâ€cell atlas approach for understanding symbiotic interactions between microbes. <i>Current Opinion in Microbiology</i> , 2021, 64, 47-59.	2.3	4
579	In the Beginning, There Was Fire: Cuatro CiÃnegas Basin (CCB) and the Long History of Life on Earth. <i>Cuatro Cielnegas Basin: an Endangered Hyperdiverse Oasis</i> , 2018, , 21-33.	0.4	8
580	Single Genus Approach to Understanding Bacterial Diversity, Niche, Distribution, and Genomics: The <i>Bacillus</i> in Cuatro CiÃnegas. <i>Cuatro Cielnegas Basin: an Endangered Hyperdiverse Oasis</i> , 2018, , 103-112.	0.4	0
588	Considering Intra-individual Genetic Heterogeneity to Understand Biodiversity. <i>History, Philosophy and Theory of the Life Sciences</i> , 2019, , 219-232.	0.4	0
589	Microbiome: Effect on Plant System, Current Application and Future Aspect. , 2019, , 119-134.		0
590	Probing the Process-Based Approach to Biodiversity: Can Plasticity Lead to the Emergence of Novel Units of Biodiversity?. <i>History, Philosophy and Theory of the Life Sciences</i> , 2019, , 247-268.	0.4	0
603	Salinity Drives Functional and Taxonomic Diversities in Global Water Metagenomes. <i>Frontiers in Microbiology</i> , 2021, 12, 719725.	1.5	6
604	Genetic detection of freshwater harmful algal blooms: A review focused on the use of environmental DNA (eDNA) in <i>Microcystis aeruginosa</i> and <i>Prymnesium parvum</i> . <i>Harmful Algae</i> , 2021, 110, 102124.	2.2	15
605	Horizontal Gene Transfer Drives the Evolution of Dependencies in Bacteria. <i>SSRN Electronic Journal</i> , 0, , .	0.4	0
606	Lipid synthesis at the trophic base as the source for energy management to build complex structures. <i>Current Opinion in Biotechnology</i> , 2022, 73, 364-373.	3.3	1
607	Predetermined clockwork microbial worlds: Current understanding of aquatic microbial diel response from model systems to complex environments. <i>Advances in Applied Microbiology</i> , 2020, 113, 163-191.	1.3	2
611	Stable Soil Microbial Functional Structure Responding to Biodiversity Loss Based on Metagenomic Evidences. <i>Frontiers in Microbiology</i> , 2021, 12, 716764.	1.5	10
612	Discovery of nondiazotrophic <i>Trichodesmium</i> species abundant and widespread in the open ocean. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2021, 118, .	3.3	31

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613	Closed microbial communities self-organize to persistently cycle carbon. Proceedings of the National Academy of Sciences of the United States of America, 2021, 118, .	3.3	13
614	Positive interactions are common among culturable bacteria. Science Advances, 2021, 7, eabi7159.	4.7	107
615	Symbiosis in Digital Evolution: Past, Present, and Future. Frontiers in Ecology and Evolution, 2021, 9, .	1.1	3
622	Design Principles of Microbial Communities: From Understanding to Engineering. Current Genomics, 2018, 19, 699.	0.7	3
623	Bacterial cooperation through horizontal gene transfer. Trends in Ecology and Evolution, 2022, 37, 223-232.	4.2	33
624	Heme auxotrophy in abundant aquatic microbial lineages. Proceedings of the National Academy of Sciences of the United States of America, 2021, 118, .	3.3	20
625	Coming full circle on diazotrophy in the marine cyanobacterium Trichodesmium. Proceedings of the National Academy of Sciences of the United States of America, 2021, 118, e2117967118.	3.3	3
626	Contribution of Lactobacillus iners to Vaginal Health and Diseases: A Systematic Review. Frontiers in Cellular and Infection Microbiology, 2021, 11, 792787.	1.8	60
627	A primer and discussion on DNA-based microbiome data and related bioinformatics analyses. , 0, 1, .		6
628	What makes a megaplasmid?. Philosophical Transactions of the Royal Society B: Biological Sciences, 2022, 377, 20200472.	1.8	44
629	Evolution of cooperation in costly institutions exhibits Red Queen and Black Queen dynamics in heterogeneous public goods. Communications Biology, 2021, 4, 1340.	2.0	6
630	The symbiosis among, and the storage stabilities of, starter lactic acid bacterial strains in biofilms. LWT - Food Science and Technology, 2022, 155, 112896.	2.5	4
631	A Genomic Perspective Across Earth's Microbiomes Reveals That Genome Size in Archaea and Bacteria Is Linked to Ecosystem Type and Trophic Strategy. Frontiers in Microbiology, 2021, 12, 761869.	1.5	29
633	Conversion of Carbon Monoxide to Chemicals Using Microbial Consortia. Advances in Biochemical Engineering/Biotechnology, 2021, , 1.	0.6	0
634	Cheating Promotes Coexistence in a Two-Species One-Substrate Culture Model. Frontiers in Ecology and Evolution, 2022, 9, .	1.1	3
635	Revisiting Leigh Van Valen's "A New Evolutionary Law" (1973). Biological Theory, 2022, 17, 120-125.	0.8	13
637	Comparative genomics reveals electron transfer and syntrophic mechanisms differentiating methanotrophic and methanogenic archaea. PLoS Biology, 2022, 20, e3001508.	2.6	62
638	<i>Prochlorococcus</i> Exudate Stimulates Heterotrophic Bacterial Competition with Rival Phytoplankton for Available Nitrogen. MBio, 2022, 13, e0257121.	1.8	6

#	ARTICLE	IF	CITATIONS
639	Comparative genomics for understanding intraspecific diversity: a case study of the cyanobacterium <i>Raphidiopsis raciborskii</i> . , 2022, , 415-434.		3
640	Habitat Adaptation Drives Speciation of a <i>Streptomyces</i> Species with Distinct Habitats and Disparate Geographic Origins. <i>MBio</i> , 2022, 13, e0278121.	1.8	15
641	Metabolically dependent consortia in biofilm: A new horizon for green agriculture. <i>Biocatalysis and Agricultural Biotechnology</i> , 2022, 39, 102256.	1.5	0
642	Genomic evidence of functional diversity in DPANN archaea, from oxic species to anoxic vampiristic consortia. <i>ISME Communications</i> , 2022, 2, .	1.7	15
643	Non-invasive monitoring of multiple wildlife health factors by fecal microbiome analysis. <i>Ecology and Evolution</i> , 2022, 12, e8564.	0.8	16
644	Dynamic Responses of Endosymbiotic Microbial Communities Within <i>Microcystis</i> Colonies in North American Lakes to Altered Nitrogen, Phosphorus, and Temperature Levels. <i>Frontiers in Microbiology</i> , 2021, 12, 781500.	1.5	3
645	The seaweed holobiont: from microecology to biotechnological applications. <i>Microbial Biotechnology</i> , 2022, 15, 738-754.	2.0	27
647	Emerging connections between gut microbiome bioenergetics and chronic metabolic diseases. <i>Cell Reports</i> , 2021, 37, 110087.	2.9	31
650	Select <i>Streptococci</i> Can Degrade <i>Candida</i> Mannan To Facilitate Growth. <i>Applied and Environmental Microbiology</i> , 2022, 88, aem0223721.	1.4	3
651	Filter Plating Method for Rendering Picocyanobacteria Cultures Free of Heterotrophic Bacterial Contaminants and Clonal. <i>Frontiers in Microbiology</i> , 2022, 13, 821803.	1.5	3
652	Convergent Loss of Prothoracicotropic Hormone, A Canonical Regulator of Development, in Social Bee Evolution. <i>Frontiers in Physiology</i> , 2022, 13, 831928.	1.3	0
653	Evolution of Phytoplankton as Estimated from Genetic Diversity. <i>Journal of Marine Science and Engineering</i> , 2022, 10, 456.	1.2	5
654	Contrasting Strategies for Sucrose Utilization in a Floral Yeast Clade. <i>MSphere</i> , 2022, 7, e0003522.	1.3	4
655	Functional and Phylogenetic Characterization of Bacteria in Bovine Rumen Using Fractionation of Ruminal Fluid. <i>Frontiers in Microbiology</i> , 2022, 13, 813002.	1.5	8
656	Biofilm through the Looking Glass: A Microbial Food Safety Perspective. <i>Pathogens</i> , 2022, 11, 346.	1.2	20
658	Microbial communities form rich extracellular metabolomes that foster metabolic interactions and promote drug tolerance. <i>Nature Microbiology</i> , 2022, 7, 542-555.	5.9	58
659	Give and take in the exometabolome. <i>Nature Microbiology</i> , 2022, 7, 484-485.	5.9	0
660	A comparative whole-genome approach identifies bacterial traits for marine microbial interactions. <i>Communications Biology</i> , 2022, 5, 276.	2.0	18

#	ARTICLE	IF	CITATIONS
661	The population genetics of adaptation through copy number variation in a fungal plant pathogen. <i>Molecular Ecology</i> , 2023, 32, 2443-2460.	2.0	14
662	Microbial metabolites in the marine carbon cycle. <i>Nature Microbiology</i> , 2022, 7, 508-523.	5.9	71
663	Cooperation increases robustness to ecological disturbance in microbial cross-feeding networks. <i>Ecology Letters</i> , 2022, 25, 1410-1420.	3.0	16
664	Noisy metabolism can promote microbial cross-feeding. <i>ELife</i> , 2022, 11, .	2.8	20
665	Reactive oxygen species in the world ocean and their impacts on marine ecosystems. <i>Redox Biology</i> , 2022, 52, 102285.	3.9	37
667	Microbial Systems Ecology to Understand Cross-Feeding in Microbiomes. <i>Frontiers in Microbiology</i> , 2021, 12, 780469.	1.5	13
668	<i>Prochlorococcus</i> have low global mutation rate and small effective population size. <i>Nature Ecology and Evolution</i> , 2022, 6, 183-194.	3.4	16
670	Resurrection of an ancient inflammatory locus reveals switch to caspase-1 specificity on a caspase-4 scaffold. <i>Journal of Biological Chemistry</i> , 2022, 298, 101931.	1.6	3
671	The Evolution of Microbial Facilitation: Sociogenesis, Symbiogenesis, and Transition in Individuality. <i>Frontiers in Ecology and Evolution</i> , 2022, 10, .	1.1	1
672	Gaia as Solaris: An Alternative Default Evolutionary Trajectory. <i>Origins of Life and Evolution of Biospheres</i> , 2022, 52, 129-147.	0.8	3
673	Sponges present a core prokaryotic community stable across Tropical Western Atlantic. <i>Science of the Total Environment</i> , 2022, 835, 155145.	3.9	7
721	Impact of Genome Reduction in Microsporidia. <i>Experientia Supplementum (2012)</i> , 2022, 114, 1-42.	0.5	14
722	Genome evolution of a nonparasitic secondary heterotroph, the diatom <i>Nitzschia putrida</i> . <i>Science Advances</i> , 2022, 8, eabi5075.	4.7	9
723	Horizontal gene transfer drives the evolution of dependencies in bacteria. <i>IScience</i> , 2022, 25, 104312.	1.9	6
725	Complex Ecotype Dynamics Evolve in Response to Fluctuating Resources. <i>MBio</i> , 2022, 13, e0346721.	1.8	7
726	Availability of vitamin B12 and its lower ligand intermediate Î±-ribazole impact prokaryotic and protist communities in oceanic systems. <i>ISME Journal</i> , 2022, 16, 2002-2014.	4.4	12
727	Exploring the onset of B ₁₂ -based mutualisms using a recently evolved <i>Chlamydomonas</i> auxotroph and B ₁₂ -producing bacteria. <i>Environmental Microbiology</i> , 2022, 24, 3134-3147.	1.8	14
729	Community Interaction Co-limitation: Nutrient Limitation in a Marine Microbial Community Context. <i>Frontiers in Microbiology</i> , 2022, 13, .	1.5	7

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730	DARHD: A sequence database for aromatic ring-hydroxylating dioxygenase analysis and primer evaluation. <i>Journal of Hazardous Materials</i> , 2022, 436, 129230.	6.5	7
732	Genome-wide identification of fitness determinants in the <i>Xanthomonas campestris</i> bacterial pathogen during early stages of plant infection. <i>New Phytologist</i> , 2022, 236, 235-248.	3.5	8
733	Higher level constructive neutral evolution. <i>Biology and Philosophy</i> , 2022, 37, .	0.7	1
735	Mutualistic interplay between bacteriophages and bacteria in the human gut. <i>Nature Reviews Microbiology</i> , 2022, 20, 737-749.	13.6	47
736	Substrate availability and toxicity shape the structure of microbial communities engaged in metabolic division of labor. , 2022, 1, 131-145.		9
737	Heterotrophic Bacteria Dominate Catalase Expression during <i>Microcystis</i> Blooms. <i>Applied and Environmental Microbiology</i> , 2022, 88, .	1.4	14
738	Nutritional interdependencies and a carbazole-dioxygenase are key elements of a bacterial consortium relying on a <i>Sphingomonas</i> for the degradation of the fungicide thiabendazole. <i>Environmental Microbiology</i> , 2022, 24, 5105-5122.	1.8	9
739	Quantitative and analytical tools to analyze the spatiotemporal population dynamics of microbial consortia. <i>Current Opinion in Biotechnology</i> , 2022, 76, 102754.	3.3	4
740	Distribution of extracellular amino acids and their potential functions in microbial cross-feeding in anaerobic digestion systems. <i>Bioresource Technology</i> , 2022, 360, 127535.	4.8	7
741	Cross-kingdom co-occurrence networks in the plant microbiome: Importance and ecological interpretations. <i>Frontiers in Microbiology</i> , 0, 13, .	1.5	15
742	Efficient management of the nitrification-anammox microbiome through intermittent aeration: absence of the NOB guild and expansion and diversity of the NOx reducing guild suggests a highly reticulated nitrogen cycle. <i>Environmental Microbiomes</i> , 2022, 17, .	2.2	1
743	Metabolism Interactions Promote the Overall Functioning of the Episymbiotic Chemosynthetic Community of <i>Shinkaia crosnieri</i> of Cold Seeps. <i>MSystems</i> , 2022, 7, .	1.7	5
744	Initial community composition determines the long-term dynamics of a microbial cross-feeding interaction by modulating niche availability. <i>ISME Communications</i> , 2022, 2, .	1.7	5
745	A Salvaging Strategy Enables Stable Metabolite Provisioning among Free-Living Bacteria. <i>MSystems</i> , 2022, 7, .	1.7	8
746	The overlooked role of a biotin precursor for marine bacteria - desthiobiotin as an escape route for biotin auxotrophy. <i>ISME Journal</i> , 2022, 16, 2599-2609.	4.4	9
747	Metabolic adaptation to vitamin auxotrophy by leaf-associated bacteria. <i>ISME Journal</i> , 2022, 16, 2712-2724.	4.4	19
749	Very early evolution from the perspective of microbial ecology. <i>Environmental Microbiology</i> , 2023, 25, 5-10.	1.8	2
750	Evolution of pathogenicity in obligate fungal pathogens and allied genera. <i>PeerJ</i> , 0, 10, e13794.	0.9	2

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751	Biodegradable microplastics impact the uptake of Cd in rice: The roles of niche breadth and assembly process. <i>Science of the Total Environment</i> , 2022, 851, 158222.	3.9	10
752	Defective Subviral Particles Modify Ecological Equilibria and Enhance Viral Coexistence. <i>Frontiers in Virology</i> , 0, 2, .	0.7	1
753	How to Completely Squeeze a Fungusâ€™ Advanced Genome Mining Tools for Novel Bioactive Substances. <i>Pharmaceutics</i> , 2022, 14, 1837.	2.0	9
754	Flavobacterial exudates disrupt cell cycle progression and metabolism of the diatom <i>Thalassiosira pseudonana</i> . <i>ISME Journal</i> , 2022, 16, 2741-2751.	4.4	8
755	High throughput genome scale modeling predicts microbial vitamin requirements contribute to gut microbiome community structure. <i>Gut Microbes</i> , 2022, 14, .	4.3	7
757	Reconciling concepts of black queen and tragedy of the commons in simulated bulk soil and rhizosphere prokaryote communities. <i>Frontiers in Microbiology</i> , 0, 13, .	1.5	1
758	Exploring Bacterial Attributes That Underpin Symbiont Life in the Monogastric Gut. <i>Applied and Environmental Microbiology</i> , 2022, 88, .	1.4	4
759	Selection, drift and community interactions shape microbial biogeographic patterns in the Pacific Ocean. <i>ISME Journal</i> , 2022, 16, 2653-2665.	4.4	27
760	Prokaryotic Pangenomes Act as Evolving Ecosystems. <i>Molecular Biology and Evolution</i> , 2023, 40, .	3.5	6
761	Insights on the bacterial composition of Parmigiano Reggiano Natural Whey Starter by a culture-dependent and 16S rRNA metabarcoding portrait. <i>Scientific Reports</i> , 2022, 12, .	1.6	5
762	Electrochemical Enrichment and Isolation of Electrogenic Bacteria from 0.22 Åµm Filtrate. <i>Microorganisms</i> , 2022, 10, 2051.	1.6	1
764	How public can public goods be? Environmental context shapes the evolutionary ecology of partially private goods. <i>PLoS Computational Biology</i> , 2022, 18, e1010666.	1.5	4
765	Guided by the principles of microbiome engineering: Accomplishments and perspectives for environmental use. , 2022, 1, 382-398.		13
767	Community context and pCO ₂ impact the transcriptome of the "helper" bacterium <i>Alteromonas</i> in co-culture with picocyanobacteria. <i>ISME Communications</i> , 2022, 2, .	1.7	2
768	Why can insects not biosynthesize cholesterol?. <i>Archives of Insect Biochemistry and Physiology</i> , 2023, 112, .	0.6	2
769	Phototroph-heterotroph interactions during growth and long-term starvation across <i>Prochlorococcus</i> and <i>Alteromonas</i> diversity. <i>ISME Journal</i> , 2023, 17, 227-237.	4.4	4
770	The mechanism of nanoparticle toxicity to cyanobacteria. <i>Archives of Microbiology</i> , 2023, 205, .	1.0	5
771	Involvement of Microbiota in Insect Physiology: Focus on B Vitamins. <i>MBio</i> , 2023, 14, .	1.8	9

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772	Adaptive genetic traits in pelagic freshwater microbes. <i>Environmental Microbiology</i> , 2023, 25, 606-641.	1.8	12
773	Exploring the Interspecific Interactions and the Metabolome of the Soil Isolate <i>Hylemonella gracilis</i> . <i>MSystems</i> , 0, , .	1.7	0
774	Upwelled plankton community modulates surface bloom succession and nutrient availability in a natural plankton assemblage. <i>Biogeosciences</i> , 2022, 19, 5911-5926.	1.3	2
775	Reply to: Erroneous predictions of auxotrophies by CarveMe. <i>Nature Ecology and Evolution</i> , 0, , .	3.4	0
776	Multi-genome metabolic modeling predicts functional inter-dependencies in the <i>Arabidopsis</i> root microbiome. <i>Microbiome</i> , 2022, 10, .	4.9	12
777	Studies of Lacustrine Phytoplankton: Current Trends and Prospects Considering Algae-Bacteria Interactions. <i>Russian Journal of Ecology</i> , 2022, 53, 478-484.	0.3	1
778	Nutrient encryption and the diversity of cobamides, siderophores, and glycans. <i>Trends in Microbiology</i> , 2023, 31, 115-119.	3.5	2
779	Not all bad: Gyromitrin has a limited distribution in the false morels as determined by a new ultra high-performance liquid chromatography method. <i>Mycologia</i> , 2023, 115, 1-15.	0.8	3
781	Gifts hidden in shadowy genome islands. <i>Cell</i> , 2023, 186, 5-7.	13.5	0
782	Warmer and drier ecosystems select for smaller bacterial genomes in global soils. , 0, , .		4
783	Mechanism for Utilization of the <i>Populus</i> -Derived Metabolite Salicin by a <i>Pseudomonas</i> – <i>Rhizobium</i> Co-Culture. <i>Metabolites</i> , 2023, 13, 140.	1.3	2
784	Site Specialization of Human Oral <i>Veillonella</i> Species. <i>Microbiology Spectrum</i> , 2023, 11, .	1.2	5
785	The origin and evolution of methanogenesis and <i>Archaea</i> are intertwined. , 2023, 2, .		7
787	Photosynthetic picoeukaryotes significantly affect global oceanic meta-metabolism: cellular and genome streamlining confer ecological success. <i>Aquatic Microbial Ecology</i> , 2023, 89, 23-41.	0.9	1
789	Reduction, evolutionary pattern and positive selection of genes encoding formate dehydrogenase in <i>Woodwardia-Ljungdahl</i> pathway of gastrointestinal acetogens suggests their adaptation to formate-rich habitats. <i>Environmental Microbiology Reports</i> , 2023, 15, 129-141.	1.0	2
790	The informational affective tie mechanism: on the role of uncertainty, context, and attention in caring. <i>Journal of Economic Psychology</i> , 2023, 97, 102625.	1.1	1
792	Mitochondrial genomes in the iconic reindeer lichens: Architecture, variation, and synteny across multiple evolutionary scales. <i>Mycologia</i> , 2023, 115, 187-205.	0.8	1
793	When biodiversity preservation meets biotechnology: The challenge of developing synthetic microbiota for resilient sustainable crop production. , 2023, 2, 5-15.		2

#	ARTICLE	IF	CITATIONS
794	Community diversity is associated with intra-species genetic diversity and gene loss in the human gut microbiome. <i>ELife</i> , 0, 12, .	2.8	9
795	Single-€ amplified genomes reveal most streamlined free-€ living marine bacteria. <i>Environmental Microbiology</i> , 2023, 25, 1136-1154.	1.8	5
796	Trait biases in microbial reference genomes. <i>Scientific Data</i> , 2023, 10, .	2.4	4
797	Cooperative virulence via the collective action of secreted pathogen effectors. <i>Nature Microbiology</i> , 2023, 8, 640-650.	5.9	16
798	Production of polyhydroxyalkanoate by mixed cultivation of <i>Brevundimonas diminuta</i> R79 and <i>Pseudomonas balearica</i> R90. <i>International Journal of Biological Macromolecules</i> , 2023, 234, 123667.	3.6	4
799	Structure-€ Thermodynamic Relationship of a Polysaccharide Gel (Alginate) as a Function of Water Content and Counterion Type (Na vs Ca). <i>Journal of Physical Chemistry B</i> , 2023, 127, 1828-1841.	1.2	0
800	Ecological divergence of syntopic marine bacterial species is shaped by gene content and expression. <i>ISME Journal</i> , 2023, 17, 813-822.	4.4	3
801	Social Diversification Driven by Mobile Genetic Elements. <i>Genes</i> , 2023, 14, 648.	1.0	2
802	Core Species Derived from Multispecies Interactions Facilitate the Immobilization of Cadmium. <i>Environmental Science & Technology</i> , 2023, 57, 4905-4914.	4.6	4
803	Microbial and Viral Genome and Proteome Nitrogen Demand Varies across Multiple Spatial Scales within a Marine Oxygen Minimum Zone. <i>MSystems</i> , 2023, 8, .	1.7	1
804	Transporter Proteins as Ecological Assets and Features of Microbial Eukaryotic Pangenomes. <i>Annual Review of Microbiology</i> , 2023, 77, 45-66.	2.9	1
805	Linking prokaryotic genome size variation to metabolic potential and environment. <i>ISME Communications</i> , 2023, 3, .	1.7	1
806	Niche Modification by Sulfate-Reducing Bacteria Drives Microbial Community Assembly in Anoxic Marine Sediments. <i>MBio</i> , 0, , .	1.8	1
807	Anti- <i>Porphyromonas gingivalis</i> nanotherapy for maintaining bacterial homeostasis in periodontitis. <i>International Journal of Antimicrobial Agents</i> , 2023, 61, 106801.	1.1	1
808	Genomic Islands in Bacterial Genome Evolution and Speciation. , 2023, , 83-109.		1
809	The role of the ecological scaffold in the origin and maintenance of whole-group trait altruism in microbial populations. <i>Bmc Ecology and Evolution</i> , 2023, 23, .	0.7	2
810	Cross-feeding in the gut microbiome: Ecology and mechanisms. <i>Cell Host and Microbe</i> , 2023, 31, 485-499.	5.1	34
811	Origins and evolution of biological novelty. <i>Biological Reviews</i> , 2023, 98, 1472-1491.	4.7	3

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813	Ecological interactions and the underlying mechanism of anammox and denitrification across the anammox enrichment with eutrophic lake sediments. <i>Microbiome</i> , 2023, 11, .	4.9	10
822	Biofilms. , 2023, , 325-335.		0
842	Progress and challenges in exploring aquatic microbial communities using non-targeted metabolomics. <i>ISME Journal</i> , 2023, 17, 2147-2159.	4.4	1