

Rudolf I Amann

List of Publications by Year in descending order

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365
papers

72,526
citations

434

131
h-index

641

256
g-index

382
all docs

382
docs citations

382
times ranked

34129
citing authors

#	ARTICLE	IF	CITATIONS
1	Highly diverse flavobacterial phages isolated from North Sea spring blooms. ISME Journal, 2022, 16, 555-568.	4.4	32
2	<i>Verrucomicrobiota</i> are specialist consumers of sulfated methyl pentoses during diatom blooms. ISME Journal, 2022, 16, 630-641.	4.4	62
3	Niche differentiation of sulfur-oxidizing bacteria (SUP05) in submarine hydrothermal plumes. ISME Journal, 2022, 16, 1479-1490.	4.4	11
4	Niche partitioning of the ubiquitous and ecologically relevant NS5 marine group. ISME Journal, 2022, 16, 1570-1582.	4.4	11
5	Strong seasonal differences of bacterial polysaccharide utilization in the North Sea over an annual cycle. Environmental Microbiology, 2022, 24, 2333-2347.	1.8	2
6	Glycoside hydrolase from the GH76 family indicates that marine <i>Salegendibacter</i> sp. Hel_I_6 consumes alpha-mannan from fungi. ISME Journal, 2022, 16, 1818-1830.	4.4	8
7	Diversity and biomass dynamics of unicellular marine fungi during a spring phytoplankton bloom. Environmental Microbiology, 2021, 23, 448-463.	1.8	22
8	Distinct ecotypes within a natural haloarchaeal population enable adaptation to changing environmental conditions without causing population sweeps. ISME Journal, 2021, 15, 1178-1191.	4.4	14
9	Quantifying fluorescent glycan uptake to elucidate strain-level variability in foraging behaviors of rumen bacteria. Microbiome, 2021, 9, 23.	4.9	16
10	Diatom fucan polysaccharide precipitates carbon during algal blooms. Nature Communications, 2021, 12, 1150.	5.8	58
11	Changing expression patterns of TonB-dependent transporters suggest shifts in polysaccharide consumption over the course of a spring phytoplankton bloom. ISME Journal, 2021, 15, 2336-2350.	4.4	42
12	Particle Collection in Imhoff Sedimentation Cones Enriches Both Motile Chemotactic and Particle-Attached Bacteria. Frontiers in Microbiology, 2021, 12, 643730.	1.5	9
13	Bacterial communities in temperate and polar coastal sands are seasonally stable. ISME Communications, 2021, 1, .	1.7	18
14	Microbial metagenome-assembled genomes of the Fram Strait from short and long read sequencing platforms. PeerJ, 2021, 9, e11721.	0.9	14
15	Release LTP_12_2020, featuring a new ARB alignment and improved 16S rRNA tree for prokaryotic type strains. Systematic and Applied Microbiology, 2021, 44, 126218.	1.2	44
16	Tight Adherence (Tad) Pilus Genes Indicate Putative Niche Differentiation in Phytoplankton Bloom Associated Rhodobacterales. Frontiers in Microbiology, 2021, 12, 718297.	1.5	16
17	North Sea spring bloom-associated Gammaproteobacteria fill diverse heterotrophic niches. Environmental Microbiomes, 2021, 16, 15.	2.2	32
18	Cultivation of particle-associated heterotrophic bacteria during a spring phytoplankton bloom in the North Sea. Systematic and Applied Microbiology, 2021, 44, 126232.	1.2	4

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19	Cultivable <i>Winogradskyella</i> species are genomically distinct from the sympatric abundant candidate species. ISME Communications, 2021, 1, .	1.7	10
20	Specific detection and quantification of the marine flavobacterial genus <i>Zobellia</i> on macroalgae using novel qPCR and CARD-FISH assays. Systematic and Applied Microbiology, 2021, 44, 126269.	1.2	8
21	In situ visualization of glycoside hydrolase family 92 genes in marine flavobacteria. ISME Communications, 2021, 1, .	1.7	1
22	Cultivation and functional characterization of 79 planctomycetes uncovers their unique biology. Nature Microbiology, 2020, 5, 126-140.	5.9	164
23	Taxonomic study of nine new <i>Winogradskyella</i> species occurring in the shallow waters of Helgoland Roads, North Sea. Proposal of <i>Winogradskyella schleiferi</i> sp. nov., <i>Winogradskyella costae</i> sp. nov., <i>Winogradskyella helgolandensis</i> sp. nov., <i>Winogradskyella vidalii</i> sp. nov., <i>Winogradskyella forsetii</i> sp. nov., <i>Winogradskyella ludwigii</i> sp. nov., <i>Winogradskyella ursingii</i> sp. nov., <i>Winogradskyella wichelsiae</i> sp. nov., and <i>Candidatus Winogradskyella atlantica</i> sp. nov.. Systematic and Applied Microbiology, 2020, 43, 126128.	1.2	38
24	Extensive Microbial Processing of Polysaccharides in the South Pacific Gyre via Selfish Uptake and Extracellular Hydrolysis. Frontiers in Microbiology, 2020, 11, 583158.	1.5	11
25	Roadmap for naming uncultivated Archaea and Bacteria. Nature Microbiology, 2020, 5, 987-994.	5.9	115
26	Bacterioplankton reveal years-long retention of Atlantic deep-ocean water by the Tropic Seamount. Scientific Reports, 2020, 10, 4715.	1.6	8
27	Short-term changes in polysaccharide utilization mechanisms of marine bacterioplankton during a spring phytoplankton bloom. Environmental Microbiology, 2020, 22, 1884-1900.	1.8	34
28	Polysaccharide niche partitioning of distinct <i>Polaribacter</i> clades during North Sea spring algal blooms. ISME Journal, 2020, 14, 1369-1383.	4.4	50
29	High-throughput cultivation of heterotrophic bacteria during a spring phytoplankton bloom in the North Sea. Systematic and Applied Microbiology, 2020, 43, 126066.	1.2	21
30	Advantages outweigh concerns about using genome sequence as type material for prokaryotic taxonomy. Environmental Microbiology, 2020, 22, 819-822.	1.8	12
31	Ancestry and adaptive radiation of Bacteroidetes as assessed by comparative genomics. Systematic and Applied Microbiology, 2020, 43, 126065.	1.2	17
32	<i>Candidatus</i> <i>Ethanoperedens</i> , a Thermophilic Genus of Archaea Mediating the Anaerobic Oxidation of Ethane. MBio, 2020, 11, .	1.8	66
33	<i>Candidatus</i> <i>Abditibacter</i> , a novel genus within the Cryomorphaceae, thriving in the North Sea. Systematic and Applied Microbiology, 2020, 43, 126088.	1.2	21
34	Polysaccharide utilization loci of North Sea <i>Flavobacteriia</i> as basis for using SusC/D-protein expression for predicting major phytoplankton glycans. ISME Journal, 2019, 13, 76-91.	4.4	139
35	Öffentliche Sequenzdaten sollten rasch wirklich frei zugänglich sein!. BioSpektrum, 2019, 25, 119-119.	0.0	0
36	In marine Bacteroidetes the bulk of glycan degradation during algae blooms is mediated by few clades using a restricted set of genes. ISME Journal, 2019, 13, 2800-2816.	4.4	125

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37	<i>In situ</i> abundance and carbon fixation activity of distinct anoxygenic phototrophs in the stratified seawater lake Rogoznica. <i>Environmental Microbiology</i> , 2019, 21, 3896-3908.	1.8	10
38	Marine Proteobacteria metabolize glycolate via the β^2 -hydroxyaspartate cycle. <i>Nature</i> , 2019, 575, 500-504.	13.7	71
39	Niche differentiation among annually recurrent coastal Marine Group II Euryarchaeota. <i>ISME Journal</i> , 2019, 13, 3024-3036.	4.4	41
40	Predominance of deterministic microbial community dynamics in salterns exposed to different light intensities. <i>Environmental Microbiology</i> , 2019, 21, 4300-4315.	1.8	20
41	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
42	Toward unrestricted use of public genomic data. <i>Science</i> , 2019, 363, 350-352.	6.0	45
43	On-Site Analysis of Bacterial Communities of the Ultraoligotrophic South Pacific Gyre. <i>Applied and Environmental Microbiology</i> , 2019, 85, .	1.4	27
44	Consent insufficient for data releaseâ€”Response. <i>Science</i> , 2019, 364, 446-446.	6.0	5
45	First description of two moderately halophilic and psychrotolerant <i>Mycoplasma</i> species isolated from cephalopods and proposal of <i>Mycoplasma marinum</i> sp. nov. and <i>Mycoplasma todarodis</i> sp. nov. <i>Systematic and Applied Microbiology</i> , 2019, 42, 457-467.	1.2	22
46	Single cell fluorescence imaging of glycan uptake by intestinal bacteria. <i>ISME Journal</i> , 2019, 13, 1883-1889.	4.4	28
47	<i>Candidatus</i> <i>Prosiliicoccus vernus</i> , a spring phytoplankton bloom associated member of the Flavobacteriaceae. <i>Systematic and Applied Microbiology</i> , 2019, 42, 41-53.	1.2	39
48	Microbial metalâ€”sulfide oxidation in inactive hydrothermal vent chimneys suggested by metagenomic and metaproteomic analyses. <i>Environmental Microbiology</i> , 2019, 21, 682-701.	1.8	50
49	Moving the cataloguing of the â€œuncultivated majorityâ€”forward. <i>Systematic and Applied Microbiology</i> , 2019, 42, 3-4.	1.2	3
50	Genomic comparison between members of the Salinibacteraceae family, and description of a new species of <i>Salinibacter</i> (<i>Salinibacter altiplanensis</i> sp. nov.) isolated from high altitude hypersaline environments of the Argentinian Altiplano. <i>Systematic and Applied Microbiology</i> , 2018, 41, 198-212.	1.2	29
51	Recurrent patterns of microdiversity in a temperate coastal marine environment. <i>ISME Journal</i> , 2018, 12, 237-252.	4.4	135
52	Reply to the commentary â€œUncultivated microbesâ€”in need of their own nomenclature?â€”. <i>ISME Journal</i> , 2018, 12, 653-654.	4.4	8
53	Unveiling the enigma of refractory carbon in the ocean. <i>National Science Review</i> , 2018, 5, 459-463.	4.6	80
54	Microbial life on a sand grain: from bulk sediment to single grains. <i>ISME Journal</i> , 2018, 12, 623-633.	4.4	99

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55	Alpha- and beta-mannan utilization by marine <i>Bacteroidetes</i> . <i>Environmental Microbiology</i> , 2018, 20, 4127-4140.	1.8	31
56	Adaptive mechanisms that provide competitive advantages to marine bacteroidetes during microalgal blooms. <i>ISME Journal</i> , 2018, 12, 2894-2906.	4.4	84
57	Metaproteogenomic Profiling of Microbial Communities Colonizing Actively Venting Hydrothermal Chimneys. <i>Frontiers in Microbiology</i> , 2018, 9, 680.	1.5	36
58	Aquatic adaptation of a laterally acquired pectin degradation pathway in marine gammaproteobacteria. <i>Environmental Microbiology</i> , 2017, 19, 2320-2333.	1.8	57
59	Determining the bacterial cell biology of Planctomycetes. <i>Nature Communications</i> , 2017, 8, 14853.	5.8	175
60	The low diverse gastric microbiome of the jellyfish <i>Cotylorhiza tuberculata</i> is dominated by four novel taxa. <i>Environmental Microbiology</i> , 2017, 19, 3039-3058.	1.8	62
61	An alternative polysaccharide uptake mechanism of marine bacteria. <i>ISME Journal</i> , 2017, 11, 1640-1650.	4.4	149
62	Niche partitioning of diverse sulfur-oxidizing bacteria at hydrothermal vents. <i>ISME Journal</i> , 2017, 11, 1545-1558.	4.4	168
63	Genomic and physiological analyses of <i>Reinekea forsetii</i> reveal a versatile opportunistic lifestyle during spring algae blooms. <i>Environmental Microbiology</i> , 2017, 19, 1209-1221.	1.8	13
64	Uncultivated microbes in need of their own taxonomy. <i>ISME Journal</i> , 2017, 11, 2399-2406.	4.4	572
65	Direct-geneFISH: a simplified protocol for the simultaneous detection and quantification of genes and rRNA in microorganisms. <i>Environmental Microbiology</i> , 2017, 19, 70-82.	1.8	51
66	Microbial Community Response to Simulated Petroleum Seepage in Caspian Sea Sediments. <i>Frontiers in Microbiology</i> , 2017, 8, 764.	1.5	19
67	Description of <i>Gramella forsetii</i> sp. nov., a marine Flavobacteriaceae isolated from North Sea water, and emended description of <i>Gramella gaetbulicola</i> Cho et al. 2011. <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2017, 67, 697-703.	0.8	17
68	Recurring patterns in bacterioplankton dynamics during coastal spring algae blooms. <i>ELife</i> , 2016, 5, e11888.	2.8	414
69	Revised phylogeny of Bacteroidetes and proposal of sixteen new taxa and two new combinations including Rhodothermaeota phyl. nov.. <i>Systematic and Applied Microbiology</i> , 2016, 39, 281-296.	1.2	214
70	Polysaccharide utilisation loci of <i>Bacteroidetes</i> from two contrasting open ocean sites in the North Atlantic. <i>Environmental Microbiology</i> , 2016, 18, 4456-4470.	1.8	56
71	After All, Only Millions?. <i>MBio</i> , 2016, 7, .	1.8	38
72	Habitat and taxon as driving forces of carbohydrate catabolism in marine heterotrophic bacteria: example of the model algae-associated bacterium <i>Zobellia galactanivorans</i> . <i>Environmental Microbiology</i> , 2016, 18, 4610-4627.	1.8	131

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73	Reply to "The Underestimation of Global Microbial Diversity". <i>MBio</i> , 2016, 7, .	1.8	6
74	Heterotrophic <i>Proteobacteria</i> in the vicinity of diffuse hydrothermal venting. <i>Environmental Microbiology</i> , 2016, 18, 4348-4368.	1.8	63
75	Chlamydial seasonal dynamics and isolation of <i>Candidatus</i> <i>Neptunochlamydia vexilliferae</i> ™ from a Tethyan coastal lake. <i>Environmental Microbiology</i> , 2016, 18, 2405-2417.	1.8	21
76	The application of "omics" technologies for the classification and identification of animals. <i>Organisms Diversity and Evolution</i> , 2016, 16, 1-12.	0.7	49
77	Colonization in the Photic Zone and Subsequent Changes during Sinking Determine Bacterial Community Composition in Marine Snow. <i>Applied and Environmental Microbiology</i> , 2015, 81, 1463-1471.	1.4	89
78	Past and future species definitions for Bacteria and Archaea. <i>Systematic and Applied Microbiology</i> , 2015, 38, 209-216.	1.2	470
79	Rapid and sensitive identification of marine bacteria by an improved in situ DNA hybridization chain reaction (quickHCR-FISH). <i>Systematic and Applied Microbiology</i> , 2015, 38, 400-405.	1.2	23
80	Taxonomy in the age of genomics. <i>Systematic and Applied Microbiology</i> , 2015, 38, 207-208.	1.2	12
81	The effect of nutrients on carbon and nitrogen fixation by the UCYN-A "haptophyte symbiosis. <i>ISME Journal</i> , 2015, 9, 1635-1647.	4.4	83
82	Community Shift from Phototrophic to Chemotrophic Sulfide Oxidation following Anoxic Holomixis in a Stratified Seawater Lake. <i>Applied and Environmental Microbiology</i> , 2015, 81, 298-308.	1.4	52
83	Niches of two polysaccharide-degrading <i>Polaribacter</i> isolates from the North Sea during a spring diatom bloom. <i>ISME Journal</i> , 2015, 9, 1410-1422.	4.4	182
84	Dilution cultivation of marine heterotrophic bacteria abundant after a spring phytoplankton bloom in the North Sea. <i>Environmental Microbiology</i> , 2015, 17, 3515-3526.	1.8	56
85	Comparison of bacterial communities on limnic versus coastal marine particles reveals profound differences in colonization. <i>Environmental Microbiology</i> , 2015, 17, 3500-3514.	1.8	148
86	High Diversity of Anaerobic Alkane-Degrading Microbial Communities in Marine Seep Sediments Based on (1-methylalkyl)succinate Synthase Genes. <i>Frontiers in Microbiology</i> , 2015, 6, 1511.	1.5	47
87	<i>Allochromatium humboldtianum</i> sp. nov., isolated from soft coastal sediments. <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2015, 65, 2980-2985.	0.8	9
88	Massive Regime Shifts and High Activity of Heterotrophic Bacteria in an Ice-Covered Lake. <i>PLoS ONE</i> , 2014, 9, e113611.	1.1	60
89	Identification and activity of acetate-assimilating bacteria in diffuse fluids venting from two deep-sea hydrothermal systems. <i>FEMS Microbiology Ecology</i> , 2014, 90, 731-746.	1.3	21
90	Functional characterization of polysaccharide utilization loci in the marine <i>Bacteroidetes</i> <i>Candidatus</i> <i>Gramella forsetii</i> ™ KT0803. <i>ISME Journal</i> , 2014, 8, 1492-1502.	4.4	177

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91	Genomic Encyclopedia of Bacteria and Archaea: Sequencing a Myriad of Type Strains. PLoS Biology, 2014, 12, e1001920.	2.6	190
92	Microbial lipids reveal carbon assimilation patterns on hydrothermal sulfide chimneys. Environmental Microbiology, 2014, 16, 3515-3532.	1.8	44
93	Distribution of a consortium between unicellular algae and the <i>N₂</i> fixing cyanobacterium <i>UCYN-A</i> in the North Atlantic Ocean. Environmental Microbiology, 2014, 16, 3153-3167.	1.8	38
94	Evaluation of the 23S rRNA gene as target for qPCR based quantification of Frankia in soils. Systematic and Applied Microbiology, 2014, 37, 229-234.	1.2	13
95	Uniting the classification of cultured and uncultured bacteria and archaea using 16S rRNA gene sequences. Nature Reviews Microbiology, 2014, 12, 635-645.	13.6	2,000
96	Diverse sulfate-reducing bacteria of the <i>Desulfosarcina/Desulfococcus</i> clade are the key alkane degraders at marine seeps. ISME Journal, 2014, 8, 2029-2044.	4.4	182
97	Indications for algae-degrading benthic microbial communities in deep-sea sediments along the Antarctic Polar Front. Deep-Sea Research Part II: Topical Studies in Oceanography, 2014, 108, 6-16.	0.6	56
98	The metagenome of the marine anammox bacterium <i>Candidatus Scalindua profunda</i> illustrates the versatility of this globally important nitrogen cycle bacterium. Environmental Microbiology, 2013, 15, 1275-1289.	1.8	246
99	Single-cell and population level viral infection dynamics revealed by phage <i>FISH</i> , a method to visualize intracellular and free viruses. Environmental Microbiology, 2013, 15, 2306-2318.	1.8	118
100	The Genome of the Alga-Associated Marine Flavobacterium <i>Formosa agariphila</i> KMM 3901 ^T Reveals a Broad Potential for Degradation of Algal Polysaccharides. Applied and Environmental Microbiology, 2013, 79, 6813-6822.	1.4	222
101	In situ identification and N ₂ and C fixation rates of uncultivated cyanobacteria populations. Systematic and Applied Microbiology, 2013, 36, 259-271.	1.2	76
102	Mapping glycoconjugate-mediated interactions of marine Bacteroidetes with diatoms. Systematic and Applied Microbiology, 2013, 36, 417-425.	1.2	43
103	Sequencing orphan species initiative (SOS): Filling the gaps in the 16S rRNA gene sequence database for all species with validly published names. Systematic and Applied Microbiology, 2013, 36, 69-73.	1.2	98
104	Complete genome, catabolic subproteomes and key metabolites of <i>Desulfobacula toluolica</i> , a marine, aromatic compound-degrading, sulfate-reducing bacterium. Environmental Microbiology, 2013, 15, 1334-1355.	1.8	96
105	Complete genome sequence of <i>Desulfocapsa sulfexigens</i> , a marine deltaproteobacterium specialized in disproportionating inorganic sulfur compounds. Standards in Genomic Sciences, 2013, 8, 58-68.	1.5	69
106	Microbial Communities of Deep-Sea Methane Seeps at Hikurangi Continental Margin (New Zealand). PLoS ONE, 2013, 8, e72627.	1.1	78
107	All-Species Living Tree Project. , 2013, , 1-11.		0
108	Microbial Community Response during the Iron Fertilization Experiment LOHAFEX. Applied and Environmental Microbiology, 2012, 78, 8803-8812.	1.4	58

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109	<i>Roseobacter</i> clade bacteria are abundant in coastal sediments and encode a novel combination of sulfur oxidation genes. <i>ISME Journal</i> , 2012, 6, 2178-2187.	4.4	125
110	HISAT-SIMS analysis of bacterial uptake of algal-derived carbon in the Río de la Plata estuary. <i>Systematic and Applied Microbiology</i> , 2012, 35, 541-548.	1.2	30
111	Two decades of fluorescence in situ hybridization in systematic and applied microbiology. <i>Systematic and Applied Microbiology</i> , 2012, 35, 483-484.	1.2	7
112	Revealing structure and assembly cues for Arabidopsis root-inhabiting bacterial microbiota. <i>Nature</i> , 2012, 488, 91-95.	13.7	2,127
113	Distribution and in situ abundance of sulfate-reducing bacteria in diverse marine hydrocarbon seep sediments. <i>Environmental Microbiology</i> , 2012, 14, 2689-2710.	1.8	128
114	Archaea of the Miscellaneous Crenarchaeotal Group are abundant, diverse and widespread in marine sediments. <i>ISME Journal</i> , 2012, 6, 1949-1965.	4.4	281
115	Crystal ball: Fluorescence in situ hybridization in the age of super-resolution microscopy. <i>Systematic and Applied Microbiology</i> , 2012, 35, 549-552.	1.2	14
116	Contrasting extracellular enzyme activities of particle-associated bacteria from distinct provinces of the North Atlantic Ocean. <i>Frontiers in Microbiology</i> , 2012, 3, 425.	1.5	52
117	Cell surface proteome of the marine planctomycete <i>Rhodopirellula baltica</i> . <i>Proteomics</i> , 2012, 12, 1781-1791.	1.3	13
118	Multiple self-splicing introns in the 16S rRNA genes of giant sulfur bacteria. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2012, 109, 4203-4208.	3.3	62
119	Substrate-Controlled Succession of Marine Bacterioplankton Populations Induced by a Phytoplankton Bloom. <i>Science</i> , 2012, 336, 608-611.	6.0	1,304
120	Quantification of Tinto River Sediment Microbial Communities: Importance of Sulfate-Reducing Bacteria and Their Role in Attenuating Acid Mine Drainage. <i>Applied and Environmental Microbiology</i> , 2012, 78, 4638-4645.	1.4	74
121	Genomic content of uncultured <i>Bacteroidetes</i> from contrasting oceanic provinces in the North Atlantic Ocean. <i>Environmental Microbiology</i> , 2012, 14, 52-66.	1.8	137
122	High abundance of novel environmental chlamydiae in a Tyrrhenian coastal lake (Lago di Paola, Italy). <i>Environmental Microbiology Reports</i> , 2012, 4, 446-452.	1.0	11
123	Conservation of proteobacterial magnetosome genes and structures in an uncultivated member of the deep-branching <i>Nitrospira</i> phylum. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2011, 108, 1134-1139.	3.3	115
124	Concepts and software for a rational design of polynucleotide probes. <i>Environmental Microbiology Reports</i> , 2011, 3, 69-78.	1.0	18
125	Novel groups of <i>Gammaproteobacteria</i> catalyse sulfur oxidation and carbon fixation in a coastal, intertidal sediment. <i>Environmental Microbiology</i> , 2011, 13, 758-774.	1.8	136
126	Response of sulfate-reducing bacteria to an artificial oil spill in a coastal marine sediment. <i>Environmental Microbiology</i> , 2011, 13, 1488-1499.	1.8	55

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127	Bacterial sulfur cycling shapes microbial communities in surface sediments of an ultramafic hydrothermal vent field. <i>Environmental Microbiology</i> , 2011, 13, 2633-2648.	1.8	51
128	Practical application of self-organizing maps to interrelate biodiversity and functional data in NGS-based metagenomics. <i>ISME Journal</i> , 2011, 5, 918-928.	4.4	50
129	Sulfur-metabolizing bacterial populations in microbial mats of the Nakabusa hot spring, Japan. <i>Systematic and Applied Microbiology</i> , 2011, 34, 293-302.	1.2	84
130	A single-cell sequencing approach to the classification of large, vacuolated sulfur bacteria. <i>Systematic and Applied Microbiology</i> , 2011, 34, 243-259.	1.2	132
131	Release LTPs104 of the All-Species Living Tree. <i>Systematic and Applied Microbiology</i> , 2011, 34, 169-170.	1.2	146
132	The genus <i>Allochromatium</i> (Chromatiales Chromatiaceae) revisited: A study on its intragenic structure based on multilocus sequence analysis (MLSA) and DNA-DNA hybridization (DDH). <i>Systematic and Applied Microbiology</i> , 2011, 34, 590-594.	1.2	4
133	Hydrogen is an energy source for hydrothermal vent symbioses. <i>Nature</i> , 2011, 476, 176-180.	13.7	251
134	Thermophilic anaerobic oxidation of methane by marine microbial consortia. <i>ISME Journal</i> , 2011, 5, 1946-1956.	4.4	185
135	Temporal Variability of Coastal Planctomycetes Clades at Kabeltonne Station, North Sea. <i>Applied and Environmental Microbiology</i> , 2011, 77, 5009-5017.	1.4	52
136	Evaluation of the use of multilocus sequence analysis (MLSA) to resolve taxonomic conflicts within the genus <i>Marichromatium</i> . <i>Systematic and Applied Microbiology</i> , 2010, 33, 116-121.	1.2	23
137	Development of a 16S rRNA-targeted probe set for Verrucomicrobia and its application for fluorescence in situ hybridization in a humic lake. <i>Systematic and Applied Microbiology</i> , 2010, 33, 139-148.	1.2	45
138	Bacterioplankton diversity and community composition in the Southern Lagoon of Venice. <i>Systematic and Applied Microbiology</i> , 2010, 33, 128-138.	1.2	30
139	Update of the All-Species Living Tree Project based on 16S and 23S rRNA sequence analyses. <i>Systematic and Applied Microbiology</i> , 2010, 33, 291-299.	1.2	441
140	Distinct flavobacterial communities in contrasting water masses of the North Atlantic Ocean. <i>ISME Journal</i> , 2010, 4, 472-487.	4.4	143
141	Fine-scale evolution: genomic, phenotypic and ecological differentiation in two coexisting <i>Salinibacter ruber</i> strains. <i>ISME Journal</i> , 2010, 4, 882-895.	4.4	81
142	Metagenome and mRNA expression analyses of anaerobic methanotrophic archaea of the ANME-1 group. <i>Environmental Microbiology</i> , 2010, 12, 422-439.	1.8	221
143	Identification of the dominant sulfate-reducing bacterial partner of anaerobic methanotrophs of the ANME-2 clade. <i>Environmental Microbiology</i> , 2010, 12, 2327-2340.	1.8	153
144	GeneFISH – an in situ technique for linking gene presence and cell identity in environmental microorganisms. <i>Environmental Microbiology</i> , 2010, 12, 3057-3073.	1.8	75

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145	A new moderately thermophilic and high sulfide tolerant biotype of <i>Marichromatium gracile</i> , isolated from tidal sediments of the German Wadden Sea: <i>Marichromatium gracile</i> biotype <i>thermosulfidophilum</i> . <i>Systematic and Applied Microbiology</i> , 2009, 32, 1-7.	1.2	14
146	Biogeography and phylogeny of the NOR5/OM60 clade of Gammaproteobacteria. <i>Systematic and Applied Microbiology</i> , 2009, 32, 124-139.	1.2	68
147	Detoxification of sulphidic African shelf waters by blooming chemolithotrophs. <i>Nature</i> , 2009, 457, 581-584.	13.7	297
148	Genome sequence of <i>Desulfobacterium autotrophicum</i> HRM2, a marine sulfate reducer oxidizing organic carbon completely to carbon dioxide. <i>Environmental Microbiology</i> , 2009, 11, 1038-1055.	1.8	100
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