

Rudolf I Amann

List of Publications by Year in Descending Order

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The third column is the impact factor (IF) of the journal, and the fourth column is the number of citations of the article.

361
papers

57,402
citations

122
h-index

235
g-index

380
ext. papers

65,152
ext. citations

7.3
avg, IF

7.49
L-index

#	Paper	IF	Citations
361	Specific detection and quantification of the marine flavobacterial genus <i>Zobellia</i> on macroalgae using novel qPCR and CARD-FISH assays. <i>Systematic and Applied Microbiology</i> , 2021 , 44, 126269	4.2	0
360	Particle Collection in Imhoff Sedimentation Cones Enriches Both Motile Chemotactic and Particle-Attached Bacteria. <i>Frontiers in Microbiology</i> , 2021 , 12, 643730	5.7	1
359	Bacterial communities in temperate and polar coastal sands are seasonally stable. <i>ISME Communications</i> , 2021 , 1,		2
358	Microbial metagenome-assembled genomes of the Fram Strait from short and long read sequencing platforms. <i>PeerJ</i> , 2021 , 9, e11721	3.1	3
357	Diversity and biomass dynamics of unicellular marine fungi during a spring phytoplankton bloom. <i>Environmental Microbiology</i> , 2021 , 23, 448-463	5.2	9
356	Distinct ecotypes within a natural haloarchaeal population enable adaptation to changing environmental conditions without causing population sweeps. <i>ISME Journal</i> , 2021 , 15, 1178-1191	11.9	3
355	Quantifying fluorescent glycan uptake to elucidate strain-level variability in foraging behaviors of rumen bacteria. <i>Microbiome</i> , 2021 , 9, 23	16.6	8
354	Diatom fucan polysaccharide precipitates carbon during algal blooms. <i>Nature Communications</i> , 2021 , 12, 1150	17.4	12
353	Changing expression patterns of TonB-dependent transporters suggest shifts in polysaccharide consumption over the course of a spring phytoplankton bloom. <i>ISME Journal</i> , 2021 , 15, 2336-2350	11.9	8
352	Release LTP_12_2020, featuring a new ARB alignment and improved 16S rRNA tree for prokaryotic type strains. <i>Systematic and Applied Microbiology</i> , 2021 , 44, 126218	4.2	8
351	Tight Adherence (Tad) Pilus Genes Indicate Putative Niche Differentiation in Phytoplankton Bloom Associated. <i>Frontiers in Microbiology</i> , 2021 , 12, 718297	5.7	2
350	North Sea spring bloom-associated Gammaproteobacteria fill diverse heterotrophic niches. <i>Environmental Microbiomes</i> , 2021 , 16, 15	5.6	2
349	Cultivation of particle-associated heterotrophic bacteria during a spring phytoplankton bloom in the North Sea. <i>Systematic and Applied Microbiology</i> , 2021 , 44, 126232	4.2	1
348	Cultivable <i>Winogradskyella</i> species are genomically distinct from the sympatric abundant candidate species. <i>ISME Communications</i> , 2021 , 1,		1
347	Highly diverse flavobacterial phages isolated from North Sea spring blooms. <i>ISME Journal</i> , 2021 ,	11.9	2
346	Verrucomicrobiota are specialist consumers of sulfated methyl pentoses during diatom blooms. <i>ISME Journal</i> , 2021 ,	11.9	5
345	Bakterielle Mechanismen der marinen Polysaccharidverwertung. <i>BioSpektrum</i> , 2020 , 26, 800-802	0.1	

344	Roadmap for naming uncultivated Archaea and Bacteria. <i>Nature Microbiology</i> , 2020 , 5, 987-994	26.6	64
343	Bacterioplankton reveal years-long retention of Atlantic deep-ocean water by the Tropic Seamount. <i>Scientific Reports</i> , 2020 , 10, 4715	4.9	4
342	Short-term changes in polysaccharide utilization mechanisms of marine bacterioplankton during a spring phytoplankton bloom. <i>Environmental Microbiology</i> , 2020 , 22, 1884-1900	5.2	11
341	Polysaccharide niche partitioning of distinct Polaribacter clades during North Sea spring algal blooms. <i>ISME Journal</i> , 2020 , 14, 1369-1383	11.9	16
340	High-throughput cultivation of heterotrophic bacteria during a spring phytoplankton bloom in the North Sea. <i>Systematic and Applied Microbiology</i> , 2020 , 43, 126066	4.2	7
339	Advantages outweigh concerns about using genome sequence as type material for prokaryotic taxonomy. <i>Environmental Microbiology</i> , 2020 , 22, 819-822	5.2	9
338	Ancestry and adaptive radiation of Bacteroidetes as assessed by comparative genomics. <i>Systematic and Applied Microbiology</i> , 2020 , 43, 126065	4.2	6
337	"Ethanoperedens," a Thermophilic Genus of Mediating the Anaerobic Oxidation of Ethane. <i>MBio</i> , 2020 , 11,	7.8	23
336	Candidatus Abditibacter, a novel genus within the Cryomorphaceae, thriving in the North Sea. <i>Systematic and Applied Microbiology</i> , 2020 , 43, 126088	4.2	3
335	Cultivation and functional characterization of 79 planctomycetes uncovers their unique biology. <i>Nature Microbiology</i> , 2020 , 5, 126-140	26.6	85
334	Taxonomic study of nine new Winogradskyella species occurring in the shallow waters of Helgoland Roads, North Sea. Proposal of Winogradskyella schleiferi sp. nov., Winogradskyella costae sp. nov., Winogradskyella helgolandensis sp. nov., Winogradskyella vidalii sp. nov., Winogradskyella forsetii sp. nov., Winogradskyella ludwigii sp. nov., Winogradskyella ursingii sp. nov., Winogradskyella	4.2	6
333	Extensive Microbial Processing of Polysaccharides in the South Pacific Gyre via Selfish Uptake and Extracellular Hydrolysis. <i>Frontiers in Microbiology</i> , 2020 , 11, 583158	5.7	3
332	Niche differentiation among annually recurrent coastal Marine Group II Euryarchaeota. <i>ISME Journal</i> , 2019 , 13, 3024-3036	11.9	18
331	Predominance of deterministic microbial community dynamics in salterns exposed to different light intensities. <i>Environmental Microbiology</i> , 2019 , 21, 4300-4315	5.2	7
330	Selfish, sharing and scavenging bacteria in the Atlantic Ocean: a biogeographical study of bacterial substrate utilisation. <i>ISME Journal</i> , 2019 , 13, 1119-1132	11.9	43
329	Toward unrestricted use of public genomic data. <i>Science</i> , 2019 , 363, 350-352	33.3	25
328	On-Site Analysis of Bacterial Communities of the Ultraoligotrophic South Pacific Gyre. <i>Applied and Environmental Microbiology</i> , 2019 , 85,	4.8	15
327	Consent insufficient for data release-Response. <i>Science</i> , 2019 , 364, 446	33.3	4

326	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	4.2	7
325	Single cell fluorescence imaging of glycan uptake by intestinal bacteria. <i>ISME Journal</i> , 2019 , 13, 1883-1889.	9	17
324	Mit modernen Methoden zu magnetischen Mikroben. <i>BioSpektrum</i> , 2019 , 25, 18-21	0.1	1
323	Polysaccharide utilization loci of North Sea Flavobacteriia as basis for using SusC/D-protein expression for predicting major phytoplankton glycans. <i>ISME Journal</i> , 2019 , 13, 76-91	11.9	64
322	In marine Bacteroidetes the bulk of glycan degradation during algae blooms is mediated by few clades using a restricted set of genes. <i>ISME Journal</i> , 2019 , 13, 2800-2816	11.9	47
321	In situ abundance and carbon fixation activity of distinct anoxygenic phototrophs in the stratified seawater lake Rogoznica. <i>Environmental Microbiology</i> , 2019 , 21, 3896-3908	5.2	6
320	Marine Proteobacteria metabolize glycolate via the ̢-hydroxyaspartate cycle. <i>Nature</i> , 2019 , 575, 500-504	50.4	31
319	Candidatus Prosiliicoccus vernus, a spring phytoplankton bloom associated member of the Flavobacteriaceae. <i>Systematic and Applied Microbiology</i> , 2019 , 42, 41-53	4.2	18
318	Microbial metal-sulfide oxidation in inactive hydrothermal vent chimneys suggested by metagenomic and metaproteomic analyses. <i>Environmental Microbiology</i> , 2019 , 21, 682-701	5.2	20
317	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	4.2	14
316	Recurrent patterns of microdiversity in a temperate coastal marine environment. <i>ISME Journal</i> , 2018 , 12, 237-252	11.9	77
315	Reply to the commentary "Uncultivated microbes-in need of their own nomenclature?". <i>ISME Journal</i> , 2018 , 12, 653-654	11.9	7
314	Unveiling the enigma of refractory carbon in the ocean. <i>National Science Review</i> , 2018 , 5, 459-463	10.8	38
313	Adaptive mechanisms that provide competitive advantages to marine bacteroidetes during microalgal blooms. <i>ISME Journal</i> , 2018 , 12, 2894-2906	11.9	43
312	Metaproteogenomic Profiling of Microbial Communities Colonizing Actively Venting Hydrothermal Chimneys. <i>Frontiers in Microbiology</i> , 2018 , 9, 680	5.7	22
311	Microbial life on a sand grain: from bulk sediment to single grains. <i>ISME Journal</i> , 2018 , 12, 623-633	11.9	53
310	Alpha- and beta-mannan utilization by marine Bacteroidetes. <i>Environmental Microbiology</i> , 2018 , 20, 4127-4140	14	8
309	Aquatic adaptation of a laterally acquired pectin degradation pathway in marine gammaproteobacteria. <i>Environmental Microbiology</i> , 2017 , 19, 2320-2333	5.2	27

308	Determining the bacterial cell biology of Planctomycetes. <i>Nature Communications</i> , 2017 , 8, 14853	17.4	127
307	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	5.2	32
306	An alternative polysaccharide uptake mechanism of marine bacteria. <i>ISME Journal</i> , 2017 , 11, 1640-1650	11.9	94
305	Niche partitioning of diverse sulfur-oxidizing bacteria at hydrothermal vents. <i>ISME Journal</i> , 2017 , 11, 1545-1558	11.9	81
304	Genomic and physiological analyses of 'Reinekea forsetii' reveal a versatile opportunistic lifestyle during spring algae blooms. <i>Environmental Microbiology</i> , 2017 , 19, 1209-1221	5.2	7
303	Uncultivated microbes in need of their own taxonomy. <i>ISME Journal</i> , 2017 , 11, 2399-2406	11.9	278
302	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	5.2	35
301	Microbial Community Response to Simulated Petroleum Seepage in Caspian Sea Sediments. <i>Frontiers in Microbiology</i> , 2017 , 8, 764	5.7	14
300	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	2.2	9
299	The application of Ebmics technologies for the classification and identification of animals. <i>Organisms Diversity and Evolution</i> , 2016 , 16, 1-12	1.7	36
298	After All, Only Millions?. <i>MBio</i> , 2016 , 7,	7.8	31
297	Habitat and taxon as driving forces of carbohydrate catabolism in marine heterotrophic bacteria: example of the model algae-associated bacterium <i>Zobellia galactanivorans</i> Dsij. <i>Environmental Microbiology</i> , 2016 , 18, 4610-4627	5.2	72
296	Reply to "The Underestimation of Global Microbial Diversity". <i>MBio</i> , 2016 , 7,	7.8	6
295	Heterotrophic Proteobacteria in the vicinity of diffuse hydrothermal venting. <i>Environmental Microbiology</i> , 2016 , 18, 4348-4368	5.2	26
294	Chlamydial seasonal dynamics and isolation of 'Candidatus Neptunochlamydia vexilliferae' from a Tyrrhenian coastal lake. <i>Environmental Microbiology</i> , 2016 , 18, 2405-17	5.2	9
293	Recurring patterns in bacterioplankton dynamics during coastal spring algae blooms. <i>ELife</i> , 2016 , 5, e11888	11.8	193
292	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, 281-96	4.2	95
291	Polysaccharide utilisation loci of Bacteroidetes from two contrasting open ocean sites in the North Atlantic. <i>Environmental Microbiology</i> , 2016 , 18, 4456-4470	5.2	35

290	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, 1463-71	4.8	54
289	Past and future species definitions for Bacteria and Archaea. <i>Systematic and Applied Microbiology</i> , 2015 , 38, 209-16	4.2	312
288	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, 400-5	4.2	18
287	Taxonomy in the age of genomics. Introduction. <i>Systematic and Applied Microbiology</i> , 2015 , 38, 207-8	4.2	6
286	The effect of nutrients on carbon and nitrogen fixation by the UCYN-A-haptophyte symbiosis. <i>ISME Journal</i> , 2015 , 9, 1635-47	11.9	61
285	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	4.8	35
284	Niches of two polysaccharide-degrading Polaribacter isolates from the North Sea during a spring diatom bloom. <i>ISME Journal</i> , 2015 , 9, 1410-22	11.9	107
283	Dilution cultivation of marine heterotrophic bacteria abundant after a spring phytoplankton bloom in the North Sea. <i>Environmental Microbiology</i> , 2015 , 17, 3515-26	5.2	35
282	Comparison of bacterial communities on limnic versus coastal marine particles reveals profound differences in colonization. <i>Environmental Microbiology</i> , 2015 , 17, 3500-14	5.2	84
281	Nucleic Acid Probes and Their Application in Environmental Microbiology 2015 , 1-28		
280	Salinibacter 2015 , 1-7		
279	Allochromatium humboldtianum sp. nov., isolated from soft coastal sediments. <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2015 , 65, 2980-2985	2.2	4
278	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	5.7	38
277	Distribution of a consortium between unicellular algae and the N ₂ fixing cyanobacterium UCYN-A in the North Atlantic Ocean. <i>Environmental Microbiology</i> , 2014 , 16, 3153-67	5.2	29
276	Evaluation of the 23S rRNA gene as target for qPCR based quantification of Frankia in soils. <i>Systematic and Applied Microbiology</i> , 2014 , 37, 229-34	4.2	10
275	Uniting the classification of cultured and uncultured bacteria and archaea using 16S rRNA gene sequences. <i>Nature Reviews Microbiology</i> , 2014 , 12, 635-45	22.2	1290
274	Diverse sulfate-reducing bacteria of the Desulfosarcina/Desulfococcus clade are the key alkane degraders at marine seeps. <i>ISME Journal</i> , 2014 , 8, 2029-44	11.9	134
273	Indications for algae-degrading benthic microbial communities in deep-sea sediments along the Antarctic Polar Front. <i>Deep-Sea Research Part II: Topical Studies in Oceanography</i> , 2014 , 108, 6-16	2.3	41

272	Massive regime shifts and high activity of heterotrophic bacteria in an ice-covered lake. <i>PLoS ONE</i> , 2014 , 9, e113611	3.7	35
271	Identification and activity of acetate-assimilating bacteria in diffuse fluids venting from two deep-sea hydrothermal systems. <i>FEMS Microbiology Ecology</i> , 2014 , 90, 731-46	4.3	16
270	Functional characterization of polysaccharide utilization loci in the marine Bacteroidetes 'Gramella forsetii' KT0803. <i>ISME Journal</i> , 2014 , 8, 1492-502	11.9	126
269	Genomic encyclopedia of bacteria and archaea: sequencing a myriad of type strains. <i>PLoS Biology</i> , 2014 , 12, e1001920	9.7	146
268	Microbial lipids reveal carbon assimilation patterns on hydrothermal sulfide chimneys. <i>Environmental Microbiology</i> , 2014 , 16, 3515-32	5.2	24
267	The metagenome of the marine anammox bacterium 'Candidatus Scalindua profunda' illustrates the versatility of this globally important nitrogen cycle bacterium. <i>Environmental Microbiology</i> , 2013 , 15, 1275-89	5.2	199
266	Single-cell and population level viral infection dynamics revealed by phageFISH, a method to visualize intracellular and free viruses. <i>Environmental Microbiology</i> , 2013 , 15, 2306-18	5.2	95
265	The genome of the alga-associated marine flavobacterium <i>Formosa agariphila</i> KMM 3901T reveals a broad potential for degradation of algal polysaccharides. <i>Applied and Environmental Microbiology</i> , 2013 , 79, 6813-22	4.8	137
264	In situ identification and N and C fixation rates of uncultivated cyanobacteria populations. <i>Systematic and Applied Microbiology</i> , 2013 , 36, 259-71	4.2	55
263	Mapping glycoconjugate-mediated interactions of marine Bacteroidetes with diatoms. <i>Systematic and Applied Microbiology</i> , 2013 , 36, 417-25	4.2	33
262	Sequencing orphan species initiative (SOS): Filling the gaps in the 16S rRNA gene sequence database for all species with validly published names. <i>Systematic and Applied Microbiology</i> , 2013 , 36, 69-73	4.2	65
261	Complete genome, catabolic sub-proteomes and key-metabolites of <i>Desulfobacula toluolica</i> Tol2, a marine, aromatic compound-degrading, sulfate-reducing bacterium. <i>Environmental Microbiology</i> , 2013 , 15, 1334-55	5.2	80
260	Complete genome sequence of <i>Desulfocapsa sulfexigens</i> , a marine deltaproteobacterium specialized in disproportionating inorganic sulfur compounds. <i>Standards in Genomic Sciences</i> , 2013 , 8, 58-68		43
259	Microbial communities of deep-sea methane seeps at Hikurangi continental margin (New Zealand). <i>PLoS ONE</i> , 2013 , 8, e72627	3.7	56
258	High abundance of novel environmental chlamydiae in a Tyrrhenian coastal lake (Lago di Paola, Italy). <i>Environmental Microbiology Reports</i> , 2012 , 4, 446-52	3.7	10
257	Roseobacter clade bacteria are abundant in coastal sediments and encode a novel combination of sulfur oxidation genes. <i>ISME Journal</i> , 2012 , 6, 2178-87	11.9	88
256	HISH-SIMS analysis of bacterial uptake of algal-derived carbon in the Río de la Plata estuary. <i>Systematic and Applied Microbiology</i> , 2012 , 35, 541-8	4.2	25
255	Revealing structure and assembly cues for Arabidopsis root-inhabiting bacterial microbiota. <i>Nature</i> , 2012 , 488, 91-5	50.4	1426

254	Distribution and in situ abundance of sulfate-reducing bacteria in diverse marine hydrocarbon seep sediments. <i>Environmental Microbiology</i> , 2012 , 14, 2689-710	5.2	96
253	Archaea of the Miscellaneous Crenarchaeotal Group are abundant, diverse and widespread in marine sediments. <i>ISME Journal</i> , 2012 , 6, 1949-65	11.9	198
252	Crystal ball: fluorescence in situ hybridization in the age of super-resolution microscopy. <i>Systematic and Applied Microbiology</i> , 2012 , 35, 549-52	4.2	12
251	Contrasting extracellular enzyme activities of particle-associated bacteria from distinct provinces of the North Atlantic Ocean. <i>Frontiers in Microbiology</i> , 2012 , 3, 425	5.7	33
250	Cell surface proteome of the marine planctomycete <i>Rhodopirellula baltica</i> . <i>Proteomics</i> , 2012 , 12, 1781-94	4.8	12
249	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, 4203-8	11.5	55
248	Substrate-controlled succession of marine bacterioplankton populations induced by a phytoplankton bloom. <i>Science</i> , 2012 , 336, 608-11	33.3	846
247	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, 4638-45	4.8	49
246	Genomic content of uncultured Bacteroidetes from contrasting oceanic provinces in the North Atlantic Ocean. <i>Environmental Microbiology</i> , 2012 , 14, 52-66	5.2	119
245	Microbial community response during the iron fertilization experiment LOHAFEX. <i>Applied and Environmental Microbiology</i> , 2012 , 78, 8803-12	4.8	42
244	Concepts and software for a rational design of polynucleotide probes. <i>Environmental Microbiology Reports</i> , 2011 , 3, 69-78	3.7	16
243	Novel groups of Gammaproteobacteria catalyze sulfur oxidation and carbon fixation in a coastal, intertidal sediment. <i>Environmental Microbiology</i> , 2011 , 13, 758-74	5.2	96
242	Response of sulfate-reducing bacteria to an artificial oil-spill in a coastal marine sediment. <i>Environmental Microbiology</i> , 2011 , 13, 1488-99	5.2	44
241	Bacterial sulfur cycling shapes microbial communities in surface sediments of an ultramafic hydrothermal vent field. <i>Environmental Microbiology</i> , 2011 , 13, 2633-48	5.2	39
240	Practical application of self-organizing maps to interrelate biodiversity and functional data in NGS-based metagenomics. <i>ISME Journal</i> , 2011 , 5, 918-28	11.9	43
239	Sulfur-metabolizing bacterial populations in microbial mats of the Nakabusa hot spring, Japan. <i>Systematic and Applied Microbiology</i> , 2011 , 34, 293-302	4.2	61
238	A single-cell sequencing approach to the classification of large, vacuolated sulfur bacteria. <i>Systematic and Applied Microbiology</i> , 2011 , 34, 243-59	4.2	78
237	Release LTPs104 of the All-Species Living Tree. <i>Systematic and Applied Microbiology</i> , 2011 , 34, 169-70	4.2	122

236	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, 590-4	4.2	4
235	Hydrogen is an energy source for hydrothermal vent symbioses. <i>Nature</i> , 2011 , 476, 176-80	50.4	175
234	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, 1134-9	11.5	99
233	Thermophilic anaerobic oxidation of methane by marine microbial consortia. <i>ISME Journal</i> , 2011 , 5, 1946-156	15.9	137
232	Temporal variability of coastal Planctomycetes clades at Kabeltonne station, North Sea. <i>Applied and Environmental Microbiology</i> , 2011 , 77, 5009-17	4.8	45
231	Distinct flavobacterial communities in contrasting water masses of the north Atlantic Ocean. <i>ISME Journal</i> , 2010 , 4, 472-87	11.9	119
230	Fine-scale evolution: genomic, phenotypic and ecological differentiation in two coexisting <i>Salinibacter ruber</i> strains. <i>ISME Journal</i> , 2010 , 4, 882-95	11.9	58
229	Metagenome and mRNA expression analyses of anaerobic methanotrophic archaea of the ANME-1 group. <i>Environmental Microbiology</i> , 2010 , 12, 422-39	5.2	181
228	Identification of the dominant sulfate-reducing bacterial partner of anaerobic methanotrophs of the ANME-2 clade. <i>Environmental Microbiology</i> , 2010 , 12, 2327-40	5.2	119
227	GeneFISH--an in situ technique for linking gene presence and cell identity in environmental microorganisms. <i>Environmental Microbiology</i> , 2010 , 12, 3057-73	5.2	61
226	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, 116-21	4.2	16
225	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, 139-48	4.2	38
224	Bacterioplankton diversity and community composition in the Southern Lagoon of Venice. <i>Systematic and Applied Microbiology</i> , 2010 , 33, 128-38	4.2	27
223	Update of the All-Species Living Tree Project based on 16S and 23S rRNA sequence analyses. <i>Systematic and Applied Microbiology</i> , 2010 , 33, 291-9	4.2	366
222	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>thermosulfidiphilum</i> . <i>Systematic and Applied Microbiology</i> , 2009 , 32, 1-7	4.2	12
221	Biogeography and phylogeny of the NOR5/OM60 clade of Gammaproteobacteria. <i>Systematic and Applied Microbiology</i> , 2009 , 32, 124-39	4.2	60
220	Detoxification of sulphidic African shelf waters by blooming chemolithotrophs. <i>Nature</i> , 2009 , 457, 581-450.4	50.4	250
219	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, 1038-55	5.2	89

218	Substrate incorporation patterns of bacterioplankton populations in stratified and mixed waters of a humic lake. <i>Environmental Microbiology</i> , 2009 , 11, 1854-65	5.2	63
217	Latitudinal distribution of prokaryotic picoplankton populations in the Atlantic Ocean. <i>Environmental Microbiology</i> , 2009 , 11, 2078-93	5.2	177
216	Revising the nitrogen cycle in the Peruvian oxygen minimum zone. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2009 , 106, 4752-7	11.5	568
215	Toward cloning of the magnetotactic metagenome: identification of magnetosome island gene clusters in uncultivated magnetotactic bacteria from different aquatic sediments. <i>Applied and Environmental Microbiology</i> , 2009 , 75, 3972-9	4.8	88
214	Single-cell identification in microbial communities by improved fluorescence in situ hybridization techniques. <i>Nature Reviews Microbiology</i> , 2008 , 6, 339-48	22.2	551
213	A microdiversity study of anammox bacteria reveals a novel Candidatus Scalindua phylotype in marine oxygen minimum zones. <i>Environmental Microbiology</i> , 2008 , 10, 3106-19	5.2	210
212	The All-Species Living Tree project: a 16S rRNA-based phylogenetic tree of all sequenced type strains. <i>Systematic and Applied Microbiology</i> , 2008 , 31, 241-50	4.2	761
211	A single-cell view on the ecophysiology of anaerobic phototrophic bacteria. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2008 , 105, 17861-6	11.5	332
210	Description of <i>Maribacter forsetii</i> sp. nov., a marine Flavobacteriaceae isolated from North Sea water, and emended description of the genus <i>Maribacter</i> . <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2008 , 58, 790-7	2.2	38
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