

Christian Rinke

List of Publications by Year in descending order

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Version: 2024-02-01

45
papers

14,125
citations

117571

34
h-index

182361

51
g-index

61
all docs

61
docs citations

61
times ranked

12431
citing authors

#	ARTICLE	IF	CITATIONS
1	GTDB: an ongoing census of bacterial and archaeal diversity through a phylogenetically consistent, rank normalized and complete genome-based taxonomy. <i>Nucleic Acids Research</i> , 2022, 50, D785-D794.	6.5	662
2	Chemotaxis shapes the microscale organization of the ocean's microbiome. <i>Nature</i> , 2022, 605, 132-138.	13.7	51
3	Insights into plastic biodegradation: community composition and functional capabilities of the superworm (<i>Zophobas morio</i>) microbiome in styrofoam feeding trials. <i>Microbial Genomics</i> , 2022, 8, .	1.0	11
4	Three families of Asgard archaeal viruses identified in metagenome-assembled genomes. <i>Nature Microbiology</i> , 2022, 7, 962-973.	5.9	21
5	A genomic catalog of Earth's microbiomes. <i>Nature Biotechnology</i> , 2021, 39, 499-509.	9.4	457
6	A standardized archaeal taxonomy for the Genome Taxonomy Database. <i>Nature Microbiology</i> , 2021, 6, 946-959.	5.9	198
7	Recoding of stop codons expands the metabolic potential of two novel Asgardarchaeota lineages. <i>ISME Communications</i> , 2021, 1, .	1.7	23
8	Editorial: Ecology, Metabolism and Evolution of Archaea-Perspectives From Proceedings of the International Workshop on Geo-Omics of Archaea. <i>Frontiers in Microbiology</i> , 2021, 12, 827229.	1.5	3
9	Microvolume DNA extraction methods for microscale amplicon and metagenomic studies. <i>ISME Communications</i> , 2021, 1, .	1.7	10
10	Undinarchaeota illuminate DPANN phylogeny and the impact of gene transfer on archaeal evolution. <i>Nature Communications</i> , 2020, 11, 3939.	5.8	102
11	A complete domain-to-species taxonomy for Bacteria and Archaea. <i>Nature Biotechnology</i> , 2020, 38, 1079-1086.	9.4	883
12	The importance of designating type material for uncultured taxa. <i>Systematic and Applied Microbiology</i> , 2019, 42, 15-21.	1.2	149
13	Defining the human gut host-phage network through single-cell viral tagging. <i>Nature Microbiology</i> , 2019, 4, 2192-2203.	5.9	95
14	A phylogenomic and ecological analysis of the globally abundant Marine Group II archaea (<i>Ca</i>). <i>Journal of Applied Microbiology</i> , 2019, 126, 1-11.	4.4	158
15	Single-Cell Genomics of Microbial Dark Matter. <i>Methods in Molecular Biology</i> , 2018, 1849, 99-111.	0.4	5
16	A standardized bacterial taxonomy based on genome phylogeny substantially revises the tree of life. <i>Nature Biotechnology</i> , 2018, 36, 996-1004.	9.4	2,615
17	Recovery of nearly 8,000 metagenome-assembled genomes substantially expands the tree of life. <i>Nature Microbiology</i> , 2017, 2, 1533-1542.	5.9	1,465
18	Minimum information about a single amplified genome (MISAG) and a metagenome-assembled genome (MIMAG) of bacteria and archaea. <i>Nature Biotechnology</i> , 2017, 35, 725-731.	9.4	1,512

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19	Diverse Marinimicrobia bacteria may mediate coupled biogeochemical cycles along eco-thermodynamic gradients. <i>Nature Communications</i> , 2017, 8, 1507.	5.8	99
20	Genomic Analysis of <i>Caldithrix abyssi</i> , the Thermophilic Anaerobic Bacterium of the Novel Bacterial Phylum Calditrarchaeota. <i>Frontiers in Microbiology</i> , 2017, 8, 195.	1.5	66
21	Comparative Genomic Analysis of the Class Epsilonproteobacteria and Proposed Reclassification to Epsilonbacteraeota (phyl. nov.). <i>Frontiers in Microbiology</i> , 2017, 8, 682.	1.5	409
22	A microfluidics-based in situ chemotaxis assay to study the behaviour of aquatic microbial communities. <i>Nature Microbiology</i> , 2017, 2, 1344-1349.	5.9	60
23	acdc â€“ Automated Contamination Detection and Confidence estimation for single-cell genome data. <i>BMC Bioinformatics</i> , 2016, 17, 543.	1.2	22
24	ProDeGe: a computational protocol for fully automated decontamination of genomes. <i>ISME Journal</i> , 2016, 10, 269-272.	4.4	65
25	Phylogeny and physiology of candidate phylum â€˜Atribacteriaâ€™ TM (OP9/J51) inferred from cultivation-independent genomics. <i>ISME Journal</i> , 2016, 10, 273-286.	4.4	166
26	Validation of picogram- and femtogram-input DNA libraries for microscale metagenomics. <i>PeerJ</i> , 2016, 4, e2486.	0.9	64
27	In Silico Analysis of the Metabolic Potential and Niche Specialization of Candidate Phylum "Latescibacteria" (WS3). <i>PLoS ONE</i> , 2015, 10, e0127499.	1.1	102
28	Microbial dark matter ecogenomics reveals complex synergistic networks in a methanogenic bioreactor. <i>ISME Journal</i> , 2015, 9, 1710-1722.	4.4	360
29	Insights into the metabolism, lifestyle and putative evolutionary history of the novel archaeal phylum â€˜Diapherotritesâ€™ TM . <i>ISME Journal</i> , 2015, 9, 447-460.	4.4	89
30	Obtaining genomes from uncultivated environmental microorganisms using FACSâ€“based single-cell genomics. <i>Nature Protocols</i> , 2014, 9, 1038-1048.	5.5	243
31	Stop codon reassignments in the wild. <i>Science</i> , 2014, 344, 909-913.	6.0	124
32	An environmental bacterial taxon with a large and distinct metabolic repertoire. <i>Nature</i> , 2014, 506, 58-62.	13.7	530
33	Impact of single-cell genomics and metagenomics on the emerging view of extremophile â€œmicrobial dark matterâ€“. <i>Extremophiles</i> , 2014, 18, 865-875.	0.9	133
34	Reconstructing each cell's genome within complex microbial communitiesÃ¢â€šâ€“â€“dream or reality?. <i>Frontiers in Microbiology</i> , 2014, 5, 771.	1.5	58
35	The Candidate Phylum Poribacteria by Single-Cell Genomics: New Insights into Phylogeny, Cell-Compartmentation, Eukaryote-Like Repeat Proteins, and Other Genomic Features. <i>PLoS ONE</i> , 2014, 9, e87353.	1.1	79
36	Insights into the phylogeny and coding potential of microbial dark matter. <i>Nature</i> , 2013, 499, 431-437.	13.7	2,239

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37	Single-cell genomics reveals complex carbohydrate degradation patterns in poribacterial symbionts of marine sponges. ISME Journal, 2013, 7, 2287-2300.	4.4	113
38	Decontamination of MDA Reagents for Single Cell Whole Genome Amplification. PLoS ONE, 2011, 6, e26161.	1.1	163
39	Cell proliferation and growth in <i>Zoothamnium niveum</i> (Oligohymenophora, Peritrichida) – Thiotrophic bacteria symbiosis. Symbiosis, 2009, 47, 43-50.	1.2	4
40	High genetic similarity between two geographically distinct strains of the sulfur-oxidizing symbiont <i>Candidatus Thiobios zoothamnicoli</i> ™. FEMS Microbiology Ecology, 2009, 67, 229-241.	1.3	35
41	Molecular characterization of the symbionts associated with marine nematodes of the genus <i>Robbea</i> [†] . Environmental Microbiology Reports, 2009, 1, 136-144.	1.0	46
42	Macro camera temperature logger array for deep-sea hydrothermal vent and benthic studies. Limnology and Oceanography: Methods, 2009, 7, 527-534.	1.0	6
43	Pathways, activities and thermal stability of anaerobic and aerobic enzymes in thermophilic vent paralvinellid worms. Marine Ecology - Progress Series, 2009, 382, 99-112.	0.9	11
44	The effects of sulphide on growth and behaviour of the thiotrophic <i>Zoothamnium niveum</i> symbiosis. Proceedings of the Royal Society B: Biological Sciences, 2007, 274, 2259-2269.	1.2	22
45	<i>Candidatus Thiobios zoothamnicoli</i> , an Ectosymbiotic Bacterium Covering the Giant Marine Ciliate <i>Zoothamnium niveum</i> . Applied and Environmental Microbiology, 2006, 72, 2014-2021.	1.4	84