

Jan Philipp Meier-Kolthoff

List of Publications by Year in descending order

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Version: 2024-02-01

53
papers

20,681
citations

126708

33
h-index

138251

58
g-index

63
all docs

63
docs citations

63
times ranked

12848
citing authors

#	ARTICLE	IF	CITATIONS
1	Genome sequence-based species delimitation with confidence intervals and improved distance functions. <i>BMC Bioinformatics</i> , 2013, 14, 60.	1.2	5,139
2	Genome-Based Taxonomic Classification of the Phylum Actinobacteria. <i>Frontiers in Microbiology</i> , 2018, 9, 2007.	1.5	2,599
3	TYGS is an automated high-throughput platform for state-of-the-art genome-based taxonomy. <i>Nature Communications</i> , 2019, 10, 2182.	5.8	1,588
4	Analysis of 1,000+ Type-Strain Genomes Substantially Improves Taxonomic Classification of Alphaproteobacteria. <i>Frontiers in Microbiology</i> , 2020, 11, 468.	1.5	1,537
5	Taxonomy, Physiology, and Natural Products of Actinobacteria. <i>Microbiology and Molecular Biology Reviews</i> , 2016, 80, 1-43.	2.9	1,395
6	Analysis of 1,000 Type-Strain Genomes Improves Taxonomic Classification of Bacteroidetes. <i>Frontiers in Microbiology</i> , 2019, 10, 2083.	1.5	1,281
7	List of Prokaryotic names with Standing in Nomenclature (LPSN) moves to the DSMZ. <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2020, 70, 5607-5612.	0.8	929
8	TYGS and LPSN: A database tandem for fast and reliable genome-based classification and nomenclature of prokaryotes. <i>Nucleic Acids Research</i> , 2022, 50, D801-D807.	6.5	728
9	Taxonomic use of DNA G+C content and DNA-DNA hybridization in the genomic age. <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2014, 64, 352-356.	0.8	526
10	Genome-Based Taxonomic Classification of Bacteroidetes. <i>Frontiers in Microbiology</i> , 2016, 7, 2003.	1.5	493
11	When should a DDH experiment be mandatory in microbial taxonomy?. <i>Archives of Microbiology</i> , 2013, 195, 413-418.	1.0	490
12	The Mouse Intestinal Bacterial Collection (miBC) provides host-specific insight into cultured diversity and functional potential of the gut microbiota. <i>Nature Microbiology</i> , 2016, 1, 16131.	5.9	465
13	Complete genome sequence of DSM 30083T, the type strain (U5/41T) of <i>Escherichia coli</i> , and a proposal for delineating subspecies in microbial taxonomy. <i>Standards in Genomic Sciences</i> , 2014, 9, 2.	1.5	454
14	VICTOR: genome-based phylogeny and classification of prokaryotic viruses. <i>Bioinformatics</i> , 2017, 33, 3396-3404.	1.8	401
15	Comparative genomics of biotechnologically important yeasts. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2016, 113, 9882-9887.	3.3	302
16	Phylogenomics of <i>Rhodobacteraceae</i> reveals evolutionary adaptation to marine and non-marine habitats. <i>ISME Journal</i> , 2017, 11, 1483-1499.	4.4	283
17	1,003 reference genomes of bacterial and archaeal isolates expand coverage of the tree of life. <i>Nature Biotechnology</i> , 2017, 35, 676-683.	9.4	222
18	Genomic insights into the taxonomic status of the <i>Bacillus cereus</i> group. <i>Scientific Reports</i> , 2015, 5, 14082.	1.6	220

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19	Genomic and Genetic Diversity within the <i>Pseudomonas fluorescens</i> Complex. PLoS ONE, 2016, 11, e0150183.	1.1	171
20	Phylogenomic Analysis of the Gammaproteobacterial Methanotrophs (Order Methylococcales) Calls for the Reclassification of Members at the Genus and Species Levels. Frontiers in Microbiology, 2018, 9, 3162.	1.5	156
21	Phylogenomic Study of Burkholderia glathei-like Organisms, Proposal of 13 Novel Burkholderia Species and Emended Descriptions of Burkholderia sordidicola, Burkholderia zhejiangensis, and Burkholderia grimmiae. Frontiers in Microbiology, 2016, 7, 877.	1.5	120
22	Genome-Scale Data Call for a Taxonomic Rearrangement of Geodermatophilaceae. Frontiers in Microbiology, 2017, 8, 2501.	1.5	105
23	Genome-based classification of micromonosporae with a focus on their biotechnological and ecological potential. Scientific Reports, 2018, 8, 525.	1.6	102
24	COPYCAT : cophylogenetic analysis tool. Bioinformatics, 2007, 23, 898-900.	1.8	92
25	Still Something to Discover: Novel Insights into Escherichia coli Phage Diversity and Taxonomy. Viruses, 2019, 11, 454.	1.5	77
26	Proposal of a type strain for Frankia alni (Woronin 1866) Von Tubeuf 1895, emended description of Frankia alni, and recognition of Frankia casuarinae sp. nov. and Frankia elaeagni sp. nov.. International Journal of Systematic and Evolutionary Microbiology, 2016, 66, 5201-5210.	0.8	68
27	Highly parallelized inference of large genome-based phylogenies. Concurrency Computation Practice and Experience, 2014, 26, 1715-1729.	1.4	63
28	First genome sequences of Achromobacter phages reveal new members of the N4 family. Virology Journal, 2014, 11, 14.	1.4	59
29	Sequence-based analysis of the genus Ruminococcus resolves its phylogeny and reveals strong host association. Microbial Genomics, 2016, 2, e000099.	1.0	57
30	Whole-Genome Sequencing Redefines Shewanella Taxonomy. Frontiers in Microbiology, 2019, 10, 1861.	1.5	46
31	Reclassification of Haloactinobacterium glaciecola as Occultella glaciecola gen. nov., comb. nov., of Haloactinobacterium album as Ruania alba comb. nov, with an emended description of the genus Ruania, recognition that the genus names Haloactinobacterium and Ruania are heterotypic synonyms and description of Occultella aeris sp. nov., a halotolerant isolate from surface soil sampled at an ancient copper smelter. International Journal of Systematic and Evolutionary Microbiology, 2021, 71, 1-11.	0.8	44
32	Genomic diversity within the haloalkaliphilic genus Thioalkalivibrio. PLoS ONE, 2017, 12, e0173517.	1.1	42
33	AxPcoords & parallel AxParafit: statistical co-phylogenetic analyses on thousands of taxa. BMC Bioinformatics, 2007, 8, 405.	1.2	39
34	Pathways and substrate-specific regulation of amino acid degradation in <i>Pseudomonas</i> <i>haeobacter</i> <i>inhibens</i> DSM 17395 (archetype of the marine <i>Rhodospirillum</i> clade). Environmental Microbiology, 2014, 16, 218-238.	1.8	28
35	Comparing polysaccharide decomposition between the type strains Gramella echinicola KMM 6050T (DSM 19838T) and Gramella portivictoriae UST040801-001T (DSM 23547T), and emended description of Gramella echinicola Nedashkovskaya et al. 2005 emend. Shahina et al. 2014 and Gramella portivictoriae Lau et al. 2005. Standards in Genomic Sciences. 2016. 11, 37.	1.5	27
36	Cobaviruses – a new globally distributed phage group infecting <i>Rhodobacteraceae</i> in marine ecosystems. ISME Journal, 2019, 13, 1404-1421.	4.4	26

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37	100-year-old enigma solved: identification, genomic characterization and biogeography of the yet uncultured <i>Planctomyces bekefii</i> . <i>Environmental Microbiology</i> , 2020, 22, 198-211.	1.8	25
38	<i>Streptomyces jeddahensis</i> sp. nov., an oleaginous bacterium isolated from desert soil. <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2017, 67, 1676-1682.	0.8	25
39	A publicly accessible database for <i>Clostridioides difficile</i> genome sequences supports tracing of transmission chains and epidemics. <i>Microbial Genomics</i> , 2020, 6, .	1.0	22
40	Comparative Genomics Suggests Mechanisms of Genetic Adaptation toward the Catabolism of the Phenylurea Herbicide Linuron in <i>Variovorax</i> . <i>Genome Biology and Evolution</i> , 2020, 12, 827-841.	1.1	21
41	High quality draft genome sequence of <i>Flavobacterium rivuli</i> type strain WB 3.3-2T (DSM 21788T), a valuable source of polysaccharide decomposing enzymes. <i>Standards in Genomic Sciences</i> , 2015, 10, 46.	1.5	16
42	Investigation of recombination-intense viral groups and their genes in the Earth's virome. <i>Scientific Reports</i> , 2018, 8, 11496.	1.6	14
43	The Biofilm Inhibitor Carolacton Enters Gram-Negative Cells: Studies Using a TolC-Deficient Strain of <i>Escherichia coli</i> . <i>MSphere</i> , 2017, 2, .	1.3	13
44	Trajectories and Drivers of Genome Evolution in Surface-Associated Marine <i>Phaeobacter</i> . <i>Genome Biology and Evolution</i> , 2017, 9, 3297-3311.	1.1	13
45	<i>Sphingomonas aliaeris</i> sp. nov., a new species isolated from pork steak packed under modified atmosphere. <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2021, 71, .	0.8	13
46	Genome sequence of the moderately thermophilic sulfur-reducing bacterium <i>Thermanaerovibrio velox</i> type strain (Z-9701T) and emended description of the genus <i>Thermanaerovibrio</i> . <i>Standards in Genomic Sciences</i> , 2013, 9, 57-70.	1.5	8
47	A single-cell genomics pipeline for environmental microbial eukaryotes. <i>IScience</i> , 2021, 24, 102290.	1.9	7
48	<i>Prevotella illustrans</i> sp. nov., derived from human oropharyngeal abscess puncture fluid. <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2021, 71, .	0.8	6
49	Genome sequence of the chemoheterotrophic soil bacterium <i>Saccharomonospora cyanea</i> type strain (NA-134T). <i>Standards in Genomic Sciences</i> , 2013, 9, 28-41.	1.5	4
50	Improving Phylogeny Reconstruction at the Strain Level Using Peptidome Datasets. <i>PLoS Computational Biology</i> , 2016, 12, e1005271.	1.5	4
51	High-quality draft genome sequence of <i>Flavobacterium suncheonense</i> GH29-5T (DSM 17707T) isolated from greenhouse soil in South Korea, and emended description of <i>Flavobacterium suncheonense</i> GH29-5T. <i>Standards in Genomic Sciences</i> , 2016, 11, 42.	1.5	3
52	Panoramic Insights into Microevolution and Macroevolution of A <i>Prevotella copri</i> -containing Lineage in Primate Guts. <i>Genomics, Proteomics and Bioinformatics</i> , 2022, 20, 334-349.	3.0	3
53	Large-Scale Co-Phylogenetic Analysis on the Grid. <i>International Journal of Grid and High Performance Computing</i> , 2009, 1, 39-54.	0.7	2