Jan Philipp Meier-Kolthoff

List of Publications by Year
in descending order

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	TYGS and LPSN: Âa database tandem for fast and reliable genome-based classification and nomenclature of prokaryotes. Nucleic Acids Research, 2022, 50, D801-D807.	6.5	728
2	Panoramic Insights into Microevolution and Macroevolution of A Prevotella copri-containing Lineage in Primate Guts. Genomics, Proteomics and Bioinformatics, 2022, 20, 334-349.	3.0	3
3	A single-cell genomics pipeline for environmental microbial eukaryotes. IScience, 2021, 24, 102290.	1.9	7
4	Reclassification of Haloactinobacterium glacieicola as Occultella glacieicola 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, .	0.8	44
5	Sphingomonas aliaeris sp. nov., a new species isolated from pork steak packed under modified atmosphere. International Journal of Systematic and Evolutionary Microbiology, 2021, 71, .	0.8	13
6	Prevotella illustrans sp. nov., derived from human oropharyngeal abscess puncture fluid. International Journal of Systematic and Evolutionary Microbiology, 2021, 71, .	0.8	6
7	100â€yearâ€old enigma solved: identification, genomic characterization and biogeography of the yet uncultured <i>Planctomyces bekefii</i>. Environmental Microbiology, 2020, 22, 198-211.	1.8	25
8	Comparative Genomics Suggests Mechanisms of Genetic Adaptation toward the Catabolism of the Phenylurea Herbicide Linuron in Variovorax. Genome Biology and Evolution, 2020, 12, 827-841.	1.1	21
9	Analysis of 1,000+ Type-Strain Genomes Substantially Improves Taxonomic Classification of Alphaproteobacteria. Frontiers in Microbiology, 2020, 11, 468.	1.5	1,537
10	List of Prokaryotic names with Standing in Nomenclature (LPSN) moves to the DSMZ. International Journal of Systematic and Evolutionary Microbiology, 2020, 70, 5607-5612.	0.8	929
11	A publicly accessible database for Clostridioides difficile genome sequences supports tracing of transmission chains and epidemics. Microbial Genomics, 2020, 6, .	1.0	22
12	Analysis of 1,000 Type-Strain Genomes Improves Taxonomic Classification of Bacteroidetes. Frontiers in Microbiology, 2019, 10, 2083.	1.5	1,281
13	Whole-Genome Sequencing Redefines Shewanella Taxonomy. Frontiers in Microbiology, 2019, 10, 1861.	1.5	46
14	TYGS is an automated high-throughput platform for state-of-the-art genome-based taxonomy. Nature Communications, 2019, 10, 2182.	5.8	1,588
15	Still Something to Discover: Novel Insights into Escherichia coli Phage Diversity and Taxonomy. Viruses, 2019, 11, 454.	1.5	77
16	Cobaviruses â€" a new globally distributed phage group infecting <i>Rhodobacteraceae</i> in marine ecosystems. ISME Journal, 2019, 13, 1404-1421.	4.4	26
17	Genome-based classification of micromonosporae with a focus on their biotechnological and ecological potential. Scientific Reports, 2018, 8, 525.	1.6	102
18	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

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19	Genome-Based Taxonomic Classification of the Phylum Actinobacteria. Frontiers in Microbiology, 2018, 9, 2007.	1.5	2,599
20	Investigation of recombination-intense viral groups and their genes in the Earth's virome. Scientific Reports, 2018, 8, 11496.	1.6	14
21	Phylogenomics of *Rhodobacteraceae* reveals evolutionary adaptation to marine and non-marine habitats. ISME Journal, 2017, 11, 1483-1499.	4.4	283
22	1,003 reference genomes of bacterial and archaeal isolates expand coverage of the tree of life. Nature Biotechnology, 2017, 35, 676-683.	9.4	222
23	VICTOR: genome-based phylogeny and classification of prokaryotic viruses. Bioinformatics, 2017, 33, 3396-3404.	1.8	401
24	The Biofilm Inhibitor Carolacton Enters Gram-Negative Cells: Studies Using a TolC-Deficient Strain of Escherichia coli. MSphere, 2017, 2, .	1.3	13
25	Trajectories and Drivers of Genome Evolution in Surface-Associated Marine Phaeobacter. Genome Biology and Evolution, 2017, 9, 3297-3311.	1.1	13
26	Genome-Scale Data Call for a Taxonomic Rearrangement of Geodermatophilaceae. Frontiers in Microbiology, 2017, 8, 2501.	1.5	105
27	Genomic diversity within the haloalkaliphilic genus Thioalkalivibrio. PLoS ONE, 2017, 12, e0173517.	1.1	42
28	Streptomyces jeddahensis sp. nov., an oleaginous bacterium isolated from desert soil. International Journal of Systematic and Evolutionary Microbiology, 2017, 67, 1676-1682.	0.8	25
29	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
30	Genome-Based Taxonomic Classification of Bacteroidetes. Frontiers in Microbiology, 2016, 7, 2003.	1.5	493
31	Comparative genomics of biotechnologically important yeasts. Proceedings of the National Academy of Sciences of the United States of America, 2016, 113, 9882-9887.	3.3	302
32	The Mouse Intestinal Bacterial Collection (miBC) provides host-specific insight into cultured diversity and functional potential of the gut microbiota. Nature Microbiology, 2016, 1, 16131.	5.9	465
33	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
34	High-quality draft genome sequence of Flavobacterium suncheonense GH29-5T (DSM 17707T) isolated from greenhouse soil in South Korea, and emended description of Flavobacterium suncheonense GH29-5T. Standards in Genomic Sciences, 2016, 11, 42.	1.5	3
35	Taxonomy, Physiology, and Natural Products of Actinobacteria. Microbiology and Molecular Biology Reviews, 2016, 80, 1-43.	2.9	1,395
36	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

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37	Sequence-based analysis of the genus Ruminococcus resolves its phylogeny and reveals strong host association. Microbial Genomics, 2016, 2, e000099.	1.0	57
38	Improving Phylogeny Reconstruction at the Strain Level Using Peptidome Datasets. PLoS Computational Biology, 2016, 12, e1005271.	1.5	4
39	Genomic and Genetic Diversity within the Pseudomonas fluorescens Complex. PLoS ONE, 2016, 11, e0150183.	1.1	171
40	Genomic insights into the taxonomic status of the Bacillus cereus group. Scientific Reports, 2015, 5, 14082.	1.6	220
41	High quality draft genome sequence of Flavobacterium rivuli type strain WB 3.3-2T (DSM 21788T), a valuable source of polysaccharide decomposing enzymes. Standards in Genomic Sciences, 2015, 10, 46.	1.5	16
42	Highly parallelized inference of large genomeâ€based phylogenies. Concurrency Computation Practice and Experience, 2014, 26, 1715-1729.	1.4	63
43	Pathways and substrateâ€specific regulation of amino acid degradation in <i><scp>P</scp>haeobacter inhibens</i>â€…<scp>DSM</scp> 17395 (archetype of the marine <i><scp>R</scp>oseobacter</i> clade). Environmental Microbiology, 2014, 16, 218-238.	1.8	28
44	First genome sequences of Achromobacter phages reveal new members of the N4 family. Virology Journal, 2014, 11, 14.	1.4	59
45	Taxonomic use of DNA G+C content and DNAâ€"DNA hybridization in the genomic age. International Journal of Systematic and Evolutionary Microbiology, 2014, 64, 352-356.	0.8	526
46	Complete genome sequence of DSM 30083T, the type strain (U5/41T) of Escherichia coli, and a proposal for delineating subspecies in microbial taxonomy. Standards in Genomic Sciences, 2014, 9, 2.	1.5	454
47	When should a DDH experiment be mandatory in microbial taxonomy?. Archives of Microbiology, 2013, 195, 413-418.	1.0	490
48	Genome sequence-based species delimitation with confidence intervals and improved distance functions. BMC Bioinformatics, 2013, 14, 60.	1.2	5,139
49	Genome sequence of the chemoheterotrophic soil bacterium Saccharomonospora cyanea type strain (NA-134T). Standards in Genomic Sciences, 2013, 9, 28-41.	1.5	4
50	Genome sequence of the moderately thermophilic sulfur-reducing bacterium Thermanaerovibrio velox type strain (Z-9701T) and emended description of the genus Thermanaerovibrio. Standards in Genomic Sciences, 2013, 9, 57-70.	1.5	8
51	Large-Scale Co-Phylogenetic Analysis on the Grid. International Journal of Grid and High Performance Computing, 2009, 1, 39-54.	0.7	2
52	COPYCAT : cophylogenetic analysis tool. Bioinformatics, 2007, 23, 898-900.	1.8	92
53	AxPcoords & parallel AxParafit: statistical co-phylogenetic analyses on thousands of taxa. BMC Bioinformatics, 2007, 8, 405.	1.2	39