

Sebastian Jaenicke

List of Publications by Year in descending order

Source: <https://exaly.com/author-pdf/10448077/publications.pdf>

Version: 2024-02-01

37
papers

3,104
citations

185998

28
h-index

329751

37
g-index

38
all docs

38
docs citations

38
times ranked

4754
citing authors

#	ARTICLE	IF	CITATIONS
1	Whole Genome Sequencing versus Traditional Genotyping for Investigation of a Mycobacterium tuberculosis Outbreak: A Longitudinal Molecular Epidemiological Study. PLoS Medicine, 2013, 10, e1001387.	3.9	425
2	Phylogenetic characterization of a biogas plant microbial community integrating clone library 16S-rDNA sequences and metagenome sequence data obtained by 454-pyrosequencing. Journal of Biotechnology, 2009, 142, 38-49.	1.9	248
3	Comparative and Joint Analysis of Two Metagenomic Datasets from a Biogas Fermenter Obtained by 454-Pyrosequencing. PLoS ONE, 2011, 6, e14519.	1.1	208
4	Profiling of the metabolically active community from a production-scale biogas plant by means of high-throughput metatranscriptome sequencing. Journal of Biotechnology, 2012, 158, 248-258.	1.9	198
5	Comparative metagenomics of biogas-producing microbial communities from production-scale biogas plants operating under wet or dry fermentation conditions. Biotechnology for Biofuels, 2015, 8, 14.	6.2	159
6	High-quality genome sequence of Pichia pastoris CBS7435. Journal of Biotechnology, 2011, 154, 312-320.	1.9	146
7	Pangenomic Study of Corynebacterium diphtheriae That Provides Insights into the Genomic Diversity of Pathogenic Isolates from Cases of Classical Diphtheria, Endocarditis, and Pneumonia. Journal of Bacteriology, 2012, 194, 3199-3215.	1.0	142
8	Unraveling the microbiome of a thermophilic biogas plant by metagenome and metatranscriptome analysis complemented by characterization of bacterial and archaeal isolates. Biotechnology for Biofuels, 2016, 9, 171.	6.2	134
9	Complete genome sequencing of Agrobacterium sp. H13-3, the former Rhizobium lupini H13-3, reveals a tripartite genome consisting of a circular and a linear chromosome and an accessory plasmid but lacking a tumor-inducing Ti-plasmid. Journal of Biotechnology, 2011, 155, 50-62.	1.9	112
10	Microbial diversity in different compartments of an aquaponics system. Archives of Microbiology, 2017, 199, 613-620.	1.0	99
11	Complete genome sequence of Streptomyces lividans TK24. Journal of Biotechnology, 2015, 199, 21-22.	1.9	96
12	ReadXplorer 2â€”detailed read mapping analysis and visualization from one single source. Bioinformatics, 2016, 32, 3702-3708.	1.8	96
13	The complete genome sequence of Corynebacterium pseudotuberculosis FRC41 isolated from a 12-year-old girl with necrotizing lymphadenitis reveals insights into gene-regulatory networks contributing to virulence. BMC Genomics, 2010, 11, 728.	1.2	89
14	Bioinformatics for NGS-based metagenomics and the application to biogas research. Journal of Biotechnology, 2017, 261, 10-23.	1.9	84
15	Exact and complete short-read alignment to microbial genomes using Graphics Processing Unit programming. Bioinformatics, 2011, 27, 1351-1358.	1.8	78
16	Effect of Long-Term Farming Practices on Agricultural Soil Microbiome Members Represented by Metagenomically Assembled Genomes (MAGs) and Their Predicted Plant-Beneficial Genes. Genes, 2019, 10, 424.	1.0	61
17	Proteorhodopsin light-enhanced growth linked to vitamin-B1 acquisition in marine Flavobacteria. ISME Journal, 2016, 10, 1102-1112.	4.4	58
18	Genomics of the Proteorhodopsin-Containing Marine Flavobacterium Dokdonia sp. Strain MED134. Applied and Environmental Microbiology, 2011, 77, 8676-8686.	1.4	56

#	ARTICLE	IF	CITATIONS
19	The <i>Sinorhizobium fredii</i> HH103 Genome: A Comparative Analysis With <i>S. fredii</i> Strains Differing in Their Symbiotic Behavior With Soybean. <i>Molecular Plant-Microbe Interactions</i> , 2015, 28, 811-824.	1.4	56
20	Complete Genome Sequence of the Hydrogenotrophic, Methanogenic Archaeon <i>Methanoculleus bourgensis</i> Strain MS2 ^T , Isolated from a Sewage Sludge Digester. <i>Journal of Bacteriology</i> , 2012, 194, 5487-5488.	1.0	55
21	Genome Sequence of the Soybean Symbiont <i>Sinorhizobium fredii</i> HH103. <i>Journal of Bacteriology</i> , 2012, 194, 1617-1618.	1.0	54
22	Complete genome sequence, lifestyle, and multi-drug resistance of the human pathogen <i>Corynebacterium resistens</i> DSM 45100 isolated from blood samples of a leukemia patient. <i>BMC Genomics</i> , 2012, 13, 141.	1.2	51
23	New insights into <i>C. hlamydomonas reinhardtii</i> hydrogen production processes by combined microarray/RNA-seq transcriptomics. <i>Plant Biotechnology Journal</i> , 2013, 11, 717-733.	4.1	47
24	Genome sequence of <i>Wickerhamomyces anomalus</i> DSM 6766 reveals genetic basis of biotechnologically important antimicrobial activities. <i>FEMS Yeast Research</i> , 2012, 12, 382-386.	1.1	40
25	Draft whole genome sequence of the cyanide-degrading bacterium <i>Pseudomonas pseudoalcaligenes</i> CECT5344. <i>Environmental Microbiology</i> , 2013, 15, 253-270.	1.8	38
26	Characterization of Bathyarchaeota genomes assembled from metagenomes of biofilms residing in mesophilic and thermophilic biogas reactors. <i>Biotechnology for Biofuels</i> , 2018, 11, 167.	6.2	38
27	An integrated metagenome and -proteome analysis of the microbial community residing in a biogas production plant. <i>Journal of Biotechnology</i> , 2016, 231, 268-279.	1.9	33
28	Expansion and re-classification of the extracytoplasmic function (ECF) σ factor family. <i>Nucleic Acids Research</i> , 2021, 49, 986-1005.	6.5	32
29	Detailed analysis of metagenome datasets obtained from biogas-producing microbial communities residing in biogas reactors does not indicate the presence of putative pathogenic microorganisms. <i>Biotechnology for Biofuels</i> , 2013, 6, 49.	6.2	31
30	Flexible metagenome analysis using the MGX framework. <i>Microbiome</i> , 2018, 6, 76.	4.9	29
31	Complete Genome Sequence of the Barley Pathogen <i>Xanthomonas translucens</i> pv. <i>translucens</i> DSM 18974 ^T (ATCC 19319 ^T). <i>Genome Announcements</i> , 2016, 4, .	0.8	24
32	Draft genome sequence of the cellulolytic <i>Clostridium thermocellum</i> wild-type strain BC1 playing a role in cellulosic biomass degradation. <i>Journal of Biotechnology</i> , 2013, 168, 62-63.	1.9	21
33	Genomics of high molecular weight plasmids isolated from an on-farm biopurification system. <i>Scientific Reports</i> , 2016, 6, 28284.	1.6	17
34	Compared to conventional, ecological intensive management promotes beneficial proteolytic soil microbial communities for agro-ecosystem functioning under climate change-induced rain regimes. <i>Scientific Reports</i> , 2020, 10, 7296.	1.6	14
35	Draft Genome Sequence of <i>Wickerhamomyces ciferrii</i> NRRL Y-1031 F-60-10. <i>Eukaryotic Cell</i> , 2012, 11, 1582-1583.	3.4	13
36	RAPYD – Rapid Annotation Platform for Yeast Data. <i>Journal of Biotechnology</i> , 2011, 155, 118-126.	1.9	10

#	ARTICLE	IF	CITATIONS
37	The structure of the <i>Cyberlindnera jadinii</i> genome and its relation to <i>Candida utilis</i> analyzed by the occurrence of single nucleotide polymorphisms. <i>Journal of Biotechnology</i> , 2015, 211, 20-30.	1.9	10