

# Sebastian Jaenicke

## List of Publications by Year in descending order

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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	Expansion and re-classification of the extracytoplasmic function (ECF) $\sigma$ factor family. <i>Nucleic Acids Research</i> , 2021, 49, 986-1005.	6.5	32
2	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
3	Effect of Long-Term Farming Practices on Agricultural Soil Microbiome Members Represented by Metagenomically Assembled Genomes (MAGs) and Their Predicted Plant-Beneficial Genes. <i>Genes</i> , 2019, 10, 424.	1.0	61
4	Flexible metagenome analysis using the MGX framework. <i>Microbiome</i> , 2018, 6, 76.	4.9	29
5	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
6	Microbial diversity in different compartments of an aquaponics system. <i>Archives of Microbiology</i> , 2017, 199, 613-620.	1.0	99
7	Bioinformatics for NGS-based metagenomics and the application to biogas research. <i>Journal of Biotechnology</i> , 2017, 261, 10-23.	1.9	84
8	Unraveling the microbiome of a thermophilic biogas plant by metagenome and metatranscriptome analysis complemented by characterization of bacterial and archaeal isolates. <i>Biotechnology for Biofuels</i> , 2016, 9, 171.	6.2	134
9	ReadXplorer 2â€™ detailed read mapping analysis and visualization from one single source. <i>Bioinformatics</i> , 2016, 32, 3702-3708.	1.8	96
10	Genomics of high molecular weight plasmids isolated from an on-farm biopurification system. <i>Scientific Reports</i> , 2016, 6, 28284.	1.6	17
11	Complete Genome Sequence of the Barley Pathogen <i>Xanthomonas translucens</i> pv. <i>translucens</i> DSM 18974 <sup>T</sup> (ATCC 19319 <sup>T</sup>). <i>Genome Announcements</i> , 2016, 4, .	0.8	24
12	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
13	Proteorhodopsin light-enhanced growth linked to vitamin-B1 acquisition in marine Flavobacteria. <i>ISME Journal</i> , 2016, 10, 1102-1112.	4.4	58
14	Comparative metagenomics of biogas-producing microbial communities from production-scale biogas plants operating under wet or dry fermentation conditions. <i>Biotechnology for Biofuels</i> , 2015, 8, 14.	6.2	159
15	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
16	Complete genome sequence of <i>Streptomyces lividans</i> TK24. <i>Journal of Biotechnology</i> , 2015, 199, 21-22.	1.9	96
17	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
18	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

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19	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
20	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
21	New insights into <i>Chlamydomonas reinhardtii</i> hydrogen production processes by combined microarray/RNA-seq transcriptomics. <i>Plant Biotechnology Journal</i> , 2013, 11, 717-733.	4.1	47
22	Whole Genome Sequencing versus Traditional Genotyping for Investigation of a <i>Mycobacterium tuberculosis</i> Outbreak: A Longitudinal Molecular Epidemiological Study. <i>PLoS Medicine</i> , 2013, 10, e1001387.	3.9	425
23	Genome Sequence of the Soybean Symbiont <i>Sinorhizobium fredii</i> HH103. <i>Journal of Bacteriology</i> , 2012, 194, 1617-1618.	1.0	54
24	Pangenomic Study of <i>Corynebacterium diphtheriae</i> That Provides Insights into the Genomic Diversity of Pathogenic Isolates from Cases of Classical Diphtheria, Endocarditis, and Pneumonia. <i>Journal of Bacteriology</i> , 2012, 194, 3199-3215.	1.0	142
25	Complete Genome Sequence of the Hydrogenotrophic, Methanogenic Archaeon <i>Methanoculleus bourgensis</i> Strain MS2 <sup>T</sup> , Isolated from a Sewage Sludge Digester. <i>Journal of Bacteriology</i> , 2012, 194, 5487-5488.	1.0	55
26	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
27	Profiling of the metabolically active community from a production-scale biogas plant by means of high-throughput metatranscriptome sequencing. <i>Journal of Biotechnology</i> , 2012, 158, 248-258.	1.9	198
28	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
29	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
30	Comparative and Joint Analysis of Two Metagenomic Datasets from a Biogas Fermenter Obtained by 454-Pyrosequencing. <i>PLoS ONE</i> , 2011, 6, e14519.	1.1	208
31	RAPYD – Rapid Annotation Platform for Yeast Data. <i>Journal of Biotechnology</i> , 2011, 155, 118-126.	1.9	10
32	Complete genome sequencing of <i>Agrobacterium</i> sp. H13-3, the former <i>Rhizobium lupini</i> 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. <i>Journal of Biotechnology</i> , 2011, 155, 50-62.	1.9	112
33	High-quality genome sequence of <i>Pichia pastoris</i> CBS7435. <i>Journal of Biotechnology</i> , 2011, 154, 312-320.	1.9	146
34	Exact and complete short-read alignment to microbial genomes using Graphics Processing Unit programming. <i>Bioinformatics</i> , 2011, 27, 1351-1358.	1.8	78
35	Genomics of the Proteorhodopsin-Containing Marine Flavobacterium <i>Dokdonia</i> sp. Strain MED134. <i>Applied and Environmental Microbiology</i> , 2011, 77, 8676-8686.	1.4	56
36	The complete genome sequence of <i>Corynebacterium pseudotuberculosis</i> FRC41 isolated from a 12-year-old girl with necrotizing lymphadenitis reveals insights into gene-regulatory networks contributing to virulence. <i>BMC Genomics</i> , 2010, 11, 728.	1.2	89

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37	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