

Andreas Bremges

List of Publications by Year in descending order

Source: <https://exaly.com/author-pdf/832562/publications.pdf>

Version: 2024-02-01

26
papers

2,030
citations

430874

18
h-index

552781

26
g-index

31
all docs

31
docs citations

31
times ranked

3055
citing authors

#	ARTICLE	IF	CITATIONS
1	Critical Assessment of Metagenome Interpretation: the second round of challenges. <i>Nature Methods</i> , 2022, 19, 429-440.	19.0	133
2	Tutorial: assessing metagenomics software with the CAMI benchmarking toolkit. <i>Nature Protocols</i> , 2021, 16, 1785-1801.	12.0	36
3	Haploflow: strain-resolved de novo assembly of viral genomes. <i>Genome Biology</i> , 2021, 22, 212.	8.8	16
4	CAMITAX: Taxon labels for microbial genomes. <i>GigaScience</i> , 2020, 9, .	6.4	6
5	Predicting antimicrobial resistance in <i>Pseudomonas aeruginosa</i> with machine learning-enabled molecular diagnostics. <i>EMBO Molecular Medicine</i> , 2020, 12, e10264.	6.9	111
6	Assessing taxonomic metagenome profilers with OPAL. <i>Genome Biology</i> , 2019, 20, 51.	8.8	67
7	CAMISIM: simulating metagenomes and microbial communities. <i>Microbiome</i> , 2019, 7, 17.	11.1	117
8	Assembly of the <i>Lactuca sativa</i> , L. cv. Tizian draft genome sequence reveals differences within major resistance complex 1 as compared to the cv. Salinas reference genome. <i>Journal of Biotechnology</i> , 2018, 267, 12-18.	3.8	13
9	Targeted <i>in situ</i> metatranscriptomics for selected taxa from mesophilic and thermophilic biogas plants. <i>Microbial Biotechnology</i> , 2018, 11, 667-679.	4.2	43
10	Critical Assessment of Metagenome Interpretation Enters the Second Round. <i>MSystems</i> , 2018, 3, .	3.8	18
11	Metagenomics and CAZyme Discovery. <i>Methods in Molecular Biology</i> , 2017, 1588, 255-277.	0.9	19
12	Critical Assessment of Metagenome Interpretation—a benchmark of metagenomics software. <i>Nature Methods</i> , 2017, 14, 1063-1071.	19.0	635
13	Characterisation of a stable laboratory co-culture of acidophilic nanoorganisms. <i>Scientific Reports</i> , 2017, 7, 3289.	3.3	57
14	Investigation of different nitrogen reduction routes and their key microbial players in wood chip-driven denitrification beds. <i>Scientific Reports</i> , 2017, 7, 17028.	3.3	33
15	Genomics and prevalence of bacterial and archaeal isolates from biogas-producing microbiomes. <i>Biotechnology for Biofuels</i> , 2017, 10, 264.	6.2	50
16	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
17	From Genomes to Phenotypes: Traitair, the Microbial Trait Analyzer. <i>MSystems</i> , 2016, 1, .	3.8	102
18	Identification and genome reconstruction of abundant distinct taxa in microbiomes from one thermophilic and three mesophilic production-scale biogas plants. <i>Biotechnology for Biofuels</i> , 2016, 9, 156.	6.2	120

#	ARTICLE	IF	CITATIONS
19	Finished genome sequence and methylome of the cyanide-degrading <i>Pseudomonas pseudoalcaligenes</i> strain CECT5344 as resolved by single-molecule real-time sequencing. <i>Journal of Biotechnology</i> , 2016, 232, 61-68.	3.8	20
20	Genomic characterization of <i>DeFluviitoga tunisiensis</i> L3, a key hydrolytic bacterium in a thermophilic biogas plant and its abundance as determined by metagenome fragment recruitment. <i>Journal of Biotechnology</i> , 2016, 232, 50-60.	3.8	53
21	MeCorS: Metagenome-enabled error correction of single cell sequencing reads. <i>Bioinformatics</i> , 2016, 32, 2199-2201.	4.1	8
22	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.	3.8	33
23	Deeply sequenced metagenome and metatranscriptome of a biogas-producing microbial community from an agricultural production-scale biogas plant. <i>GigaScience</i> , 2015, 4, 33.	6.4	68
24	Bioboxes: standardised containers for interchangeable bioinformatics software. <i>GigaScience</i> , 2015, 4, 47.	6.4	84
25	Fractionation of biogas plant sludge material improves metaproteomic characterization to investigate metabolic activity of microbial communities. <i>Proteomics</i> , 2015, 15, 3585-3589.	2.2	14
26	Complete genome sequence of the cyanide-degrading bacterium <i>Pseudomonas pseudoalcaligenes</i> CECT5344. <i>Journal of Biotechnology</i> , 2014, 175, 67-68.	3.8	28