

Christian Brandt

List of Publications by Year in descending order

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Version: 2024-02-01

29
papers

801
citations

623188

14
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552369

26
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44
all docs

44
docs citations

44
times ranked

1319
citing authors

#	ARTICLE	IF	CITATIONS
1	Phage Genome Diversity in a Biogas-Producing Microbiome Analyzed by Illumina and Nanopore GridION Sequencing. <i>Microorganisms</i> , 2022, 10, 368.	1.6	8
2	Evaluation of microbiome enrichment and host DNA depletion in human vaginal samples using Oxford Nanopore's adaptive sequencing. <i>Scientific Reports</i> , 2022, 12, 4000.	1.6	32
3	Near Chromosome-Level Genome Assembly and Annotation of <i>Rhodotorula babjevae</i> Strains Reveals High Intraspecific Divergence. <i>Journal of Fungi (Basel, Switzerland)</i> , 2022, 8, 323.	1.5	1
4	D,L-Lysine-Acetylsalicylate + Glycine (LASAG) Reduces SARS-CoV-2 Replication and Shows an Additive Effect with Remdesivir. <i>International Journal of Molecular Sciences</i> , 2022, 23, 6880.	1.8	1
5	Computational strategies to combat COVID-19: useful tools to accelerate SARS-CoV-2 and coronavirus research. <i>Briefings in Bioinformatics</i> , 2021, 22, 642-663.	3.2	110
6	Metagenomics workflow for hybrid assembly, differential coverage binning, metatranscriptomics and pathway analysis (MUFFIN). <i>PLoS Computational Biology</i> , 2021, 17, e1008716.	1.5	18
7	SARS-CoV-2 Causes Severe Epithelial Inflammation and Barrier Dysfunction. <i>Journal of Virology</i> , 2021, 95, .	1.5	70
8	Severe clinical relapse in an immunocompromised host with persistent SARS-CoV-2 infection. <i>Leukemia</i> , 2021, 35, 920-923.	3.3	38
9	WGS based analysis of acquired antimicrobial resistance in human and non-human <i>Acinetobacter baumannii</i> isolates from a German perspective. <i>BMC Microbiology</i> , 2021, 21, 210.	1.3	12
10	poreCov-An Easy to Use, Fast, and Robust Workflow for SARS-CoV-2 Genome Reconstruction via Nanopore Sequencing. <i>Frontiers in Genetics</i> , 2021, 12, 711437.	1.1	24
11	Chromosome-level genome assembly and transcriptome-based annotation of the oleaginous yeast <i>Rhodotorula toruloides</i> CBS 14. <i>Genomics</i> , 2021, 113, 4022-4027.	1.3	9
12	Context-aware genomic surveillance reveals hidden transmission of a carbapenemase-producing <i>Klebsiella pneumoniae</i> . <i>Microbial Genomics</i> , 2021, 7, .	1.0	9
13	Abundance Tracking by Long-Read Nanopore Sequencing of Complex Microbial Communities in Samples from 20 Different Biogas/Wastewater Plants. <i>Applied Sciences (Switzerland)</i> , 2020, 10, 7518.	1.3	15
14	Spatio-Temporal Distribution of <i>Acinetobacter baumannii</i> in Germany—A Comprehensive Systematic Review of Studies on Resistance Development in Humans (2000–2018). <i>Microorganisms</i> , 2020, 8, 375.	1.6	16
15	A Genotype-Phenotype Correlation Study of SHV β -Lactamases Offers New Insight into SHV Resistance Profiles. <i>Antimicrobial Agents and Chemotherapy</i> , 2020, 64, .	1.4	5
16	Assessing genetic diversity and similarity of 435 KPC-carrying plasmids. <i>Scientific Reports</i> , 2019, 9, 11223.	1.6	30
17	Use of MALDI-TOF mass spectrometry to detect nosocomial outbreaks of <i>Serratia marcescens</i> and <i>Citrobacter freundii</i> . <i>European Journal of Clinical Microbiology and Infectious Diseases</i> , 2019, 38, 581-591.	1.3	14
18	ESBL colonization and acquisition in a hospital population: The molecular epidemiology and transmission of resistance genes. <i>PLoS ONE</i> , 2019, 14, e0208505.	1.1	38

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19	A Nosocomial Foodborne Outbreak of a VIM Carbapenemase-Expressing <i>Citrobacter freundii</i> . <i>Clinical Infectious Diseases</i> , 2018, 67, 58-64.	2.9	35
20	In silico serine β -lactamases analysis reveals a huge potential resistome in environmental and pathogenic species. <i>Scientific Reports</i> , 2017, 7, 43232.	1.6	65
21	Whole Genome Sequencing of 39 Invasive <i>Streptococcus pneumoniae</i> Sequence Type 199 Isolates Revealed Switches from Serotype 19A to 15B. <i>PLoS ONE</i> , 2017, 12, e0169370.	1.1	19
22	Development of a rapid diagnostic assay based on magnetic bead purification of OXA- β -lactamase mRNA. <i>Future Microbiology</i> , 2016, 11, 617-629.	1.0	4
23	Multidrug-resistant organisms detected in refugee patients admitted to a University Hospital, Germany June–December 2015. <i>Eurosurveillance</i> , 2016, 21, .	3.9	82
24	Direct RNA-based detection of CTX-M β -lactamases in human blood samples. <i>International Journal of Medical Microbiology</i> , 2015, 305, 370-377.	1.5	4
25	Mutagenesis of the CTX-M-type ESBLs is MIC-guided treatment according to the new EUCAST recommendations a safe approach?. <i>Journal of Antimicrobial Chemotherapy</i> , 2015, 70, 2528-2535.	1.3	8
26	The bigger picture: The history of antibiotics and antimicrobial resistance displayed by scientometric data. <i>International Journal of Antimicrobial Agents</i> , 2014, 44, 424-430.	1.1	43
27	Direct RNA-Based Detection and Differentiation of CTX-M-Type Extended-Spectrum β -Lactamases (ESBL). <i>PLoS ONE</i> , 2013, 8, e80079.	1.1	5
28	Global spread of New Delhi metallo- β -lactamase 1. <i>Lancet Infectious Diseases</i> , The, 2010, 10, 828-829.	4.6	50
29	DarkQ: continuous genomic monitoring using message queues. <i>F1000Research</i> , 0, 10, 998.	0.8	1