

Silke Peter

List of Publications by Year in descending order

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Version: 2024-02-01

28
papers

838
citations

623188

14
h-index

500791

28
g-index

32
all docs

32
docs citations

32
times ranked

1396
citing authors

#	ARTICLE	IF	CITATIONS
1	Application of shotgun metagenomics sequencing and targeted sequence capture to detect circulating porcine viruses in the Dutch-German border region. <i>Transboundary and Emerging Diseases</i> , 2022, 69, 2306-2319.	1.3	5
2	Impact of single-room contact precautions on acquisition and transmission of vancomycin-resistant enterococci on haematological and oncological wards, multicentre cohort-study, Germany, January-December 2016. <i>Eurosurveillance</i> , 2022, 27, .	3.9	10
3	High Plasticity of the Amicetin Biosynthetic Pathway in <i>Streptomyces</i> sp. SHP 22-7 Led to the Discovery of Streptocytosine P and Cytosaminomycins F and G and Facilitated the Production of 12F-Plicacetin. <i>Journal of Natural Products</i> , 2022, 85, 530-539.	1.5	6
4	Signature of Alzheimer's Disease in Intestinal Microbiome: Results From the AlzBiom Study. <i>Frontiers in Neuroscience</i> , 2022, 16, 792996.	1.4	12
5	Detection of a small IncX4 plasmid carrying the mcr-1.1 gene in a pig oral fluid sample by shotgun metagenomic sequencing. <i>Journal of Global Antimicrobial Resistance</i> , 2021, 24, 205-206.	0.9	1
6	First detection of porcine respirovirus 1 in Germany and the Netherlands. <i>Transboundary and Emerging Diseases</i> , 2021, 68, 3120-3125.	1.3	15
7	<i>Acinetobacter geminorum</i> sp. nov., isolated from human throat swabs. <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2021, 71, .	0.8	10
8	Evaluation of whole-genome sequence data analysis approaches for short- and long-read sequencing of <i>Mycobacterium tuberculosis</i> . <i>Microbial Genomics</i> , 2021, 7, .	1.0	13
9	Assessment of Viral Targeted Sequence Capture Using Nanopore Sequencing Directly from Clinical Samples. <i>Viruses</i> , 2020, 12, 1358.	1.5	13
10	Tracking of Antibiotic Resistance Transfer and Rapid Plasmid Evolution in a Hospital Setting by Nanopore Sequencing. <i>MSphere</i> , 2020, 5, .	1.3	51
11	Evaluation of two rapid molecular test systems to establish an algorithm for fast identification of bacterial pathogens from positive blood cultures. <i>European Journal of Clinical Microbiology and Infectious Diseases</i> , 2020, 39, 1147-1157.	1.3	19
12	Molecular Evolution of Extensively Drug-Resistant (XDR) <i>Pseudomonas aeruginosa</i> Strains From Patients and Hospital Environment in a Prolonged Outbreak. <i>Frontiers in Microbiology</i> , 2019, 10, 1742.	1.5	10
13	Distinct impact of antibiotics on the gut microbiome and resistome: a longitudinal multicenter cohort study. <i>BMC Biology</i> , 2019, 17, 76.	1.7	92
14	Controlling intestinal colonization of high-risk haematology patients with ESBL-producing Enterobacteriaceae: a randomized, placebo-controlled, multicentre, Phase II trial (CLEAR). <i>Journal of Antimicrobial Chemotherapy</i> , 2019, 74, 2065-2074.	1.3	8
15	Expansion of Vancomycin-Resistant <i>Enterococcus faecium</i> in an Academic Tertiary Hospital in Southwest Germany: a Large-Scale Whole-Genome-Based Outbreak Investigation. <i>Antimicrobial Agents and Chemotherapy</i> , 2019, 63, .	1.4	37
16	Critical steps in clinical shotgun metagenomics for the concomitant detection and typing of microbial pathogens. <i>Scientific Reports</i> , 2018, 8, 13767.	1.6	70
17	A simple statistical test of taxonomic or functional homogeneity using replicated microbiome sequencing samples. <i>Journal of Biotechnology</i> , 2017, 250, 45-50.	1.9	1
18	Evaluation of the Accelerate Pheno System for Fast Identification and Antimicrobial Susceptibility Testing from Positive Blood Cultures in Bloodstream Infections Caused by Gram-Negative Pathogens. <i>Journal of Clinical Microbiology</i> , 2017, 55, 2116-2126.	1.8	135

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19	Susceptibility to cephalosporin combinations and aztreonam/avibactam among third-generation cephalosporin-resistant Enterobacteriaceae recovered on hospital admission. <i>International Journal of Antimicrobial Agents</i> , 2017, 49, 239-242.	1.1	16
20	Protracted Regional Dissemination of GIM-1-Producing <i>Serratia marcescens</i> in Western Germany. <i>Antimicrobial Agents and Chemotherapy</i> , 2017, 61, .	1.4	6
21	Screening and contact precautions – A survey on infection control measures for multidrug-resistant bacteria in German university hospitals. <i>Antimicrobial Resistance and Infection Control</i> , 2017, 6, 37.	1.5	9
22	Translational metagenomics and the human resistome: confronting the menace of the new millennium. <i>Journal of Molecular Medicine</i> , 2017, 95, 41-51.	1.7	20
23	Susceptibility to penicillin derivatives among third-generation cephalosporin-resistant Enterobacteriaceae recovered on hospital admission. <i>Diagnostic Microbiology and Infectious Disease</i> , 2017, 87, 71-73.	0.8	7
24	Genomic characterisation of clinical and environmental <i>Pseudomonas putida</i> group strains and determination of their role in the transfer of antimicrobial resistance genes to <i>Pseudomonas aeruginosa</i> . <i>BMC Genomics</i> , 2017, 18, 859.	1.2	48
25	Analysis of a long-term outbreak of XDR <i>Pseudomonas aeruginosa</i> : a molecular epidemiological study. <i>Journal of Antimicrobial Chemotherapy</i> , 2015, 70, 1322-1330.	1.3	46
26	Antibiotic Selection Pressure Determination through Sequence-Based Metagenomics. <i>Antimicrobial Agents and Chemotherapy</i> , 2015, 59, 7335-7345.	1.4	61
27	Clinical and treatment-related risk factors for nosocomial colonisation with extensively drug-resistant <i>Pseudomonas aeruginosa</i> in a haematological patient population: a matched case control study. <i>BMC Infectious Diseases</i> , 2014, 14, 650.	1.3	20
28	A multicentre cohort study on colonization and infection with ESBL-producing Enterobacteriaceae in high-risk patients with haematological malignancies. <i>Journal of Antimicrobial Chemotherapy</i> , 2014, 69, 3387-3392.	1.3	84