

Sebastian Bruchmann

List of Publications by Year in descending order

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Version: 2024-02-01

14
papers

842
citations

840776

11
h-index

1058476

14
g-index

15
all docs

15
docs citations

15
times ranked

1530
citing authors

#	ARTICLE	IF	CITATIONS
1	PowerBacGWAS: a computational pipeline to perform power calculations for bacterial genome-wide association studies. <i>Communications Biology</i> , 2022, 5, 266.	4.4	4
2	Mining zebrafish microbiota reveals key community-level resistance against fish pathogen infection. <i>ISME Journal</i> , 2021, 15, 702-719.	9.8	49
3	Identifying virulence determinants of multidrug-resistant <i>Klebsiella pneumoniae</i> in <i>Galleria mellonella</i> . <i>Pathogens and Disease</i> , 2021, 79, .	2.0	27
4	Mutation rate dynamics reflect ecological change in an emerging zoonotic pathogen. <i>PLoS Genetics</i> , 2021, 17, e1009864.	3.5	5
5	Discordant bioinformatic predictions of antimicrobial resistance from whole-genome sequencing data of bacterial isolates: an inter-laboratory study. <i>Microbial Genomics</i> , 2020, 6, .	2.0	69
6	Spatiotemporal control of FlgZ activity impacts <i>Pseudomonas aeruginosa</i> flagellar motility. <i>Molecular Microbiology</i> , 2019, 111, 1544-1557.	2.5	12
7	Importance of flagella in acute and chronic <i>Pseudomonas aeruginosa</i> infections. <i>Environmental Microbiology</i> , 2019, 21, 883-897.	3.8	23
8	BACTOME—a reference database to explore the sequence- and gene expression-variation landscape of <i>Pseudomonas aeruginosa</i> clinical isolates. <i>Nucleic Acids Research</i> , 2019, 47, D716-D720.	14.5	38
9	Transcriptome Profiling of Antimicrobial Resistance in <i>Pseudomonas aeruginosa</i> . <i>Antimicrobial Agents and Chemotherapy</i> , 2016, 60, 4722-4733.	3.2	67
10	Deep transcriptome profiling of clinical <i>Klebsiella pneumoniae</i> isolates reveals strain and sequence type-specific adaptation. <i>Environmental Microbiology</i> , 2015, 17, 4690-4710.	3.8	31
11	Elucidation of Sigma Factor-Associated Networks in <i>Pseudomonas aeruginosa</i> Reveals a Modular Architecture with Limited and Function-Specific Crosstalk. <i>PLoS Pathogens</i> , 2015, 11, e1004744.	4.7	134
12	<i>Pseudomonas aeruginosa</i> Ceftolozane-Tazobactam Resistance Development Requires Multiple Mutations Leading to Overexpression and Structural Modification of AmpC. <i>Antimicrobial Agents and Chemotherapy</i> , 2014, 58, 3091-3099.	3.2	197
13	Radically different phylogeographies and patterns of genetic variation in two European brown frogs, genus <i>Rana</i> . <i>Molecular Phylogenetics and Evolution</i> , 2013, 68, 657-670.	2.7	56
14	Quantitative Contributions of Target Alteration and Decreased Drug Accumulation to <i>Pseudomonas aeruginosa</i> Fluoroquinolone Resistance. <i>Antimicrobial Agents and Chemotherapy</i> , 2013, 57, 1361-1368.	3.2	130