

Matthias Preuß

List of Publications by Year in descending order

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Version: 2024-02-01

19
papers

566
citations

687363

13
h-index

794594

19
g-index

20
all docs

20
docs citations

20
times ranked

995
citing authors

#	ARTICLE	IF	CITATIONS
1	Genetically diverse <i>Pseudomonas aeruginosa</i> populations display similar transcriptomic profiles in a cystic fibrosis explanted lung. <i>Nature Communications</i> , 2019, 10, 3397.	12.8	68
2	Transcriptome Profiling of Antimicrobial Resistance in <i>Pseudomonas aeruginosa</i> . <i>Antimicrobial Agents and Chemotherapy</i> , 2016, 60, 4722-4733.	3.2	67
3	Packaging of <i>Dinoroseobacter shibae</i> DNA into Gene Transfer Agent Particles Is Not Random. <i>Genome Biology and Evolution</i> , 2018, 10, 359-369.	2.5	55
4	Regulation of Flagellum Biosynthesis in Response to Cell Envelope Stress in <i>Salmonella enterica</i> Serovar Typhimurium. <i>MBio</i> , 2018, 9, .	4.1	53
5	RNAseq expression analysis of resistant and susceptible mice after influenza A virus infection identifies novel genes associated with virus replication and important for host resistance to infection. <i>BMC Genomics</i> , 2015, 16, 655.	2.8	46
6	Parallel evolutionary paths to produce more than one <i>Pseudomonas aeruginosa</i> biofilm phenotype. <i>Npj Biofilms and Microbiomes</i> , 2020, 6, 2.	6.4	36
7	Itaconate and derivatives reduce interferon responses and inflammation in influenza A virus infection. <i>PLoS Pathogens</i> , 2022, 18, e1010219.	4.7	35
8	Infection- and procedure-dependent effects on pulmonary gene expression in the early phase of influenza A virus infection in mice. <i>BMC Microbiology</i> , 2013, 13, 293.	3.3	32
9	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
10	Establishment of an induced memory response in <i>Pseudomonas aeruginosa</i> during infection of a eukaryotic host. <i>ISME Journal</i> , 2019, 13, 2018-2030.	9.8	26
11	Importance of flagella in acute and chronic <i>Pseudomonas aeruginosa</i> infections. <i>Environmental Microbiology</i> , 2019, 21, 883-897.	3.8	23
12	Host Genetic Background Strongly Affects Pulmonary microRNA Expression before and during Influenza A Virus Infection. <i>Frontiers in Immunology</i> , 2017, 8, 246.	4.8	20
13	Environment-driven changes of mRNA and protein levels in <i>Pseudomonas aeruginosa</i> . <i>Environmental Microbiology</i> , 2018, 20, 3952-3963.	3.8	19
14	Genetic determinants of <i>Pseudomonas aeruginosa</i> fitness during biofilm growth. <i>Biofilm</i> , 2020, 2, 100023.	3.8	16
15	Dual Effect: High NADH Levels Contribute to Efflux-Mediated Antibiotic Resistance but Drive Lethality Mediated by Reactive Oxygen Species. <i>MBio</i> , 2022, 13, e0243421.	4.1	12
16	Single-Nucleotide Polymorphism-Based Genetic Diversity Analysis of Clinical <i>Pseudomonas aeruginosa</i> Isolates. <i>Genome Biology and Evolution</i> , 2020, 12, 396-406.	2.5	10
17	The immunogenic potential of bacterial flagella for <i>Salmonella</i> -mediated tumor therapy. <i>International Journal of Cancer</i> , 2020, 147, 448-460.	5.1	7
18	Host-induced spermidine production in motile <i>Pseudomonas aeruginosa</i> triggers phagocytic uptake. <i>ELife</i> , 2020, 9, .	6.0	6

#	ARTICLE	IF	CITATIONS
19	Analysis of the organization and expression patterns of the convergent <i>Pseudomonas aeruginosa</i> <i>lasR</i> / <i>rsaL</i> gene pair uncovers mutual influence. <i>Molecular Microbiology</i> , 2021, 115, 643-657.	2.5	4