

# Miranda E Pitt

## List of Publications by Year in descending order

Source: <https://exaly.com/author-pdf/6345912/publications.pdf>

Version: 2024-02-01

11  
papers

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citations

1039406

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times ranked

761  
citing authors

#	ARTICLE	IF	CITATIONS
1	Computational analysis and prediction of PE_PGRS proteins using machine learning. <i>Computational and Structural Biotechnology Journal</i> , 2022, 20, 662-674.	1.9	12
2	Long-Read RNA Sequencing Identifies Polyadenylation Elongation and Differential Transcript Usage of Host Transcripts During SARS-CoV-2 In Vitro Infection. <i>Frontiers in Immunology</i> , 2022, 13, 832223.	2.2	9
3	Transcriptional and epi-transcriptional dynamics of SARS-CoV-2 during cellular infection. <i>Cell Reports</i> , 2021, 35, 109108.	2.9	25
4	Evaluating the genome and resistome of extensively drug-resistant <i>Klebsiella pneumoniae</i> using native DNA and RNA Nanopore sequencing. <i>GigaScience</i> , 2020, 9, .	3.3	22
5	Complete Genome Sequences of Clinical <i>Pandoraea fibrosis</i> Isolates. <i>Microbiology Resource Announcements</i> , 2020, 9, .	0.3	1
6	Rapid diagnosis of <i>Capnocytophaga canimorsus</i> septic shock in an immunocompetent individual using real-time Nanopore sequencing: a case report. <i>BMC Infectious Diseases</i> , 2019, 19, 660.	1.3	16
7	Octapeptin C4 and polymyxin resistance occur via distinct pathways in an epidemic XDR <i>Klebsiella pneumoniae</i> ST258 isolate. <i>Journal of Antimicrobial Chemotherapy</i> , 2019, 74, 582-593.	1.3	16
8	Multifactorial chromosomal variants regulate polymyxin resistance in extensively drug-resistant <i>Klebsiella pneumoniae</i> . <i>Microbial Genomics</i> , 2018, 4, .	1.0	39
9	Can octapeptin antibiotics combat extensively drug-resistant (XDR) bacteria?. <i>Expert Review of Anti-Infective Therapy</i> , 2018, 16, 485-499.	2.0	16
10	Inflammation-driven bone formation in a mouse model of ankylosing spondylitis: sequential not parallel processes. <i>Arthritis Research and Therapy</i> , 2016, 18, 35.	1.6	46
11	Fluorescent Trimethoprim Conjugate Probes To Assess Drug Accumulation in Wild Type and Mutant <i>Escherichia coli</i> . <i>ACS Infectious Diseases</i> , 2016, 2, 688-701.	1.8	45