

Clinical utilization of genomics data produced by the *Pseudomonas aeruginosa* consortium

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Citation Report

#	ARTICLE	IF	CITATIONS
1	Habitat-associated skew of clone abundance in the <i>Pseudomonas aeruginosa</i> population. <i>Environmental Microbiology Reports</i> , 2015, 7, 955-960.	1.0	43
2	Commentary: Clinical utilization of genomics data produced by the international <i>Pseudomonas aeruginosa</i> consortium. <i>Frontiers in Microbiology</i> , 2016, 7, 770.	1.5	3
3	Genomic Rearrangements and Functional Diversification of <i>lecA</i> and <i>lecB</i> Lectin-Coding Regions Impacting the Efficacy of Glycomimetics Directed against <i>Pseudomonas aeruginosa</i> . <i>Frontiers in Microbiology</i> , 2016, 7, 811.	1.5	39
4	Phenotype and toxicity of the recently discovered <i>exlA</i> -positive <i>Pseudomonas aeruginosa</i> strains collected worldwide. <i>Environmental Microbiology</i> , 2016, 18, 3425-3439.	1.8	63
5	Comparative analysis of the volatile metabolomes of <i>Pseudomonas aeruginosa</i> clinical isolates. <i>Journal of Breath Research</i> , 2016, 10, 047102.	1.5	83
6	Genomic analyses of multidrug resistant <i>Pseudomonas aeruginosa</i> PA1 resequenced by single-molecule real-time sequencing. <i>Bioscience Reports</i> , 2016, 36, .	1.1	13
7	SNP synteny analysis of <i>Staphylococcus aureus</i> and <i>Pseudomonas aeruginosa</i> population genomics. <i>FEMS Microbiology Letters</i> , 2016, 363, fnw229.	0.7	2
8	Enhanced annotations and features for comparing thousands of <i>Pseudomonas</i> genomes in the <i>Pseudomonas</i> genome database. <i>Nucleic Acids Research</i> , 2016, 44, D646-D653.	6.5	929
9	Microbial genomics and antimicrobial susceptibility testing. <i>Expert Review of Molecular Diagnostics</i> , 2017, 17, 257-269.	1.5	36
10	A <i>Pseudomonas aeruginosa</i> <i>TIR</i> effector mediates immune evasion by targeting <i>UBAP1</i> and <i>TLR</i> adaptors. <i>EMBO Journal</i> , 2017, 36, 1869-1887.	3.5	31
11	<i>Pseudomonas aeruginosa</i> adaptation and diversification in the non-cystic fibrosis bronchiectasis lung. <i>European Respiratory Journal</i> , 2017, 49, 1602108.	3.1	75
12	Correlation between phenotypic antibiotic susceptibility and the resistome in <i>Pseudomonas aeruginosa</i> . <i>International Journal of Antimicrobial Agents</i> , 2017, 50, 210-218.	1.1	65
13	A Pan-Genomic Approach to Understand the Basis of Host Adaptation in <i>Achromobacter</i> . <i>Genome Biology and Evolution</i> , 2017, 9, 1030-1046.	1.1	40
14	Long-term clinical outcomes of the Prairie Epidemic Strain™ <i>Pseudomonas aeruginosa</i> infection in adults with cystic fibrosis. <i>Thorax</i> , 2017, 72, 333-339.	2.7	17
15	Draft Genome Sequences of 10 Environmental <i>Pseudomonas aeruginosa</i> Strains Isolated from Soils, Sediments, and Waters. <i>Genome Announcements</i> , 2017, 5, .	0.8	8
16	Evolution of the <i>Pseudomonas aeruginosa</i> mutational resistome in an international Cystic Fibrosis clone. <i>Scientific Reports</i> , 2017, 7, 5555.	1.6	117
17	Comparative genomics of a drug-resistant <i>Pseudomonas aeruginosa</i> panel and the challenges of antimicrobial resistance prediction from genomes. <i>FEMS Microbiology Letters</i> , 2017, 364, .	0.7	40
18	Evolved Aztreonam Resistance Is Multifactorial and Can Produce Hypervirulence in <i>Pseudomonas aeruginosa</i> . <i>MBio</i> , 2017, 8, .	1.8	65

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20	Antimicrobial resistance surveillance in the genomic age. Annals of the New York Academy of Sciences, 2017, 1388, 78-91.	1.8	71
21	Genomic characterization of environmental Pseudomonas aeruginosa isolated from dental unit waterlines revealed the insertion sequence ISPa11 as a chaotropic element. FEMS Microbiology Ecology, 2017, 93, .	1.3	21
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23	A Syst-OMICS Approach to Ensuring Food Safety and Reducing the Economic Burden of Salmonellosis. Frontiers in Microbiology, 2017, 8, 996.	1.5	42
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25	cAMP and Vfr Control Exolysin Expression and Cytotoxicity of Pseudomonas aeruginosa Taxonomic Outliers. Journal of Bacteriology, 2018, 200, .	1.0	29
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27	PAMDB: a comprehensive Pseudomonas aeruginosa metabolome database. Nucleic Acids Research, 2018, 46, D575-D580.	6.5	45
28	Environmental reservoirs for <i>exoS</i> and <i>exoU</i> strains of <i>Pseudomonas aeruginosa</i> . Environmental Microbiology Reports, 2018, 10, 485-492.	1.0	25
29	Unexpected diversity in the mobilome of a Pseudomonas aeruginosa strain isolated from a dental unit waterline revealed by SMRT Sequencing. Genome, 2018, 61, 359-365.	0.9	2
30	Gallium disrupts bacterial iron metabolism and has therapeutic effects in mice and humans with lung infections. Science Translational Medicine, 2018, 10, .	5.8	214
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34	For the Safety of Fresh Produce: Regulatory Considerations for Canada on the Use of Whole Genome Sequencing to Subtype Salmonella. Frontiers in Sustainable Food Systems, 2018, 2, .	1.8	0
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38	Genomic characterisation of an international <i>Pseudomonas aeruginosa</i> reference panel indicates that the two major groups draw upon distinct mobile gene pools. <i>FEMS Microbiology Letters</i> , 2018, 365, .	0.7	67
39	Antibiotic resistance in <i>Pseudomonas aeruginosa</i> – Mechanisms, epidemiology and evolution. <i>Drug Resistance Updates</i> , 2019, 44, 100640.	6.5	269
40	The Population Structure of <i>Pseudomonas aeruginosa</i> Is Characterized by Genetic Isolation of <i>exoU</i> ⁺ and <i>exoS</i> ⁺ Lineages. <i>Genome Biology and Evolution</i> , 2019, 11, 1780-1796.	1.1	74
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47	Major Release of 161 Whole-Genome Sequences from the International <i>Pseudomonas</i> Consortium Database. <i>Microbiology Resource Announcements</i> , 2019, 8, .	0.3	2
48	The <i>Pseudomonas aeruginosa</i> Population among Cystic Fibrosis Patients in Quebec, Canada: a Disease Hot Spot without Known Epidemic Isolates. <i>Journal of Clinical Microbiology</i> , 2019, 57, .	1.8	2
49	Comparative Genomic Analyses Reveal Core-Genome-Wide Genes Under Positive Selection and Major Regulatory Hubs in Outlier Strains of <i>Pseudomonas aeruginosa</i> . <i>Frontiers in Microbiology</i> , 2019, 10, 53.	1.5	36
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54	Genomics of antibiotic resistance prediction in <i>Pseudomonas aeruginosa</i> . <i>Annals of the New York Academy of Sciences</i> , 2019, 1435, 5-17.	1.8	51
55	Comparative Genomic and Metabolomic Analyses of Two <i>Pseudomonas aeruginosa</i> Strains With Different Antifungal Activities. <i>Frontiers in Microbiology</i> , 2020, 11, 1841.	1.5	15

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57	Comparative Analysis of the Core Proteomes among the <i>Pseudomonas</i> Major Evolutionary Groups Reveals Species-Specific Adaptations for <i>Pseudomonas aeruginosa</i> and <i>Pseudomonas chlororaphis</i> . <i>Diversity</i> , 2020, 12, 289.	0.7	37
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59	Acquired fluoroquinolone resistance genes in corneal isolates of <i>Pseudomonas aeruginosa</i> . <i>Infection, Genetics and Evolution</i> , 2020, 85, 104574.	1.0	19
60	Hit Identification of New Potent PqsR Antagonists as Inhibitors of Quorum Sensing in Planktonic and Biofilm Grown <i>Pseudomonas aeruginosa</i> . <i>Frontiers in Chemistry</i> , 2020, 8, 204.	1.8	29
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77	Phosphorus stress induces the synthesis of novel glycolipids in <i>Pseudomonas aeruginosa</i> that confer protection against a last-resort antibiotic. <i>ISME Journal</i> , 2021, 15, 3303-3314.	4.4	20
78	Heterogenous Susceptibility to R-Pyocins in Populations of <i>Pseudomonas aeruginosa</i> Sourced from Cystic Fibrosis Lungs. <i>MBio</i> , 2021, 12, .	1.8	16
79	Applications of Machine Learning to the Problem of Antimicrobial Resistance: an Emerging Model for Translational Research. <i>Journal of Clinical Microbiology</i> , 2021, 59, e0126020.	1.8	70
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81	Gene-Gene Interactions Dictate Ciprofloxacin Resistance in <i>Pseudomonas aeruginosa</i> and Facilitate Prediction of Resistance Phenotype from Genome Sequence Data. <i>Antimicrobial Agents and Chemotherapy</i> , 2021, 65, e0269620.	1.4	16
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98	Antimicrobial Resistance and Genomic Characterization of Six New Sequence Types in Multidrug-Resistant <i>Pseudomonas aeruginosa</i> Clinical Isolates from Pakistan. <i>Antibiotics</i> , 2021, 10, 1386.	1.5	5
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122	Aminoglycoside-Modifying Enzymes Are Sufficient to Make <i>Pseudomonas aeruginosa</i> Clinically Resistant to Key Antibiotics. <i>Antibiotics</i> , 2022, 11, 884.	1.5	7
124	Genomic diversity and molecular epidemiology of a multidrug-resistant <i>Pseudomonas aeruginosa</i> DMC30b isolated from a hospitalized burn patient in Bangladesh. <i>Journal of Global Antimicrobial Resistance</i> , 2022, 31, 110-118.	0.9	7
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134	Artificial Intelligence for Antimicrobial Resistance Prediction: Challenges and Opportunities towards Practical Implementation. <i>Antibiotics</i> , 2023, 12, 523.	1.5	13
136	Genomic surveillance of bacterial pathogens. , 2023, , 71-117.		1
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