

Tatum D Mortimer

List of Publications by Year in descending order

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Version: 2024-02-01

25
papers

674
citations

706676

14
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721071

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41
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41
docs citations

41
times ranked

1169
citing authors

#	ARTICLE	IF	CITATIONS
1	Loci for prediction of penicillin and tetracycline susceptibility in <i>Neisseria gonorrhoeae</i> : a genome-wide association study. <i>Lancet Microbe</i> , The, 2022, 3, e376-e381.	3.4	11
2	Interactions between Loci Contributing to Antimicrobial Resistance and Virulence in <i>Neisseria gonorrhoeae</i> . <i>MBio</i> , 2022, , e0041222.	1.8	0
3	The Distribution and Spread of Susceptible and Resistant <i>Neisseria gonorrhoeae</i> Across Demographic Groups in a Major Metropolitan Center. <i>Clinical Infectious Diseases</i> , 2021, 73, e3146-e3155.	2.9	19
4	Emergence and evolution of antimicrobial resistance genes and mutations in <i>Neisseria gonorrhoeae</i> . <i>Genome Medicine</i> , 2021, 13, 51.	3.6	25
5	Draft Genome Sequences of Three Penicillin-Resistant <i>Neisseria gonorrhoeae</i> Strains Isolated in Cincinnati, Ohio, in 1994. <i>Microbiology Resource Announcements</i> , 2021, 10, .	0.3	1
6	A community-driven resource for genomic epidemiology and antimicrobial resistance prediction of <i>Neisseria gonorrhoeae</i> at Pathogenwatch. <i>Genome Medicine</i> , 2021, 13, 61.	3.6	63
7	Disseminated Gonococcal Infection Complicated by Prosthetic Joint Infection: Case Report and Genomic and Phylogenetic Analysis. <i>Open Forum Infectious Diseases</i> , 2021, 8, ofaa632.	0.4	5
8	Increased power from conditional bacterial genome-wide association identifies macrolide resistance mutations in <i>Neisseria gonorrhoeae</i> . <i>Nature Communications</i> , 2020, 11, 5374.	5.8	40
9	Efflux Pump Antibiotic Binding Site Mutations Are Associated with Azithromycin Nonsusceptibility in Clinical <i>Neisseria gonorrhoeae</i> Isolates. <i>MBio</i> , 2020, 11, .	1.8	12
10	Adaptation to the cervical environment is associated with increased antibiotic susceptibility in <i>Neisseria gonorrhoeae</i> . <i>Nature Communications</i> , 2020, 11, 4126.	5.8	51
11	Lateral Gene Transfer Shapes Diversity of <i>Gardnerella</i> spp.. <i>Frontiers in Cellular and Infection Microbiology</i> , 2020, 10, 293.	1.8	18
12	RNA polymerase mutations cause cephalosporin resistance in clinical <i>Neisseria gonorrhoeae</i> isolates. <i>ELife</i> , 2020, 9, .	2.8	31
13	Targeted surveillance strategies for efficient detection of novel antibiotic resistance variants. <i>ELife</i> , 2020, 9, .	2.8	6
14	Using rapid point-of-care tests to inform antibiotic choice to mitigate drug resistance in gonorrhoea. <i>Eurosurveillance</i> , 2020, 25, .	3.9	8
15	Applications of genomics to slow the spread of multidrug-resistant <i>Neisseria gonorrhoeae</i> . <i>Annals of the New York Academy of Sciences</i> , 2019, 1435, 93-109.	1.8	31
16	Signatures of Selection at Drug Resistance Loci in <i>Mycobacterium tuberculosis</i> . <i>MSystems</i> , 2018, 3, .	1.7	32
17	Epidemiological and genomic determinants of tuberculosis outbreaks in First Nations communities in Canada. <i>BMC Medicine</i> , 2018, 16, 128.	2.3	17
18	A molecular portrait of maternal sepsis from Byzantine Troy. <i>ELife</i> , 2017, 6, .	2.8	46

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19	Evolutionary thrift: mycobacteria repurpose plasmid diversity during adaptation of type VII secretion systems. <i>Genome Biology and Evolution</i> , 2017, 9, 398-413.	1.1	33
20	Adaptation in a Fibronectin Binding Autolysin of <i>Staphylococcus saprophyticus</i> . <i>MSphere</i> , 2017, 2, .	1.3	9
21	Estimation of Gene Insertion/Deletion Rates with Missing Data. <i>Genetics</i> , 2016, 204, 513-529.	1.2	3
22	Diversity of <i>Mycobacterium tuberculosis</i> across Evolutionary Scales. <i>PLoS Pathogens</i> , 2015, 11, e1005257.	2.1	70
23	Genomic Signatures of Distributive Conjugal Transfer among <i>Mycobacteria</i> . <i>Genome Biology and Evolution</i> , 2014, 6, 2489-2500.	1.1	48
24	A Novel Nonhuman Primate Model for Influenza Transmission. <i>PLoS ONE</i> , 2013, 8, e78750.	1.1	57
25	Rapid adaptation of a complex trait during experimental evolution of <i>Mycobacterium tuberculosis</i> . <i>ELife</i> , 0, 11, .	2.8	9