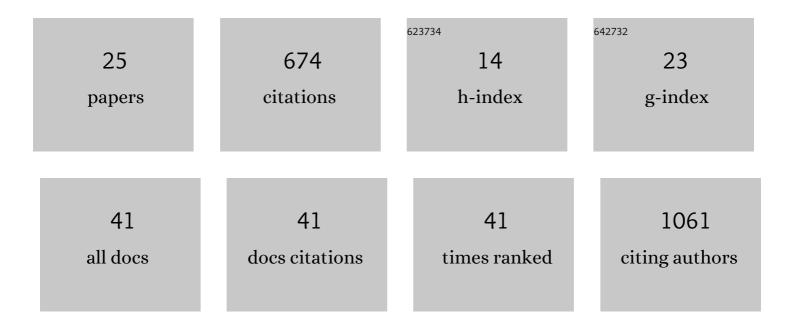
Tatum D Mortimer

List of Publications by Year in descending order

Source: https://exaly.com/author-pdf/600901/publications.pdf Version: 2024-02-01



#	Article	IF	CITATIONS
1	Diversity of Mycobacterium tuberculosis across Evolutionary Scales. PLoS Pathogens, 2015, 11, e1005257.	4.7	70
2	A community-driven resource for genomic epidemiology and antimicrobial resistance prediction of Neisseria gonorrhoeae at Pathogenwatch. Genome Medicine, 2021, 13, 61.	8.2	63
3	A Novel Nonhuman Primate Model for Influenza Transmission. PLoS ONE, 2013, 8, e78750.	2.5	57
4	Adaptation to the cervical environment is associated with increased antibiotic susceptibility in Neisseria gonorrhoeae. Nature Communications, 2020, 11, 4126.	12.8	51
5	Genomic Signatures of Distributive Conjugal Transfer among Mycobacteria. Genome Biology and Evolution, 2014, 6, 2489-2500.	2.5	48
6	A molecular portrait of maternal sepsis from Byzantine Troy. ELife, 2017, 6, .	6.0	46
7	Increased power from conditional bacterial genome-wide association identifies macrolide resistance mutations in Neisseria gonorrhoeae. Nature Communications, 2020, 11, 5374.	12.8	40
8	Evolutionary thrift: mycobacteria repurpose plasmid diversity during adaptation of type VII secretion systems. Genome Biology and Evolution, 2017, 9, 398-413.	2.5	33
9	Signatures of Selection at Drug Resistance Loci in Mycobacterium tuberculosis. MSystems, 2018, 3, .	3.8	32
10	Applications of genomics to slow the spread of multidrugâ€resistant <i>Neisseria gonorrhoeae</i> . Annals of the New York Academy of Sciences, 2019, 1435, 93-109.	3.8	31
11	RNA polymerase mutations cause cephalosporin resistance in clinical Neisseria gonorrhoeae isolates. ELife, 2020, 9, .	6.0	31
12	Emergence and evolution of antimicrobial resistance genes and mutations in Neisseria gonorrhoeae. Genome Medicine, 2021, 13, 51.	8.2	25
13	The Distribution and Spread of Susceptible and Resistant <i>Neisseria gonorrhoeae</i> Across Demographic Groups in a Major Metropolitan Center. Clinical Infectious Diseases, 2021, 73, e3146-e3155.	5.8	19
14	Lateral Gene Transfer Shapes Diversity of Gardnerella spp Frontiers in Cellular and Infection Microbiology, 2020, 10, 293.	3.9	18
15	Epidemiological and genomic determinants of tuberculosis outbreaks in First Nations communities in Canada. BMC Medicine, 2018, 16, 128.	5.5	17
16	Efflux Pump Antibiotic Binding Site Mutations Are Associated with Azithromycin Nonsusceptibility in Clinical Neisseria gonorrhoeae Isolates. MBio, 2020, 11, .	4.1	12
17	Loci for prediction of penicillin and tetracycline susceptibility in Neisseria gonorrhoeae: a genome-wide association study. Lancet Microbe, The, 2022, 3, e376-e381.	7.3	11
18	Adaptation in a Fibronectin Binding Autolysin of Staphylococcus saprophyticus. MSphere, 2017, 2, .	2.9	9

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#	Article	IF	CITATIONS
19	Rapid adaptation of a complex trait during experimental evolution of Mycobacterium tuberculosis. ELife, 0, 11, .	6.0	9
20	Using rapid point-of-care tests to inform antibiotic choice to mitigate drug resistance in gonorrhoea. Eurosurveillance, 2020, 25, .	7.0	8
21	Targeted surveillance strategies for efficient detection of novel antibiotic resistance variants. ELife, 2020, 9, .	6.0	6
22	Disseminated Gonococcal Infection Complicated by Prosthetic Joint Infection: Case Report and Genomic and Phylogenetic Analysis. Open Forum Infectious Diseases, 2021, 8, ofaa632.	0.9	5
23	Estimation of Gene Insertion/Deletion Rates with Missing Data. Genetics, 2016, 204, 513-529.	2.9	3
24	Draft Genome Sequences of Three Penicillin-Resistant Neisseria gonorrhoeae Strains Isolated in Cincinnati, Ohio, in 1994. Microbiology Resource Announcements, 2021, 10, .	0.6	1
25	Interactions between Loci Contributing to Antimicrobial Resistance and Virulence in Neisseria gonorrhoeae. MBio, 2022. , e0041222.	4.1	0