

Claudio U Käser

List of Publications by Year in descending order

Source: <https://exaly.com/author-pdf/2506099/publications.pdf>

Version: 2024-02-01

67
papers

4,589
citations

172457

29
h-index

110387

64
g-index

70
all docs

70
docs citations

70
times ranked

5444
citing authors

#	ARTICLE	IF	CITATIONS
1	Ancient and recent differences in the intrinsic susceptibility of <i>Mycobacterium tuberculosis</i> complex to pretomanid. <i>Journal of Antimicrobial Chemotherapy</i> , 2022, 77, 1685-1693.	3.0	34
2	The 2021 WHO catalogue of <i>Mycobacterium tuberculosis</i> complex mutations associated with drug resistance: a genotypic analysis. <i>Lancet Microbe</i> , The, 2022, 3, e265-e273.	7.3	114
3	Updating the approaches to define susceptibility and resistance to anti-tuberculosis agents: implications for diagnosis and treatment. <i>European Respiratory Journal</i> , 2022, 59, 2200166.	6.7	15
4	On the Consequences of Poorly Defined Breakpoints for Rifampin Susceptibility Testing of <i>Mycobacterium tuberculosis</i> Complex. <i>Journal of Clinical Microbiology</i> , 2021, 59, .	3.9	14
5	Targeted next-generation sequencing: a Swiss army knife for mycobacterial diagnostics?. <i>European Respiratory Journal</i> , 2021, 57, 2004077.	6.7	15
6	Is the new WHO definition of extensively drug-resistant tuberculosis easy to apply in practice?. <i>European Respiratory Journal</i> , 2021, 58, 2100959.	6.7	5
7	Role of Epistasis in Amikacin, Kanamycin, Bedaquiline, and Clofazimine Resistance in <i>Mycobacterium tuberculosis</i> Complex. <i>Antimicrobial Agents and Chemotherapy</i> , 2021, 65, e0116421.	3.2	35
8	Guidance is needed to mitigate the consequences of analytic errors during antimicrobial susceptibility testing for TB. <i>International Journal of Tuberculosis and Lung Disease</i> , 2021, 25, 791-794.	1.2	4
9	Impact of the bacillary load on the accuracy of rifampicin resistance results by Xpert® MTB/RIF. <i>International Journal of Tuberculosis and Lung Disease</i> , 2021, 25, 881-885.	1.2	2
10	What is the role of the EUCAST reference method for MIC testing of the <i>Mycobacterium tuberculosis</i> complex?. <i>Clinical Microbiology and Infection</i> , 2020, 26, 1453-1455.	6.0	14
11	MDR <i>M. tuberculosis</i> outbreak clone in Eswatini missed by Xpert has elevated bedaquiline resistance dated to the pre-treatment era. <i>Genome Medicine</i> , 2020, 12, 104.	8.2	50
12	How To Optimally Combine Genotypic and Phenotypic Drug Susceptibility Testing Methods for Pyrazinamide. <i>Antimicrobial Agents and Chemotherapy</i> , 2020, 64, .	3.2	18
13	Systematic review of mutations associated with resistance to the new and repurposed <i>Mycobacterium tuberculosis</i> drugs bedaquiline, clofazimine, linezolid, delamanid and pretomanid. <i>Journal of Antimicrobial Chemotherapy</i> , 2020, 75, 2031-2043.	3.0	124
14	Phylogenetically informative mutations in genes implicated in antibiotic resistance in <i>Mycobacterium tuberculosis</i> complex. <i>Genome Medicine</i> , 2020, 12, 27.	8.2	58
15	Prevalence and genetic profiles of isoniazid resistance in tuberculosis patients: A multicountry analysis of cross-sectional data. <i>PLoS Medicine</i> , 2020, 17, e1003008.	8.4	74
16	Genomic identification of cryptic susceptibility to penicillins and β -lactamase inhibitors in methicillin-resistant <i>Staphylococcus aureus</i> . <i>Nature Microbiology</i> , 2019, 4, 1680-1691.	13.3	47
17	Revised Interpretation of the Hain Lifescience GenoType MTBC To Differentiate <i>Mycobacterium canettii</i> and Members of the <i>Mycobacterium tuberculosis</i> Complex. <i>Antimicrobial Agents and Chemotherapy</i> , 2019, 63, .	3.2	20
18	Isoniazid Resistance in <i>Mycobacterium tuberculosis</i> Is a Heterogeneous Phenotype Composed of Overlapping MIC Distributions with Different Underlying Resistance Mechanisms. <i>Antimicrobial Agents and Chemotherapy</i> , 2019, 63, .	3.2	32

#	ARTICLE	IF	CITATIONS
19	Standards for MIC testing that apply to the majority of bacterial pathogens should also be enforced for <i>Mycobacterium tuberculosis</i> complex. <i>Clinical Microbiology and Infection</i> , 2019, 25, 403-405.	6.0	24
20	“Those who cannot remember the past are condemned to repeat it”: Drug-susceptibility testing for bedaquiline and delamanid. <i>International Journal of Infectious Diseases</i> , 2019, 80, S32-S35.	3.3	33
21	World Tuberculosis Day March 24th 2019 Theme: “It’s TIME” International Journal of Infectious Diseases Tuberculosis Theme Series. <i>International Journal of Infectious Diseases</i> , 2019, 80, S1-S5.	3.3	3
22	Evolution of Programmatic Definitions Used in Tuberculosis Prevention and Care. <i>Clinical Infectious Diseases</i> , 2019, 68, 1787-1789.	5.8	24
23	Limited Evidence for the Need for Region-Specific, Genotypic Drug-Susceptibility Assays for <i>Mycobacterium tuberculosis</i> . <i>Clinical Infectious Diseases</i> , 2018, 66, 1481-1482.	5.8	2
24	What Is Resistance? Impact of Phenotypic versus Molecular Drug Resistance Testing on Therapy for Multi- and Extensively Drug-Resistant Tuberculosis. <i>Antimicrobial Agents and Chemotherapy</i> , 2018, 62, .	3.2	83
25	<sc>d</sc>-Cycloserine Pharmacokinetics/Pharmacodynamics, Susceptibility, and Dosing Implications in Multidrug-resistant Tuberculosis: A Faustian Deal. <i>Clinical Infectious Diseases</i> , 2018, 67, S308-S316.	5.8	45
26	Reply to Dookie et al., “Whole-Genome Sequencing To Guide the Selection of Treatment for Drug-Resistant Tuberculosis” <i>Antimicrobial Agents and Chemotherapy</i> , 2018, 62, .	3.2	1
27	Some Synonymous and Nonsynonymous <i>gyrA</i> Mutations in <i>Mycobacterium tuberculosis</i> Lead to Systematic False-Positive Fluoroquinolone Resistance Results with the Hain GenoType MTBDR <i>sls</i> Assays. <i>Antimicrobial Agents and Chemotherapy</i> , 2017, 61, .	3.2	29
28	<i>Mycobacterium tuberculosis</i> resistance prediction and lineage classification from genome sequencing: comparison of automated analysis tools. <i>Scientific Reports</i> , 2017, 7, 46327.	3.3	82
29	Role of Alanine Racemase Mutations in <i>Mycobacterium tuberculosis</i> <sc>d</sc>-Cycloserine Resistance. <i>Antimicrobial Agents and Chemotherapy</i> , 2017, 61, .	3.2	24
30	<i>Mycobacterium tuberculosis</i> drug-resistance testing: challenges, recent developments and perspectives. <i>Clinical Microbiology and Infection</i> , 2017, 23, 154-160.	6.0	150
31	The role of whole genome sequencing in antimicrobial susceptibility testing of bacteria: report from the EUCAST Subcommittee. <i>Clinical Microbiology and Infection</i> , 2017, 23, 2-22.	6.0	428
32	A standardised method for interpreting the association between mutations and phenotypic drug resistance in <i>Mycobacterium tuberculosis</i> . <i>European Respiratory Journal</i> , 2017, 50, 1701354.	6.7	273
33	Convergent evolution and topologically disruptive polymorphisms among multidrug-resistant tuberculosis in Peru. <i>PLoS ONE</i> , 2017, 12, e0189838.	2.5	19
34	<i>dfrA thyA</i> Double Deletion in <i>para</i> -Aminosalicylic Acid-Resistant <i>Mycobacterium tuberculosis</i> Beijing Strains. <i>Antimicrobial Agents and Chemotherapy</i> , 2016, 60, 3864-3867.	3.2	20
35	Whole-genome sequencing of multidrug-resistant <i>Mycobacterium tuberculosis</i> isolates from Myanmar. <i>Journal of Global Antimicrobial Resistance</i> , 2016, 6, 113-117.	2.2	28
36	Wild-Type and Non-Wild-Type <i>Mycobacterium tuberculosis</i> MIC Distributions for the Novel Fluoroquinolone Antofloxacin Compared with Those for Ofloxacin, Levofloxacin, and Moxifloxacin. <i>Antimicrobial Agents and Chemotherapy</i> , 2016, 60, 5232-5237.	3.2	15

#	ARTICLE	IF	CITATIONS
37	Emergent and evolving antimicrobial resistance cassettes in community-associated fusidic acid and methicillin-resistant <i>Staphylococcus aureus</i> . <i>International Journal of Antimicrobial Agents</i> , 2015, 45, 477-484.	2.5	39
38	Drug-resistance mechanisms and tuberculosis drugs. <i>Lancet, The</i> , 2015, 385, 305-307.	13.7	22
39	Genome sequencing defines phylogeny and spread of methicillin-resistant <i>Staphylococcus aureus</i> in a high transmission setting. <i>Genome Research</i> , 2015, 25, 111-118.	5.5	111
40	Comment on: Characterization of the embB gene in <i>Mycobacterium tuberculosis</i> isolates from Barcelona and rapid detection of main mutations related to ethambutol resistance using a low-density DNA array. <i>Journal of Antimicrobial Chemotherapy</i> , 2014, 69, 2298-2299.	3.0	8
41	Phylogenetic polymorphisms in antibiotic resistance genes of the <i>Mycobacterium tuberculosis</i> complex. <i>Journal of Antimicrobial Chemotherapy</i> , 2014, 69, 1205-1210.	3.0	76
42	Rapid single-colony whole-genome sequencing of bacterial pathogens. <i>Journal of Antimicrobial Chemotherapy</i> , 2014, 69, 1275-1281.	3.0	49
43	New methods for identifying infectious diseases. <i>British Medical Bulletin</i> , 2014, 112, 27-35.	6.9	14
44	Whole-genome sequencing to control antimicrobial resistance. <i>Trends in Genetics</i> , 2014, 30, 401-407.	6.7	232
45	Genetic diversity within <i>Mycobacterium tuberculosis</i> complex impacts on the accuracy of genotypic pyrazinamide drug-susceptibility assay. <i>Tuberculosis</i> , 2014, 94, 451-453.	1.9	11
46	Rapid Bacterial Whole-Genome Sequencing to Enhance Diagnostic and Public Health Microbiology. <i>JAMA Internal Medicine</i> , 2013, 173, 1397.	5.1	181
47	Whole-Genome Sequencing for Rapid Susceptibility Testing of <i>M. tuberculosis</i> . <i>New England Journal of Medicine</i> , 2013, 369, 290-292.	27.0	195
48	<i>Mycobacterium canettii</i> is intrinsically resistant to both pyrazinamide and pyrazinoic acid. <i>Journal of Antimicrobial Chemotherapy</i> , 2013, 68, 1439-1440.	3.0	42
49	Rapid Whole-Genome Sequencing for Investigation of a Suspected Tuberculosis Outbreak. <i>Journal of Clinical Microbiology</i> , 2013, 51, 611-614.	3.9	80
50	A pilot study of rapid whole-genome sequencing for the investigation of a <i>Legionella</i> outbreak. <i>BMJ Open</i> , 2013, 3, e002175.	1.9	105
51	Consequences of <i>whiB7</i> (<i>Rv3197A</i>) Mutations in Beijing Genotype Isolates of the <i>Mycobacterium tuberculosis</i> Complex. <i>Antimicrobial Agents and Chemotherapy</i> , 2013, 57, 3461-3461.	3.2	17
52	Routine Use of Microbial Whole Genome Sequencing in Diagnostic and Public Health Microbiology. <i>PLoS Pathogens</i> , 2012, 8, e1002824.	4.7	450
53	Importance of the Genetic Diversity within the <i>Mycobacterium tuberculosis</i> Complex for the Development of Novel Antibiotics and Diagnostic Tests of Drug Resistance. <i>Antimicrobial Agents and Chemotherapy</i> , 2012, 56, 6080-6087.	3.2	55
54	Rapid Whole-Genome Sequencing for Investigation of a Neonatal MRSA Outbreak. <i>New England Journal of Medicine</i> , 2012, 366, 2267-2275.	27.0	609

#	ARTICLE	IF	CITATIONS
55	Overview of errors in the reference sequence and annotation of <i>Mycobacterium tuberculosis</i> H37Rv, and variation amongst its isolates. <i>Infection, Genetics and Evolution</i> , 2012, 12, 807-810.	2.3	6
56	Microbial sequences benefit health now. <i>Nature</i> , 2011, 471, 578-578.	27.8	5
57	Impact of <i>fgd1</i> and <i>ddn</i> Diversity in <i>Mycobacterium tuberculosis</i> Complex on <i>In Vitro</i> Susceptibility to PA-824. <i>Antimicrobial Agents and Chemotherapy</i> , 2011, 55, 5718-5722.	3.2	60
58	Comment on: Isoniazid and rifampicin resistance-associated mutations in <i>Mycobacterium tuberculosis</i> isolates from Yangon, Myanmar: implications for rapid molecular testing. <i>Journal of Antimicrobial Chemotherapy</i> , 2011, 66, 686-687.	3.0	2
59	Thr270Ile in <i>embC</i> (<i>Rv3793</i>) Is Not a Marker for Ethambutol Resistance in the <i>Mycobacterium tuberculosis</i> Complex. <i>Antimicrobial Agents and Chemotherapy</i> , 2011, 55, 1825-1825.	3.2	7
60	Polymorphisms in Isoniazid and Prothionamide Resistance Genes of the <i>Mycobacterium tuberculosis</i> Complex. <i>Antimicrobial Agents and Chemotherapy</i> , 2011, 55, 4408-4411.	3.2	15
61	Role of changes in the L3 loop of the active site in the evolution of enzymatic activity of VIM-type metallo- β -lactamases—authors' response. <i>Journal of Antimicrobial Chemotherapy</i> , 2011, 66, 686-686.	3.0	4
62	Read Length and Repeat Resolution: Exploring Prokaryote Genomes Using Next-Generation Sequencing Technologies. <i>PLoS ONE</i> , 2010, 5, e11518.	2.5	49
63	Thr202Ala in <i>thyA</i> Is a Marker for the Latin American Mediterranean Lineage of the <i>Mycobacterium tuberculosis</i> Complex Rather than <i>Para</i> -Aminosalicylic Acid Resistance. <i>Antimicrobial Agents and Chemotherapy</i> , 2010, 54, 4794-4798.	3.2	19
64	Role of the Dihydrofolate Reductase DfrA (<i>Rv2763c</i>) in Trimethoprim-Sulfamethoxazole (Co-Trimoxazole) Resistance in <i>Mycobacterium tuberculosis</i> . <i>Antimicrobial Agents and Chemotherapy</i> , 2010, 54, 4951-4952.	3.2	11
65	Role of Mutations in Dihydrofolate Reductase DfrA (<i>Rv2763c</i>) and Thymidylate Synthase ThyA (<i>Rv2764c</i>) in <i>Mycobacterium tuberculosis</i> Drug Resistance. <i>Antimicrobial Agents and Chemotherapy</i> , 2010, 54, 4522-4525.	3.2	8
66	Single-Nucleotide Polymorphisms in <i>Rv2629</i> Are Specific for <i>Mycobacterium tuberculosis</i> Genotypes Beijing and Ghana but Not Associated with Rifampin Resistance. <i>Journal of Clinical Microbiology</i> , 2009, 47, 223-226.	3.9	16
67	Genomic Diversity among Drug Sensitive and Multidrug Resistant Isolates of <i>Mycobacterium tuberculosis</i> with Identical DNA Fingerprints. <i>PLoS ONE</i> , 2009, 4, e7407.	2.5	128