

Thomas A Kohl

List of Publications by Year in descending order

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97
papers

7,101
citations

94433

37
h-index

69250

77
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114
all docs

114
docs citations

114
times ranked

6612
citing authors

#	ARTICLE	IF	CITATIONS
1	Whole-genome sequencing for prediction of Mycobacterium tuberculosis drug susceptibility and resistance: a retrospective cohort study. <i>Lancet Infectious Diseases</i> , The, 2015, 15, 1193-1202.	9.1	553
2	Rapid antibiotic-resistance predictions from genome sequence data for Staphylococcus aureus and Mycobacterium tuberculosis. <i>Nature Communications</i> , 2015, 6, 10063.	12.8	479
3	Evolutionary history and global spread of the Mycobacterium tuberculosis Beijing lineage. <i>Nature Genetics</i> , 2015, 47, 242-249.	21.4	466
4	Whole Genome Sequencing versus Traditional Genotyping for Investigation of a Mycobacterium tuberculosis Outbreak: A Longitudinal Molecular Epidemiological Study. <i>PLoS Medicine</i> , 2013, 10, e1001387.	8.4	425
5	Prediction of Susceptibility to First-Line Tuberculosis Drugs by DNA Sequencing. <i>New England Journal of Medicine</i> , 2018, 379, 1403-1415.	27.0	405
6	Rapid, comprehensive, and affordable mycobacterial diagnosis with whole-genome sequencing: a prospective study. <i>Lancet Respiratory Medicine</i> , the, 2016, 4, 49-58.	10.7	282
7	PhyResSE: a Web Tool Delineating Mycobacterium tuberculosis Antibiotic Resistance and Lineage from Whole-Genome Sequencing Data. <i>Journal of Clinical Microbiology</i> , 2015, 53, 1908-1914.	3.9	257
8	Whole genome sequencing of Mycobacterium tuberculosis: current standards and open issues. <i>Nature Reviews Microbiology</i> , 2019, 17, 533-545.	28.6	237
9	Global outbreak of severe Mycobacterium chimaera disease after cardiac surgery: a molecular epidemiological study. <i>Lancet Infectious Diseases</i> , The, 2017, 17, 1033-1041.	9.1	198
10	Emended description of Mycobacterium abscessus, Mycobacterium abscessus subsp. abscessus and Mycobacterium abscessus subsp. bolletii and designation of Mycobacterium abscessus subsp. massiliense comb. nov.. <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2016, 66, 4471-4479.	1.7	190
11	Detoxifying Escherichia coli for endotoxin-free production of recombinant proteins. <i>Microbial Cell Factories</i> , 2015, 14, 57.	4.0	178
12	Whole-Genome-Based Mycobacterium tuberculosis Surveillance: a Standardized, Portable, and Expandable Approach. <i>Journal of Clinical Microbiology</i> , 2014, 52, 2479-2486.	3.9	175
13	MTBseq: a comprehensive pipeline for whole genome sequence analysis of Mycobacterium tuberculosis complex isolates. <i>PeerJ</i> , 2018, 6, e5895.	2.0	148
14	Delamanid and Bedaquiline Resistance in Mycobacterium tuberculosis Ancestral Beijing Genotype Causing Extensively Drug-Resistant Tuberculosis in a Tibetan Refugee. <i>American Journal of Respiratory and Critical Care Medicine</i> , 2016, 193, 337-340.	5.6	125
15	Genetic sequencing for surveillance of drug resistance in tuberculosis in highly endemic countries: a multi-country population-based surveillance study. <i>Lancet Infectious Diseases</i> , The, 2018, 18, 675-683.	9.1	119
16	Whole Genome Sequencing Reveals Complex Evolution Patterns of Multidrug-Resistant Mycobacterium tuberculosis Beijing Strains in Patients. <i>PLoS ONE</i> , 2013, 8, e82551.	2.5	117
17	The 2021 WHO catalogue of Mycobacterium tuberculosis complex mutations associated with drug resistance: a genotypic analysis. <i>Lancet Microbe</i> , The, 2022, 3, e265-e273.	7.3	114
18	The relationship between transmission time and clustering methods in Mycobacterium tuberculosis epidemiology. <i>EBioMedicine</i> , 2018, 37, 410-416.	6.1	106

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19	Antibiotic resistance prediction for <i>Mycobacterium tuberculosis</i> from genome sequence data with Mykrobe. Wellcome Open Research, 2019, 4, 191.	1.8	103
20	Compensatory evolution drives multidrug-resistant tuberculosis in Central Asia. <i>ELife</i> , 2018, 7, .	6.0	93
21	The GlxR regulon of the amino acid producer <i>Corynebacterium glutamicum</i> : In silico and in vitro detection of DNA binding sites of a global transcription regulator. <i>Journal of Biotechnology</i> , 2008, 135, 340-350.	3.8	89
22	Library preparation for next generation sequencing: A review of automation strategies. <i>Biotechnology Advances</i> , 2020, 41, 107537.	11.7	88
23	<i>rplC</i> T460C Identified as a Dominant Mutation in Linezolid-Resistant <i>Mycobacterium tuberculosis</i> Strains. <i>Antimicrobial Agents and Chemotherapy</i> , 2012, 56, 2743-2745.	3.2	83
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	The phylogenetic landscape and nosocomial spread of the multidrug-resistant opportunist <i>Stenotrophomonas maltophilia</i> . <i>Nature Communications</i> , 2020, 11, 2044.	12.8	76
26	High Interlaboratory Reproducibility and Accuracy of Next-Generation-Sequencing-Based Bacterial Genotyping in a Ring Trial. <i>Journal of Clinical Microbiology</i> , 2017, 55, 908-913.	3.9	75
27	Integrating standardized whole genome sequence analysis with a global <i>Mycobacterium tuberculosis</i> antibiotic resistance knowledgebase. <i>Scientific Reports</i> , 2018, 8, 15382.	3.3	75
28	Application of machine learning techniques to tuberculosis drug resistance analysis. <i>Bioinformatics</i> , 2019, 35, 2276-2282.	4.1	71
29	The GlxR regulon of the amino acid producer <i>Corynebacterium glutamicum</i> : Detection of the corynebacterial core regulon and integration into the transcriptional regulatory network model. <i>Journal of Biotechnology</i> , 2009, 143, 239-246.	3.8	67
30	<i>Mycobacterium abscessus</i> in patients with cystic fibrosis: low impact of inter-human transmission in Italy. <i>European Respiratory Journal</i> , 2017, 50, 1602525.	6.7	63
31	Whole genome sequencing for M/XDR tuberculosis surveillance and for resistance testing. <i>Clinical Microbiology and Infection</i> , 2017, 23, 161-166.	6.0	61
32	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
33	Tracing <i>Mycobacterium tuberculosis</i> transmission by whole genome sequencing in a high incidence setting: a retrospective population-based study in East Greenland. <i>Scientific Reports</i> , 2016, 6, 33180.	3.3	51
34	International Society of Cardiovascular Infectious Diseases Guidelines for the Diagnosis, Treatment and Prevention of Disseminated <i>Mycobacterium chimaera</i> Infection Following Cardiac Surgery with Cardiopulmonary Bypass. <i>Journal of Hospital Infection</i> , 2020, 104, 214-235.	2.9	50
35	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
36	Rapid genomic first- and second-line drug resistance prediction from clinical <i>Mycobacterium tuberculosis</i> specimens using Deeplex-MycTB. <i>European Respiratory Journal</i> , 2021, 57, 2001796.	6.7	47

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37	High-resolution detection of DNA binding sites of the global transcriptional regulator GlxR in <i>Corynebacterium glutamicum</i> . <i>Microbiology (United Kingdom)</i> , 2013, 159, 12-22.	1.8	44
38	The Evolution of Strain Typing in the <i>Mycobacterium tuberculosis</i> Complex. <i>Advances in Experimental Medicine and Biology</i> , 2017, 1019, 43-78.	1.6	43
39	Harmonized Genome Wide Typing of Tubercle Bacilli Using a Web-Based Gene-By-Gene Nomenclature System. <i>EBioMedicine</i> , 2018, 34, 131-138.	6.1	42
40	Towards standardisation: comparison of five whole genome sequencing (WGS) analysis pipelines for detection of epidemiologically linked tuberculosis cases. <i>Eurosurveillance</i> , 2019, 24, .	7.0	42
41	Tracing the Spread of <i>Clostridium difficile</i> Ribotype 027 in Germany Based on Bacterial Genome Sequences. <i>PLoS ONE</i> , 2015, 10, e0139811.	2.5	40
42	From <i>Corynebacterium glutamicum</i> to <i>Mycobacterium tuberculosis</i> —towards transfers of gene regulatory networks and integrated data analyses with MycoRegNet. <i>Nucleic Acids Research</i> , 2009, 37, e97-e97.	14.5	39
43	Analysis of Phylogenetic Variation of <i>Stenotrophomonas maltophilia</i> Reveals Human-Specific Branches. <i>Frontiers in Microbiology</i> , 2018, 9, 806.	3.5	39
44	DeepAMR for predicting co-occurrent resistance of <i>Mycobacterium tuberculosis</i> . <i>Bioinformatics</i> , 2019, 35, 3240-3249.	4.1	38
45	New <i>Mycobacterium tuberculosis</i> Complex Sublineage, Brazzaville, Congo. <i>Emerging Infectious Diseases</i> , 2017, 23, 423-429.	4.3	35
46	Comparative genomics of <i>Mycobacterium africanum</i> Lineage 5 and Lineage 6 from Ghana suggests distinct ecological niches. <i>Scientific Reports</i> , 2018, 8, 11269.	3.3	34
47	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
48	Perspectives for personalized therapy for patients with multidrug-resistant tuberculosis. <i>Journal of Internal Medicine</i> , 2018, 284, 163-188.	6.0	33
49	Phenylacetic Acid Catabolism and Its Transcriptional Regulation in <i>Corynebacterium glutamicum</i> . <i>Applied and Environmental Microbiology</i> , 2012, 78, 5796-5804.	3.1	32
50	Detection of transrenal DNA for the diagnosis of pulmonary tuberculosis and treatment monitoring. <i>Infection</i> , 2017, 45, 269-276.	4.7	32
51	Genetic Diversity of Multi- and Extensively Drug-Resistant <i>Mycobacterium tuberculosis</i> Isolates in the Capital of Iran, Revealed by Whole-Genome Sequencing. <i>Journal of Clinical Microbiology</i> , 2019, 57, .	3.9	29
52	Phenotypic Heterogeneity Affects <i>Stenotrophomonas maltophilia</i> K279a Colony Morphotypes and β -Lactamase Expression. <i>Frontiers in Microbiology</i> , 2015, 6, 1373.	3.5	27
53	Use of a Whole Genome Sequencing-based approach for <i>Mycobacterium tuberculosis</i> surveillance in Europe in 2017–2019: an ECDC pilot study. <i>European Respiratory Journal</i> , 2021, 57, 2002272.	6.7	27
54	Impact of Genetic Diversity on the Biology of <i>Mycobacterium tuberculosis</i> Complex Strains. <i>Microbiology Spectrum</i> , 2016, 4, .	3.0	26

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55	<i>Mycobacterium abscessus</i> subsp. <i>abscessus</i> Is Capable of Degrading <i>Pseudomonas aeruginosa</i> Quinolone Signals. <i>Frontiers in Microbiology</i> , 2017, 8, 339.	3.5	26
56	A joint cross-border investigation of a cluster of multidrug-resistant tuberculosis in Austria, Romania and Germany in 2014 using classic, genotyping and whole genome sequencing methods: lessons learnt. <i>Eurosurveillance</i> , 2017, 22, .	7.0	26
57	GenomeMap: Within-Species Genome-Wide dN/dS Estimation from over 10,000 Genomes. <i>Molecular Biology and Evolution</i> , 2020, 37, 2450-2460.	8.9	25
58	Role of Alanine Racemase Mutations in <i>Mycobacterium tuberculosis</i> <i>hspR</i> -Cycloserine Resistance. <i>Antimicrobial Agents and Chemotherapy</i> , 2017, 61, .	3.2	24
59	The Genetic Transformation of <i>Chlamydia pneumoniae</i> . <i>MSphere</i> , 2018, 3, .	2.9	23
60	Multidrug- and Extensively Drug-Resistant <i>Mycobacterium tuberculosis</i> Beijing Clades, Ukraine, 2015. <i>Emerging Infectious Diseases</i> , 2020, 26, 481-490.	4.3	23
61	A publicly accessible database for <i>Clostridioides difficile</i> genome sequences supports tracing of transmission chains and epidemics. <i>Microbial Genomics</i> , 2020, 6, .	2.0	22
62	Insertion and deletion evolution reflects antibiotics selection pressure in a <i>Mycobacterium tuberculosis</i> outbreak. <i>PLoS Pathogens</i> , 2020, 16, e1008357.	4.7	22
63	Accuracy of whole-genome sequencing to determine recent tuberculosis transmission: an 11-year population-based study in Hamburg, Germany. <i>European Respiratory Journal</i> , 2019, 54, 1901154.	6.7	21
64	Design of Multidrug-Resistant Tuberculosis Treatment Regimens Based on DNA Sequencing. <i>Clinical Infectious Diseases</i> , 2021, 73, 1194-1202.	5.8	21
65	<i>Mycobacterium abscessus</i> , a taxonomic puzzle. <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2018, 68, 467-469.	1.7	21
66	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
67	Comparative analysis of phenotypic and genotypic antibiotic susceptibility patterns in <i>Mycobacterium avium</i> complex. <i>International Journal of Infectious Diseases</i> , 2020, 93, 320-328.	3.3	19
68	Adipose Gene Expression Response of Lean and Obese Mice to Short-term Dietary Restriction*. <i>Obesity</i> , 2006, 14, 974-979.	3.0	18
69	Antimicrobial Susceptibility and Phylogenetic Relations in a German Cohort Infected with <i>Mycobacterium abscessus</i> . <i>Journal of Clinical Microbiology</i> , 2020, 58, .	3.9	18
70	Drug-resistance profiling and transmission dynamics of multidrug-resistant <i>Mycobacterium tuberculosis</i> in Saudi Arabia revealed by whole genome sequencing. <i>Infection and Drug Resistance</i> , 2018, Volume 11, 2219-2229.	2.7	17
71	Direct DNA Extraction from <i>Mycobacterium tuberculosis</i> Frozen Stocks as a Reculture-Independent Approach to Whole-Genome Sequencing. <i>Journal of Clinical Microbiology</i> , 2015, 53, 2716-2719.	3.9	16
72	Shaping the niche in macrophages: Genetic diversity of the <i>M. tuberculosis</i> complex and its consequences for the infected host. <i>International Journal of Medical Microbiology</i> , 2018, 308, 118-128.	3.6	14

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73	Detection of low-frequency resistance-mediating SNPs in next-generation sequencing data of <i>Mycobacterium tuberculosis</i> complex strains with binoSNP. <i>Scientific Reports</i> , 2020, 10, 7874.	3.3	14
74	The global outbreak of <i>Mycobacterium chimaera</i> infections in cardiac surgery—a systematic review of whole-genome sequencing studies and joint analysis. <i>Clinical Microbiology and Infection</i> , 2021, 27, 1613-1620.	6.0	14
75	Implementation of whole genome sequencing for tuberculosis diagnostics in a low-middle income, high MDR-TB burden country. <i>Scientific Reports</i> , 2021, 11, 15333.	3.3	13
76	Origin and Global Expansion of <i>Mycobacterium tuberculosis</i> Complex Lineage 3. <i>Genes</i> , 2022, 13, 990.	2.4	13
77	<i>Mycobacterium bovis</i> Persistence in Two Different Captive Wild Animal Populations in Germany: a Longitudinal Molecular Epidemiological Study Revealing Pathogen Transmission by Whole-Genome Sequencing. <i>Journal of Clinical Microbiology</i> , 2018, 56, .	3.9	12
78	Phenotypic and Transcriptomic Analyses of Seven Clinical <i>Stenotrophomonas maltophilia</i> Isolates Identify a Small Set of Shared and Commonly Regulated Genes Involved in the Biofilm Lifestyle. <i>Applied and Environmental Microbiology</i> , 2020, 86, .	3.1	12
79	Population Structure of <i>Mycobacterium bovis</i> in Germany: a Long-Term Study Using Whole-Genome Sequencing Combined with Conventional Molecular Typing Methods. <i>Journal of Clinical Microbiology</i> , 2020, 58, .	3.9	10
80	Phylogenomic Perspective on a Unique <i>Mycobacterium bovis</i> Clade Dominating Bovine Tuberculosis Infections among Cattle and Buffalos in Northern Brazil. <i>Scientific Reports</i> , 2020, 10, 1747.	3.3	9
81	Improving tuberculosis surveillance by detecting international transmission using publicly available whole genome sequencing data. <i>Eurosurveillance</i> , 2021, 26, .	7.0	9
82	MotifAdjuster: a tool for computational reassessment of transcription factor binding site annotations. <i>Genome Biology</i> , 2009, 10, R46.	9.6	8
83	Fast update of undetected <i>Mycobacterium chimaera</i> infections to reveal unsuspected cases. <i>Journal of Hospital Infection</i> , 2018, 100, 451-455.	2.9	8
84	Longitudinal Outbreak of Multidrug-Resistant Tuberculosis in a Hospital Setting, Serbia. <i>Emerging Infectious Diseases</i> , 2019, 25, 555-558.	4.3	8
85	No Evidence for Acquired Mutations Associated with Cytochrome <i>bc₁</i> Inhibitor Resistance in 13,559 Clinical <i>Mycobacterium tuberculosis</i> Complex Isolates. <i>Antimicrobial Agents and Chemotherapy</i> , 2019, 63, .	3.2	7
86	MoRAine—a web server for fast computational transcription factor binding motif re-annotation. <i>Journal of Integrative Bioinformatics</i> , 2008, 5, .	1.5	6
87	Reply: Call for Regular Susceptibility Testing of Bedaquiline and Delamanid. <i>American Journal of Respiratory and Critical Care Medicine</i> , 2016, 194, 1171-1172.	5.6	5
88	Extent of transmission captured by contact tracing in a tuberculosis high endemic setting. <i>European Respiratory Journal</i> , 2017, 49, 1601851.	6.7	5
89	Whole-Genome Sequencing for Risk Assessment of Long-term Shiga Toxin-producing <i>Escherichia coli</i> . <i>Emerging Infectious Diseases</i> , 2014, 20, 732-733.	4.3	4
90	Transmission patterns of rifampicin resistant <i>Mycobacterium tuberculosis</i> complex strains in Cameroon: a genomic epidemiological study. <i>BMC Infectious Diseases</i> , 2021, 21, 891.	2.9	3

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91	Loss of Mobile Genomic Islands in Metal-Resistant, Hydrogen-Oxidizing <i>Cupriavidus metallidurans</i> . <i>Applied and Environmental Microbiology</i> , 2022, 88, AEM0204821.	3.1	3
92	Sub-Lineage Specific Phenolic Glycolipid Patterns in the <i>Mycobacterium tuberculosis</i> Complex Lineage 1. <i>Frontiers in Microbiology</i> , 2022, 13, 832054.	3.5	3
93	Aortic Endograft Infection with <i>Mycobacterium chimaera</i> and <i>Granulicatella adiacens</i> , Switzerland, 2014. <i>Emerging Infectious Diseases</i> , 2018, 24, 1700-1704.	4.3	2
94	Secretome characterization of clinical isolates from the <i>Mycobacterium abscessus</i> complex provides insight into antigenic differences. <i>BMC Genomics</i> , 2021, 22, 385.	2.8	2
95	Understanding <i>Mycobacterium tuberculosis</i> evolution in times of antibiotic treatment – A whole genome approach. <i>International Journal of Mycobacteriology</i> , 2015, 4, 2.	0.6	1
96	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
97	Multicentre study to establish interpretive criteria for clofazimine drug susceptibility testing. <i>International Journal of Tuberculosis and Lung Disease</i> , 2019, 23, 594-599.	1.2	1