Thomas A Kohl

List of Publications by Year
in descending order

97	7,101	94433	69250
papers	citations	37	77
		h-index	g-index

114	114	114	6612
all docs	docs citations	times ranked	citing authors

#	Article	IF	Citations
1	Loss of Mobile Genomic Islands in Metal-Resistant, Hydrogen-Oxidizing Cupriavidus metallidurans. Applied and Environmental Microbiology, 2022, 88, AEM0204821.	3.1	3
2	Sub-Lineage Specific Phenolic Glycolipid Patterns in the Mycobacterium tuberculosis Complex Lineage 1. Frontiers in Microbiology, 2022, 13, 832054.	3.5	3
3	Ancient and recent differences in the intrinsic susceptibility of *Mycobacterium tuberculosis* complex to pretomanid. Journal of Antimicrobial Chemotherapy, 2022, 77, 1685-1693.	3.0	34
4	The 2021 WHO catalogue of Mycobacterium tuberculosis complex mutations associated with drug resistance: a genotypic analysis. Lancet Microbe, The, 2022, 3, e265-e273.	7.3	114
5	Origin and Global Expansion of Mycobacterium tuberculosis Complex Lineage 3. Genes, 2022, 13, 990.	2.4	13
6	Use of a Whole Genome Sequencing-based approach for Mycobacterium tuberculosis surveillance in Europe in 2017â€"2019: an ECDC pilot study. European Respiratory Journal, 2021, 57, 2002272.	6.7	27
7	Rapid genomic first- and second-line drug resistance prediction from clinical *Mycobacterium tuberculosis* specimens using Deeplex-MycTB. European Respiratory Journal, 2021, 57, 2001796.	6.7	47
8	Improving tuberculosis surveillance by detecting international transmission using publicly available whole genome sequencing data. Eurosurveillance, 2021, 26, .	7.0	9
9	Design of Multidrug-Resistant Tuberculosis Treatment Regimens Based on DNA Sequencing. Clinical Infectious Diseases, 2021, 73, 1194-1202.	5.8	21
10	Secretome characterization of clinical isolates from the Mycobacterium abscessus complex provides insight into antigenic differences. BMC Genomics, 2021, 22, 385.	2.8	2
11	Implementation of whole genome sequencing for tuberculosis diagnostics in a low-middle income, high MDR-TB burden country. Scientific Reports, 2021, 11, 15333.	3.3	13
12	The global outbreak of Mycobacterium chimaera infections in cardiac surgeryâ€"a systematic review of whole-genome sequencing studies and joint analysis. Clinical Microbiology and Infection, 2021, 27, 1613-1620.	6.0	14
13	Transmission patterns of rifampicin resistant Mycobacterium tuberculosis complex strains in Cameroon: a genomic epidemiological study. BMC Infectious Diseases, 2021, 21, 891.	2.9	3
14	International Society of Cardiovascular Infectious Diseases Guidelines for the Diagnosis, Treatment and Prevention of Disseminated Mycobacterium chimaera Infection Following Cardiac Surgery with Cardiopulmonary Bypass. Journal of Hospital Infection, 2020, 104, 214-235.	2.9	50
15	MDR M. tuberculosis outbreak clone in Eswatini missed by Xpert has elevated bedaquiline resistance dated to the pre-treatment era. Genome Medicine, 2020, 12, 104.	8.2	50
16	Antimicrobial Susceptibility and Phylogenetic Relations in a German Cohort Infected with Mycobacterium abscessus. Journal of Clinical Microbiology, 2020, 58, .	3.9	18
17	Phenotypic and Transcriptomic Analyses of Seven Clinical Stenotrophomonas maltophilia Isolates Identify a Small Set of Shared and Commonly Regulated Genes Involved in the Biofilm Lifestyle. Applied and Environmental Microbiology, 2020, 86, .	3.1	12
18	Population Structure of Mycobacterium bovis in Germany: a Long-Term Study Using Whole-Genome Sequencing Combined with Conventional Molecular Typing Methods. Journal of Clinical Microbiology, 2020, 58, .	3.9	10

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19	Detection of low-frequency resistance-mediating SNPs in next-generation sequencing data of Mycobacterium tuberculosis complex strains with binoSNP. Scientific Reports, 2020, 10, 7874.	3.3	14
20	Phylogenetically informative mutations in genes implicated in antibiotic resistance in Mycobacterium tuberculosis complex. Genome Medicine, 2020, 12, 27.	8.2	58
21	Comparative analysis of phenotypic and genotypic antibiotic susceptibility patterns in Mycobacterium avium complex. International Journal of Infectious Diseases, 2020, 93, 320-328.	3.3	19
22	Library preparation for next generation sequencing: A review of automation strategies. Biotechnology Advances, 2020, 41, 107537.	11.7	88
23	GenomegaMap: Within-Species Genome-Wide dN/dS Estimation from over 10,000 Genomes. Molecular Biology and Evolution, 2020, 37, 2450-2460.	8.9	25
24	Phylogenomic Perspective on a Unique Mycobacterium bovis Clade Dominating Bovine Tuberculosis Infections among Cattle and Buffalos in Northern Brazil. Scientific Reports, 2020, 10, 1747.	3.3	9
25	Multidrug- and Extensively Drug-Resistant <i>Mycobacterium tuberculosis</i> Beijing Clades, Ukraine, 2015. Emerging Infectious Diseases, 2020, 26, 481-490.	4.3	23
26	The phylogenetic landscape and nosocomial spread of the multidrug-resistant opportunist Stenotrophomonas maltophilia. Nature Communications, 2020, 11, 2044.	12.8	76
27	A publicly accessible database for Clostridioides difficile genome sequences supports tracing of transmission chains and epidemics. Microbial Genomics, 2020, 6, .	2.0	22
28	Insertion and deletion evolution reflects antibiotics selection pressure in a Mycobacterium tuberculosis outbreak. PLoS Pathogens, 2020, 16, e1008357.	4.7	22
29	Accuracy of whole-genome sequencing to determine recent tuberculosis transmission: an 11-year population-based study in Hamburg, Germany. European Respiratory Journal, 2019, 54, 1901154.	6.7	21
30	Multicentre study to establish interpretive criteria for clofazimine drug susceptibility testing. International Journal of Tuberculosis and Lung Disease, 2019, 23, 594-599.	1.2	1
31	Whole genome sequencing of Mycobacterium tuberculosis: current standards and open issues. Nature Reviews Microbiology, 2019, 17, 533-545.	28.6	237
32	Revised Interpretation of the Hain Lifescience GenoType MTBC To Differentiate Mycobacterium canettii and Members of the Mycobacterium tuberculosis Complex. Antimicrobial Agents and Chemotherapy, 2019, 63, .	3.2	20
33	DeepAMR for predicting co-occurrent resistance of <i>Mycobacterium tuberculosis</i>. Bioinformatics, 2019, 35, 3240-3249.	4.1	38
34	Longitudinal Outbreak of Multidrug-Resistant Tuberculosis in a Hospital Setting, Serbia. Emerging Infectious Diseases, 2019, 25, 555-558.	4.3	8
35	Genetic Diversity of Multi- and Extensively Drug-Resistant Mycobacterium tuberculosis Isolates in the Capital of Iran, Revealed by Whole-Genome Sequencing. Journal of Clinical Microbiology, 2019, 57, .	3.9	29
36	Application of machine learning techniques to tuberculosis drug resistance analysis. Bioinformatics, 2019, 35, 2276-2282.	4.1	71

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37	No Evidence for Acquired Mutations Associated with Cytochrome bc_1 Inhibitor Resistance in 13,559 Clinical Mycobacterium tuberculosis Complex Isolates. Antimicrobial Agents and Chemotherapy, 2019, 63, .	3.2	7
38	Antibiotic resistance prediction for Mycobacterium tuberculosis from genome sequence data with Mykrobe. Wellcome Open Research, 2019, 4, 191.	1.8	103
39	Towards standardisation: comparison of five whole genome sequencing (WGS) analysis pipelines for detection of epidemiologically linked tuberculosis cases. Eurosurveillance, 2019, 24, .	7.0	42
40	Genetic sequencing for surveillance of drug resistance in tuberculosis in highly endemic countries: a multi-country population-based surveillance study. Lancet Infectious Diseases, The, 2018, 18, 675-683.	9.1	119
41	Shaping the niche in macrophages: Genetic diversity of the M. tuberculosis complex and its consequences for the infected host. International Journal of Medical Microbiology, 2018, 308, 118-128.	3.6	14
42	What Is Resistance? Impact of Phenotypic versus Molecular Drug Resistance Testing on Therapy for Multi- and Extensively Drug-Resistant Tuberculosis. Antimicrobial Agents and Chemotherapy, 2018, 62, .	3.2	83
43	MTBseq: a comprehensive pipeline for whole genome sequence analysis of *Mycobacterium tuberculosis* complex isolates. PeerJ, 2018, 6, e5895.	2.0	148
44	The Genetic Transformation of Chlamydia pneumoniae. MSphere, 2018, 3, .	2.9	23
45	Drug-resistance profiling and transmission dynamics of multidrug-resistant *Mycobacterium tuberculosis* in Saudi Arabia revealed by whole genome sequencing. Infection and Drug Resistance, 2018, Volume 11, 2219-2229.	2.7	17
46	Prediction of Susceptibility to First-Line Tuberculosis Drugs by DNA Sequencing. New England Journal of Medicine, 2018, 379, 1403-1415.	27.0	405
47	Integrating standardized whole genome sequence analysis with a global Mycobacterium tuberculosis antibiotic resistance knowledgebase. Scientific Reports, 2018, 8, 15382.	3.3	75
48	The relationship between transmission time and clustering methods in Mycobacterium tuberculosis epidemiology. EBioMedicine, 2018, 37, 410-416.	6.1	106
49	Fast update of undetected Mycobacterium chimaera infections to reveal unsuspected cases. Journal of Hospital Infection, 2018, 100, 451-455.	2.9	8
50	Perspectives for personalized therapy for patients with multidrugâ€resistant tuberculosis. Journal of Internal Medicine, 2018, 284, 163-188.	6.0	33
51	Mycobacterium bovis Persistence in Two Different Captive Wild Animal Populations in Germany: a Longitudinal Molecular Epidemiological Study Revealing Pathogen Transmission by Whole-Genome Sequencing. Journal of Clinical Microbiology, 2018, 56, .	3.9	12
52	Comparative genomics of Mycobacterium africanum Lineage 5 and Lineage 6 from Ghana suggests distinct ecological niches. Scientific Reports, 2018, 8, 11269.	3.3	34
53	Reply to Dookie et al., â€œWhole-Genome Sequencing To Guide the Selection of Treatment for Drug-Resistant Tuberculosisâ€. Antimicrobial Agents and Chemotherapy, 2018, 62, .	3.2	1
54	Analysis of Phylogenetic Variation of Stenotrophomonas maltophilia Reveals Human-Specific Branches. Frontiers in Microbiology, 2018, 9, 806.	3.5	39

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55	Aortic Endograft Infection with Mycobacterium chimaera and Granulicatella adiacens, Switzerland, 2014. Emerging Infectious Diseases, 2018, 24, 1700-1704.	4.3	2
56	Harmonized Genome Wide Typing of Tubercle Bacilli Using a Web-Based Gene-By-Gene Nomenclature System. EBioMedicine, 2018, 34, 131-138.	6.1	42
57	Mycobacterium abscessus, a taxonomic puzzle. International Journal of Systematic and Evolutionary Microbiology, 2018, 68, 467-469.	1.7	21
58	Compensatory evolution drives multidrug-resistant tuberculosis in Central Asia. ELife, 2018, 7, .	6.0	93
59	High Interlaboratory Reproducibility and Accuracy of Next-Generation-Sequencing-Based Bacterial Genotyping in a Ring Trial. Journal of Clinical Microbiology, 2017, 55, 908-913.	3.9	75
60	Extent of transmission captured by contact tracing in a tuberculosis high endemic setting. European Respiratory Journal, 2017, 49, 1601851.	6.7	5
61	Role of Alanine Racemase Mutations in Mycobacterium tuberculosis <scp>d</scp> -Cycloserine Resistance. Antimicrobial Agents and Chemotherapy, 2017, 61, .	3.2	24
62	Global outbreak of severe Mycobacterium chimaera disease after cardiac surgery: a molecular epidemiological study. Lancet Infectious Diseases, The, 2017, 17, 1033-1041.	9.1	198
63	<i>Mycobacterium abscessus</i> in patients with cystic fibrosis: low impact of inter-human transmission in Italy. European Respiratory Journal, 2017, 50, 1602525.	6.7	63
64	The Evolution of Strain Typing in the Mycobacterium tuberculosis Complex. Advances in Experimental Medicine and Biology, 2017, 1019, 43-78.	1.6	43
65	Detection of transrenal DNA for the diagnosis of pulmonary tuberculosis and treatment monitoring. Infection, 2017, 45, 269-276.	4.7	32
66	Whole genome sequencing for M/XDR tuberculosis surveillance and for resistance testing. Clinical Microbiology and Infection, 2017, 23, 161-166.	6.0	61
67	Mycobacterium abscessus subsp. abscessus Is Capable of Degrading Pseudomonas aeruginosa Quinolone Signals. Frontiers in Microbiology, 2017, 8, 339.	3.5	26
68	New<i>Mycobacterium tuberculosis</i>Complex Sublineage, Brazzaville, Congo. Emerging Infectious Diseases, 2017, 23, 423-429.	4.3	35
69	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. Eurosurveillance, 2017, 22, .	7.0	26
70	Impact of Genetic Diversity on the Biology of <i>Mycobacterium tuberculosis</i> Complex Strains. Microbiology Spectrum, 2016, 4, .	3.0	26
71	Tracing Mycobacterium tuberculosis transmission by whole genome sequencing in a high incidence setting: a retrospective population-based study in East Greenland. Scientific Reports, 2016, 6, 33180.	3.3	51
72	Reply: Call for Regular Susceptibility Testing of Bedaquiline and Delamanid. American Journal of Respiratory and Critical Care Medicine, 2016, 194, 1171-1172.	5.6	5

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73	Rapid, comprehensive, and affordable mycobacterial diagnosis with whole-genome sequencing: a prospective study. Lancet Respiratory Medicine,the, 2016, 4, 49-58.	10.7	282
74	Delamanid and Bedaquiline Resistance in <i>Mycobacterium tuberculosis</i> Ancestral Beijing Genotype Causing Extensively Drug-Resistant Tuberculosis in a Tibetan Refugee. American Journal of Respiratory and Critical Care Medicine, 2016, 193, 337-340.	5.6	125
75	Emended description of Mycobacterium abscessus, Mycobacterium abscessus subsp. abscessus and Mycobacterium abscessus subsp. bolletii and designation of Mycobacterium abscessus subsp. massiliense comb. nov.. International Journal of Systematic and Evolutionary Microbiology, 2016, 66, 4471-4479.	1.7	190
76	Phenotypic Heterogeneity Affects Stenotrophomonas maltophilia K279a Colony Morphotypes and Î²-Lactamase Expression. Frontiers in Microbiology, 2015, 6, 1373.	3.5	27
77	Rapid antibiotic-resistance predictions from genome sequence data for Staphylococcus aureus and Mycobacterium tuberculosis. Nature Communications, 2015, 6, 10063.	12.8	479
78	Evolutionary history and global spread of the Mycobacterium tuberculosis Beijing lineage. Nature Genetics, 2015, 47, 242-249.	21.4	466
79	Direct DNA Extraction from Mycobacterium tuberculosis Frozen Stocks as a Reculture-Independent Approach to Whole-Genome Sequencing. Journal of Clinical Microbiology, 2015, 53, 2716-2719.	3.9	16
80	Whole-genome sequencing for prediction of Mycobacterium tuberculosis drug susceptibility and resistance: a retrospective cohort study. Lancet Infectious Diseases, The, 2015, 15, 1193-1202.	9.1	553
81	Detoxifying Escherichia coli for endotoxin-free production of recombinant proteins. Microbial Cell Factories, 2015, 14, 57.	4.0	178
82	PhyResSE: a Web Tool Delineating Mycobacterium tuberculosis Antibiotic Resistance and Lineage from Whole-Genome Sequencing Data. Journal of Clinical Microbiology, 2015, 53, 1908-1914.	3.9	257
83	Understanding Mycobacterium tuberculosis evolution in times of antibiotic treatment â€" A whole genome approach. International Journal of Mycobacteriology, 2015, 4, 2.	0.6	1
84	Tracing the Spread of Clostridium difficile Ribotype 027 in Germany Based on Bacterial Genome Sequences. PLoS ONE, 2015, 10, e0139811.	2.5	40
85	Whole-Genome Sequencing for Risk Assessment of Long-term Shiga Toxinâ€"producing<i>Escherichia coli</i>. Emerging Infectious Diseases, 2014, 20, 732-733.	4.3	4
86	Whole-Genome-Based Mycobacterium tuberculosis Surveillance: a Standardized, Portable, and Expandable Approach. Journal of Clinical Microbiology, 2014, 52, 2479-2486.	3.9	175
87	High-resolution detection of DNA binding sites of the global transcriptional regulator GlxR in Corynebacterium glutamicum. Microbiology (United Kingdom), 2013, 159, 12-22.	1.8	44
88	Whole Genome Sequencing versus Traditional Genotyping for Investigation of a Mycobacterium tuberculosis Outbreak: A Longitudinal Molecular Epidemiological Study. PLoS Medicine, 2013, 10, e1001387.	8.4	425
89	Whole Genome Sequencing Reveals Complex Evolution Patterns of Multidrug-Resistant Mycobacterium tuberculosis Beijing Strains in Patients. PLoS ONE, 2013, 8, e82551.	2.5	117
90	<i>rplC</i> T460C Identified as a Dominant Mutation in Linezolid-Resistant Mycobacterium tuberculosis Strains. Antimicrobial Agents and Chemotherapy, 2012, 56, 2743-2745.	3.2	83

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91	Phenylacetic Acid Catabolism and Its Transcriptional Regulation in Corynebacterium glutamicum. Applied and Environmental Microbiology, 2012, 78, 5796-5804.	3.1	32
92	From Corynebacterium glutamicum to Mycobacterium tuberculosis--towards transfers of gene regulatory networks and integrated data analyses with MycoRegNet. Nucleic Acids Research, 2009, 37, e97-e97.	14.5	39
93	The GlxR regulon of the amino acid producer Corynebacterium glutamicum: Detection of the corynebacterial core regulon and integration into the transcriptional regulatory network model. Journal of Biotechnology, 2009, 143, 239-246.	3.8	67
94	MotifAdjuster: a tool for computational reassessment of transcription factor binding site annotations. Genome Biology, 2009, 10, R46.	9.6	8
95	The GlxR regulon of the amino acid producer Corynebacterium glutamicum: In silico and in vitro detection of DNA binding sites of a global transcription regulator. Journal of Biotechnology, 2008, 135, 340-350.	3.8	89
96	MoRAine--a web server for fast computational transcription factor binding motif re-annotation. Journal of Integrative Bioinformatics, 2008, 5, .	1.5	6
97	Adipose Gene Expression Response of Lean and Obese Mice to Short-term Dietary Restriction*. Obesity, 2006, 14, 974-979.	3.0	18