

# Vitali Sintchenko

## List of Publications by Year in descending order

Source: <https://exaly.com/author-pdf/6827083/publications.pdf>

Version: 2024-02-01

196  
papers

6,222  
citations

87843

38  
h-index

110317

64  
g-index

216  
all docs

216  
docs citations

216  
times ranked

8476  
citing authors

#	ARTICLE	IF	CITATIONS
1	Prediction of Susceptibility to First-Line Tuberculosis Drugs by DNA Sequencing. <i>New England Journal of Medicine</i> , 2018, 379, 1403-1415.	13.9	405
2	Revealing COVID-19 transmission in Australia by SARS-CoV-2 genome sequencing and agent-based modeling. <i>Nature Medicine</i> , 2020, 26, 1398-1404.	15.2	283
3	Global Population Structure and Evolution of <i>Bordetella pertussis</i> and Their Relationship with Vaccination. <i>MBio</i> , 2014, 5, e01074.	1.8	257
4	Intercontinental dissemination of azithromycin-resistant shigellosis through sexual transmission: a cross-sectional study. <i>Lancet Infectious Diseases</i> , The, 2015, 15, 913-921.	4.6	204
5	Rapid Increase in Pertactin-deficient <i>Bordetella pertussis</i> Isolates, Australia. <i>Emerging Infectious Diseases</i> , 2014, 20, 626-33.	2.0	151
6	Newly Emerging Clones of <i>Bordetella pertussis</i> Carrying prn2 and ptxP3 Alleles Implicated in Australian Pertussis Epidemic in 2008–2010. <i>Journal of Infectious Diseases</i> , 2012, 205, 1220-1224.	1.9	148
7	Resistance Mutations in SARS-CoV-2 Delta Variant after Sotrovimab Use. <i>New England Journal of Medicine</i> , 2022, 386, 1477-1479.	13.9	134
8	An emergent clade of SARS-CoV-2 linked to returned travellers from Iran. <i>Virus Evolution</i> , 2020, 6, veaa027.	2.2	119
9	Community-wide Screening for Tuberculosis in a High-Prevalence Setting. <i>New England Journal of Medicine</i> , 2019, 381, 1347-1357.	13.9	116
10	The global establishment of a highly-fluoroquinolone resistant <i>Salmonella enterica</i> serotype Kentucky ST198 strain. <i>Frontiers in Microbiology</i> , 2013, 4, 395.	1.5	114
11	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.	3.4	114
12	Cell-based Culture Informs Infectivity and Safe De-Isolation Assessments in Patients with Coronavirus Disease 2019. <i>Clinical Infectious Diseases</i> , 2021, 73, e2952-e2959.	2.9	109
13	SARS-CoV-2 neutralizing antibodies: Longevity, breadth, and evasion by emerging viral variants. <i>PLoS Medicine</i> , 2021, 18, e1003656.	3.9	109
14	Antibiotic resistance prediction for <i>Mycobacterium tuberculosis</i> from genome sequence data with Mykrobe. <i>Wellcome Open Research</i> , 2019, 4, 191.	0.9	103
15	Handheld Computer-based Decision Support Reduces Patient Length of Stay and Antibiotic Prescribing in Critical Care. <i>Journal of the American Medical Informatics Association: JAMIA</i> , 2005, 12, 398-402.	2.2	100
16	Epidemiologic Evidence for Airborne Transmission of SARS-CoV-2 during Church Singing, Australia, 2020. <i>Emerging Infectious Diseases</i> , 2021, 27, 1677-1680.	2.0	97
17	Pertactin negative <i>Bordetella pertussis</i> demonstrates higher fitness under vaccine selection pressure in a mixed infection model. <i>Vaccine</i> , 2015, 33, 6277-6281.	1.7	93
18	Insight into Evolution of <i>Bordetella pertussis</i> from Comparative Genomic Analysis: Evidence of Vaccine-Driven Selection. <i>Molecular Biology and Evolution</i> , 2011, 28, 707-715.	3.5	78

#	ARTICLE	IF	CITATIONS
19	Delineating Community Outbreaks of <i>Salmonella enterica</i> Serovar Typhimurium by Use of Whole-Genome Sequencing: Insights into Genomic Variability within an Outbreak. <i>Journal of Clinical Microbiology</i> , 2015, 53, 1063-1071.	1.8	76
20	Pathogen profiling for disease management and surveillance. <i>Nature Reviews Microbiology</i> , 2007, 5, 464-470.	13.6	71
21	Comparative Impact of Guidelines, Clinical Data, and Decision Support on Prescribing Decisions: An Interactive Web Experiment with Simulated Cases. <i>Journal of the American Medical Informatics Association: JAMIA</i> , 2004, 11, 71-77.	2.2	70
22	Impact of a web-based personally controlled health management system on influenza vaccination and health services utilization rates: a randomized controlled trial. <i>Journal of the American Medical Informatics Association: JAMIA</i> , 2012, 19, 719-727.	2.2	64
23	Co-infection with SARS-CoV-2 Omicron and Delta variants revealed by genomic surveillance. <i>Nature Communications</i> , 2022, 13, 2745.	5.8	64
24	Proficiency testing for bacterial whole genome sequencing: an end-user survey of current capabilities, requirements and priorities. <i>BMC Infectious Diseases</i> , 2015, 15, 174.	1.3	62
25	The role of pathogen genomics in assessing disease transmission. <i>BMJ, The</i> , 2015, 350, h1314-h1314.	3.0	59
26	Clinical Microbiology Informatics. <i>Clinical Microbiology Reviews</i> , 2014, 27, 1025-1047.	5.7	57
27	Identification of non-tuberculous mycobacteria: utility of the GenoType Mycobacterium CM/AS assay compared with HPLC and 16S rRNA gene sequencing. <i>Journal of Medical Microbiology</i> , 2009, 58, 900-904.	0.7	55
28	<i>Francisella tularensis</i> Subspecies <i>holarctica</i> , Tasmania, Australia, 2011. <i>Emerging Infectious Diseases</i> , 2012, 18, 1484-1486.	2.0	55
29	Genomics-informed responses in the elimination of COVID-19 in Victoria, Australia: an observational, genomic epidemiological study. <i>Lancet Public Health, The</i> , 2021, 6, e547-e556.	4.7	53
30	Decision support systems for antibiotic prescribing. <i>Current Opinion in Infectious Diseases</i> , 2008, 21, 573-579.	1.3	52
31	Genomic dissection of Australian <i>Bordetella pertussis</i> isolates from the 2008–2012 epidemic. <i>Journal of Infection</i> , 2016, 72, 468-477.	1.7	52
32	Multidrug-Resistant <i>Salmonella enterica</i> Sequence Type 34, New South Wales, Australia, 2016–2017. <i>Emerging Infectious Diseases</i> , 2018, 24, 751-753.	2.0	52
33	Which clinical decisions benefit from automation? A task complexity approach. <i>International Journal of Medical Informatics</i> , 2003, 70, 309-316.	1.6	49
34	<i>Francisella tularensis</i> ssp. <i>holarctica</i> in Ringtail Possums, Australia. <i>Emerging Infectious Diseases</i> , 2017, 23, 1198-1201.	2.0	49
35	Advances in Clinical Sample Preparation for Identification and Characterization of Bacterial Pathogens Using Metagenomics. <i>Frontiers in Public Health</i> , 2018, 6, 363.	1.3	48
36	The Antibody Response to SARS-CoV-2 Infection. <i>Open Forum Infectious Diseases</i> , 2020, 7, ofaa387.	0.4	45

#	ARTICLE	IF	CITATIONS
37	Whole Genome Sequencing Demonstrates Limited Transmission within Identified Mycobacterium tuberculosis Clusters in New South Wales, Australia. <i>PLoS ONE</i> , 2016, 11, e0163612.	1.1	44
38	Selection and emergence of pertussis toxin promoter ptxP3 allele in the evolution of <i>Bordetella pertussis</i> . <i>Infection, Genetics and Evolution</i> , 2012, 12, 492-495.	1.0	42
39	Nontoxic Metal-Cyclam Complexes, a New Class of Compounds with Potency against Drug-Resistant <i>Mycobacterium tuberculosis</i> . <i>Journal of Medicinal Chemistry</i> , 2016, 59, 5917-5921.	2.9	42
40	Better colonisation of newly emerged <i>Bordetella pertussis</i> in the co-infection mouse model study. <i>Vaccine</i> , 2016, 34, 3967-3971.	1.7	40
41	Are we measuring the right end-points? Variables that affect the impact of computerised decision support on patient outcomes: A systematic review. <i>Informatics for Health and Social Care</i> , 2007, 32, 225-240.	1.0	38
42	Improving resolution of public health surveillance for human <i>Salmonella enterica</i> serovar Typhimurium infection: 3 years of prospective multiple-locus variable-number tandem-repeat analysis (MLVA). <i>BMC Infectious Diseases</i> , 2012, 12, 78.	1.3	38
43	DeepAMR for predicting co-occurrent resistance of <i>Mycobacterium tuberculosis</i> . <i>Bioinformatics</i> , 2019, 35, 3240-3249.	1.8	38
44	Mutations in rpoB gene and rifabutin susceptibility of multidrug-resistant mycobacterium tuberculosis strains isolated in Australia. <i>Pathology</i> , 1999, 31, 257-260.	0.3	37
45	secA1 Gene Sequence Polymorphisms for Species Identification of <i>Nocardia</i> Species and Recognition of Intraspecies Genetic Diversity. <i>Journal of Clinical Microbiology</i> , 2010, 48, 3928-3934.	1.8	37
46	Added value of whole-genome sequencing for management of highly drug-resistant TB. <i>Journal of Antimicrobial Chemotherapy</i> , 2014, 70, 1198-202.	1.3	36
47	Characterisation of the <i>Bordetella pertussis</i> secretome under different media. <i>Journal of Proteomics</i> , 2017, 158, 43-51.	1.2	34
48	Potent Antimycobacterial Activity of the Pyridoxal Isonicotinoyl Hydrazone Analog 2-Pyridylcarboxaldehyde Isonicotinoyl Hydrazone: A Lipophilic Transport Vehicle for Isonicotinic Acid Hydrazide. <i>Molecular Pharmacology</i> , 2014, 85, 269-278.	1.0	33
49	SARS-CoV-2 Genome Sequencing Methods Differ in Their Abilities To Detect Variants from Low-Viral-Load Samples. <i>Journal of Clinical Microbiology</i> , 2021, 59, e0104621.	1.8	33
50	Laboratory-Guided Detection of Disease Outbreaks: Three Generations of Surveillance Systems. <i>Archives of Pathology and Laboratory Medicine</i> , 2009, 133, 916-925.	1.2	33
51	<i>Bordetella pertussis</i> Clones Identified by Multilocus Variable-Number Tandem-Repeat Analysis. <i>Emerging Infectious Diseases</i> , 2010, 16, 297-300.	2.0	32
52	The relationship between <i>Bordetella pertussis</i> genotype and clinical severity in Australian children with pertussis. <i>Journal of Infection</i> , 2016, 72, 171-178.	1.7	32
53	Whole Genome Sequencing of Australian <i>Candida glabrata</i> Isolates Reveals Genetic Diversity and Novel Sequence Types. <i>Frontiers in Microbiology</i> , 2018, 9, 2946.	1.5	31
54	Mutations associated with in vitro resistance to bedaquiline in <i>Mycobacterium tuberculosis</i> isolates in Australia. <i>Tuberculosis</i> , 2018, 111, 31-34.	0.8	31

#	ARTICLE	IF	CITATIONS
55	Value of routine whole genome sequencing for Mycobacterium tuberculosis drug resistance detection. International Journal of Infectious Diseases, 2021, 113, S48-S54.	1.5	31
56	Effectiveness of Hospital-Wide Methicillin-Resistant Staphylococcus aureus (MRSA) Infection Control Policies Differs by Ward Specialty. PLoS ONE, 2013, 8, e83099.	1.1	30
57	Defining the Core Genome of Salmonella enterica Serovar Typhimurium for Genomic Surveillance and Epidemiological Typing. Journal of Clinical Microbiology, 2015, 53, 2530-2538.	1.8	29
58	Whole genome sequencing of Salmonella Typhimurium illuminates distinct outbreaks caused by an endemic multi-locus variable number tandem repeat analysis type in Australia, 2014. BMC Microbiology, 2016, 16, 211.	1.3	29
59	Proteomic Adaptation of Australian Epidemic <i>Bordetella pertussis</i> . Proteomics, 2018, 18, e1700237.	1.3	29
60	Pertactin-Negative and Filamentous Hemagglutinin-Negative <i>Bordetella pertussis</i> , Australia, 2013–2017. Emerging Infectious Diseases, 2019, 25, 1196-1199.	2.0	29
61	Seven <i>Salmonella</i> Typhimurium Outbreaks in Australia Linked by Trace-Back and Whole Genome Sequencing. Foodborne Pathogens and Disease, 2018, 15, 285-292.	0.8	27
62	Comparative genomics of Australian and international isolates of Salmonella Typhimurium: correlation of core genome evolution with CRISPR and prophage profiles. Scientific Reports, 2017, 7, 9733.	1.6	26
63	Tracking a moving user in indoor environments using Bluetooth low energy beacons. Journal of Biomedical Informatics, 2019, 98, 103288.	2.5	26
64	Inaccurate Ascertainment of Morbidity and Mortality due to Influenza in Administrative Databases: A Population-Based Record Linkage Study. PLoS ONE, 2014, 9, e98446.	1.1	25
65	It Is Not All about Single Nucleotide Polymorphisms: Comparison of Mobile Genetic Elements and Deletions in Listeria monocytogenes Genomes Links Cases of Hospital-Acquired Listeriosis to the Environmental Source. Journal of Clinical Microbiology, 2015, 53, 3492-3500.	1.8	24
66	Whole Genome Sequencing of <i>Candida glabrata</i> for Detection of Markers of Antifungal Drug Resistance. Journal of Visualized Experiments, 2017, .	0.2	24
67	Incorporating Whole-Genome Sequencing into Public Health Surveillance: Lessons from Prospective Sequencing of Salmonella Typhimurium in Australia. Foodborne Pathogens and Disease, 2018, 15, 161-167.	0.8	24
68	Relentless spread and adaptation of non-typeable vanA vancomycin-resistant Enterococcus faecium: a genome-wide investigation. Journal of Antimicrobial Chemotherapy, 2018, 73, 1487-1491.	1.3	24
69	Identifying Likely Transmission Pathways within a 10-Year Community Outbreak of Tuberculosis by High-Depth Whole Genome Sequencing. PLoS ONE, 2016, 11, e0150550.	1.1	24
70	Assignment of Reference 5'-end 16S rDNA Sequences and Species-Specific Sequence Polymorphisms Improves Species Identification of Nocardia. Open Microbiology Journal, 2009, 3, 97-105.	0.2	24
71	Genetic Relationships of Phage Types and Single Nucleotide Polymorphism Typing of Salmonella enterica Serovar Typhimurium. Journal of Clinical Microbiology, 2012, 50, 727-734.	1.8	23
72	Editorial Commentary: The "How" of Polymerase Chain Reaction Testing for Bordetella pertussis Depends on the "Why". Clinical Infectious Diseases, 2013, 56, 332-334.	2.9	23

#	ARTICLE	IF	CITATIONS
73	Antibiotic susceptibility of diverse <i>Mycobacterium abscessus</i> complex strains in New South Wales, Australia. <i>Pathology</i> , 2015, 47, 678-682.	0.3	23
74	Genomic Variability of Serial Human Isolates of <i>Salmonella enterica</i> Serovar Typhimurium Associated with Prolonged Carriage. <i>Journal of Clinical Microbiology</i> , 2015, 53, 3507-3514.	1.8	23
75	Genome-wide comparison of <i>Corynebacterium diphtheriae</i> isolates from Australia identifies differences in the Pan-genomes between respiratory and cutaneous strains. <i>BMC Genomics</i> , 2018, 19, 869.	1.2	23
76	Genome-wide analysis of single nucleotide polymorphisms in <i>Bordetella pertussis</i> using comparative genomic sequencing. <i>Research in Microbiology</i> , 2008, 159, 602-608.	1.0	22
77	Rapid Identification of Methicillin-Resistant <i>Staphylococcus aureus</i> Transmission in Hospitals by Use of Phage-Derived Open Reading Frame Typing Enhanced by Multiplex PCR and Reverse Line Blot Assay. <i>Journal of Clinical Microbiology</i> , 2010, 48, 2741-2748.	1.8	22
78	Prospective Genotyping of Hospital-Acquired Methicillin-Resistant <i>Staphylococcus aureus</i> Isolates by Use of a Novel, Highly Discriminatory Binary Typing System. <i>Journal of Clinical Microbiology</i> , 2012, 50, 3513-3519.	1.8	22
79	Influenza Outbreak during Sydney World Youth Day 2008: The Utility of Laboratory Testing and Case Definitions on Mass Gathering Outbreak Containment. <i>PLoS ONE</i> , 2009, 4, e6620.	1.1	22
80	Comparison of Single- and Multilocus Sequence Typing and Toxin Gene Profiling for Characterization of Methicillin-Resistant <i>Staphylococcus aureus</i> . <i>Journal of Clinical Microbiology</i> , 2007, 45, 3302-3308.	1.8	21
81	Genome sequencing reveals novel deletions associated with secondary resistance to pyrazinamide in MDR <i>Mycobacterium tuberculosis</i> . <i>Journal of Antimicrobial Chemotherapy</i> , 2015, 70, 2511-2514.	1.3	21
82	Identification of Pathogenic <i>Nocardia</i> Species by Reverse Line Blot Hybridization Targeting the 16S rRNA and 16S-23S rRNA Gene Spacer Regions. <i>Journal of Clinical Microbiology</i> , 2010, 48, 503-511.	1.8	20
83	<i>dhfrA 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.	1.4	20
84	SnpFilt: A pipeline for reference-free assembly-based identification of SNPs in bacterial genomes. <i>Computational Biology and Chemistry</i> , 2016, 65, 178-184.	1.1	19
85	Cross-Border Movement of Highly Drug-Resistant <i>Mycobacterium tuberculosis</i> from Papua New Guinea to Australia through Torres Strait Protected Zone, 2010–2015. <i>Emerging Infectious Diseases</i> , 2019, 25, 406-415.	2.0	19
86	Computational Bacterial Genome-Wide Analysis of Phylogenetic Profiles Reveals Potential Virulence Genes of <i>Streptococcus agalactiae</i> . <i>PLoS ONE</i> , 2011, 6, e17964.	1.1	18
87	Temporal dynamics of <i>Mycobacterium tuberculosis</i> genotypes in New South Wales, Australia. <i>BMC Infectious Diseases</i> , 2014, 14, 455.	1.3	18
88	Improved Identification of Rapidly Growing <i>Mycobacteria</i> by a 16S–23S Internal Transcribed Spacer Region PCR and Capillary Gel Electrophoresis. <i>PLoS ONE</i> , 2014, 9, e102290.	1.1	18
89	Utility of genotyping of <i>Mycobacterium tuberculosis</i> in the contact investigation: A decision analysis. <i>Tuberculosis</i> , 2007, 87, 176-184.	0.8	17
90	Fluoroquinolone resistance in non-multidrug-resistant tuberculosis—a surveillance study in New South Wales, Australia, and a review of global resistance rates. <i>International Journal of Infectious Diseases</i> , 2014, 26, 149-153.	1.5	17

#	ARTICLE	IF	CITATIONS
91	Improved identification of <i>Gordonia</i> , <i>Rhodococcus</i> and <i>Tsukamurella</i> species by 5'-end 16S rRNA gene sequencing. <i>Pathology</i> , 2011, 43, 58-63.	0.3	16
92	<i>Burkholderia lata</i> Infections from Intrinsically Contaminated Chlorhexidine Mouthwash, Australia, 2016. <i>Emerging Infectious Diseases</i> , 2018, 24, 2109-2111.	2.0	16
93	Recurrence of tuberculosis in a low-incidence setting: a retrospective cross-sectional study augmented by whole genome sequencing. <i>BMC Infectious Diseases</i> , 2018, 18, 265.	1.3	16
94	Long-term Impact of Pneumococcal Conjugate Vaccines on Invasive Disease and Pneumonia Hospitalizations in Indigenous and Non-Indigenous Australians. <i>Clinical Infectious Diseases</i> , 2020, 70, 2607-2615.	2.9	16
95	Enhancing genomics-based outbreak detection of endemic <i>Salmonella enterica</i> serovar Typhimurium using dynamic thresholds. <i>Microbial Genomics</i> , 2021, 7, .	1.0	16
96	Rapid and accurate typing of <i>Bordetella pertussis</i> targeting genes encoding acellular vaccine antigens using real time PCR and High Resolution Melt analysis. <i>Journal of Microbiological Methods</i> , 2009, 77, 326-329.	0.7	15
97	Detection and incidence of <i>Bordetella holmesii</i> in respiratory specimens from patients with pertussis-like symptoms in New South Wales, Australia. <i>Pathology</i> , 2018, 50, 322-326.	0.3	15
98	Whole-genome sequencing reveals genetic signature of bedaquiline resistance in a clinical isolate of <i>Mycobacterium tuberculosis</i> . <i>Journal of Global Antimicrobial Resistance</i> , 2018, 15, 103-104.	0.9	15
99	Clinical and public health utility of <i>Mycobacterium tuberculosis</i> whole genome sequencing. <i>International Journal of Infectious Diseases</i> , 2021, 113, S40-S42.	1.5	15
100	COVID-19 Infection With the Omicron SARS-CoV-2 Variant in a Cohort of Kidney and Kidney Pancreas Transplant Recipients: Clinical Features, Risk Factors, and Outcomes. <i>Transplantation</i> , 2022, 106, 1860-1866.	0.5	15
101	Biosurveillance of emerging biothreats using scalable genotype clustering. <i>Journal of Biomedical Informatics</i> , 2009, 42, 66-73.	2.5	14
102	Use of the 5' untranslated region and VP1 region to examine the molecular diversity in enterovirus B species. <i>Journal of Medical Microbiology</i> , 2014, 63, 1339-1355.	0.7	14
103	Genome-wide analysis of <i>Streptococcus pneumoniae</i> serogroup 19 in the decade after the introduction of pneumococcal conjugate vaccines in Australia. <i>Scientific Reports</i> , 2018, 8, 16969.	1.6	14
104	<i>Mycobacterium tuberculosis</i> Drug Resistance and Transmission among Human Immunodeficiency Virus-Infected Patients in Ho Chi Minh City, Vietnam. <i>American Journal of Tropical Medicine and Hygiene</i> , 2018, 99, 1397-1406.	0.6	14
105	Towards bioinformatics assisted infectious disease control. <i>BMC Bioinformatics</i> , 2009, 10, S10.	1.2	13
106	A new multiplex PCR-based reverse line-blot hybridization (mPCR/RLB) assay for rapid staphylococcal cassette chromosome mec (SCCmec) typing. <i>Journal of Medical Microbiology</i> , 2009, 58, 1045-1057.	0.7	13
107	Three-year longitudinal study of genotypes of <i>Mycobacterium tuberculosis</i> in a low prevalence population. <i>Pathology</i> , 2010, 42, 267-272.	0.3	13
108	Implications of Isoniazid Resistance in <i>Mycobacterium bovis</i> Bacillus Calmette-Guerin used for Immunotherapy in Bladder Cancer. <i>Clinical Infectious Diseases</i> , 2011, 52, 86-88.	2.9	13

#	ARTICLE	IF	CITATIONS
109	Aiming for zero tuberculosis transmission in low-burden countries. <i>Lancet Respiratory Medicine</i> , 2017, 5, 846-848.	5.2	13
110	Is <i>Bordetella pertussis</i> susceptibility to erythromycin changing? MIC trends among Australian isolates 1971-2006. <i>Journal of Antimicrobial Chemotherapy</i> , 2007, 60, 1178-1179.	1.3	12
111	Transmission of multi-drug resistant tuberculosis in Mongolia is driven by Beijing strains of <i>Mycobacterium tuberculosis</i> resistant to all first-line drugs. <i>Tuberculosis</i> , 2016, 101, 49-53.	0.8	12
112	Comparison of the Whole Cell Proteome and Secretome of Epidemic <i>Bordetella pertussis</i> Strains From the 2008-2012 Australian Epidemic Under Sulfate-Modulating Conditions. <i>Frontiers in Microbiology</i> , 2018, 9, 2851.	1.5	12
113	Surfaceome analysis of Australian epidemic <i>Bordetella pertussis</i> reveals potential vaccine antigens. <i>Vaccine</i> , 2020, 38, 539-548.	1.7	12
114	Genetic Heterogeneity of Australian <i>Candida auris</i> Isolates: Insights From a Nonoutbreak Setting Using Whole-Genome Sequencing. <i>Open Forum Infectious Diseases</i> , 2020, 7, ofaa158.	0.4	12
115	Community perspectives on the benefits and risks of technologically enhanced communicable disease surveillance systems: a report on four community juries. <i>BMC Medical Ethics</i> , 2020, 21, 31.	1.0	12
116	Novel multiplex PCR assay for identification and subtyping of enteroinvasive <i>Escherichia coli</i> and differentiation from <i>Shigella</i> based on target genes selected by comparative genomics. <i>Journal of Medical Microbiology</i> , 2018, 67, 1257-1264.	0.7	12
117	Multilevel genome typing: genomics-guided scalable resolution typing of microbial pathogens. <i>Eurosurveillance</i> , 2020, 25, .	3.9	12
118	An outbreak of pulmonary tuberculosis in young Australians. <i>Medical Journal of Australia</i> , 2007, 186, 240-242.	0.8	11
119	Multiplex PCR and Reverse Line Blot Hybridization Assay (mPCR/RLB). <i>Journal of Visualized Experiments</i> , 2011, .	0.2	11
120	Drug resistance and <i>Mycobacterium tuberculosis</i> strain diversity in TB/HIV co-infected patients in Ho Chi Minh city, Vietnam. <i>Journal of Global Antimicrobial Resistance</i> , 2017, 10, 154-160.	0.9	11
121	A PubMed-Wide Associational Study of Infectious Diseases. <i>PLoS ONE</i> , 2010, 5, e9535.	1.1	11
122	Investigating genome reduction of <i>Bordetella pertussis</i> using a multiplex PCR-based reverse line blot assay (mPCR/RLB). <i>BMC Research Notes</i> , 2014, 7, 727.	0.6	10
123	Whole-genome sequencing of <i>Mycobacterium tuberculosis</i> for rapid diagnostics: feasibility of a decentralised model. <i>Lancet Respiratory Medicine</i> , 2016, 4, e13-e14.	5.2	10
124	Genotype heterogeneity of <i>Mycobacterium tuberculosis</i> within geospatial hotspots suggests foci of imported infection in Sydney, Australia. <i>Infection, Genetics and Evolution</i> , 2016, 40, 346-351.	1.0	10
125	Genome Sequencing Links Persistent Outbreak of Legionellosis in Sydney (New South Wales, Australia) to an Emerging Clone of <i>Legionella pneumophila</i> Sequence Type 211. <i>Applied and Environmental Microbiology</i> , 2018, 84, .	1.4	10
126	Bengamides display potent activity against drug-resistant <i>Mycobacterium tuberculosis</i> . <i>Scientific Reports</i> , 2019, 9, 14396.	1.6	10

#	ARTICLE	IF	CITATIONS
127	The importance of public health genomics for ensuring health security for Australia. Medical Journal of Australia, 2019, 210, 295.	0.8	10
128	World Tuberculosis Day 2021 Theme “The Clock is Ticking™” and the world is running out of time to deliver the United Nations General Assembly commitments to End TB due to the COVID-19 pandemic. International Journal of Infectious Diseases, 2021, 113, S1-S6.	1.5	10
129	Cost of whole genome sequencing for non-typhoidal Salmonella enterica. PLoS ONE, 2021, 16, e0248561.	1.1	10
130	Complete microbial genomes for public health in Australia and the Southwest Pacific. Microbial Genomics, 2020, 6, .	1.0	10
131	Protocol for a randomised controlled trial examining the impact of a web-based personally controlled health management system on the uptake of influenza vaccination rates. BMC Health Services Research, 2012, 12, 86.	0.9	9
132	Genomic Epidemiology of Clostridium botulinum Isolates from Temporally Related Cases of Infant Botulism in New South Wales, Australia. Journal of Clinical Microbiology, 2015, 53, 2846-2853.	1.8	9
133	Cluster of invasive Mycobacteria chimaera infections following cardiac surgery demonstrating novel clinical features and risks of aortic valve replacement. Internal Medicine Journal, 2018, 48, 1514-1520.	0.5	9
134	Network properties of salmonella epidemics. Scientific Reports, 2019, 9, 6159.	1.6	9
135	Highly Sensitive and Specific Detection and Serotyping of Five Prevalent Salmonella Serovars by Multiple Cross-Displacement Amplification. Journal of Molecular Diagnostics, 2020, 22, 708-719.	1.2	9
136	Elucidation of global and national genomic epidemiology of Salmonella enterica serovar Enteritidis through multilevel genome typing. Microbial Genomics, 2021, 7, .	1.0	9
137	The re-emergence of pertussis: implications for diagnosis and surveillance. NSW Public Health Bulletin, 2008, 19, 143.	0.3	9
138	Defining Reference Sequences for Nocardia Species by Similarity and Clustering Analyses of 16S rRNA Gene Sequence Data. PLoS ONE, 2011, 6, e19517.	1.1	9
139	Epidemiology of Peripheral Lymph Node Tuberculosis and Genotyping of M. tuberculosis Strains: A Case-Control Study. PLoS ONE, 2015, 10, e0132400.	1.1	9
140	Antibiotic therapy of ventilator-associated pneumonia—a reappraisal of rationale in the era of bacterial resistance. International Journal of Antimicrobial Agents, 2001, 18, 223-229.	1.1	8
141	Reverse line blot hybridization and DNA sequencing studies of the 16S-23S rRNA gene intergenic spacer regions of five emerging pathogenic Nocardia species. Journal of Medical Microbiology, 2010, 59, 548-555.	0.7	8
142	Evolution of Variable Number Tandem Repeats and Its Relationship with Genomic Diversity in Salmonella Typhimurium. Frontiers in Microbiology, 2016, 7, 2002.	1.5	8
143	Epidemic spread of multidrug-resistant tuberculosis in China. Lancet Infectious Diseases, The, 2017, 17, 238-239.	4.6	8
144	Effect of two alternative methods of pooling sputum prior to testing for tuberculosis with genexpert MTB/RIF. BMC Infectious Diseases, 2019, 19, 347.	1.3	8

#	ARTICLE	IF	CITATIONS
145	Optimization of sample preparation for culture-independent sequencing of <i>Bordetella pertussis</i> . <i>Microbial Genomics</i> , 2020, 6, .	1.0	8
146	Genome-wide networks reveal emergence of epidemic strains of <i>Salmonella Enteritidis</i> . <i>International Journal of Infectious Diseases</i> , 2022, 117, 65-73.	1.5	8
147	Screening for antibiotic resistant Gram-negative bacteria. <i>Lancet Infectious Diseases</i> , The, 2006, 6, 316-317.	4.6	7
148	Use of GeneXpert MTB/RIF on a single pooled sputum specimen to exclude pulmonary tuberculosis among hospital inpatients placed in respiratory isolation. <i>International Journal of Infectious Diseases</i> , 2020, 92, 175-180.	1.5	7
149	Whole genome sequencing based differentiation between re-infection and relapse in Indian patients with tuberculosis recurrence, with and without HIV co-infection. <i>International Journal of Infectious Diseases</i> , 2021, 113, S43-S47.	1.5	7
150	A case of urinary tuberculosis due to <i>Mycobacterium bovis</i> subspecies <i>caprae</i> . <i>Pathology</i> , 2006, 38, 376-378.	0.3	6
151	Novel <i>Salmonella enterica</i> Serovar Typhimurium Genotype Levels as Herald of Seasonal Salmonellosis Epidemics. <i>Emerging Infectious Diseases</i> , 2018, 24, 1079-1082.	2.0	6
152	Pathogen Genome Bioinformatics. <i>Methods in Molecular Biology</i> , 2014, 1168, 173-193.	0.4	6
153	Decision complexity affects the extent and type of decision support use. <i>AMIA ... Annual Symposium proceedings</i> , 2006, , 724-8.	0.2	6
154	<i>Mycobacterium tuberculosis</i> <i>rpoB</i> gene DNA sequencing: implications for detection of rifamycin resistance. <i>Journal of Antimicrobial Chemotherapy</i> , 1999, 44, 294-295.	1.3	5
155	Is it time to replace the petri dish with pcr? application of culture-independent nucleic acid amplification in diagnostic bacteriology: expectations and reality. <i>Pathology</i> , 1999, 31, 436-439.	0.3	5
156	Rolling circle amplification and multiplex allele-specific PCR for rapid detection of <i>katG</i> and <i>inhA</i> gene mutations in <i>Mycobacterium tuberculosis</i> . <i>International Journal of Medical Microbiology</i> , 2009, 299, 574-581.	1.5	5
157	Commonly used molecular epidemiology markers of <i>Streptococcus agalactiae</i> do not appear to predict virulence. <i>Pathology</i> , 2009, 41, 576-581.	0.3	5
158	Software for selecting the most informative sets of genomic loci for multi-target microbial typing. <i>BMC Bioinformatics</i> , 2013, 14, 148.	1.2	5
159	Nontuberculosis mycobacteria infections: would there be pharmacodynamics without pharmacokinetics?. <i>European Respiratory Journal</i> , 2019, 54, 1901508.	3.1	5
160	Genomic Surveillance Enables Suitability Assessment of <i>Salmonella</i> Gene Targets Used for Culture-Independent Diagnostic Testing. <i>Journal of Clinical Microbiology</i> , 2020, 58, .	1.8	5
161	Listeriosis cluster in Sydney linked to hospital food. <i>Medical Journal of Australia</i> , 2015, 202, 448-449.	0.8	4
162	Acquired Drug Resistance: Recognizing the Potential of Repurposed Drugs. <i>Clinical Infectious Diseases</i> , 2019, 69, 2038-2039.	2.9	4

#	ARTICLE	IF	CITATIONS
163	Microbial Genomics as a Catalyst for Targeted Antivirulence Therapeutics. <i>Frontiers in Medicine</i> , 2021, 8, 641260.	1.2	4
164	16S-23S Internal Transcribed Spacer Region PCR and Sequencer-Based Capillary Gel Electrophoresis has Potential as an Alternative to High Performance Liquid Chromatography for Identification of Slowly Growing Nontuberculous Mycobacteria. <i>PLoS ONE</i> , 2016, 11, e0164138.	1.1	4
165	Documenting elimination of co-circulating COVID-19 clusters using genomics in New South Wales, Australia. <i>BMC Research Notes</i> , 2021, 14, 415.	0.6	4
166	Assessment of Inter-Laboratory Differences in SARS-CoV-2 Consensus Genome Assemblies between Public Health Laboratories in Australia. <i>Viruses</i> , 2022, 14, 185.	1.5	4
167	Genomic dissection of the microevolution of Australian epidemic <i>Bordetella pertussis</i> . <i>Emerging Microbes and Infections</i> , 2022, 11, 1460-1473.	3.0	4
168	SARS-CoV-2 Within-Host and in vitro Genomic Variability and Sub-Genomic RNA Levels Indicate Differences in Viral Expression Between Clinical Cohorts and in vitro Culture. <i>Frontiers in Microbiology</i> , 2022, 13, .	1.5	4
169	In silico prioritisation of candidate genes for prokaryotic gene function discovery: an application of phylogenetic profiles. <i>BMC Bioinformatics</i> , 2009, 10, 86.	1.2	3
170	Unexpected Diversity of Staphylococcal Cassette Chromosome mec Type IV in Methicillin-Resistant <i>Staphylococcus aureus</i> Strains. <i>Journal of Clinical Microbiology</i> , 2010, 48, 3628-3634.	1.8	3
171	Assignment of <i>recA</i> reference sequence types for enhanced identification of the <i>Burkholderia cepacia</i> complex. <i>Pathology</i> , 2012, 44, 373-375.	0.3	3
172	Tuberculosis risk factors and <i>Mycobacterium tuberculosis</i> transmission among HIV-infected patients in Vietnam. <i>Tuberculosis</i> , 2019, 115, 67-75.	0.8	3
173	Genome Sequences of Enteroinvasive <i>Escherichia coli</i> Sequence Type 6, 99, and 311 Strains Acquired in Asia Pacific. <i>Microbiology Resource Announcements</i> , 2019, 8, .	0.3	3
174	Hospital MRSA outbreaks: Multiplex PCR-reverse line blot binary typing as a screening method for WGS, and the role of the environment in transmission. <i>Infection, Disease and Health</i> , 2020, 25, 268-276.	0.5	3
175	Inferring evolutionary pathways and directed genotype networks of foodborne pathogens. <i>PLoS Computational Biology</i> , 2020, 16, e1008401.	1.5	3
176	Are clinicians' information needs and decision support affected by different models of care? Experimental study. <i>Studies in Health Technology and Informatics</i> , 2007, 129, 895-9.	0.2	3
177	Developing Decision Support Systems in Clinical Bioinformatics. <i>Methods in Molecular Medicine</i> , 2008, 141, 331-351.	0.8	2
178	Linear normalised hash function for clustering gene sequences and identifying reference sequences from multiple sequence alignments. <i>Microbial Informatics and Experimentation</i> , 2012, 2, 2.	7.6	2
179	Quantitative Estimation of the Stability of Methicillin-Resistant <i>Staphylococcus aureus</i> Strain-Typing Systems by Use of Kaplan-Meier Survival Analysis. <i>Journal of Clinical Microbiology</i> , 2013, 51, 112-116.	1.8	2
180	Genomic heterogeneity of <i>Salmonella enterica</i> serovar Typhimurium bacteriuria from chronic infection. <i>Infection, Genetics and Evolution</i> , 2017, 51, 17-20.	1.0	2

#	ARTICLE	IF	CITATIONS
181	Extensive Homoplasmy but No Evidence of Convergent Evolution of Repeat Numbers at MIRU Loci in Modern Mycobacterium tuberculosis Lineages. <i>Frontiers in Public Health</i> , 2020, 8, 455.	1.3	2
182	Antibiotic Use Associated with Confirmed Influenza, Pertussis, and Nontyphoidal Salmonella Infections. <i>Microbial Drug Resistance</i> , 2020, 26, 1482-1490.	0.9	2
183	Editorial: Pathogen Genomics: Empowering Infectious Disease Surveillance and Outbreak Investigations. <i>Frontiers in Public Health</i> , 2020, 8, 179.	1.3	2
184	The use of mycobacterial interspersed repetitive unit typing and whole genome sequencing to inform tuberculosis prevention and control activities. <i>NSW Public Health Bulletin</i> , 2013, 24, 10.	0.3	2
185	Retrospective use of whole genome sequencing to better understand an outbreak of Salmonella enterica serovar Mbandaka in New South Wales, Australia. <i>Western Pacific Surveillance and Response Journal: WPSAR</i> , 2018, 9, 20-25.	0.3	2
186	Search Space Reduction Technique for Distributed Multiple Sequence Alignment. , 2009, , .		1
187	Translational web robots for pathogen genome analysis. <i>Microbial Informatics and Experimentation</i> , 2011, 1, 10.	7.6	1
188	Evaluation of the BioGX BD-Max PCR assay for detection of pathogenic Bordetella. <i>Pathology</i> , 2019, 51, 323-324.	0.3	1
189	Informatics for Infectious Disease Research and Control. , 2010, , 1-26.		1
190	Migration and descent, adaptations to altitude and tuberculosis in Nepalis and Tibetans. <i>Evolution, Medicine and Public Health</i> , 2022, 10, 189-201.	1.1	1
191	Inferring evolutionary pathways and directed genotype networks of foodborne pathogens. , 2020, 16, e1008401.		0
192	Inferring evolutionary pathways and directed genotype networks of foodborne pathogens. , 2020, 16, e1008401.		0
193	Inferring evolutionary pathways and directed genotype networks of foodborne pathogens. , 2020, 16, e1008401.		0
194	Inferring evolutionary pathways and directed genotype networks of foodborne pathogens. , 2020, 16, e1008401.		0
195	Inferring evolutionary pathways and directed genotype networks of foodborne pathogens. , 2020, 16, e1008401.		0
196	Inferring evolutionary pathways and directed genotype networks of foodborne pathogens. , 2020, 16, e1008401.		0