

# Vitali Sintchenko

## List of Publications by Year in descending order

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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	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
2	Genome-wide networks reveal emergence of epidemic strains of <i>Salmonella</i> Enteritidis. <i>International Journal of Infectious Diseases</i> , 2022, 117, 65-73.	1.5	8
3	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
4	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
5	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
6	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
7	Co-infection with SARS-CoV-2 Omicron and Delta variants revealed by genomic surveillance. <i>Nature Communications</i> , 2022, 13, 2745.	5.8	64
8	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
9	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
10	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
11	Value of routine whole genome sequencing for <i>Mycobacterium tuberculosis</i> drug resistance detection. <i>International Journal of Infectious Diseases</i> , 2021, 113, S48-S54.	1.5	31
12	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
13	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
14	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. <i>International Journal of Infectious Diseases</i> , 2021, 113, S1-S6.	1.5	10
15	Cost of whole genome sequencing for non-typhoidal <i>Salmonella enterica</i> . <i>PLoS ONE</i> , 2021, 16, e0248561.	1.1	10
16	Microbial Genomics as a Catalyst for Targeted Antivirulence Therapeutics. <i>Frontiers in Medicine</i> , 2021, 8, 641260.	1.2	4
17	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
18	Elucidation of global and national genomic epidemiology of <i>Salmonella enterica</i> serovar Enteritidis through multilevel genome typing. <i>Microbial Genomics</i> , 2021, 7, .	1.0	9

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19	SARS-CoV-2 neutralizing antibodies: Longevity, breadth, and evasion by emerging viral variants. <i>PLoS Medicine</i> , 2021, 18, e1003656.	3.9	109
20	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
21	Genomics-informed responses in the elimination of COVID-19 in Victoria, Australia: an observational, genomic epidemiological study. <i>Lancet Public Health</i> , The, 2021, 6, e547-e556.	4.7	53
22	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
23	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
24	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
25	Surfaceome analysis of Australian epidemic <i>Bordetella pertussis</i> reveals potential vaccine antigens. <i>Vaccine</i> , 2020, 38, 539-548.	1.7	12
26	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
27	The Antibody Response to SARS-CoV-2 Infection. <i>Open Forum Infectious Diseases</i> , 2020, 7, ofaa387.	0.4	45
28	Extensive Homoplasmy but No Evidence of Convergent Evolution of Repeat Numbers at MIRU Loci in Modern <i>Mycobacterium tuberculosis</i> Lineages. <i>Frontiers in Public Health</i> , 2020, 8, 455.	1.3	2
29	Antibiotic Use Associated with Confirmed Influenza, Pertussis, and Nontyphoidal <i>Salmonella</i> Infections. <i>Microbial Drug Resistance</i> , 2020, 26, 1482-1490.	0.9	2
30	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
31	Editorial: Pathogen Genomics: Empowering Infectious Disease Surveillance and Outbreak Investigations. <i>Frontiers in Public Health</i> , 2020, 8, 179.	1.3	2
32	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
33	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
34	Highly Sensitive and Specific Detection and Serotyping of Five Prevalent <i>Salmonella</i> Serovars by Multiple Cross-Displacement Amplification. <i>Journal of Molecular Diagnostics</i> , 2020, 22, 708-719.	1.2	9
35	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
36	An emergent clade of SARS-CoV-2 linked to returned travellers from Iran. <i>Virus Evolution</i> , 2020, 6, veaa027.	2.2	119

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37	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
38	Optimization of sample preparation for culture-independent sequencing of <i>Bordetella pertussis</i> . <i>Microbial Genomics</i> , 2020, 6, .	1.0	8
39	Complete microbial genomes for public health in Australia and the Southwest Pacific. <i>Microbial Genomics</i> , 2020, 6, .	1.0	10
40	Multilevel genome typing: genomics-guided scalable resolution typing of microbial pathogens. <i>Eurosurveillance</i> , 2020, 25, .	3.9	12
41	Inferring evolutionary pathways and directed genotype networks of foodborne pathogens. <i>PLoS Computational Biology</i> , 2020, 16, e1008401.	1.5	3
42	Inferring evolutionary pathways and directed genotype networks of foodborne pathogens. , 2020, 16, e1008401.		0
43	Inferring evolutionary pathways and directed genotype networks of foodborne pathogens. , 2020, 16, e1008401.		0
44	Inferring evolutionary pathways and directed genotype networks of foodborne pathogens. , 2020, 16, e1008401.		0
45	Inferring evolutionary pathways and directed genotype networks of foodborne pathogens. , 2020, 16, e1008401.		0
46	Inferring evolutionary pathways and directed genotype networks of foodborne pathogens. , 2020, 16, e1008401.		0
47	Inferring evolutionary pathways and directed genotype networks of foodborne pathogens. , 2020, 16, e1008401.		0
48	Tracking a moving user in indoor environments using Bluetooth low energy beacons. <i>Journal of Biomedical Informatics</i> , 2019, 98, 103288.	2.5	26
49	Community-wide Screening for Tuberculosis in a High-Prevalence Setting. <i>New England Journal of Medicine</i> , 2019, 381, 1347-1357.	13.9	116
50	Bengamides display potent activity against drug-resistant <i>Mycobacterium tuberculosis</i> . <i>Scientific Reports</i> , 2019, 9, 14396.	1.6	10
51	Pertactin-Negative and Filamentous Hemagglutinin-Negative <i>Bordetella pertussis</i> , Australia, 2013–2017. <i>Emerging Infectious Diseases</i> , 2019, 25, 1196-1199.	2.0	29
52	Network properties of salmonella epidemics. <i>Scientific Reports</i> , 2019, 9, 6159.	1.6	9
53	Effect of two alternative methods of pooling sputum prior to testing for tuberculosis with genexpert MTB/RIF. <i>BMC Infectious Diseases</i> , 2019, 19, 347.	1.3	8
54	Acquired Drug Resistance: Recognizing the Potential of Repurposed Drugs. <i>Clinical Infectious Diseases</i> , 2019, 69, 2038-2039.	2.9	4

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55	DeepAMR for predicting co-occurrent resistance of <i>Mycobacterium tuberculosis</i> . <i>Bioinformatics</i> , 2019, 35, 3240-3249.	1.8	38
56	The importance of public health genomics for ensuring health security for Australia. <i>Medical Journal of Australia</i> , 2019, 210, 295.	0.8	10
57	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
58	Evaluation of the BioGX BD-Max PCR assay for detection of pathogenic <i>Bordetella</i> . <i>Pathology</i> , 2019, 51, 323-324.	0.3	1
59	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
60	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
61	Nontuberculosis mycobacteria infections: would there be pharmacodynamics without pharmacokinetics?. <i>European Respiratory Journal</i> , 2019, 54, 1901508.	3.1	5
62	Antibiotic resistance prediction for <i>Mycobacterium tuberculosis</i> from genome sequence data with Mykrobe. Wellcome Open Research, 2019, 4, 191.	0.9	103
63	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
64	Proteomic Adaptation of Australian Epidemic <i>Bordetella pertussis</i> . <i>Proteomics</i> , 2018, 18, e1700237.	1.3	29
65	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
66	Incorporating Whole-Genome Sequencing into Public Health Surveillance: Lessons from Prospective Sequencing of <i>Salmonella</i> Typhimurium in Australia. <i>Foodborne Pathogens and Disease</i> , 2018, 15, 161-167.	0.8	24
67	Seven <i>Salmonella</i> Typhimurium Outbreaks in Australia Linked by Trace-Back and Whole Genome Sequencing. <i>Foodborne Pathogens and Disease</i> , 2018, 15, 285-292.	0.8	27
68	Relentless spread and adaptation of non-typeable vanA vancomycin-resistant <i>Enterococcus faecium</i> : a genome-wide investigation. <i>Journal of Antimicrobial Chemotherapy</i> , 2018, 73, 1487-1491.	1.3	24
69	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
70	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
71	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
72	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

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73	Cluster of invasive <i>Mycobacteria chimaera</i> infections following cardiac surgery demonstrating novel clinical features and risks of aortic valve replacement. <i>Internal Medicine Journal</i> , 2018, 48, 1514-1520.	0.5	9
74	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
75	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
76	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
77	<i>Burkholderia lata</i> Infections from Intrinsically Contaminated Chlorhexidine Mouthwash, Australia, 2016. <i>Emerging Infectious Diseases</i> , 2018, 24, 2109-2111.	2.0	16
78	Multidrug-Resistant <i>Salmonella enterica</i> 4,[5],12:i:- Sequence Type 34, New South Wales, Australia, 2016–2017. <i>Emerging Infectious Diseases</i> , 2018, 24, 751-753.	2.0	52
79	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
80	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
81	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
82	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
83	<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
84	Retrospective use of whole genome sequencing to better understand an outbreak of <i>Salmonella enterica</i> serovar Mbandaka in New South Wales, Australia. <i>Western Pacific Surveillance and Response Journal: WPSAR</i> , 2018, 9, 20-25.	0.3	2
85	Characterisation of the <i>Bordetella pertussis</i> secretome under different media. <i>Journal of Proteomics</i> , 2017, 158, 43-51.	1.2	34
86	Epidemic spread of multidrug-resistant tuberculosis in China. <i>Lancet Infectious Diseases</i> , The, 2017, 17, 238-239.	4.6	8
87	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
88	Aiming for zero tuberculosis transmission in low-burden countries. <i>Lancet Respiratory Medicine</i> , the, 2017, 5, 846-848.	5.2	13
89	Comparative genomics of Australian and international isolates of <i>Salmonella Typhimurium</i> : correlation of core genome evolution with CRISPR and prophage profiles. <i>Scientific Reports</i> , 2017, 7, 9733.	1.6	26
90	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

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91	Whole Genome Sequencing of <i>Candida glabrata</i> for Detection of Markers of Antifungal Drug Resistance. <i>Journal of Visualized Experiments</i> , 2017, .	0.2	24
92	<i>Francisella tularensis</i> ssp. <i>holarctica</i> in Ringtail Possums, Australia. <i>Emerging Infectious Diseases</i> , 2017, 23, 1198-1201.	2.0	49
93	Evolution of Variable Number Tandem Repeats and Its Relationship with Genomic Diversity in <i>Salmonella</i> Typhimurium. <i>Frontiers in Microbiology</i> , 2016, 7, 2002.	1.5	8
94	Whole genome sequencing of <i>Salmonella</i> Typhimurium illuminates distinct outbreaks caused by an endemic multi-locus variable number tandem repeat analysis type in Australia, 2014. <i>BMC Microbiology</i> , 2016, 16, 211.	1.3	29
95	Whole Genome Sequencing Demonstrates Limited Transmission within Identified <i>Mycobacterium tuberculosis</i> Clusters in New South Wales, Australia. <i>PLoS ONE</i> , 2016, 11, e0163612.	1.1	44
96	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
97	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
98	<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.	1.4	20
99	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
100	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
101	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
102	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
103	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
104	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
105	Identifying Likely Transmission Pathways within a 10-Year Community Outbreak of Tuberculosis by High-Depth Whole Genome Sequencing. <i>PLoS ONE</i> , 2016, 11, e0150550.	1.1	24
106	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 <i>Mycobacteria</i> . <i>PLoS ONE</i> , 2016, 11, e0164138.	1.1	4
107	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
108	Listeriosis cluster in Sydney linked to hospital food. <i>Medical Journal of Australia</i> , 2015, 202, 448-449.	0.8	4

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109	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
110	Defining the Core Genome of <i>Salmonella enterica</i> Serovar Typhimurium for Genomic Surveillance and Epidemiological Typing. <i>Journal of Clinical Microbiology</i> , 2015, 53, 2530-2538.	1.8	29
111	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
112	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
113	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
114	The role of pathogen genomics in assessing disease transmission. <i>BMJ</i> , The, 2015, 350, h1314-h1314.	3.0	59
115	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
116	It Is Not All about Single Nucleotide Polymorphisms: Comparison of Mobile Genetic Elements and Deletions in <i>Listeria monocytogenes</i> Genomes Links Cases of Hospital-Acquired Listeriosis to the Environmental Source. <i>Journal of Clinical Microbiology</i> , 2015, 53, 3492-3500.	1.8	24
117	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
118	Genomic Epidemiology of <i>Clostridium botulinum</i> Isolates from Temporally Related Cases of Infant Botulism in New South Wales, Australia. <i>Journal of Clinical Microbiology</i> , 2015, 53, 2846-2853.	1.8	9
119	Epidemiology of Peripheral Lymph Node Tuberculosis and Genotyping of <i>M. tuberculosis</i> Strains: A Case-Control Study. <i>PLoS ONE</i> , 2015, 10, e0132400.	1.1	9
120	Inaccurate Ascertainment of Morbidity and Mortality due to Influenza in Administrative Databases: A Population-Based Record Linkage Study. <i>PLoS ONE</i> , 2014, 9, e98446.	1.1	25
121	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
122	Rapid Increase in Pertactin-deficient <i>Bordetella pertussis</i> Isolates, Australia. <i>Emerging Infectious Diseases</i> , 2014, 20, 626-33.	2.0	151
123	Global Population Structure and Evolution of <i>Bordetella pertussis</i> and Their Relationship with Vaccination. <i>MBio</i> , 2014, 5, e01074.	1.8	257
124	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
125	Temporal dynamics of <i>Mycobacterium tuberculosis</i> genotypes in New South Wales, Australia. <i>BMC Infectious Diseases</i> , 2014, 14, 455.	1.3	18
126	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



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127	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
128	Clinical Microbiology Informatics. <i>Clinical Microbiology Reviews</i> , 2014, 27, 1025-1047.	5.7	57
129	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
130	Pathogen Genome Bioinformatics. <i>Methods in Molecular Biology</i> , 2014, 1168, 173-193.	0.4	6
131	Improved Identification of Rapidly Growing Mycobacteria by a 16S rRNA Internal Transcribed Spacer Region PCR and Capillary Gel Electrophoresis. <i>PLoS ONE</i> , 2014, 9, e102290.	1.1	18
132	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
133	Editorial Commentary: The "How" of Polymerase Chain Reaction Testing for <i>Bordetella pertussis</i> Depends on the "Why". <i>Clinical Infectious Diseases</i> , 2013, 56, 332-334.	2.9	23
134	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
135	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
136	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
137	Effectiveness of Hospital-Wide Methicillin-Resistant <i>Staphylococcus aureus</i> (MRSA) Infection Control Policies Differs by Ward Specialty. <i>PLoS ONE</i> , 2013, 8, e83099.	1.1	30
138	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
139	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
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