

Sebastiaan J Van Hal

List of Publications by Year in descending order

Source: <https://exaly.com/author-pdf/407894/publications.pdf>

Version: 2024-02-01

53
papers

1,714
citations

304368

22
h-index

301761

39
g-index

57
all docs

57
docs citations

57
times ranked

2790
citing authors

#	ARTICLE	IF	CITATIONS
1	Emerging therapeutic drug monitoring of anti-infective agents in Australian hospitals: Availability, performance and barriers to implementation. <i>British Journal of Clinical Pharmacology</i> , 2022, 88, 669-679.	1.1	23
2	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
3	The interplay between community and hospital <i>Enterococcus faecium</i> clones within health-care settings: a genomic analysis. <i>Lancet Microbe</i> , The, 2022, 3, e133-e141.	3.4	17
4	SARS-CoV-2 N-gene mutation leading to Xpert Xpress SARS-CoV-2 assay instability. <i>Pathology</i> , 2022, , .	0.3	8
5	Multidrug-resistant OXA-48/CTX-M-15 <i>Klebsiella pneumoniae</i> cluster in a COVID-19 intensive care unit: salient lessons for infection prevention and control during the COVID-19 pandemic. <i>Journal of Hospital Infection</i> , 2022, 126, 64-69.	1.4	3
6	Persistent high-level shedding of cultivable SARS-CoV-2 Delta virus 33 days after onset of COVID-19 in a hospitalized patient with pneumonia. <i>Journal of Medical Virology</i> , 2022, 94, 4043-4046.	2.5	4
7	Platform for isolation and characterization of SARS-CoV-2 variants enables rapid characterization of Omicron in Australia. <i>Nature Microbiology</i> , 2022, 7, 896-908.	5.9	32
8	The <i>Staphylococcus aureus</i> Network Adaptive Platform Trial Protocol: New Tools for an Old Foe. <i>Clinical Infectious Diseases</i> , 2022, 75, 2027-2034.	2.9	27
9	Risk factors for candidaemia: A prospective multi-centre case-control study. <i>Mycoses</i> , 2021, 64, 257-263.	1.8	23
10	Respiratory viral co-infections among SARS-CoV-2 cases confirmed by virome capture sequencing. <i>Scientific Reports</i> , 2021, 11, 3934.	1.6	55
11	The global dissemination of hospital clones of <i>Enterococcus faecium</i> . <i>Genome Medicine</i> , 2021, 13, 52.	3.6	33
12	Predictive Performance of Bayesian Vancomycin Monitoring in the Critically Ill*. <i>Critical Care Medicine</i> , 2021, 49, e952-e960.	0.4	13
13	Centralised or Localised Pathogen Whole Genome Sequencing: Lessons Learnt From Implementation in a Clinical Diagnostic Laboratory. <i>Frontiers in Cellular and Infection Microbiology</i> , 2021, 11, 636290.	1.8	2
14	Bayesian Forecasting for Intravenous Tobramycin Dosing in Adults With Cystic Fibrosis Using One Versus Two Serum Concentrations in a Dosing Interval. <i>Therapeutic Drug Monitoring</i> , 2021, 43, 505-511.	1.0	9
15	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
16	Whole genome sequencing identifies opportunistic non-typeable <i>Haemophilus influenzae</i> rather than a hypervirulent clone. <i>Pathology</i> , 2021, 53, 540-541.	0.3	2
17	A vanA vancomycin-resistant <i>Enterococcus faecium</i> ST80 outbreak resulting from a single importation event. <i>Journal of Antimicrobial Chemotherapy</i> , 2021, , .	1.3	5
18	Consensus guidelines for the diagnosis and management of invasive aspergillosis, 2021. <i>Internal Medicine Journal</i> , 2021, 51, 143-176.	0.5	51

#	ARTICLE	IF	CITATIONS
19	SUBA-Itraconazole for Primary Antifungal Prophylaxis After Allogeneic Hematopoietic Cell Transplantation. <i>Open Forum Infectious Diseases</i> , 2021, 8, ofab502.	0.4	2
20	Therapeutic drug monitoring of commonly used anti-infective agents: A nationwide cross-sectional survey of Australian hospital practices. <i>International Journal of Antimicrobial Agents</i> , 2020, 56, 106180.	1.1	17
21	Analytical validity of nanopore sequencing for rapid SARS-CoV-2 genome analysis. <i>Nature Communications</i> , 2020, 11, 6272.	5.8	183
22	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
23	Clinical characteristics and outcomes of invasive <i>Lomentospora prolificans</i> infections: Analysis of patients in the FungiScope registry. <i>Mycoses</i> , 2020, 63, 437-442.	1.8	41
24	Effect of Vancomycin or Daptomycin With vs Without an Antistaphylococcal β -Lactam on Mortality, Bacteremia, Relapse, or Treatment Failure in Patients With MRSA Bacteremia. <i>JAMA - Journal of the American Medical Association</i> , 2020, 323, 527.	3.8	169
25	A multicentre outbreak of ST45 MRSA containing deletions in the <i>spa</i> gene in New South Wales, Australia. <i>Journal of Antimicrobial Chemotherapy</i> , 2020, 75, 1112-1116.	1.3	10
26	Clinical experience with new formulation SUBA [®] -itraconazole for prophylaxis in patients undergoing stem cell transplantation or treatment for haematological malignancies. <i>Journal of Antimicrobial Chemotherapy</i> , 2019, 74, 3049-3055.	1.3	25
27	Prolonged Immunosuppression in Relapsed, Refractory Multiple Myeloma Leading to Cerebral Toxoplasmosis and Progressive Multifocal Leukoencephalopathy. <i>Clinical Lymphoma, Myeloma and Leukemia</i> , 2019, 19, e625-e628.	0.2	8
28	Identification of multiple species and subpopulations among Australian clinical <i>Sporothrix</i> isolates using whole genome sequencing. <i>Medical Mycology</i> , 2019, 57, 905-908.	0.3	11
29	Defining the Role of the Environment in the Emergence and Persistence of <i>vanA</i> Vancomycin-Resistant <i>Enterococcus</i> (VRE) in an Intensive Care Unit: A Molecular Epidemiological Study. <i>Infection Control and Hospital Epidemiology</i> , 2018, 39, 668-675.	1.0	32
30	Morbidity from in-hospital complications is greater than treatment failure in patients with <i>Staphylococcus aureus</i> bacteraemia. <i>BMC Infectious Diseases</i> , 2018, 18, 107.	1.3	26
31	Relentless spread and adaptation of non-typeable <i>vanA</i> vancomycin-resistant <i>Enterococcus faecium</i> : a genome-wide investigation. <i>Journal of Antimicrobial Chemotherapy</i> , 2018, 73, 1487-1491.	1.3	24
32	Failure of daptomycin β -Lactam combination therapy to prevent resistance emergence in <i>Enterococcus faecium</i> . <i>Diagnostic Microbiology and Infectious Disease</i> , 2018, 90, 120-122.	0.8	8
33	Invasive Fungal Sinusitis Presenting as Acute Posterior Ischemic Optic Neuropathy. <i>Neuro-Ophthalmology</i> , 2018, 42, 209-214.	0.4	10
34	Evaluation of Tobramycin Exposure Predictions in Three Bayesian Forecasting Programmes Compared with Current Clinical Practice in Children and Adults with Cystic Fibrosis. <i>Clinical Pharmacokinetics</i> , 2018, 57, 1017-1027.	1.6	17
35	Bayesian therapeutic drug monitoring software: past, present and future. <i>International Journal of Pharmacokinetics</i> , 2018, 3, 109-114.	0.5	20
36	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

#	ARTICLE	IF	CITATIONS
37	Recommendations To Address the Difficulties Encountered When Determining Linezolid Resistance from Whole-Genome Sequencing Data. <i>Antimicrobial Agents and Chemotherapy</i> , 2018, 62, .	1.4	9
38	Global Scale Dissemination of ST93: A Divergent <i>Staphylococcus aureus</i> Epidemic Lineage That Has Recently Emerged From Remote Northern Australia. <i>Frontiers in Microbiology</i> , 2018, 9, 1453.	1.5	29
39	Personalized Medicine and Infectious Disease Management. <i>Trends in Microbiology</i> , 2017, 25, 875-876.	3.5	13
40	Epidemiology and Mortality of <i>Staphylococcus aureus</i> Bacteremia in Australian and New Zealand Children. <i>JAMA Pediatrics</i> , 2016, 170, 979.	3.3	102
41	When sepsis persists: a review of MRSA bacteraemia salvage therapy. <i>Journal of Antimicrobial Chemotherapy</i> , 2016, 71, 576-586.	1.3	61
42	Combination of Vancomycin and β -Lactam Therapy for Methicillin-Resistant <i>Staphylococcus aureus</i> Bacteremia: A Pilot Multicenter Randomized Controlled Trial. <i>Clinical Infectious Diseases</i> , 2016, 62, 173-180.	2.9	149
43	Evolutionary dynamics of <i>Enterococcus faecium</i> reveals complex genomic relationships between isolates with independent emergence of vancomycin resistance. <i>Microbial Genomics</i> , 2016, 2, .	1.0	50
44	Whole Genome Sequencing in Real-Time Investigation and Management of a <i>Pseudomonas aeruginosa</i> Outbreak on a Neonatal Intensive Care Unit. <i>Infection Control and Hospital Epidemiology</i> , 2015, 36, 1058-1064.	1.0	40
45	Treatment of Methicillin-Resistant <i>Staphylococcus aureus</i> : Vancomycin and Beyond. <i>Seminars in Respiratory and Critical Care Medicine</i> , 2015, 36, 017-030.	0.8	50
46	The use of whole-genome sequencing for molecular epidemiology and antimicrobial surveillance: identifying the role of IncX3 plasmids and the spread of <i>bla</i> _{NDM-4} -like genes in the Enterobacteriaceae. <i>Journal of Clinical Pathology</i> , 2015, 68, 835-838.	1.0	44
47	“Tolerance” of Misused Terminology? Enforcing Standardized Phenotypic Definitions. <i>MBio</i> , 2015, 6, e00446-15.	1.8	2
48	Ceftaroline fosamil salvage therapy: an option for reduced-vancomycin-susceptible MRSA bacteraemia. <i>Journal of Antimicrobial Chemotherapy</i> , 2015, 70, 797-801.	1.3	10
49	Therapeutic Options for Resistant Gram Positives. <i>Current Treatment Options in Infectious Diseases</i> , 2014, 6, 439-455.	0.8	0
50	Reply to Parra-Ruiz. <i>Clinical Infectious Diseases</i> , 2013, 57, 1219-1220.	2.9	3
51	Is It Time to Replace Vancomycin in the Treatment of Methicillin-Resistant <i>Staphylococcus aureus</i> Infections?. <i>Clinical Infectious Diseases</i> , 2013, 56, 1779-1788.	2.9	105
52	HIV-1 integrase polymorphisms are associated with prior antiretroviral drug exposure. <i>Retrovirology</i> , 2009, 6, 12.	0.9	22
53	Lymphogranuloma venereum: an emerging anorectal disease in Australia. <i>Medical Journal of Australia</i> , 2007, 187, 309-310.	0.8	11