

Arshad Ismail

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The third column is the impact factor (IF) of the journal, and the fourth column is the number of citations of the article.

87
papers

2,345
citations

17
h-index

48
g-index

102
ext. papers

4,589
ext. citations

8.1
avg, IF

4.63
L-index

#	Paper	IF	Citations
87	Detection of a SARS-CoV-2 variant of concern in South Africa. <i>Nature</i> , 2021 , 592, 438-443	50.4	685
86	Emergence and rapid spread of a new severe acute respiratory syndrome-related coronavirus 2 (SARS-CoV-2) lineage with multiple spike mutations in South Africa		446
85	Sixteen novel lineages of SARS-CoV-2 in South Africa. <i>Nature Medicine</i> , 2021 , 27, 440-446	50.5	206
84	Rapid epidemic expansion of the SARS-CoV-2 Omicron variant in southern Africa.. <i>Nature</i> , 2022 ,	50.4	205
83	Early assessment of the clinical severity of the SARS-CoV-2 omicron variant in South Africa: a data linkage study.. <i>Lancet, The</i> , 2022 ,	40	152
82	Outbreak of in South Africa, 2017-2018: Laboratory Activities and Experiences Associated with Whole-Genome Sequencing Analysis of Isolates. <i>Foodborne Pathogens and Disease</i> , 2019 , 16, 524-530	3.8	71
81	Outbreak of Listeriosis in South Africa Associated with Processed Meat. <i>New England Journal of Medicine</i> , 2020 , 382, 632-643	59.2	65
80	Ability to develop broadly neutralizing HIV-1 antibodies is not restricted by the germline Ig gene repertoire. <i>Journal of Immunology</i> , 2015 , 194, 4371-8	5.3	58
79	A year of genomic surveillance reveals how the SARS-CoV-2 pandemic unfolded in Africa. <i>Science</i> , 2021 , 374, 423-431	33.3	35
78	Genome Sequencing of Extended-Spectrum β Lactamase (ESBL)-Producing Isolated from Pigs and Abattoir Workers in Cameroon. <i>Frontiers in Microbiology</i> , 2018 , 9, 188	5.7	26
77	Whole-Genome Sequences of <i>Listeria monocytogenes</i> Sequence Type 6 Isolates Associated with a Large Foodborne Outbreak in South Africa, 2017 to 2018. <i>Genome Announcements</i> , 2018 , 6,		23
76	Emergence and phenotypic characterization of C.1.2, a globally detected lineage that rapidly accumulated mutations of concern		23
75	Genomic analysis of methicillin-resistant <i>Staphylococcus aureus</i> isolated from poultry and occupational farm workers in Umgungundlovu District, South Africa. <i>Science of the Total Environment</i> , 2019 , 670, 704-716	10.2	21
74	Rapid epidemic expansion of the SARS-CoV-2 Omicron variant in southern Africa. <i>Nature</i> ,	50.4	20
73	Human Blastomycosis in South Africa Caused by and sp. nov., 1967 to 2014. <i>Journal of Clinical Microbiology</i> , 2020 , 58,	9.7	20
72	HIV-1 and SARS-CoV-2: Patterns in the evolution of two pandemic pathogens. <i>Cell Host and Microbe</i> , 2021 , 29, 1093-1110	23.4	19
71	Whole Genome Sequencing of Extended Spectrum β Lactamase (ESBL)-producing <i>Klebsiella pneumoniae</i> Isolated from Hospitalized Patients in KwaZulu-Natal, South Africa. <i>Scientific Reports</i> , 2019 , 9, 6266	4.9	17

70	V2-Directed Vaccine-like Antibodies from HIV-1 Infection Identify an Additional K169-Binding Light Chain Motif with Broad ADCC Activity. <i>Cell Reports</i> , 2018 , 25, 3123-3135.e6	10.6	17
69	Rapid replacement of the Beta variant by the Delta variant in South Africa		17
68	Genomic Analysis of CarbapenemaseProducing Extensively Drug-Resistant Isolates Reveals the Horizontal Spread of p18-43_01 Plasmid Encoding in South Africa. <i>Microorganisms</i> , 2020 , 8,	4.9	14
67	Phenotypic and genotypic characterisation of a unique indigenous hypersaline unicellular cyanobacterium, <i>Euhalothece</i> sp.nov. <i>Microbiological Research</i> , 2018 , 211, 47-56	5.3	12
66	Rapid epidemic expansion of the SARS-CoV-2 Omicron variant in southern Africa		12
65	Genomic characterisation of <i>Klebsiella michiganensis</i> co-producing OXA-181 and NDM-1 carbapenemases isolated from a cancer patient in uMgungundlovu District, KwaZulu-Natal Province, South Africa. <i>South African Medical Journal</i> , 2018 , 109, 7-8	1.5	11
64	Genome Sequence for Shiga Toxin-Producing O26:H11, Associated with a Cluster of Hemolytic-Uremic Syndrome Cases in South Africa, 2017. <i>Genome Announcements</i> , 2017 , 5,		9
63	Biological crusts of serpentine and non-serpentine soils from the Barberton Greenstone Belt of South Africa. <i>Ecological Research</i> , 2018 , 33, 629-640	1.9	9
62	Genome Mining and Comparative Pathogenomic Analysis of An Endemic Methicillin-Resistant (MRSA) Clone, ST612-CC8-t1257-SCCmec_IVd(2B), Isolated in South Africa. <i>Pathogens</i> , 2019 , 8,	4.5	8
61	Major new lineages of SARS-CoV-2 emerge and spread in South Africa during lockdown		8
60	A novel adenovirus isolated from the Egyptian fruit bat in South Africa is closely related to recent isolates from China. <i>Scientific Reports</i> , 2018 , 8, 9584	4.9	8
59	Genomic Insights of Multidrug-Resistant From Wastewater Sources and Their Association With Clinical Pathogens in South Africa. <i>Frontiers in Veterinary Science</i> , 2021 , 8, 636715	3.1	7
58	Extended-spectrum beta-lactamase-producing <i>Escherichia coli</i> harbouring <i>mcr-1</i> gene isolated from pigs in South Africa. <i>South African Medical Journal</i> , 2018 , 108, 796-797	1.5	7
57	Antifungal Resistance of <i>Candida auris</i> Isolates from Bloodstream Infections, South Africa. <i>Antimicrobial Agents and Chemotherapy</i> , 2021 , 65, e0051721	5.9	7
56	Genome analysis of methicillin-resistant <i>Staphylococcus aureus</i> isolated from pigs: Detection of the clonal lineage ST398 in Cameroon and South Africa. <i>Zoonoses and Public Health</i> , 2019 , 66, 512-525	2.9	5
55	Human surveillance and phylogeny of highly pathogenic avian influenza A(H5N8) during an outbreak in poultry in South Africa, 2017. <i>Influenza and Other Respiratory Viruses</i> , 2020 , 14, 266-273	5.6	5
54	Genome Sequencing of a Severe Acute Respiratory Syndrome Coronavirus 2 Isolate Obtained from a South African Patient with Coronavirus Disease 2019. <i>Microbiology Resource Announcements</i> , 2020 , 9,	1.3	5
53	Genomic epidemiology of SARS-CoV-2 in Mauritius reveals a new wave of infections dominated by the B.1.1.318, a variant under investigation		5

52	Bacterial diversity and functional profile of microbial populations on surfaces in public hospital environments in South Africa: A high throughput metagenomic analysis. <i>Science of the Total Environment</i> , 2020 , 719, 137360	10.2	4
51	Pathogenomic Analysis of a Novel Extensively Drug-Resistant Isolate Carrying a bla Carbapenemase in South Africa. <i>Pathogens</i> , 2020 , 9,	4.5	4
50	Comparative evaluation of the microbial community in biological processes treating industrial and domestic wastewaters. <i>Journal of Applied Microbiology</i> , 2008 , 104, 353-63	4.7	4
49	Shiga toxin-producing O26:H11 associated with a cluster of haemolytic uraemic syndrome cases in South Africa, 2017. <i>Access Microbiology</i> , 2019 , 1, e000061	1	4
48	Antibody Isotype Switching as a Mechanism to Counter HIV Neutralization Escape. <i>Cell Reports</i> , 2020 , 33, 108430	10.6	4
47	Clade distribution of in South Africa using whole genome sequencing of clinical and environmental isolates. <i>Emerging Microbes and Infections</i> , 2021 , 10, 1300-1308	18.9	4
46	Mobile genetic elements-mediated Enterobacterales-associated carbapenemase antibiotic resistance genes propagation between the environment and humans: A One Health South African study. <i>Science of the Total Environment</i> , 2022 , 806, 150641	10.2	4
45	Draft Genome Sequence of <i>Providencia rettgeri</i> APW139_S1, an NDM-18-Producing Clinical Strain Originating from Hospital Effluent in South Africa. <i>Microbiology Resource Announcements</i> , 2019 , 8,	1.3	3
44	Draft genome sequence of DSM 9356 isolated from the termite. <i>Genomics Data</i> , 2017 , 12, 76-78		3
43	Draft Genome Sequence of a Multidrug-Resistant Strain, Isolated from a Patient with Peritoneal Cancer in South Africa. <i>Genome Announcements</i> , 2017 , 5,		3
42	Using respirometric techniques and fluorescent in situ hybridization to evaluate the heterotrophic active biomass in activated sludge. <i>Biotechnology and Bioengineering</i> , 2007 , 98, 561-8	4.9	3
41	An outbreak of cutaneous abscesses caused by Panton-Valentine leukocidin-producing methicillin-susceptible <i>Staphylococcus aureus</i> among gold mine workers, South Africa, November 2017 to March 2018. <i>BMC Infectious Diseases</i> , 2020 , 20, 621	4	3
40	<i>Enterococcus faecalis</i> ST21 harbouring Tn6009 isolated from a carriage sample in South Africa. <i>South African Medical Journal</i> , 2021 , 111, 98-99	1.5	3
39	Emergence and phenotypic characterization of the global SARS-CoV-2 C.1.2 lineage.. <i>Nature Communications</i> , 2022 , 13, 1976	17.4	3
38	Phylogenetic Analysis of Ebola Virus Disease Transmission in Sierra Leone. <i>Viruses</i> , 2019 , 11,	6.2	2
37	Genome Sequences of <i>Bacillus sporothermodurans</i> Strains Isolated from Ultra-High-Temperature Milk. <i>Microbiology Resource Announcements</i> , 2019 , 8,	1.3	2
36	Genome Sequence of <i>Escherichia coli</i> Clone O25:H4 Sequence Type 131, Isolated from a Sudanese Patient with Urinary Tract Infection. <i>Microbiology Resource Announcements</i> , 2020 , 9,	1.3	2
35	Whole-Genome Sequence of a Isolate from a Pediatric Patient in South Africa. <i>Genome Announcements</i> , 2018 , 6,		2

34	Draft genome sequences of extended-spectrum β -lactamase-producing <i>Enterobacter aerogenes</i> isolated from swine and human. <i>Journal of Global Antimicrobial Resistance</i> , 2018 , 14, 70-71	3.4	2
33	Whole-Genome Sequence of <i>Acinetobacter baumannii</i> Strain NUBRI-A, Isolated from a Hospitalized Patient in Khartoum, Sudan. <i>Microbiology Resource Announcements</i> , 2019 , 8,	1.3	2
32	Whole-Genome Sequence of a Novel Sequence Type 3136 Carbapenem-Resistant <i>Klebsiella pneumoniae</i> Strain Isolated from a Hospitalized Patient in Durban, South Africa. <i>Microbiology Resource Announcements</i> , 2018 , 7,	1.3	2
31	Whole-Genome Shotgun Sequence of Drug-Resistant <i>Staphylococcus aureus</i> Strain SA9, Isolated from a Slaughterhouse Chicken Carcass in South Africa. <i>Microbiology Resource Announcements</i> , 2019 , 8,	1.3	1
30	Comparative Pathogenomics of from Pigs in South Africa: Dominance of the Novel ST657 Clone. <i>Microorganisms</i> , 2020 , 8,	4.9	1
29	First report of a clinical multidrug-resistant <i>Pseudomonas aeruginosa</i> ST532 isolate harbouring a ciprofloxacin-modifying enzyme (CrpP) in South Africa. <i>Journal of Global Antimicrobial Resistance</i> , 2020 , 22, 145-146	3.4	1
28	Complete Genome Sequences of Virus Strains Isolated from Bottle A of the South African Live Attenuated Bluetongue Virus Vaccine. <i>Microbiology Resource Announcements</i> , 2020 , 9,	1.3	1
27	First Whole-Genome Sequence of a Highly Resistant <i>Klebsiella pneumoniae</i> Sequence Type 14 Strain Isolated from Sudan. <i>Microbiology Resource Announcements</i> , 2019 , 8,	1.3	1
26	Strain Specific Anti-HIV Antibody Evolution during Acute Infection and Viral Escape. <i>AIDS Research and Human Retroviruses</i> , 2014 , 30, A210-A210	1.6	1
25	Draft Genome Sequence of Isolated from an HIV-Positive Patient in South Africa. <i>Genome Announcements</i> , 2017 , 5,		1
24	Detection and genome characterization of Middelburg virus strains isolated from CSF and whole blood samples of humans with neurological manifestations in South Africa.. <i>PLoS Neglected Tropical Diseases</i> , 2022 , 16, e0010020	4.8	1
23	Genomic analysis of antibiotic-resistant <i>Enterococcus</i> spp. reveals novel enterococci strains and the spread of plasmid-borne Tet(M), Tet(L) and Erm(B) genes from chicken litter to agricultural soil in South Africa. <i>Journal of Environmental Management</i> , 2022 , 302, 114101	7.9	1
22	Lung microbiome of stable and exacerbated COPD patients in Tshwane, South Africa. <i>Scientific Reports</i> , 2021 , 11, 19758	4.9	1
21	Whole-Genome Sequence of High-Risk Clone Sequence Type 111 of <i>Pseudomonas aeruginosa</i> Strain NUBRI-P, Isolated from a Wounded Sudanese Patient. <i>Microbiology Resource Announcements</i> , 2019 , 8,	1.3	1
20	Comparative Genome Analysis of with Its Closest Phylogenetic Neighbor, , and and Groups. <i>Microorganisms</i> , 2020 , 8,	4.9	1
19	Genome Sequences of Five Novel <i>Neisseria gonorrhoeae</i> Sequence Types Isolated in KwaZulu-Natal, South Africa. <i>Microbiology Resource Announcements</i> , 2021 , 10,	1.3	1
18	Ward-specific clustering of methicillin-resistant <i>Staphylococcus aureus</i> spa-type t037 and t045 in two hospitals in South Africa: 2013 to 2017. <i>PLoS ONE</i> , 2021 , 16, e0253883	3.7	1
17	Genomic Analysis of spp. Isolated From a Wastewater Treatment Plant and Its Associated Waters in Umgungundlovu District, South Africa. <i>Frontiers in Microbiology</i> , 2021 , 12, 648454	5.7	1

16	First confirmed case of infant botulism in Africa, caused by a dual-toxin-producing <i>Clostridium botulinum</i> strain. <i>International Journal of Infectious Diseases</i> , 2021 , 103, 164-166	10.5	1
15	Draft genome sequence of a methicillin-resistant <i>Staphylococcus epidermidis</i> isolate from swine. <i>Journal of Global Antimicrobial Resistance</i> , 2018 , 15, 250-251	3.4	1
14	Draft genome sequence of an extended-spectrum β -lactamase (CTX-M-15)-producing <i>Escherichia coli</i> ST10 isolated from a nasal sample of an abattoir worker in Cameroon. <i>Journal of Global Antimicrobial Resistance</i> , 2018 , 14, 68-69	3.4	1
13	Antimicrobial Resistance Mechanisms, Multilocus Sequence Typing, and NG-STAR Sequence Types of Diverse <i>Neisseria gonorrhoeae</i> Isolates in KwaZulu-Natal, South Africa. <i>Antimicrobial Agents and Chemotherapy</i> , 2021 , 65, e0075921	5.9	1
12	Nasopharyngeal Dysbiosis Precedes the Development of Lower Respiratory Tract Infections in Young Infants, a Longitudinal Infant Cohort Study. <i>Gates Open Research</i> , 2021 , 6, 48	2.4	1
11	The dynamic gut microbiota of zoophilic members of the <i>Anopheles gambiae</i> complex (Diptera: Culicidae).. <i>Scientific Reports</i> , 2022 , 12, 1495	4.9	0
10	High-Resolution Melting Analysis to Detect Antimicrobial Resistance Determinants in South African Clinical Isolates and Specimens.. <i>International Journal of Microbiology</i> , 2022 , 2022, 9094328	3.6	0
9	First genome sequence of <i>Aeromonas hydrophila</i> novel sequence type 658 strain isolated from livestock in South Africa. <i>Journal of Global Antimicrobial Resistance</i> , 2021 , 24, 175-177	3.4	0
8	Genomic characterisation of <i>Staphylococcus aureus</i> ST121 isolated from hospitalised patients in South Africa. <i>South African Medical Journal</i> , 2018 , 108, 1007-1008	1.5	0
7	Process Performance and Microbial Community Structures in Three Anammox-Mediated Systems with Different Mixing Conditions. <i>Journal of Environmental Chemical Engineering</i> , 2021 , 10, 106466	6.8	0
6	Whole Genome Sequencing of Extended-Spectrum- and AmpC- β -Lactamase-Positive Enterobacterales Isolated From Spinach Production in Gauteng Province, South Africa. <i>Frontiers in Microbiology</i> , 2021 , 12, 734649	5.7	0
5	Deep sequencing of the HIV-1 polymerase gene for characterisation of cytotoxic T-lymphocyte epitopes during early and chronic disease stages.. <i>Virology Journal</i> , 2022 , 19, 56	6.1	0
4	Profiling of emerging pathogens, antibiotic resistance genes and mobile genetic elements in different biological wastewater treatment plants. <i>Journal of Environmental Chemical Engineering</i> , 2022 , 10, 107596	6.8	0
3	Draft genome sequence of a clinical <i>Acinetobacter haemolyticus</i> isolate from South Africa. <i>Journal of Global Antimicrobial Resistance</i> , 2020 , 20, 16-17	3.4	0
2	Investigation of Possible Nosocomial-Associated Invasive Group B Streptococcus Disease Using Whole-Genome Sequencing: A Report of 3 Cases. <i>Journal of the Pediatric Infectious Diseases Society</i> , 2021 , 10, 880-882	4.8	0
1	Near-Complete Genome Sequence of Ndumu Virus from Garissa, Kenya, 1997. <i>Microbiology Resource Announcements</i> , 2021 , 10, e0055121	1.3	0