

Arshad Ismail

List of Publications by Year in descending order

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Version: 2024-02-01

90
papers

5,904
citations

448610

19
h-index

134545

62
g-index

102
all docs

102
docs citations

102
times ranked

10602
citing authors

#	ARTICLE	IF	CITATIONS
1	Detection of a SARS-CoV-2 variant of concern in South Africa. <i>Nature</i> , 2021, 592, 438-443.	13.7	1,381
2	Rapid epidemic expansion of the SARS-CoV-2 Omicron variant in southern Africa. <i>Nature</i> , 2022, 603, 679-686.	13.7	1,210
3	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, 399, 437-446.	6.3	818
4	Sixteen novel lineages of SARS-CoV-2 in South Africa. <i>Nature Medicine</i> , 2021, 27, 440-446.	15.2	326
5	A year of genomic surveillance reveals how the SARS-CoV-2 pandemic unfolded in Africa. <i>Science</i> , 2021, 374, 423-431.	6.0	144
6	Outbreak of <i>Listeria monocytogenes</i> 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.	0.8	142
7	Outbreak of Listeriosis in South Africa Associated with Processed Meat. <i>New England Journal of Medicine</i> , 2020, 382, 632-643.	13.9	139
8	Ability To Develop Broadly Neutralizing HIV-1 Antibodies Is Not Restricted by the Germline Ig Gene Repertoire. <i>Journal of Immunology</i> , 2015, 194, 4371-4378.	0.4	85
9	HIV-1 and SARS-CoV-2: Patterns in the evolution of two pandemic pathogens. <i>Cell Host and Microbe</i> , 2021, 29, 1093-1110.	5.1	73
10	Rapid epidemic expansion of the SARS-CoV-2 Omicron variant in southern Africa. <i>Nature</i> , 0, , .	13.7	61
11	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, .	0.8	39
12	Genome Sequencing of Extended-Spectrum β -Lactamase (ESBL)-Producing <i>Klebsiella pneumoniae</i> Isolated from Pigs and Abattoir Workers in Cameroon. <i>Frontiers in Microbiology</i> , 2018, 9, 188.	1.5	38
13	<i>In Vitro</i> Antifungal Resistance of <i>Candida auris</i> Isolates from Bloodstream Infections, South Africa. <i>Antimicrobial Agents and Chemotherapy</i> , 2021, 65, e0051721.	1.4	38
14	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.	1.6	36
15	Human Blastomycosis in South Africa Caused by <i>Blastomyces percursor</i> and <i>Blastomyces emzantsi</i> sp. nov., 1967 to 2014. <i>Journal of Clinical Microbiology</i> , 2020, 58, .	1.8	35
16	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.	3.9	33
17	Emergence and phenotypic characterization of the global SARS-CoV-2 C.1.2 lineage. <i>Nature Communications</i> , 2022, 13, 1976.	5.8	27
18	Genomic Analysis of Carbapenemase-Producing Extensively Drug-Resistant <i>Klebsiella pneumoniae</i> Isolates Reveals the Horizontal Spread of p18-43_01 Plasmid Encoding bla _{NDM-1} in South Africa. <i>Microorganisms</i> , 2020, 8, 137.	1.6	25

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19	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.	2.9	23
20	Identification of SARS-CoV-2 Omicron variant using spike gene target failure and genotyping assays, Gauteng, South Africa, 2021. <i>Journal of Medical Virology</i> , 2022, 94, 3676-3684.	2.5	23
21	Genomic Insights of Multidrug-Resistant <i>Escherichia coli</i> From Wastewater Sources and Their Association With Clinical Pathogens in South Africa. <i>Frontiers in Veterinary Science</i> , 2021, 8, 636715.	0.9	22
22	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.	3.9	21
23	Phenotypic and genotypic characterisation of an unique indigenous hypersaline unicellular cyanobacterium, <i>Euhalothece</i> sp.nov. <i>Microbiological Research</i> , 2018, 211, 47-56.	2.5	17
24	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.	0.2	17
25	Biological crusts of serpentine and non-serpentine soils from the Barberton Greenstone Belt of South Africa. <i>Ecological Research</i> , 2018, 33, 629-640.	0.7	16
26	Antibody Isotype Switching as a Mechanism to Counter HIV Neutralization Escape. <i>Cell Reports</i> , 2020, 33, 108430.	2.9	16
27	Clade distribution of <i>Candida auris</i> in South Africa using whole genome sequencing of clinical and environmental isolates. <i>Emerging Microbes and Infections</i> , 2021, 10, 1300-1308.	3.0	15
28	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.	3.3	14
29	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.	1.6	13
30	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.	0.9	13
31	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.	3.8	12
32	Lung microbiome of stable and exacerbated COPD patients in Tshwane, South Africa. <i>Scientific Reports</i> , 2021, 11, 19758.	1.6	11
33	Genome Sequence for Shiga Toxin-Producing <i>Escherichia coli</i> O26:H11, Associated with a Cluster of Hemolytic-Uremic Syndrome Cases in South Africa, 2017. <i>Genome Announcements</i> , 2017, 5, .	0.8	10
34	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.	3.9	10
35	Pathogenomic Analysis of a Novel Extensively Drug-Resistant <i>Citrobacter freundii</i> Isolate Carrying a blaNDM-1 Carbapenemase in South Africa. <i>Pathogens</i> , 2020, 9, 89.	1.2	10
36	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.	1.4	10

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37	Genome Mining and Comparative Pathogenomic Analysis of An Endemic Methicillin-Resistant Staphylococcus Aureus (MRSA) Clone, ST612-CC8-t1257-SCCmec_IVd(2B), Isolated in South Africa. Pathogens, 2019, 8, 166.	1.2	9
38	Human surveillance and phylogeny of highly pathogenic avian influenza A(H5N8) during an outbreak in poultry in South Africa, 2017. Influenza and Other Respiratory Viruses, 2020, 14, 266-273.	1.5	9
39	Genomic Analysis of Enterococcus spp. Isolated From a Wastewater Treatment Plant and Its Associated Waters in Umgungundlovu District, South Africa. Frontiers in Microbiology, 2021, 12, 648454.	1.5	9
40	Extended-spectrum beta-lactamase-producing Escherichia coli harbouring mcr-1 gene isolated from pigs in South Africa. South African Medical Journal, 2018, 108, 796.	0.2	8
41	Genome Sequencing of a Severe Acute Respiratory Syndrome Coronavirus 2 Isolate Obtained from a South African Patient with Coronavirus Disease 2019. Microbiology Resource Announcements, 2020, 9, .	0.3	8
42	An outbreak of cutaneous abscesses caused by Panton-Valentine leukocidin-producing methicillin-susceptible Staphylococcus aureus among gold mine workers, South Africa, November 2017 to March 2018. BMC Infectious Diseases, 2020, 20, 621.	1.3	8
43	Enterococcus faecalis ST21 harbouring Tn6009 isolated from a carriage sample in South Africa. South African Medical Journal, 2021, 111, 98.	0.2	7
44	Draft genome sequence of Bacillus oleronius DSM 9356 isolated from the termite Reticulitermes santonensis. Genomics Data, 2017, 12, 76-78.	1.3	6
45	Comparative Pathogenomics of Aeromonas veronii from Pigs in South Africa: Dominance of the Novel ST657 Clone. Microorganisms, 2020, 8, 2008.	1.6	6
46	First report of a clinical multidrug-resistant Pseudomonas aeruginosa ST532 isolate harbouring a ciprofloxacin-modifying enzyme (CrpP) in South Africa. Journal of Global Antimicrobial Resistance, 2020, 22, 145-146.	0.9	6
47	First confirmed case of infant botulism in Africa, caused by a dual-toxin-producing Clostridium botulinum strain. International Journal of Infectious Diseases, 2021, 103, 164-166.	1.5	6
48	Whole Genome Sequencing of Extended-Spectrum- and AmpC- β -Lactamase-Positive Enterobacterales Isolated From Spinach Production in Gauteng Province, South Africa. Frontiers in Microbiology, 2021, 12, 734649.	1.5	6
49	Shiga toxin-producing Escherichia coli O26:H11 associated with a cluster of haemolytic uraemic syndrome cases in South Africa, 2017. Access Microbiology, 2019, 1, e000061.	0.2	6
50	Comparative evaluation of the microbial community in biological processes treating industrial and domestic wastewaters. Journal of Applied Microbiology, 2007, 104, 071008041820012-???.	1.4	5
51	Draft genome sequence of an extended-spectrum β -lactamase (CTX-M-15)-producing Escherichia coli ST10 isolated from a nasal sample of an abattoir worker in Cameroon. Journal of Global Antimicrobial Resistance, 2018, 14, 68-69.	0.9	5
52	Draft Genome Sequence of a Multidrug-Resistant Serratia marcescens Strain, Isolated from a Patient with Peritoneal Cancer in South Africa. Genome Announcements, 2017, 5, .	0.8	4
53	Draft Genome Sequence of Providencia rettgeri APW139_S1, an NDM-18-Producing Clinical Strain Originating from Hospital Effluent in South Africa. Microbiology Resource Announcements, 2019, 8, .	0.3	4
54	Genome Sequences of Bacillus sporothermodurans Strains Isolated from Ultra-High-Temperature Milk. Microbiology Resource Announcements, 2019, 8, .	0.3	4

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55	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.	1.3	4
56	Using respirometric techniques and fluorescent in situ hybridization to evaluate the heterotrophic active biomass in activated sludge. <i>Biotechnology and Bioengineering</i> , 2007, 98, 561-568.	1.7	3
57	Draft Genome Sequence of <i>Mycobacterium peregrinum</i> Isolated from an HIV-Positive Patient in South Africa. <i>Genome Announcements</i> , 2017, 5, .	0.8	3
58	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, .	0.3	3
59	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, .	0.3	3
60	Phylogenetic Analysis of Ebola Virus Disease Transmission in Sierra Leone. <i>Viruses</i> , 2019, 11, 71.	1.5	3
61	Genome Sequences of Five Novel <i>Neisseria gonorrhoeae</i> Sequence Types Isolated in KwaZulu-Natal, South Africa. <i>Microbiology Resource Announcements</i> , 2021, 10, .	0.3	3
62	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.	1.1	3
63	The dynamic gut microbiota of zoophilic members of the <i>Anopheles gambiae</i> complex (Diptera: Tj ETQq1 1 0.784314 rgBT / Qverlock 1.6 3	1.6	3
64	Whole-Genome Sequence of a <i>Mycobacterium goodii</i> Isolate from a Pediatric Patient in South Africa. <i>Genome Announcements</i> , 2018, 6, .	0.8	2
65	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.	0.9	2
66	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, .	0.3	2
67	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.	0.9	2
68	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, .	0.3	2
69	Comparative Genome Analysis of <i>Bacillus sporothermodurans</i> with Its Closest Phylogenetic Neighbor, <i>Bacillus oleronius</i> , and <i>Bacillus cereus</i> and <i>Bacillus subtilis</i> Groups. <i>Microorganisms</i> , 2020, 8, 1185.	1.6	2
70	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, .	0.3	2
71	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, .	0.3	2
72	Genome Sequence of a Novel <i>Enterococcus faecalis</i> Sequence Type 922 Strain Isolated from a Door Handle in the Intensive Care Unit of a District Hospital in Durban, South Africa. <i>Microbiology Resource Announcements</i> , 2019, 8, .	0.3	2

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73	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.	1.4	2
74	Nasopharyngeal Dysbiosis Precedes the Development of Lower Respiratory Tract Infections in Young Infants, a Longitudinal Infant Cohort Study. <i>Gates Open Research</i> , 0, 6, 48.	2.0	2
75	Phylogenetic Characterisation of the Full Genome of a Bagaza Virus Isolate from Bird Fatalities in South Africa. <i>Viruses</i> , 2022, 14, 1476.	1.5	2
76	Strain Specific Anti-HIV Antibody Evolution during Acute Infection and Viral Escape. <i>AIDS Research and Human Retroviruses</i> , 2014, 30, A210-A210.	0.5	1
77	Genomic characterisation of <i>Staphylococcus aureus</i> ST121 isolated from hospitalised patients in South Africa. <i>South African Medical Journal</i> , 2018, 108, 1007.	0.2	1
78	Whole-Genome Sequences of Two Multidrug-Resistant <i>Acinetobacter baumannii</i> Strains Isolated from Patients with Urinary Tract Infection in Ghana. <i>Microbiology Resource Announcements</i> , 2019, 8, .	0.3	1
79	Whole-Genome Sequencing of a <i>Mycobacterium tuberculosis</i> Strain Belonging to Lineage 1 (Indo-Oceanic) and the East African Indian Spoligotype, Isolated in Jazan, Saudi Arabia. <i>Microbiology Resource Announcements</i> , 2020, 9, .	0.3	1
80	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.	0.9	1
81	Process Performance and Microbial Community Structures in Three Anammox-Mediated Systems with Different Mixing Conditions. <i>Journal of Environmental Chemical Engineering</i> , 2021, , 106466.	3.3	1
82	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, .	0.3	1
83	High-Resolution Melting Analysis to Detect Antimicrobial Resistance Determinants in South African <i>Neisseria gonorrhoeae</i> Clinical Isolates and Specimens. <i>International Journal of Microbiology</i> , 2022, 1-9.	0.9	1
84	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.	0.9	0
85	Investigation of Possible Nosocomial-Associated Invasive Group B <i>Streptococcus</i> Disease Using Whole-Genome Sequencing: A Report of 3 Cases. <i>Journal of the Pediatric Infectious Diseases Society</i> , 2021, 10, 880-882.	0.6	0
86	Near-Complete Genome Sequence of Ndumu Virus from Garissa, Kenya, 1997. <i>Microbiology Resource Announcements</i> , 2021, 10, e0055121.	0.3	0
87	Extended-spectrum beta-lactamase-producing <i>Klebsiella pneumoniae</i> isolated from an abattoir worker in Cameroon. <i>South African Medical Journal</i> , 2019, 109, 820.	0.2	0
88	Complete Genome Sequence of a <i>Staphylococcus aureus</i> Isolate from a Nasopharyngeal Swab from a Mine Worker in South Africa. <i>Microbiology Resource Announcements</i> , 2019, 8, .	0.3	0
89	Methicillin-resistant <i>Staphylococcus haemolyticus</i> ST25 isolated from carriage samples in uMgungundlovu district, South Africa. <i>South African Medical Journal</i> , 2020, 110, 959.	0.2	0
90	Extraintestinal pathogenic <i>Escherichia coli</i> (ExPEC) ST221 isolated in the microbiome of swine in South Africa. <i>South African Medical Journal</i> , 2020, 111, 5.	0.2	0