

Arshad Ismail

List of Publications by Year in descending order

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Version: 2024-02-01

90
papers

5,904
citations

394421

19
h-index

118850

62
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102
all docs

102
docs citations

102
times ranked

9973
citing authors

#	ARTICLE	IF	CITATIONS
1	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.	8.0	21
2	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.	7.8	12
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.	13.7	818
4	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.	3.0	4
5	The dynamic gut microbiota of zoophilic members of the <i>Anopheles gambiae</i> complex (Diptera: Tj ETQq1 1 0.784314 rgBT /Overlock 10	3.3	3
6	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, 2022, 1-9.	2.3	1
7	Rapid epidemic expansion of the SARS-CoV-2 Omicron variant in southern Africa. <i>Nature</i> , 2022, 603, 679-686.	27.8	1,210
8	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.	3.4	2
9	Emergence and phenotypic characterization of the global SARS-CoV-2 C.1.2 lineage. <i>Nature Communications</i> , 2022, 13, 1976.	12.8	27
10	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.	6.7	14
11	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.	5.0	23
12	Phylogenetic Characterisation of the Full Genome of a Bagaza Virus Isolate from Bird Fatalities in South Africa. <i>Viruses</i> , 2022, 14, 1476.	3.3	2
13	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.	3.3	6
14	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.	6.5	15
15	<i>Enterococcus faecalis</i> ST21 harbouring Tn6009 isolated from a carriage sample in South Africa. <i>South African Medical Journal</i> , 2021, 111, 98.	0.6	7
16	Sixteen novel lineages of SARS-CoV-2 in South Africa. <i>Nature Medicine</i> , 2021, 27, 440-446.	30.7	326
17	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.	2.2	22
18	Detection of a SARS-CoV-2 variant of concern in South Africa. <i>Nature</i> , 2021, 592, 438-443.	27.8	1,381

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19	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.	2.2	1
20	Genome Sequences of Five Novel <i>Neisseria gonorrhoeae</i> Sequence Types Isolated in KwaZulu-Natal, South Africa. <i>Microbiology Resource Announcements</i> , 2021, 10, .	0.6	3
21	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.	1.3	0
22	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.	2.5	3
23	Genomic Analysis of <i>Enterococcus</i> spp. Isolated From a Wastewater Treatment Plant and Its Associated Waters in Umgungundlovu District, South Africa. <i>Frontiers in Microbiology</i> , 2021, 12, 648454.	3.5	9
24	HIV-1 and SARS-CoV-2: Patterns in the evolution of two pandemic pathogens. <i>Cell Host and Microbe</i> , 2021, 29, 1093-1110.	11.0	73
25	<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.	3.2	38
26	Near-Complete Genome Sequence of Ndumu Virus from Garissa, Kenya, 1997. <i>Microbiology Resource Announcements</i> , 2021, 10, e0055121.	0.6	0
27	Process Performance and Microbial Community Structures in Three Anammox-Mediated Systems with Different Mixing Conditions. <i>Journal of Environmental Chemical Engineering</i> , 2021, , 106466.	6.7	1
28	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.	3.2	10
29	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.	3.5	6
30	A year of genomic surveillance reveals how the SARS-CoV-2 pandemic unfolded in Africa. <i>Science</i> , 2021, 374, 423-431.	12.6	144
31	Lung microbiome of stable and exacerbated COPD patients in Tshwane, South Africa. <i>Scientific Reports</i> , 2021, 11, 19758.	3.3	11
32	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.	2.2	0
33	Human Blastomycosis in South Africa Caused by <i>Blastomyces percursus</i> and <i>Blastomyces emzantsi</i> sp. nov., 1967 to 2014. <i>Journal of Clinical Microbiology</i> , 2020, 58, .	3.9	35
34	Antibody Isotype Switching as a Mechanism to Counter HIV Neutralization Escape. <i>Cell Reports</i> , 2020, 33, 108430.	6.4	16
35	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.	3.6	2
36	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, .	0.6	8

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37	Whole-Genome Sequencing of a Mycobacterium tuberculosis Strain Belonging to Lineage 1 (Indo-Oceanic) and the East African Indian Spoligotype, Isolated in Jazan, Saudi Arabia. Microbiology Resource Announcements, 2020, 9, .	0.6	1
38	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.	2.9	8
39	Comparative Pathogenomics of Aeromonas veronii from Pigs in South Africa: Dominance of the Novel ST657 Clone. Microorganisms, 2020, 8, 2008.	3.6	6
40	Genome Sequence of Escherichia coli Clone O25:H4 Sequence Type 131, Isolated from a Sudanese Patient with Urinary Tract Infection. Microbiology Resource Announcements, 2020, 9, .	0.6	2
41	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.	2.2	6
42	Complete Genome Sequences of Virus Strains Isolated from Bottle A of the South African Live Attenuated Bluetongue Virus Vaccine. Microbiology Resource Announcements, 2020, 9, .	0.6	2
43	Bacterial diversity and functional profile of microbial populations on surfaces in public hospital environments in South Africa: A high throughput metagenomic analysis. Science of the Total Environment, 2020, 719, 137360.	8.0	10
44	Outbreak of Listeriosis in South Africa Associated with Processed Meat. New England Journal of Medicine, 2020, 382, 632-643.	27.0	139
45	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.	3.4	9
46	Genomic Analysis of Carbapenemase-Producing Extensively Drug-Resistant Klebsiella pneumoniae Isolates Reveals the Horizontal Spread of p18-43_01 Plasmid Encoding blaNDM-1 in South Africa. Microorganisms, 2020, 8, 137.	3.6	25
47	Pathogenomic Analysis of a Novel Extensively Drug-Resistant Citrobacter freundii Isolate Carrying a blaNDM-1 Carbapenemase in South Africa. Pathogens, 2020, 9, 89.	2.8	10
48	Methicillin-resistant Staphylococcus haemolyticus ST25 isolated from carriage samples in uMgungundlovu district, South Africa. South African Medical Journal, 2020, 110, 959.	0.6	0
49	Extraintestinal pathogenic Escherichia coli (ExPEC) ST221 isolated in the microbiome of swine in South Africa. South African Medical Journal, 2020, 111, 5.	0.6	0
50	Whole-Genome Sequences of Two Multidrug-Resistant Acinetobacter baumannii Strains Isolated from Patients with Urinary Tract Infection in Ghana. Microbiology Resource Announcements, 2019, 8, .	0.6	1
51	Whole-Genome Sequence of Acinetobacter baumannii Strain NUBRI-A, Isolated from a Hospitalized Patient in Khartoum, Sudan. Microbiology Resource Announcements, 2019, 8, .	0.6	3
52	First Whole-Genome Sequence of a Highly Resistant Klebsiella pneumoniae Sequence Type 14 Strain Isolated from Sudan. Microbiology Resource Announcements, 2019, 8, .	0.6	3
53	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.	2.8	9
54	Phylogenetic Analysis of Ebola Virus Disease Transmission in Sierra Leone. Viruses, 2019, 11, 71.	3.3	3

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55	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.	2.2	13
56	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, .	0.6	4
57	Genome Sequences of <i>Bacillus sporothermodurans</i> Strains Isolated from Ultra-High-Temperature Milk. <i>Microbiology Resource Announcements</i> , 2019, 8, .	0.6	4
58	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, .	0.6	2
59	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.	1.8	142
60	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.	3.3	36
61	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.	8.0	33
62	Shiga toxin-producing <i>Escherichia coli</i> O26:H11 associated with a cluster of haemolytic uraemic syndrome cases in South Africa, 2017. <i>Access Microbiology</i> , 2019, 1, e000061.	0.5	6
63	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, .	0.6	2
64	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.	0.6	0
65	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, .	0.6	0
66	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, .	0.6	1
67	Phenotypic and genotypic characterisation of an unique indigenous hypersaline unicellular cyanobacterium, <i>Euhalothece</i> sp.nov. <i>Microbiological Research</i> , 2018, 211, 47-56.	5.3	17
68	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
69	Biological crusts of serpentine and non-serpentine soils from the Barberton Greenstone Belt of South Africa. <i>Ecological Research</i> , 2018, 33, 629-640.	1.5	16
70	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.	0.6	17
71	Genomic characterisation of <i>Staphylococcus aureus</i> ST121 isolated from hospitalised patients in South Africa. <i>South African Medical Journal</i> , 2018, 108, 1007.	0.6	1
72	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.	2.2	2

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73	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.	0.6	8
74	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.	6.4	23
75	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, .	0.6	2
76	Draft genome sequence of an extended-spectrum \hat{I}^2 -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.	2.2	5
77	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.	3.3	13
78	Draft genome sequences of extended-spectrum \hat{I}^2 -lactamase-producing <i>Enterobacter aerogenes</i> isolated from swine and human. <i>Journal of Global Antimicrobial Resistance</i> , 2018, 14, 70-71.	2.2	2
79	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
80	Genome Sequencing of Extended-Spectrum \hat{I}^2 -Lactamase (ESBL)-Producing <i>Klebsiella pneumoniae</i> Isolated from Pigs and Abattoir Workers in Cameroon. <i>Frontiers in Microbiology</i> , 2018, 9, 188.	3.5	38
81	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
82	Draft genome sequence of <i>Bacillus oleronius</i> DSM 9356 isolated from the termite <i>Reticulitermesantonensis</i> . <i>Genomics Data</i> , 2017, 12, 76-78.	1.3	6
83	Draft Genome Sequence of a Multidrug-Resistant <i>Serratia marcescens</i> Strain, Isolated from a Patient with Peritoneal Cancer in South Africa. <i>Genome Announcements</i> , 2017, 5, .	0.8	4
84	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
85	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.	0.8	85
86	Strain Specific Anti-HIV Antibody Evolution during Acute Infection and Viral Escape. <i>AIDS Research and Human Retroviruses</i> , 2014, 30, A210-A210.	1.1	1
87	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.	3.3	3
88	Comparative evaluation of the microbial community in biological processes treating industrial and domestic wastewaters. <i>Journal of Applied Microbiology</i> , 2007, 104, 071008041820012-???	3.1	5
89	Rapid epidemic expansion of the SARS-CoV-2 Omicron variant in southern Africa. <i>Nature</i> , 0, , .	27.8	61
90	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.	1.1	2