

# 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  
g-index

102  
all docs

102  
docs citations

102  
times ranked

9973  
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.  | 27.8 | 1,381     |
| 2  | Rapid epidemic expansion of the SARS-CoV-2 Omicron variant in southern Africa. <i>Nature</i> , 2022, 603, 679-686.   | 27.8 | 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.  | 13.7 | 818       |
| 4  | Sixteen novel lineages of SARS-CoV-2 in South Africa. <i>Nature Medicine</i> , 2021, 27, 440-446.  | 30.7 | 326       |
| 5  | 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       |
| 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.                | 1.8  | 142       |
| 7  | Outbreak of Listeriosis in South Africa Associated with Processed Meat. <i>New England Journal of Medicine</i> , 2020, 382, 632-643.   | 27.0 | 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.  | 0.8  | 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.   | 11.0 | 73        |
| 10 | Rapid epidemic expansion of the SARS-CoV-2 Omicron variant in southern Africa. <i>Nature</i> , 0, , .  | 27.8 | 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 $\beta$ -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        |
| 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.   | 3.2  | 38        |
| 14 | Whole Genome Sequencing of Extended Spectrum $\beta$ -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        |
| 15 | 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        |
| 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.                    | 8.0  | 33        |
| 17 | Emergence and phenotypic characterization of the global SARS-CoV-2 C.1.2 lineage. <i>Nature Communications</i> , 2022, 13, 1976.   | 12.8 | 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 <sub>NDM-1</sub> in South Africa. <i>Microorganisms</i> , 2020, 8, 137. | 3.6  | 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.  | 6.4 | 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.  | 5.0 | 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.  | 2.2 | 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.   | 8.0 | 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.  | 5.3 | 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.                                | 0.6 | 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.  | 1.5 | 16        |
| 26 | Antibody Isotype Switching as a Mechanism to Counter HIV Neutralization Escape. <i>Cell Reports</i> , 2020, 33, 108430.   | 6.4 | 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.   | 6.5 | 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.  | 6.7 | 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.  | 3.3 | 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.  | 2.2 | 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. | 7.8 | 12        |
| 32 | Lung microbiome of stable and exacerbated COPD patients in Tshwane, South Africa. <i>Scientific Reports</i> , 2021, 11, 19758.  | 3.3 | 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.   | 8.0 | 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.  | 2.8 | 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.   | 3.2 | 10        |

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|----|---|-----|-----------|
| 37 | Genome Mining and Comparative Pathogenomic Analysis of An Endemic Methicillin-Resistant <i>Staphylococcus Aureus</i> (MRSA) Clone, ST612-CC8-t1257-SCCmec_IVd(2B), Isolated in South Africa. <i>Pathogens</i> , 2019, 8, 166.                               | 2.8 | 9         |
| 38 | 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.  | 3.4 | 9         |
| 39 | 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         |
| 40 | Extended-spectrum beta-lactamase-producing <i>Escherichia coli</i> harbouring mcr-1 gene isolated from pigs in South Africa. <i>South African Medical Journal</i> , 2018, 108, 796.   | 0.6 | 8         |
| 41 | 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         |
| 42 | 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. | 2.9 | 8         |
| 43 | <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         |
| 44 | Draft genome sequence of <i>Bacillus oleronius</i> DSM 9356 isolated from the termite <i>Reticulitermes santonensis</i> . <i>Genomics Data</i> , 2017, 12, 76-78.   | 1.3 | 6         |
| 45 | Comparative Pathogenomics of <i>Aeromonas veronii</i> from Pigs in South Africa: Dominance of the Novel ST657 Clone. <i>Microorganisms</i> , 2020, 8, 2008.   | 3.6 | 6         |
| 46 | 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.                       | 2.2 | 6         |
| 47 | 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         |
| 48 | Whole Genome Sequencing of Extended-Spectrum- and AmpC- $\beta$ -Lactamase-Positive Enterobacterales Isolated From Spinach Production in Gauteng Province, South Africa. <i>Frontiers in Microbiology</i> , 2021, 12, 734649.                               | 3.5 | 6         |
| 49 | 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         |
| 50 | 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         |
| 51 | Draft genome sequence of an extended-spectrum $\beta$ -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         |
| 52 | 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         |
| 53 | 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         |
| 54 | Genome Sequences of <i>Bacillus sporothermodurans</i> Strains Isolated from Ultra-High-Temperature Milk. <i>Microbiology Resource Announcements</i> , 2019, 8, .  | 0.6 | 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. PLoS Neglected Tropical Diseases, 2022, 16, e0010020.    | 3.0 | 4         |
| 56 | Using respirometric techniques and fluorescent in situ hybridization to evaluate the heterotrophic active biomass in activated sludge. Biotechnology and Bioengineering, 2007, 98, 561-568.                                      | 3.3 | 3         |
| 57 | Draft Genome Sequence of Mycobacterium peregrinum Isolated from an HIV-Positive Patient in South Africa. Genome Announcements, 2017, 5, .  | 0.8 | 3         |
| 58 | 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         |
| 59 | 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         |
| 60 | Phylogenetic Analysis of Ebola Virus Disease Transmission in Sierra Leone. Viruses, 2019, 11, 71.  | 3.3 | 3         |
| 61 | Genome Sequences of Five Novel Neisseria gonorrhoeae Sequence Types Isolated in KwaZulu-Natal, South Africa. Microbiology Resource Announcements, 2021, 10, .  | 0.6 | 3         |
| 62 | Ward-specific clustering of methicillin-resistant Staphylococcus aureus spa-type t037 and t045 in two hospitals in South Africa: 2013 to 2017. PLoS ONE, 2021, 16, e0253883.   | 2.5 | 3         |
| 63 | The dynamic gut microbiota of zoophilic members of the Anopheles gambiae complex (Diptera: Tj ETQq1 1 0.784314 rgBT /Qverlock  | 3.3 | 3         |
| 64 | Whole-Genome Sequence of a Mycobacterium goodii Isolate from a Pediatric Patient in South Africa. Genome Announcements, 2018, 6, .   | 0.8 | 2         |
| 65 | Draft genome sequence of a methicillin-resistant Staphylococcus epidermidis isolate from swine. Journal of Global Antimicrobial Resistance, 2018, 15, 250-251.   | 2.2 | 2         |
| 66 | Whole-Genome Sequence of a Novel Sequence Type 3136 Carbapenem-Resistant Klebsiella pneumoniae Strain Isolated from a Hospitalized Patient in Durban, South Africa. Microbiology Resource Announcements, 2018, 7, .              | 0.6 | 2         |
| 67 | Draft genome sequences of extended-spectrum $\beta$ -lactamase-producing Enterobacter aerogenes isolated from swine and human. Journal of Global Antimicrobial Resistance, 2018, 14, 70-71.                                      | 2.2 | 2         |
| 68 | Whole-Genome Shotgun Sequence of Drug-Resistant Staphylococcus aureus Strain SA9, Isolated from a Slaughterhouse Chicken Carcass in South Africa. Microbiology Resource Announcements, 2019, 8, .                                | 0.6 | 2         |
| 69 | Comparative Genome Analysis of Bacillus sporothermodurans with Its Closest Phylogenetic Neighbor, Bacillus oleronius, and Bacillus cereus and Bacillus subtilis Groups. Microorganisms, 2020, 8, 1185.                           | 3.6 | 2         |
| 70 | 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         |
| 71 | 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         |
| 72 | Genome Sequence of a Novel Enterococcus faecalis Sequence Type 922 Strain Isolated from a Door Handle in the Intensive Care Unit of a District Hospital in Durban, South Africa. Microbiology Resource Announcements, 2019, 8, . | 0.6 | 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.   | 3.4 | 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.  | 1.1 | 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.   | 3.3 | 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.   | 1.1 | 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.   | 0.6 | 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, .                                | 0.6 | 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, . | 0.6 | 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.   | 2.2 | 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.   | 6.7 | 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, .                                 | 0.6 | 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, 2022, 1-9.               | 2.3 | 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.   | 2.2 | 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.            | 1.3 | 0         |
| 86 | Near-Complete Genome Sequence of Ndumu Virus from Garissa, Kenya, 1997. <i>Microbiology Resource Announcements</i> , 2021, 10, e0055121.  | 0.6 | 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.  | 0.6 | 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, .   | 0.6 | 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.  | 0.6 | 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.  | 0.6 | 0         |