

Mushal Allam

List of Publications by Year in descending order

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85
papers

3,635
citations

516215

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93
docs citations

93
times ranked

8306
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.	3.9	21
2	The dynamic gut microbiota of zoophilic members of the <i>Anopheles gambiae</i> complex (Diptera: Tj ETQq0 0 0 rgBT /Overlock ₃ 10 Tf 50 7	1.6	3
3	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.	0.9	1
4	Characteristics in the whole-genome sequence of <i>Klebsiella pneumoniae</i> ST147 from Turkey. <i>Acta Microbiologica Et Immunologica Hungarica</i> , 2022, , .	0.4	1
5	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
6	Whole-Genome Sequencing of a Colistin-Resistant <i>Acinetobacter baumannii</i> Strain Isolated at a Tertiary Health Facility in Pretoria, South Africa. <i>Antibiotics</i> , 2022, 11, 594.	1.5	8
7	Genome Analysis of ESBL-Producing <i>Escherichia coli</i> Isolated from Pigs. <i>Pathogens</i> , 2022, 11, 776.	1.2	7
8	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
9	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.	1.5	6
10	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
11	Distribution and Genetic Diversity of <i>Aedes aegypti</i> Subspecies across the Sahelian Belt in Sudan. <i>Pathogens</i> , 2021, 10, 78.	1.2	8
12	<i>Enterococcus faecalis</i> ST21 harbouring Tn6009 isolated from a carriage sample in South Africa. <i>South African Medical Journal</i> , 2021, 111, 98.	0.2	7
13	Sixteen novel lineages of SARS-CoV-2 in South Africa. <i>Nature Medicine</i> , 2021, 27, 440-446.	15.2	326
14	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
15	Detection of a SARS-CoV-2 variant of concern in South Africa. <i>Nature</i> , 2021, 592, 438-443.	13.7	1,381
16	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
17	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
18	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

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19	Genomic Analysis of Enterococcus spp. Isolated From a Wastewater Treatment Plant and Its Associated Waters in Umgungundlovu District, South Africa. <i>Frontiers in Microbiology</i> , 2021, 12, 648454.	1.5	9
20	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
21	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
22	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
23	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.	1.5	6
24	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
25	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
26	Human Blastomycosis in South Africa Caused by <i>Blastomyces percursorus</i> and <i>Blastomyces emzantsi</i> sp. nov., 1967 to 2014. <i>Journal of Clinical Microbiology</i> , 2020, 58, .	1.8	35
27	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
28	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, .	0.3	8
29	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
30	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.	1.3	8
31	Convalescent plasma as a treatment modality for coronavirus disease 2019 in Sudan. <i>Transfusion and Apheresis Science</i> , 2020, 59, 102918.	0.5	7
32	Comparative Pathogenomics of <i>Aeromonas veronii</i> from Pigs in South Africa: Dominance of the Novel ST657 Clone. <i>Microorganisms</i> , 2020, 8, 2008.	1.6	6
33	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
34	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.	0.9	6
35	Outbreak of Listeriosis in South Africa Associated with Processed Meat. <i>New England Journal of Medicine</i> , 2020, 382, 632-643.	13.9	139
36	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.	1.5	9

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37	Genomic Analysis of Carbapenemase-Producing Extensively Drug-Resistant <i>Klebsiella pneumoniae</i> Isolates Reveals the Horizontal Spread of p18-43_01 Plasmid Encoding blaNDM-1 in South Africa. <i>Microorganisms</i> , 2020, 8, 137.	1.6	25
38	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
39	Inflammatory markers as predictors of mortality in COVID-19 infection. <i>African Journal of Laboratory Medicine</i> , 2020, 9, 1298.	0.2	12
40	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
41	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
42	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
43	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
44	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.	1.2	9
45	Phylogenetic Analysis of Ebola Virus Disease Transmission in Sierra Leone. <i>Viruses</i> , 2019, 11, 71.	1.5	3
46	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
47	Genomic characterization of multidrug-resistant ESBL-producing <i>Klebsiella pneumoniae</i> isolated from a Ghanaian teaching hospital. <i>International Journal of Infectious Diseases</i> , 2019, 85, 117-123.	1.5	28
48	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, .	0.3	4
49	Genome Sequences of <i>Bacillus sporothermodurans</i> Strains Isolated from Ultra-High-Temperature Milk. <i>Microbiology Resource Announcements</i> , 2019, 8, .	0.3	4
50	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
51	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
52	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
53	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
54	Evidence for both Intermittent and Persistent Compartmentalization of HIV-1 in the Female Genital Tract. <i>Journal of Virology</i> , 2019, 93, .	1.5	9

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55	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.	0.2	6
56	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
57	Genomic differences among carriage and invasive nontypeable pneumococci circulating in South Africa. <i>Microbial Genomics</i> , 2019, 5, .	1.0	0
58	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
59	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
60	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
61	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
62	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
63	Invasive Disease Caused Simultaneously by Dual Serotypes of <i>Streptococcus pneumoniae</i> . <i>Journal of Clinical Microbiology</i> , 2018, 56, .	1.8	13
64	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
65	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
66	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
67	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.	0.2	8
68	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
69	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.	0.9	5
70	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
71	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
72	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

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73	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
74	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
75	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
76	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
77	Molecular characterization of invasive capsule null <i>Neisseria meningitidis</i> in South Africa. <i>BMC Microbiology</i> , 2017, 17, 40.	1.3	17
78	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
79	Molecular Characterization of <i>Corynebacterium diphtheriae</i> Outbreak Isolates, South Africa, March–June 2015. <i>Emerging Infectious Diseases</i> , 2017, 23, 1308-1315.	2.0	36
80	Two cases of serotypeable and non-serotypeable variants of <i>Streptococcus pneumoniae</i> detected simultaneously during invasive disease. <i>BMC Microbiology</i> , 2016, 16, 126.	1.3	2
81	Genomic analysis of nontypeable pneumococci causing invasive pneumococcal disease in South Africa, 2003–2013. <i>BMC Genomics</i> , 2016, 17, 470.	1.2	15
82	Identification and characterization of microRNAs expressed in the African malaria vector <i>Anopheles funestus</i> life stages using high throughput sequencing. <i>Malaria Journal</i> , 2016, 15, 542.	0.8	11
83	Phylogenetic Analysis of Invasive Serotype 1 <i>Pneumococcus</i> in South Africa, 1989 to 2013. <i>Journal of Clinical Microbiology</i> , 2016, 54, 1326-1334.	1.8	16
84	Hyper-reactive Malarial Splenomegaly (HMS) in malaria endemic area in Eastern Sudan. <i>Acta Tropica</i> , 2008, 105, 196-199.	0.9	12
85	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