Gerald Mboowa

List of Publications by Year
in descending order

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45

papers

756

citations

687363

13

h-index

580821

25

g-index

55

all docs

55

docs citations

55

times ranked

1362

citing authors

#	Article	IF	Citations
1	Bioinformatics mentorship in a resource limited setting. Briefings in Bioinformatics, 2022, 23, .	6.5	8
2	Genetic Diversity, Distribution, and Genomic Characterization of Antibiotic Resistance and Virulence of Clinical Pseudomonas aeruginosa Strains in Kenya. Frontiers in Microbiology, 2022, 13, 835403.	3.5	12
3	First report of whole-genome analysis of an extensively drug-resistant Mycobacterium tuberculosis clinical isolate with bedaquiline, linezolid and clofazimine resistance from Uganda. Antimicrobial Resistance and Infection Control, 2022, 11, 68.	4.1	8
4	Unmapped exome reads implicate a role for Anelloviridae in childhood HIV-1 long-term non-progression. Npj Genomic Medicine, 2021, 6, 24.	3.8	3
5	Genomics and bioinformatics capacity in Africa: no continent is left behind. Genome, 2021, 64, 503-513.	2.0	8
6	Gastrointestinal Tract Colonization Rate of Extended-Spectrum Beta-Lactamase-Producing Gram-Negative Bacteria and Associated Factors Among Orthopaedic Patients in a Tertiary Hospital in Tanzania: Implications for Infection Prevention. Infection and Drug Resistance, 2021, Volume 14, 1733-1745.	2.7	6
7	Increasing Antimicrobial Resistance in Surgical Wards at Mulago National Referral Hospital, Uganda, from 2014 to 2018â€”Cause for Concern?. Tropical Medicine and Infectious Disease, 2021, 6, 82.	2.3	4
8	Efficacy of Face Masks Used in Uganda: A Laboratory-Based Inquiry during the COVID-19 Pandemic. American Journal of Tropical Medicine and Hygiene, 2021, 104, 1703-1708.	1.4	5
9	Knowledge and attitude of secondary school students in Nakaseke, Uganda towards HIV transmission and treatment. AAS Open Research, 2021, 4, 23.	1.5	0
10	rMAP: the Rapid Microbial Analysis Pipeline for ESKAPE bacterial group whole-genome sequence data. Microbial Genomics, 2021, 7, .	2.0	6
11	Knowledge and attitude of secondary school students in Nakaseke, Uganda towards HIV transmission and treatment. AAS Open Research, 2021, 4, 23.	1.5	0
12	Whole-genome sequencing of SARS-CoV-2 in Uganda: implementation of the low-cost ARTIC protocol in resource-limited settings. F1000Research, 2021, 10, 598.	1.6	7
13	Transmission Dynamics of Antimicrobial Resistance at a National Referral Hospital in Uganda. American Journal of Tropical Medicine and Hygiene, 2021, 105, 498-506.	1.4	6
14	High prevalence of phenotypic pyrazinamide resistance and its association with pncA gene mutations in Mycobacterium tuberculosis isolates from Uganda. PLoS ONE, 2020, 15, e0232543.	2.5	12
15	Variations in Trim5Î± and Cyclophilin A genes among HIV-1 elite controllers and non controllers in Uganda: a laboratory-based cross-sectional study. Retrovirology, 2020, 17, 19.	2.0	0
16	Current and emerging diagnostic tests available for the novel COVID-19 global pandemic. AAS Open Research, 2020, 3, 8.	1.5	11
17	Face-Masking, an Acceptable Protective Measure against COVID-19 in Ugandan High-Risk Groups. American Journal of Tropical Medicine and Hygiene, 2020, , .	1.4	14
18	blaVIM- and blaOXA-mediated carbapenem resistance among Acinetobacter baumannii and Pseudomonas aeruginosa isolates from the Mulago hospital intensive care unit in Kampala, Uganda. BMC Infectious Diseases, 2019, 19, 853.	2.9	29

#	ARTICLE	IF	CITATIONS
19	Role of genomics literacy in reducing the burden of common genetic diseases in Africa. Molecular Genetics & Genomic Medicine, 2019, 7, e00776.	1.2	16
20	Investigating colistin drug resistance: The role of high-throughput sequencing and bioinformatics. F1000Research, 2019, 8, 150.	1.6	9
21	Investigating colistin drug resistance: The role of high-throughput sequencing and bioinformatics. F1000Research, 2019, 8, 150.	1.6	6
22	Whole-Exome Sequencing Reveals Uncaptured Variation and Distinct Ancestry in the Southern African Population of Botswana. American Journal of Human Genetics, 2018, 102, 731-743.	6.2	38
23	Human Genomic Loci Important in Common Infectious Diseases: Role of High-Throughput Sequencing and Genome-Wide Association Studies. Canadian Journal of Infectious Diseases and Medical Microbiology, 2018, 2018, 1-9.	1.9	10
24	Microbial contaminants isolated from items and work surfaces in the post- operative ward at Kawolo general hospital, Uganda. BMC Infectious Diseases, 2018, 18, 68.	2.9	27
25	The Collaborative African Genomics Network (CAfGEN): Applying Genomic technologies to probe host factors important to the progression of HIV and HIV-tuberculosis infection in sub-Saharan Africa. AAS Open Research, 2018, 1, 3.	1.5	10
26	The Collaborative African Genomics Network (CAfGEN): Applying Genomic technologies to probe host factors important to the progression of HIV and HIV-tuberculosis infection in sub-Saharan Africa. AAS Open Research, 2018, 1, 3.	1.5	15
27	The collaborative African genomics network training program: a trainee perspective on training the next generation of African scientists. Genetics in Medicine, 2017, 19, 826-833.	2.4	29
28	Serological and molecular investigation for brucellosis in swine in selected districts of Uganda. Tropical Animal Health and Production, 2016, 48, 1147-1155.	1.4	15
29	High Genotypic Discordance of Concurrent Mycobacterium tuberculosis Isolates from Sputum and Blood of HIV-Infected Individuals. PLoS ONE, 2015, 10, e0132581.	2.5	15
30	Isolation and Molecular Characterization of<i>Brucella</i>Isolates in Cattle Milk in Uganda. BioMed Research International, 2015, 2015, 1-9.	1.9	32
31	Improving the Sensitivity of the Xpert MTB/RIF Assay on Sputum Pellets by Decreasing the Amount of Added Sample Reagent: a Laboratory and Clinical Evaluation. Journal of Clinical Microbiology, 2015, 53, 1258-1263.	3.9	4
32	Feasibility of establishing a biosafety level 3 tuberculosis culture laboratory of acceptable quality standards in a resource-limited setting: an experience from Uganda. Health Research Policy and Systems, 2015, 13, 4.	2.8	20
33	Cough Aerosol Cultures of Mycobacterium tuberculosis: Insights on TST / IGRA Discordance and Transmission Dynamics. PLoS ONE, 2015, 10, e0138358.	2.5	16
34	Seroprevalence of Syphilis among Human Immunodeficiency Virus Positive Individuals Attending Immune Suppressed Syndrome Clinic at International Hospital Kampala, Uganda. International STD Research & Reviews, 2015, 3, 84-90.	0.2	2
35	Periodontopathogenic bacterial species among patients with periodontal diseases at Mulago Hospital Dental Clinic in Kampala, Uganda: A cross-section study. Journal of Dentistry and Oral Hygiene, 2014, 6, 58-63.	0.2	4
36	Sensititre MYCOTB MIC Plate for Testing Mycobacterium tuberculosis Susceptibility to First- and Second-Line Drugs. Antimicrobial Agents and Chemotherapy, 2014, 58, 11-18.	3.2	86

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37	Rifampicin resistance mutations in the 81Âbp RRDR of rpoB gene in Mycobacterium tuberculosis clinical isolates using XpertÂ®MTB/RIF in Kampala, Uganda: a retrospective study. BMC Infectious Diseases, 2014, 14, 481.	2.9	48
38	Tuberculosis and Genetics of Sub-Saharan Africa Human Population. Mycobacterial Diseases: Tuberculosis & Leprosy, 2014, 04, .	0.1	1
39	Genetics of Sub-Saharan African Human Population: Implications for HIV/AIDS, Tuberculosis, and Malaria. International Journal of Evolutionary Biology, 2014, 2014, 1-8.	1.0	13
40	Clinico-pathological features of tuberculosis due to Mycobacterium tuberculosis Uganda genotype in patients with tuberculous lymphadenitis: a cross sectional study. BMC Clinical Pathology, 2014, 14, 14.	1.8	10
41	Species and genotypic diversity of non-tuberculous mycobacteria isolated from children investigated for pulmonary tuberculosis in rural Uganda. BMC Infectious Diseases, 2013, 13, 88.	2.9	37
42	Cough Aerosols of <i>Mycobacterium tuberculosis</i> Predict New Infection. A Household Contact Study. American Journal of Respiratory and Critical Care Medicine, 2013, 187, 1007-1015.	5.6	132
43	An Early Morning Sputum Sample Is Necessary for the Diagnosis of Pulmonary Tuberculosis, Even with More Sensitive Techniques: A Prospective Cohort Study among Adolescent TB-Suspects in Uganda. Tuberculosis Research and Treatment, 2012, 2012, 1-6.	0.6	14
44	Whole-genome sequence analysis ofÂVibrio cholerae from three outbreaks in Uganda, 2014 - 2016. F1000Research, 0, 8, 1340.	1.6	1
45	Re-thinking antimicrobial resistance transmission dynamics: a meta-analysis of cross-sectional studies at referral hospitals in Uganda. F1000Research, 0, 9, 878.	1.6	0