

# Chrispin Chaguza

## List of Publications by Year in descending order

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Version: 2024-02-01

35  
papers

638  
citations

687363

13  
h-index

642732

23  
g-index

40  
all docs

40  
docs citations

40  
times ranked

1080  
citing authors

#	ARTICLE	IF	CITATIONS
1	RCandy: an R package for visualizing homologous recombinations in bacterial genomes. <i>Bioinformatics</i> , 2022, 38, 1450-1451.	4.1	5
2	Widespread sharing of pneumococcal strains in a rural African setting: proximate villages are more likely to share similar strains that are carried at multiple timepoints. <i>Microbial Genomics</i> , 2022, 8, .	2.0	1
3	A new perspective on ancient Mitis group streptococcal genetics. <i>Microbial Genomics</i> , 2022, 8, .	2.0	4
4	A <i>Streptococcus pneumoniae</i> lineage usually associated with pneumococcal conjugate vaccine (PCV) serotypes is the most common cause of serotype 35B invasive disease in South Africa, following routine use of PCV. <i>Microbial Genomics</i> , 2022, 8, .	2.0	4
5	Serotype 1 pneumococcus: epidemiology, genomics, and disease mechanisms. <i>Trends in Microbiology</i> , 2022, 30, 581-592.	7.7	5
6	Comparative Genomics of Disease and Carriage Serotype 1 Pneumococci. <i>Genome Biology and Evolution</i> , 2022, 14, .	2.5	3
7	Pneumococcal Colonization and Virulence Factors Identified Via Experimental Evolution in Infection Models. <i>Molecular Biology and Evolution</i> , 2021, 38, 2209-2226.	8.9	9
8	Whole genomic comparative analysis of <i>Streptococcus pneumoniae</i> serotype 1 isolates causing invasive and non-invasive infections among children under 5 years in Casablanca, Morocco. <i>BMC Genomics</i> , 2021, 22, 39.	2.8	2
9	Metagenomics for surveillance of respiratory pathogens. <i>Nature Reviews Microbiology</i> , 2021, 19, 285-285.	28.6	8
10	Complete Genome Sequence of <i>Streptococcus pneumoniae</i> Strain BVJ1JL, a Serotype 1 Carriage Isolate from Malawi. <i>Microbiology Resource Announcements</i> , 2021, 10, e0071521.	0.6	1
11	<i>Streptococcus pneumoniae</i> serotypes that frequently colonise the human nasopharynx are common recipients of penicillin-binding protein gene fragments from <i>Streptococcus mitis</i> . <i>Microbial Genomics</i> , 2021, 7, .	2.0	5
12	Early Signals of Vaccine-driven Perturbation Seen in Pneumococcal Carriage Population Genomic Data. <i>Clinical Infectious Diseases</i> , 2020, 70, 1294-1303.	5.8	9
13	Bacterial survival: evolve and adapt or perish. <i>Nature Reviews Microbiology</i> , 2020, 18, 5-5.	28.6	6
14	Hypervirulent pneumococcal serotype 1 harbours two pneumolysin variants with differential haemolytic activity. <i>Scientific Reports</i> , 2020, 10, 17313.	3.3	7
15	Rotavirus Genotypes in Hospitalized Children With Acute Gastroenteritis Before and After Rotavirus Vaccine Introduction in Blantyre, Malawi, 1997â€“2019. <i>Journal of Infectious Diseases</i> , 2020, , .	4.0	13
16	Within-host microevolution of <i>Streptococcus pneumoniae</i> is rapid and adaptive during natural colonisation. <i>Nature Communications</i> , 2020, 11, 3442.	12.8	39
17	Bacterial genome-wide association study of hyper-virulent pneumococcal serotype 1 identifies genetic variation associated with neurotropism. <i>Communications Biology</i> , 2020, 3, 559.	4.4	11
18	Using genomics to improve preparedness and response of future epidemics or pandemics in Africa. <i>Lancet Microbe</i> , The, 2020, 1, e275-e276.	7.3	2

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19	Carriage Dynamics of Pneumococcal Serotypes in Naturally Colonized Infants in a Rural African Setting During the First Year of Life. <i>Frontiers in Pediatrics</i> , 2020, 8, 587730.	1.9	8
20	Lower Density and Shorter Duration of Nasopharyngeal Carriage by Pneumococcal Serotype 1 (ST217) May Explain Its Increased Invasiveness over Other Serotypes. <i>MBio</i> , 2020, 11, .	4.1	4
21	Molecular epidemiology of G12 rotavirus strains during eight consecutive epidemic seasons in the Basque Country (North of Spain), 2010–2018. <i>Infection, Genetics and Evolution</i> , 2019, 71, 67-75.	2.3	6
22	Genomic analysis of <i>Klebsiella pneumoniae</i> isolates from Malawi reveals acquisition of multiple ESBL determinants across diverse lineages. <i>Journal of Antimicrobial Chemotherapy</i> , 2019, 74, 1223-1232.	3.0	36
23	Emergence of Double- and Triple-Gene Reassortant G1P[8] Rotaviruses Possessing a DS-1-Like Backbone after Rotavirus Vaccine Introduction in Malawi. <i>Journal of Virology</i> , 2018, 92, .	3.4	61
24	Genomic Epidemiology of Penicillin-Nonsusceptible Pneumococci with Nonvaccine Serotypes Causing Invasive Disease in the United States. <i>Journal of Clinical Microbiology</i> , 2017, 55, 1104-1115.	3.9	44
25	The global distribution and diversity of protein vaccine candidate antigens in the highly virulent <i>Streptococcus pneumoniae</i> serotype 1. <i>Vaccine</i> , 2017, 35, 972-980.	3.8	27
26	Genomic landscape of extended-spectrum $\beta$ -lactamase resistance in <i>Escherichia coli</i> from an urban African setting. <i>Journal of Antimicrobial Chemotherapy</i> , 2017, 72, 1602-1609.	3.0	46
27	Comparative Genomic Analysis and In Vivo Modeling of <i>Streptococcus pneumoniae</i> ST3081 and ST618 Isolates Reveal Key Genetic and Phenotypic Differences Contributing to Clonal Replacement of Serotype 1 in The Gambia. <i>Journal of Infectious Diseases</i> , 2017, 216, 1318-1327.	4.0	11
28	Population genetic structure, antibiotic resistance, capsule switching and evolution of invasive pneumococci before conjugate vaccination in Malawi. <i>Vaccine</i> , 2017, 35, 4594-4602.	3.8	27
29	Adaptation... that's what you need?. <i>Nature Reviews Microbiology</i> , 2017, 15, 452-452.	28.6	0
30	Recombination in <i>Streptococcus pneumoniae</i> Lineages Increase with Carriage Duration and Size of the Polysaccharide Capsule. <i>MBio</i> , 2016, 7, .	4.1	50
31	Understanding pneumococcal serotype 1 biology through population genomic analysis. <i>BMC Infectious Diseases</i> , 2016, 16, 649.	2.9	22
32	High multiple carriage and emergence of <i>Streptococcus pneumoniae</i> vaccine serotype variants in Malawian children. <i>BMC Infectious Diseases</i> , 2015, 15, 234.	2.9	56
33	Mechanisms and impact of genetic recombination in the evolution of <i>Streptococcus pneumoniae</i> . <i>Computational and Structural Biotechnology Journal</i> , 2015, 13, 241-247.	4.1	50
34	Comparative Genomic Analysis of Meningitis- and Bacteremia-Causing Pneumococci Identifies a Common Core Genome. <i>Infection and Immunity</i> , 2015, 83, 4165-4173.	2.2	23
35	Region-specific diversification of the highly virulent serotype 1 <i>Streptococcus pneumoniae</i> . <i>Microbial Genomics</i> , 2015, 1, e000027.	2.0	27