

Rebecca A Gladstone

List of Publications by Year in descending order

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Version: 2024-02-01

52
papers

2,579
citations

331670

21
h-index

233421

45
g-index

66
all docs

66
docs citations

66
times ranked

2721
citing authors

#	ARTICLE	IF	CITATIONS
1	Producing polished prokaryotic pangenomes with the Panaroo pipeline. <i>Genome Biology</i> , 2020, 21, 180.	8.8	419
2	Fast and flexible bacterial genomic epidemiology with PopPUNK. <i>Genome Research</i> , 2019, 29, 304-316.	5.5	258
3	A New Pneumococcal Capsule Type, 10D, is the 100th Serotype and Has a Large <i>cps</i> Fragment from an Oral <i>Streptococcus</i> . <i>MBio</i> , 2020, 11, .	4.1	219
4	International genomic definition of pneumococcal lineages, to contextualise disease, antibiotic resistance and vaccine impact. <i>EBioMedicine</i> , 2019, 43, 338-346.	6.1	168
5	Pneumococcal lineages associated with serotype replacement and antibiotic resistance in childhood invasive pneumococcal disease in the post-PCV13 era: an international whole-genome sequencing study. <i>Lancet Infectious Diseases</i> , The, 2019, 19, 759-769.	9.1	165
6	Strain features and distributions in pneumococci from children with invasive disease before and after 13-valent conjugate vaccine implementation in the USA. <i>Clinical Microbiology and Infection</i> , 2016, 22, 60.e9-60.e29.	6.0	161
7	Five winters of pneumococcal serotype replacement in UK carriage following PCV introduction. <i>Vaccine</i> , 2015, 33, 2015-2021.	3.8	130
8	Joint sequencing of human and pathogen genomes reveals the genetics of pneumococcal meningitis. <i>Nature Communications</i> , 2019, 10, 2176.	12.8	83
9	Global emergence and population dynamics of divergent serotype 3 CC180 pneumococci. <i>PLoS Pathogens</i> , 2018, 14, e1007438.	4.7	74
10	Current methods for capsular typing of <i>Streptococcus pneumoniae</i> . <i>Journal of Microbiological Methods</i> , 2015, 113, 41-49.	1.6	70
11	Apparent nosocomial adaptation of <i>Enterococcus faecalis</i> predates the modern hospital era. <i>Nature Communications</i> , 2021, 12, 1523.	12.8	69
12	The rise and fall of pneumococcal serotypes carried in the PCV era. <i>Vaccine</i> , 2017, 35, 1293-1298.	3.8	68
13	SeroBA: rapid high-throughput serotyping of <i>Streptococcus pneumoniae</i> from whole genome sequence data. <i>Microbial Genomics</i> , 2018, 4, .	2.0	68
14	Continued control of pneumococcal disease in the UK – the impact of vaccination. <i>Journal of Medical Microbiology</i> , 2011, 60, 1-8.	1.8	56
15	Effect on nasopharyngeal pneumococcal carriage of replacing PCV7 with PCV13 in the Expanded Programme of Immunization in The Gambia. <i>Vaccine</i> , 2015, 33, 7144-7151.	3.8	48
16	Emergence and dissemination of antimicrobial resistance in <i>Escherichia coli</i> causing bloodstream infections in Norway in 2002–17: a nationwide, longitudinal, microbial population genomic study. <i>Lancet Microbe</i> , The, 2021, 2, e331-e341.	7.3	43
17	Persistence of Nasopharyngeal Pneumococcal Vaccine Serotypes and Increase of Nonvaccine Serotypes Among Vaccinated Infants and Their Mothers 5 Years After Introduction of Pneumococcal Conjugate Vaccine 13 in The Gambia. <i>Clinical Infectious Diseases</i> , 2019, 68, 1512-1521.	5.8	41
18	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

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19	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
20	Pre-vaccine serotype composition within a lineage signposts its serotype replacement – a carriage study over 7 years following pneumococcal conjugate vaccine use in the UK. <i>Microbial Genomics</i> , 2017, 3, e000119.	2.0	26
21	Visualizing variation within Global Pneumococcal Sequence Clusters (GPSCs) and country population snapshots to contextualize pneumococcal isolates. <i>Microbial Genomics</i> , 2020, 6, .	2.0	25
22	Clonal Expansion within Pneumococcal Serotype 6C after Use of Seven-Valent Vaccine. <i>PLoS ONE</i> , 2013, 8, e64731.	2.5	21
23	The role of interspecies recombination in the evolution of antibiotic-resistant pneumococci. <i>ELife</i> , 2021, 10, .	6.0	21
24	Pneumococcal 13-valent conjugate vaccine for the prevention of invasive pneumococcal disease in children and adults. <i>Expert Review of Vaccines</i> , 2012, 11, 889-902.	4.4	18
25	Phylogenetic Analysis of Invasive Serotype 1 Pneumococcus in South Africa, 1989 to 2013. <i>Journal of Clinical Microbiology</i> , 2016, 54, 1326-1334.	3.9	16
26	Patients with Chronic Obstructive Pulmonary Disease harbour a variation of Haemophilus species. <i>Scientific Reports</i> , 2018, 8, 14734.	3.3	14
27	Putative novel cps loci in a large global collection of pneumococci. <i>Microbial Genomics</i> , 2019, 5, .	2.0	14
28	Invasive Disease Caused Simultaneously by Dual Serotypes of Streptococcus pneumoniae. <i>Journal of Clinical Microbiology</i> , 2018, 56, .	3.9	13
29	A high-throughput multiplexing and selection strategy to complete bacterial genomes. <i>GigaScience</i> , 2021, 10, .	6.4	13
30	Global Distribution of Invasive Serotype 35D Streptococcus pneumoniae Isolates following Introduction of 13-Valent Pneumococcal Conjugate Vaccine. <i>Journal of Clinical Microbiology</i> , 2018, 56, .	3.9	12
31	A mosaic tetracycline resistance gene tet(S/M) detected in an MDR pneumococcal CC230 lineage that underwent capsular switching in South Africa. <i>Journal of Antimicrobial Chemotherapy</i> , 2020, 75, 512-520.	3.0	12
32	Pneumococcal vaccine impacts on the population genomics of non-typeable Haemophilus influenzae. <i>Microbial Genomics</i> , 2018, 4, .	2.0	12
33	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
34	Sampling methods for the study of pneumococcal carriage: A systematic review. <i>Vaccine</i> , 2012, 30, 6738-6744.	3.8	9
35	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
36	Using genomics to examine the persistence of Streptococcus pneumoniae serotype 19A in Ireland and the emergence of a sub-clade associated with vaccine failures. <i>Vaccine</i> , 2021, 39, 5064-5073.	3.8	9

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37	Comparative Genomics of Carriage and Disease Isolates of <i>Streptococcus pneumoniae</i> Serotype 22F Reveals Lineage-Specific Divergence and Niche Adaptation. <i>Genome Biology and Evolution</i> , 2016, 8, 1243-1251.	2.5	8
38	Population genetic structure, serotype distribution and antibiotic resistance of <i>Streptococcus pneumoniae</i> causing invasive disease in children in Argentina. <i>Microbial Genomics</i> , 2021, 7, .	2.0	8
39	<i>Streptococcus pneumoniae</i> genomic datasets from an Indian population describing pre-vaccine evolutionary epidemiology using a whole genome sequencing approach. <i>Microbial Genomics</i> , 2021, 7, .	2.0	8
40	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
41	Genomic surveillance of invasive <i>Streptococcus pneumoniae</i> isolates in the period pre-PCV10 and post-PCV10 introduction in Brazil. <i>Microbial Genomics</i> , 2021, 7, .	2.0	6
42	Genetic stability of pneumococcal isolates during 35 days of human experimental carriage. <i>Vaccine</i> , 2015, 33, 3342-3345.	3.8	5
43	Key features of invasive pneumococcal isolates recovered in Lima, Peru determined through whole genome sequencing. <i>International Journal of Medical Microbiology</i> , 2017, 307, 415-421.	3.6	5
44	Antimicrobial resistance determinants and susceptibility profiles of pneumococcal isolates recovered in Trinidad and Tobago. <i>Journal of Global Antimicrobial Resistance</i> , 2017, 11, 148-151.	2.2	4
45	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
46	Population genomics of pneumococcal carriage in South Africa following the introduction of the 13-valent pneumococcal conjugate vaccine (PCV13) immunization. <i>Microbial Genomics</i> , 2022, 8, .	2.0	4
47	Mass drug administration with azithromycin for trachoma elimination and the population structure of <i>Streptococcus pneumoniae</i> in the nasopharynx. <i>Clinical Microbiology and Infection</i> , 2021, 27, 864-870.	6.0	3
48	Comparative Genomics of Disease and Carriage Serotype 1 Pneumococci. <i>Genome Biology and Evolution</i> , 2022, 14, .	2.5	3
49	“M systems go on the offensive. <i>Nature Reviews Microbiology</i> , 2015, 13, 131-131.	28.6	2
50	Antimicrobial resistance genes and clonal success in <i>Escherichia coli</i> isolates causing bloodstream infection – Authors’ reply. <i>Lancet Microbe</i> , The, 2021, 2, e493.	7.3	1
51	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
52	Phylogeography and resistome of pneumococcal meningitis in West Africa before and after vaccine introduction. <i>Microbial Genomics</i> , 2021, 7, .	2.0	0