

Odile Barbara Harrison

List of Publications by Year in descending order

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Version: 2024-02-01

55
papers

2,149
citations

279798

23
h-index

243625

44
g-index

74
all docs

74
docs citations

74
times ranked

2406
citing authors

#	ARTICLE	IF	CITATIONS
1	Ribosomal multilocus sequence typing: universal characterization of bacteria from domain to strain. <i>Microbiology (United Kingdom)</i> , 2012, 158, 1005-1015.	1.8	497
2	Description and Nomenclature of <i>Neisseria meningitidis</i> Capsule Locus. <i>Emerging Infectious Diseases</i> , 2013, 19, 566-573.	4.3	259
3	Phasevarions Mediate Random Switching of Gene Expression in Pathogenic <i>Neisseria</i> . <i>PLoS Pathogens</i> , 2009, 5, e1000400.	4.7	170
4	Resolution of a Meningococcal Disease Outbreak from Whole-Genome Sequence Data with Rapid Web-Based Analysis Methods. <i>Journal of Clinical Microbiology</i> , 2012, 50, 3046-3053.	3.9	72
5	Genomic epidemiology of age-associated meningococcal lineages in national surveillance: an observational cohort study. <i>Lancet Infectious Diseases</i> , The, 2015, 15, 1420-1428.	9.1	63
6	Influence of the combination and phase variation status of the haemoglobin receptors HmbR and HpuAB on meningococcal virulence. <i>Microbiology (United Kingdom)</i> , 2011, 157, 1446-1456.	1.8	58
7	Identifying <i>Neisseria</i> Species by Use of the 50S Ribosomal Protein L6 (<i>rplF</i>) Gene. <i>Journal of Clinical Microbiology</i> , 2014, 52, 1375-1381.	3.9	55
8	Genomic analyses of <i>Neisseria gonorrhoeae</i> reveal an association of the gonococcal genetic island with antimicrobial resistance. <i>Journal of Infection</i> , 2016, 73, 578-587.	3.3	54
9	Pan-GWAS of <i>Streptococcus agalactiae</i> Highlights Lineage-Specific Genes Associated with Virulence and Niche Adaptation. <i>MBio</i> , 2020, 11, .	4.1	47
10	Identification of Novel <i>Neisseria gonorrhoeae</i> Lineages Harboring Resistance Plasmids in Coastal Kenya. <i>Journal of Infectious Diseases</i> , 2018, 218, 801-808.	4.0	40
11	Distribution and diversity of the haemoglobin haptoglobin iron-acquisition systems in pathogenic and non-pathogenic <i>Neisseria</i> . <i>Microbiology (United Kingdom)</i> , 2013, 159, 1920-1930.	1.8	39
12	High diversity of invasive <i>Haemophilus influenzae</i> isolates in France and the emergence of resistance to third generation cephalosporins by alteration of <i>ftsI</i> gene. <i>Journal of Infection</i> , 2019, 79, 7-14.	3.3	39
13	Population and Functional Genomics of <i>Neisseria</i> Revealed with Gene-by-Gene Approaches. <i>Journal of Clinical Microbiology</i> , 2016, 54, 1949-1955.	3.9	38
14	<i>Neisseria gonorrhoeae</i> Population Genomics: Use of the Gonococcal Core Genome to Improve Surveillance of Antimicrobial Resistance. <i>Journal of Infectious Diseases</i> , 2020, 222, 1816-1825.	4.0	36
15	Epidemiological Evidence for the Role of the Hemoglobin Receptor, HmbR, in Meningococcal Virulence. <i>Journal of Infectious Diseases</i> , 2009, 200, 94-98.	4.0	34
16	Molecular typing methods for outbreak detection and surveillance of invasive disease caused by <i>Neisseria meningitidis</i> , <i>Haemophilus influenzae</i> and <i>Streptococcus pneumoniae</i> , a review. <i>Microbiology (United Kingdom)</i> , 2011, 157, 2181-2195.	1.8	32
17	Distribution of the type III DNA methyltransferases <i>modA</i> , <i>modB</i> and <i>modD</i> among <i>Neisseria meningitidis</i> genotypes: implications for gene regulation and virulence. <i>Scientific Reports</i> , 2016, 6, 21015.	3.3	32
18	Household transmission of <i>Neisseria meningitidis</i> in the African meningitis belt: a longitudinal cohort study. <i>The Lancet Global Health</i> , 2016, 4, e989-e995.	6.3	30

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19	Genomic characterization of novel <i>Neisseria</i> species. <i>Scientific Reports</i> , 2019, 9, 13742.	3.3	29
20	Variation and molecular evolution of HmbR, the <i>Neisseria meningitidis</i> haemoglobin receptor. <i>Microbiology (United Kingdom)</i> , 2010, 156, 1384-1393.	1.8	28
21	Genomic analyses of the <i>Chlamydia trachomatis</i> core genome show an association between chromosomal genome, plasmid type and disease. <i>BMC Genomics</i> , 2018, 19, 130.	2.8	27
22	Isolation and characterization of <i>Neisseria musculi</i> sp. nov., from the wild house mouse. <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2016, 66, 3585-3593.	1.7	27
23	Genomic analysis of urogenital and rectal <i>Neisseria meningitidis</i> isolates reveals encapsulated hyperinvasive meningococci and coincident multidrug-resistant gonococci. <i>Sexually Transmitted Infections</i> , 2017, 93, 445-451.	1.9	26
24	Distribution of transferrin binding protein B gene (tbpB) variants among <i>Neisseria</i> species. <i>BMC Microbiology</i> , 2008, 8, 66.	3.3	25
25	Emergence and evolution of antimicrobial resistance genes and mutations in <i>Neisseria gonorrhoeae</i> . <i>Genome Medicine</i> , 2021, 13, 51.	8.2	25
26	Meningococcal carriage in periods of high and low invasive meningococcal disease incidence in the UK: comparison of UKMenCar1â€“4 cross-sectional survey results. <i>Lancet Infectious Diseases</i> , The, 2021, 21, 677-687.	9.1	24
27	Acquisition of the capsule locus by horizontal gene transfer in <i>Neisseria meningitidis</i> is often accompanied by the loss of UDP-GalNAc synthesis. <i>Scientific Reports</i> , 2017, 7, 44442.	3.3	23
28	<i>Neisseria</i> genomics: current status and future perspectives. <i>Pathogens and Disease</i> , 2017, 75, .	2.0	23
29	Association of <i>Neisseria gonorrhoeae</i> Plasmids With Distinct Lineages and The Economic Status of Their Country of Origin. <i>Journal of Infectious Diseases</i> , 2020, 222, 1826-1836.	4.0	22
30	Genomic Analysis of the Evolution and Global Spread of Hyper-invasive Meningococcal Lineage 5. <i>EBioMedicine</i> , 2015, 2, 234-243.	6.1	20
31	Impact of meningococcal ACWY conjugate vaccines on pharyngeal carriage in adolescents: evidence for herd protection from the UK MenACWY programme. <i>Clinical Microbiology and Infection</i> , 2022, 28, 1649.e1-1649.e8.	6.0	20
32	Molecular characterization of invasive capsule null <i>Neisseria meningitidis</i> in South Africa. <i>BMC Microbiology</i> , 2017, 17, 40.	3.3	17
33	Toward a Global Genomic Epidemiology of Meningococcal Disease. <i>Journal of Infectious Diseases</i> , 2019, 220, S266-S273.	4.0	16
34	Genetic determinants of genus-level glycan diversity in a bacterial protein glycosylation system. <i>PLoS Genetics</i> , 2019, 15, e1008532.	3.5	16
35	Characterization of capsule genes in non-pathogenic <i>Neisseria</i> species. <i>Microbial Genomics</i> , 2018, 4, .	2.0	16
36	Hierarchical genomic analysis of carried and invasive serogroup A <i>Neisseria meningitidis</i> during the 2011 epidemic in Chad. <i>BMC Genomics</i> , 2017, 18, 398.	2.8	15

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37	Molecular diagnostic assays for the detection of common bacterial meningitis pathogens: A narrative review. <i>EBioMedicine</i> , 2021, 65, 103274.	6.1	15
38	Genome-wide association studies reveal the role of polymorphisms affecting factor H binding protein expression in host invasion by <i>Neisseria meningitidis</i> . <i>PLoS Pathogens</i> , 2021, 17, e1009992.	4.7	15
39	Integrated Bioinformatic Analyses and Immune Characterization of New <i>Neisseria gonorrhoeae</i> Vaccine Antigens Expressed during Natural Mucosal Infection. <i>Vaccines</i> , 2019, 7, 153.	4.4	14
40	The global meningitis genome partnership. <i>Journal of Infection</i> , 2020, 81, 510-520.	3.3	13
41	Genomic Analysis of Serogroup Y <i>Neisseria meningitidis</i> Isolates Reveals Extensive Similarities Between Carriage-Associated and Disease-Associated Organisms. <i>Journal of Infectious Diseases</i> , 2016, 213, 1777-1785.	4.0	12
42	Development of a PCR algorithm to detect and characterize <i>Neisseria meningitidis</i> carriage isolates in the African meningitis belt. <i>PLoS ONE</i> , 2018, 13, e0206453.	2.5	12
43	The Genus <i>Neisseria</i> . , 2014, , 881-900.		12
44	Localized Hypermutation is the Major Driver of Meningococcal Genetic Variability during Persistent Asymptomatic Carriage. <i>MBio</i> , 2020, 11, .	4.1	11
45	The <i>Neisseria gonorrhoeae</i> Accessory Genome and Its Association with the Core Genome and Antimicrobial Resistance. <i>Microbiology Spectrum</i> , 2022, 10, .	3.0	9
46	Evolution of Sequence Type 4821 Clonal Complex Hyperinvasive and Quinolone-Resistant Meningococci. <i>Emerging Infectious Diseases</i> , 2021, 27, 1110-1122.	4.3	7
47	Invasive meningococcal disease in Shanghai, China from 1950 to 2016: implications for serogroup B vaccine implementation. <i>Scientific Reports</i> , 2018, 8, 12334.	3.3	6
48	<i>Neisseria meningitidis</i> has acquired sequences within the capsule locus by horizontal genetic transfer. <i>Wellcome Open Research</i> , 2019, 4, 99.	1.8	6
49	Typing complex meningococcal vaccines to understand diversity and population structure of key vaccine antigens. <i>Wellcome Open Research</i> , 2018, 3, 151.	1.8	5
50	Genomic epidemiology of group B streptococci spanning 10 years in an Irish maternity hospital, 2008–2017. <i>Journal of Infection</i> , 2021, 83, 37-45.	3.3	4
51	Recent advances in understanding and combatting <i>Neisseria gonorrhoeae</i> : a genomic perspective. <i>Faculty Reviews</i> , 2021, 10, 65.	3.9	4
52	<i>Neisseria meningitidis</i> has acquired sequences within the capsule locus by horizontal genetic transfer. <i>Wellcome Open Research</i> , 2019, 4, 99.	1.8	3
53	Complete genome and methylome analysis of <i>Neisseria meningitidis</i> associated with increased serogroup Y disease. <i>Scientific Reports</i> , 2020, 10, 3644.	3.3	2
54	Genome Sequencing and Interrogation of Genome Databases: A Guide to <i>Neisseria meningitidis</i> Genomics. <i>Methods in Molecular Biology</i> , 2019, 1969, 51-82.	0.9	1

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55	Mobile antimicrobial resistance in <i>Neisseria gonorrhoeae</i> . <i>Access Microbiology</i> , 2022, 4, .	0.5	0