

Xin Wang

List of Publications by Year in descending order

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88
papers

3,244
citations

126708

33
h-index

161609

54
g-index

89
all docs

89
docs citations

89
times ranked

2295
citing authors

#	ARTICLE	IF	CITATIONS
1	Infection With the US <i>Neisseria meningitidis</i> Urethritis Clade Does Not Lower Future Risk of Urethral Gonorrhoea. <i>Clinical Infectious Diseases</i> , 2022, 74, 2159-2165.	2.9	2
2	Evaluation of Urethrotropic-Clade Meningococcal Infection by Urine Metagenomic Shotgun Sequencing. <i>Journal of Clinical Microbiology</i> , 2022, 60, JCM0173221.	1.8	2
3	Risk Factors for Invasive Meningococcal Disease Belonging to a Novel Urethritis Clade of <i>Neisseria meningitidis</i> United States, 2013–2017. <i>Open Forum Infectious Diseases</i> , 2022, 9, ofac035.	0.4	3
4	Antimicrobial Susceptibility Survey of Invasive <i>Neisseria meningitidis</i> , United States 2012–2016. <i>Journal of Infectious Diseases</i> , 2022, 225, 1871-1875.	1.9	12
5	Genomic Insights on Variation Underlying Capsule Expression in Meningococcal Carriage Isolates From University Students, United States, 2015–2016. <i>Frontiers in Microbiology</i> , 2022, 13, 815044.	1.5	2
6	Enhancing Meningococcal Genomic Surveillance in the Meningitis Belt Using High-Resolution Culture-Free Whole-Genome Sequencing. <i>Journal of Infectious Diseases</i> , 2022, 226, 729-737.	1.9	6
7	Direct Real-Time PCR for the Detection and Serotyping of <i>Haemophilus influenzae</i> without DNA Extraction. <i>Journal of Clinical Microbiology</i> , 2022, 60, e0211121.	1.8	3
8	Phylogenetic Structure and Comparative Genomics of Multi-National Invasive <i>Haemophilus influenzae</i> Serotype a Isolates. <i>Frontiers in Microbiology</i> , 2022, 13, 856884.	1.5	3
9	<i>Neisseria meningitidis</i> Serogroup C Clonal Complex 10217 Outbreak in West Kpendjal Prefecture, Togo 2019. <i>Microbiology Spectrum</i> , 2022, , e0192321.	1.2	1
10	Antimicrobial Susceptibility Survey of Invasive <i>Haemophilus influenzae</i> in the United States in 2016. <i>Microbiology Spectrum</i> , 2022, 10, e0257921.	1.2	7
11	Epidemiology of Invasive <i>Haemophilus influenzae</i> Serotype a Disease United States, 2008–2017. <i>Clinical Infectious Diseases</i> , 2021, 73, e371-e379.	2.9	27
12	Molecular diagnostic assays for the detection of common bacterial meningitis pathogens: A narrative review. <i>EBioMedicine</i> , 2021, 65, 103274.	2.7	15
13	Acquisition of Ciprofloxacin Resistance Among an Expanding Clade of β -Lactamase-Positive, Serogroup Y <i>Neisseria meningitidis</i> in the United States. <i>Clinical Infectious Diseases</i> , 2021, 73, 1185-1193.	2.9	17
14	Using <i>Neisseria meningitidis</i> genomic diversity to inform outbreak strain identification. <i>PLoS Pathogens</i> , 2021, 17, e1009586.	2.1	6
15	Genetic Diversity of Meningococcal Serogroup B Vaccine Antigens among Carriage Isolates Collected from Students at Three Universities in the United States, 2015–2016. <i>MBio</i> , 2021, 12, .	1.8	3
16	Next generation rapid diagnostic tests for meningitis diagnosis. <i>Journal of Infection</i> , 2020, 81, 712-718.	1.7	16
17	Transmission Dynamics and Microevolution of <i>Neisseria meningitidis</i> During Carriage and Invasive Disease in High School Students in Georgia and Maryland, 2006–2007. <i>Journal of Infectious Diseases</i> , 2020, 223, 2038-2047.	1.9	6
18	Full Molecular Typing of <i>Neisseria meningitidis</i> Directly from Clinical Specimens for Outbreak Investigation. <i>Journal of Clinical Microbiology</i> , 2020, 58, .	1.8	19

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19	Web-Based Genome Analysis of Bacterial Meningitis Pathogens for Public Health Applications Using the Bacterial Meningitis Genomic Analysis Platform (BMGAP). <i>Frontiers in Genetics</i> , 2020, 11, 601870.	1.1	4
20	Meningococcal carriage 7 years after introduction of a serogroup A meningococcal conjugate vaccine in Burkina Faso: results from four cross-sectional carriage surveys. <i>Lancet Infectious Diseases</i> , The, 2020, 20, 1418-1425.	4.6	12
21	Oropharyngeal microbiome of a college population following a meningococcal disease outbreak. <i>Scientific Reports</i> , 2020, 10, 632.	1.6	7
22	Insights on Population Structure and Within-Host Genetic Changes among Meningococcal Carriage Isolates from U.S. Universities. <i>MSphere</i> , 2020, 5, .	1.3	3
23	Detection of Ciprofloxacin-Resistant, β -Lactamase-Producing <i>Neisseria meningitidis</i> Serogroup Y Isolates in the United States, 2019-2020. <i>Morbidity and Mortality Weekly Report</i> , 2020, 69, 735-739.	9.0	36
24	Molecular insights into meningococcal carriage isolates from Burkina Faso 7 years after introduction of a serogroup A meningococcal conjugate vaccine. <i>Microbial Genomics</i> , 2020, 6, .	1.0	0
25	Epidemiology of Meningococcal Disease Outbreaks in the United States, 2009-2013. <i>Clinical Infectious Diseases</i> , 2019, 68, 580-585.	2.9	29
26	Genomic characterization of <i>Haemophilus influenzae</i> : a focus on the capsule locus. <i>BMC Genomics</i> , 2019, 20, 733.	1.2	29
27	Epidemiology of Bacterial Meningitis in the Nine Years Since Meningococcal Serogroup A Conjugate Vaccine Introduction, Niger, 2010-2018. <i>Journal of Infectious Diseases</i> , 2019, 220, S206-S215.	1.9	11
28	Bacterial Meningitis Epidemiology in Five Countries in the Meningitis Belt of Sub-Saharan Africa, 2015-2017. <i>Journal of Infectious Diseases</i> , 2019, 220, S165-S174.	1.9	54
29	A New Sequence Type of <i>Neisseria meningitidis</i> Serogroup C Associated With a 2016 Meningitis Outbreak in Mali. <i>Journal of Infectious Diseases</i> , 2019, 220, S190-S197.	1.9	12
30	Toward a Global Genomic Epidemiology of Meningococcal Disease. <i>Journal of Infectious Diseases</i> , 2019, 220, S266-S273.	1.9	16
31	The Strengthening of Laboratory Systems in the Meningitis Belt to Improve Meningitis Surveillance, 2008-2018: A Partners Perspective. <i>Journal of Infectious Diseases</i> , 2019, 220, S175-S181.	1.9	19
32	MenAfriNet: A Network Supporting Case-Based Meningitis Surveillance and Vaccine Evaluation in the Meningitis Belt of Africa. <i>Journal of Infectious Diseases</i> , 2019, 220, S148-S154.	1.9	33
33	Genetic Similarity of Gonococcal Homologs to Meningococcal Outer Membrane Proteins of Serogroup B Vaccine. <i>MBio</i> , 2019, 10, .	1.8	29
34	Distribution of <i>Neisseria meningitidis</i> serogroup b (NmB) vaccine antigens in meningococcal disease causing isolates in the United States during 2009-2014, prior to NmB vaccine licensure. <i>Journal of Infection</i> , 2019, 79, 426-434.	1.7	8
35	Phylogenetic relationships and regional spread of meningococcal strains in the meningitis belt, 2011-2016. <i>EBioMedicine</i> , 2019, 41, 488-496.	2.7	17
36	Meningococcal Disease Among College-Aged Young Adults: 2014-2016. <i>Pediatrics</i> , 2019, 143, .	1.0	33

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37	Whole-Genome Sequencing for Characterization of Capsule Locus and Prediction of Serogroup of Invasive Meningococcal Isolates. <i>Journal of Clinical Microbiology</i> , 2019, 57, .	1.8	18
38	Heteroresistance to the model antimicrobial peptide polymyxin B in the emerging <i>Neisseria meningitidis</i> lineage 11.2 urethritis clade: mutations in the <i>pilMNOPQ</i> operon. <i>Molecular Microbiology</i> , 2019, 111, 254-268.	1.2	15
39	Triplex real-time PCR assay for the detection of <i>Streptococcus pneumoniae</i> , <i>Neisseria meningitidis</i> and <i>Haemophilus influenzae</i> directly from clinical specimens without extraction of DNA. <i>Diagnostic Microbiology and Infectious Disease</i> , 2019, 93, 188-190.	0.8	15
40	Current Epidemiology and Trends in Invasive <i>Haemophilus influenzae</i> Disease—United States, 2009–2015. <i>Clinical Infectious Diseases</i> , 2018, 67, 881-889.	2.9	106
41	Meningococcal carriage among a university student population — United States, 2015. <i>Vaccine</i> , 2018, 36, 29-35.	1.7	40
42	Current Epidemiology and Trends in Meningococcal Disease—United States, 1996–2015. <i>Clinical Infectious Diseases</i> , 2018, 66, 1276-1281.	2.9	101
43	Expansion of a urethritis-associated <i>Neisseria meningitidis</i> clade in the United States with concurrent acquisition of <i>N. gonorrhoeae</i> alleles. <i>BMC Genomics</i> , 2018, 19, 176.	1.2	61
44	Predicting the Susceptibility of Meningococcal Serogroup B Isolates to Bactericidal Antibodies Elicited by Bivalent rLP2086, a Novel Prophylactic Vaccine. <i>MBio</i> , 2018, 9, .	1.8	53
45	Draft Genome Sequences for a Diverse Set of Seven <i>Haemophilus</i> and <i>Aggregatibacter</i> Species. <i>Microbiology Resource Announcements</i> , 2018, 7, .	0.3	1
46	Whole genome sequencing for investigations of meningococcal outbreaks in the United States: a retrospective analysis. <i>Scientific Reports</i> , 2018, 8, 15803.	1.6	20
47	Outbreak of <i>Neisseria meningitidis</i> serogroup C outside the meningitis belt—Liberia, 2017: an epidemiological and laboratory investigation. <i>Lancet Infectious Diseases</i> , The, 2018, 18, 1360-1367.	4.6	20
48	Triplex Real-Time PCR without DNA Extraction for the Monitoring of Meningococcal Disease. <i>Diagnostics</i> , 2018, 8, 58.	1.3	4
49	Distinct evolutionary patterns of <i>Neisseria meningitidis</i> serogroup B disease outbreaks at two universities in the USA. <i>Microbial Genomics</i> , 2018, 4, .	1.0	4
50	Population structure of invasive <i>Neisseria meningitidis</i> in the United States, 2011–15. <i>Journal of Infection</i> , 2018, 77, 427-434.	1.7	19
51	Molecular characterization of invasive meningococcal isolates in Burkina Faso as the relative importance of serogroups X and W increases, 2008–2012. <i>BMC Infectious Diseases</i> , 2018, 18, 337.	1.3	8
52	BMScan: using whole genome similarity to rapidly and accurately identify bacterial meningitis causing species. <i>BMC Infectious Diseases</i> , 2018, 18, 405.	1.3	13
53	Emergence of a new <i>Neisseria meningitidis</i> clonal complex 11 lineage 11.2 clade as an effective urogenital pathogen. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2017, 114, 4237-4242.	3.3	79
54	Large Cluster of <i>Neisseria meningitidis</i> Urethritis in Columbus, Ohio, 2015. <i>Clinical Infectious Diseases</i> , 2017, 65, 92-99.	2.9	52

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55	Increased Risk for Meningococcal Disease Among Men Who Have Sex With Men in the United States, 2012–2015. <i>Clinical Infectious Diseases</i> , 2017, 65, 756-763.	2.9	55
56	<i>Neisseria</i> genomics: current status and future perspectives. <i>Pathogens and Disease</i> , 2017, 75, .	0.8	23
57	Meningococcal Carriage Evaluation in Response to a Serogroup B Meningococcal Disease Outbreak and Mass Vaccination Campaign at a College—Rhode Island, 2015–2016. <i>Clinical Infectious Diseases</i> , 2017, 64, 1115-1122.	2.9	85
58	Meningococcal Carriage Following a Vaccination Campaign With MenB-4C and MenB-FHbp in Response to a University Serogroup B Meningococcal Disease Outbreak—Oregon, 2015–2016. <i>Journal of Infectious Diseases</i> , 2017, 216, 1130-1140.	1.9	67
59	High Risk for Invasive Meningococcal Disease Among Patients Receiving Eculizumab (Soliris) Despite Receipt of Meningococcal Vaccine. <i>Morbidity and Mortality Weekly Report</i> , 2017, 66, 734-737.	9.0	227
60	Whole-Genome Characterization of Epidemic <i>Neisseria meningitidis</i> Serogroup C and Resurgence of Serogroup W, Niger, 2015. <i>Emerging Infectious Diseases</i> , 2016, 22, 1762-1768.	2.0	53
61	Notes from the Field: Increase in <i>Neisseria meningitidis</i> Associated Urethritis Among Men at Two Sentinel Clinics—Columbus, Ohio, and Oakland County, Michigan, 2015. <i>Morbidity and Mortality Weekly Report</i> , 2016, 65, 550-552.	9.0	53
62	Development of Real-Time PCR Methods for the Detection of Bacterial Meningitis Pathogens without DNA Extraction. <i>PLoS ONE</i> , 2016, 11, e0147765.	1.1	56
63	Comparative Genomic Analysis of <i>Haemophilus haemolyticus</i> and Nontypeable <i>Haemophilus influenzae</i> and a New Testing Scheme for Their Discrimination. <i>Journal of Clinical Microbiology</i> , 2016, 54, 3010-3017.	1.8	12
64	Emergence of epidemic <i>Neisseria meningitidis</i> serogroup C in Niger, 2015: an analysis of national surveillance data. <i>Lancet Infectious Diseases</i> , The, 2016, 16, 1288-1294.	4.6	71
65	The Establishment and Diversification of Epidemic-Associated Serogroup W <i>Meningococcus</i> in the African Meningitis Belt, 1994 to 2012. <i>MSphere</i> , 2016, 1, .	1.3	29
66	Genomic Investigation Reveals Highly Conserved, Mosaic, Recombination Events Associated with Capsular Switching among Invasive <i>Neisseria meningitidis</i> Serogroup W Sequence Type (ST)-11 Strains. <i>Genome Biology and Evolution</i> , 2016, 8, 2065-2075.	1.1	30
67	Comparison of Phenotypic and Genotypic Approaches to Capsule Typing of <i>Neisseria meningitidis</i> by Use of Invasive and Carriage Isolate Collections. <i>Journal of Clinical Microbiology</i> , 2016, 54, 25-34.	1.8	27
68	Changes in the Population Structure of Invasive <i>Neisseria meningitidis</i> in the United States After Quadrivalent Meningococcal Conjugate Vaccine Licensure. <i>Journal of Infectious Diseases</i> , 2015, 211, 1887-1894.	1.9	30
69	First Use of a Serogroup B Meningococcal Vaccine in the US in Response to a University Outbreak. <i>Pediatrics</i> , 2015, 135, 798-804.	1.0	109
70	Genomic Epidemiology of Hypervirulent Serogroup W, ST-11 <i>Neisseria meningitidis</i> . <i>EBioMedicine</i> , 2015, 2, 1447-1455.	2.7	51
71	Population-Based Surveillance of <i>Neisseria meningitidis</i> Antimicrobial Resistance in the United States. <i>Open Forum Infectious Diseases</i> , 2015, 2, ofv117.	0.4	47
72	Serogroup B Meningococcal Disease Outbreak and Carriage Evaluation at a College - Rhode Island, 2015. <i>Morbidity and Mortality Weekly Report</i> , 2015, 64, 606-7.	9.0	56

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73	Invasive <i>Haemophilus influenzae</i> Disease in Adults ≥65 Years, United States, 2011. <i>Open Forum Infectious Diseases</i> , 2014, 1, ofu044.	0.4	37
74	A five-year field assessment of rapid diagnostic tests for meningococcal meningitis in Niger by using the combination of conventional and real-time PCR assays as a gold standard. <i>Transactions of the Royal Society of Tropical Medicine and Hygiene</i> , 2014, 108, 6-12.	0.7	14
75	Prolonged University Outbreak of Meningococcal Disease Associated With a Serogroup B Strain Rarely Seen in the United States. <i>Clinical Infectious Diseases</i> , 2013, 57, 344-348.	2.9	63
76	A Multi-country Evaluation of <i>Neisseria meningitidis</i> Serogroup B Factor H-Binding Proteins and Implications for Vaccine Coverage in Different Age Groups. <i>Pediatric Infectious Disease Journal</i> , 2013, 32, 1096-1101.	1.1	36
77	<i>Haemophilus haemolyticus</i> Isolates Causing Clinical Disease. <i>Journal of Clinical Microbiology</i> , 2012, 50, 2462-2465.	1.8	57
78	Evaluation of New Biomarker Genes for Differentiating <i>Haemophilus influenzae</i> from <i>Haemophilus haemolyticus</i> . <i>Journal of Clinical Microbiology</i> , 2012, 50, 1422-1424.	1.8	33
79	Clinical Validation of Multiplex Real-Time PCR Assays for Detection of Bacterial Meningitis Pathogens. <i>Journal of Clinical Microbiology</i> , 2012, 50, 702-708.	1.8	116
80	Molecular Characterization of Invasive Meningococcal Isolates from Countries in the African Meningitis Belt before Introduction of a Serogroup A Conjugate Vaccine. <i>PLoS ONE</i> , 2012, 7, e46019.	1.1	46
81	Detection of bacterial pathogens in Mongolia meningitis surveillance with a new real-time PCR assay to detect <i>Haemophilus influenzae</i> . <i>International Journal of Medical Microbiology</i> , 2011, 301, 303-309.	1.5	98
82	Prevalence and genetic diversity of candidate vaccine antigens among invasive <i>Neisseria meningitidis</i> isolates in the United States. <i>Vaccine</i> , 2011, 29, 4739-4744.	1.7	98
83	sodC-Based Real-Time PCR for Detection of <i>Neisseria meningitidis</i> . <i>PLoS ONE</i> , 2011, 6, e19361.	1.1	88
84	Preclinical evidence for the potential of a bivalent fHBP vaccine to prevent <i>Neisseria meningitidis</i> Serogroup C Disease. <i>Hum Vaccin</i> , 2011, 7, 68-74.	2.4	43
85	Genome Sequences for Five Strains of the Emerging Pathogen <i>Haemophilus haemolyticus</i> . <i>Journal of Bacteriology</i> , 2011, 193, 5879-5880.	1.0	20
86	Population Structure and Capsular Switching of Invasive <i>Neisseria meningitidis</i> Isolates in the Pre-Meningococcal Conjugate Vaccine Era—United States, 2000–2005. <i>Journal of Infectious Diseases</i> , 2010, 201, 1208-1224.	1.9	92
87	Sequence Diversity of the Factor H Binding Protein Vaccine Candidate in Epidemiologically Relevant Strains of Serogroup B <i>Neisseria meningitidis</i> . <i>Journal of Infectious Diseases</i> , 2009, 200, 379-389.	1.9	180
88	Meningococcus genome informatics platform: a system for analyzing multilocus sequence typing data. <i>Nucleic Acids Research</i> , 2009, 37, W606-W611.	6.5	11