## **Guiqing Wang**

## List of Publications by Year in Descending Order

Source: https://exaly.com/author-pdf/761084/guiqing-wang-publications-by-year.pdf

Version: 2024-04-28

This document has been generated based on the publications and citations recorded by exaly.com. For the latest version of this publication list, visit the link given above.

The third column is the impact factor (IF) of the journal, and the fourth column is the number of citations of the article.

46
papers

1,999
citations

44
g-index

47
ext. papers

2,312
ext. citations

6.2
avg, IF
L-index

#	Paper	IF	Citations
46	Biennial Upsurge and Molecular Epidemiology of Enterovirus D68 Infection in New York, USA, 2014 to 2018. <i>Journal of Clinical Microbiology</i> , <b>2020</b> , 58,	9.7	6
45	The Lyme Disease Biobank: Characterization of 550 Patient and Control Samples from the East Coast and Upper Midwest of the United States. <i>Journal of Clinical Microbiology</i> , <b>2020</b> , 58,	9.7	10
44	Integrated Genome-Wide Analysis of an Isogenic Pair of Clinical Isolates with Differential Antimicrobial Resistance to Ceftolozane/Tazobactam, Ceftazidime/Avibactam, and Piperacillin/Tazobactam. <i>International Journal of Molecular Sciences</i> , <b>2020</b> , 21,	6.3	2
43	Precision Infection Prevention (PIP) as a New Standard of Practice Within Longitudinal Infection Prevention and Surveillance. <i>Infection Control and Hospital Epidemiology</i> , <b>2020</b> , 41, s449-s450	2	
42	Co-infections in Persons with Early Lyme Disease, New York, USA. <i>Emerging Infectious Diseases</i> , <b>2019</b> , 25, 748-752	10.2	19
41	Optimizing a Whole-Genome Sequencing Data Processing Pipeline for Precision Surveillance of Health Care-Associated Infections. <i>Microorganisms</i> , <b>2019</b> , 7,	4.9	1
40	531. Practical and Evidence-Based Considerations for Implementation of Bacterial Whole-Genome Sequencing Within Longitudinal Infection Control Practice. <i>Open Forum Infectious Diseases</i> , <b>2019</b> , 6, S2	.55 <sup>1</sup> -S25	5 <sup>78</sup>
39	Optimizing a Metatranscriptomic Next-Generation Sequencing Protocol for Bronchoalveolar Lavage Diagnostics. <i>Journal of Molecular Diagnostics</i> , <b>2019</b> , 21, 251-261	5.1	6
38	Congenital Babesiosis After Maternal Infection With Borrelia burgdorferi and Babesia microti. <i>Journal of the Pediatric Infectious Diseases Society</i> , <b>2018</b> , 7, e1-e5	4.8	18
37	Comparison of the Severity of Respiratory Disease in Children Testing Positive for Enterovirus D68 and Human Rhinovirus. <i>Journal of Pediatrics</i> , <b>2018</b> , 197, 147-153.e1	3.6	1
36	Complete Genome Sequences of Four Toxigenic Clinical Isolates from Patients of the Lower Hudson Valley, New York, USA. <i>Genome Announcements</i> , <b>2018</b> , 6,		3
35	1248. Genomic Sequencing and Clinical Data Integration for Next-Generation Infection Prevention. <i>Open Forum Infectious Diseases</i> , <b>2018</b> , 5, S379-S380	1	78
34	Evolution and mutations predisposing to daptomycin resistance in vancomycin-resistant Enterococcus faecium ST736 strains. <i>PLoS ONE</i> , <b>2018</b> , 13, e0209785	3.7	15
33	Enterovirus D68 Subclade B3 Strain Circulating and Causing an Outbreak in the United States in 2016. <i>Scientific Reports</i> , <b>2017</b> , 7, 1242	4.9	44
32	Emergence and Evolution of Multidrug-Resistant Klebsiella pneumoniae with both and Integrated in the Chromosome. <i>Antimicrobial Agents and Chemotherapy</i> , <b>2017</b> , 61,	5.9	35
31	Use of a Perianal Swab Compared With a Stool Sample to Detect Symptomatic Clostridium difficile Infection. <i>Infection Control and Hospital Epidemiology</i> , <b>2017</b> , 38, 658-662	2	3
30	Complete Genome Sequence of a Colistin-Resistant Strain Harboring on an IncHI2 Plasmid in the United States. <i>Genome Announcements</i> , <b>2017</b> , 5,		14

## (2008-2016)

29	Insights into Borrelia miyamotoi infection from an untreated case demonstrating relapsing fever, monocytosis and a positive C6 Lyme serology. <i>Diagnostic Microbiology and Infectious Disease</i> , <b>2016</b> , 86, 93-6	2.9	27
28	Assessing next-generation sequencing and 4 bioinformatics tools for detection of Enterovirus D68 and other respiratory viruses in clinical samples. <i>Diagnostic Microbiology and Infectious Disease</i> , <b>2016</b> , 85, 26-9	2.9	6
27	Identification of spp. from Cardiac Tissue by 16S rRNA PCR in a Patient with Culture-Negative Device-Associated Endocarditis: A Case Report and Review of the Literature. <i>Case Reports in Infectious Diseases</i> , <b>2016</b> , 2016, 8935052	0.9	3
26	Complete Genome Sequences of Nine Enterovirus D68 Strains from Patients of the Lower Hudson Valley, New York, 2016. <i>Genome Announcements</i> , <b>2016</b> , 4,		8
25	Neutropenia in Congenital and Adult Babesiosis. American Journal of Clinical Pathology, 2015, 144, 94-6	1.9	15
24	Comparison of a quantitative PCR assay with peripheral blood smear examination for detection and quantitation of Babesia microti infection in humans. <i>Diagnostic Microbiology and Infectious Disease</i> , <b>2015</b> , 82, 109-13	2.9	29
23	Evaluation of a Real-Time Reverse Transcription-PCR Assay for Detection of Enterovirus D68 in Clinical Samples from an Outbreak in New York State in 2014. <i>Journal of Clinical Microbiology</i> , <b>2015</b> , 53, 1915-20	9.7	22
22	Borrelia burgdorferi and Other Borrelia Species <b>2015</b> , 1867-1909		4
21	Borrelia <b>2015</b> , 1-21		2
20	Whole-Genome Sequence Analysis Reveals the Enterovirus D68 Isolates during the United States 2014 Outbreak Mainly Belong to a Novel Clade. <i>Scientific Reports</i> , <b>2015</b> , 5, 15223	4.9	38
19	Utilization of a real-time PCR assay for diagnosis of Babesia microti infection in clinical practice. <i>Ticks and Tick-borne Diseases</i> , <b>2015</b> , 6, 376-82	3.6	34
18	A Novel, High-Sensitivity, Quantitative Hepatitis C Virus Assay. <i>American Journal of Clinical Pathology</i> , <b>2015</b> , 144, A223-A223	1.9	
17	Molecular Typing of Borrelia burgdorferi. Current Protocols in Microbiology, 2014, 34, 12C.5.1-31	7.1	31
16	Identification of a novel clone, ST736, among Enterococcus faecium clinical isolates and its association with daptomycin nonsusceptibility. <i>Antimicrobial Agents and Chemotherapy</i> , <b>2014</b> , 58, 4848-	5 <del>4</del> 9	13
15	CTX-M Elactamase-producing Klebsiella pneumoniae in suburban New York City, New York, USA. <i>Emerging Infectious Diseases</i> , <b>2013</b> , 19, 1803-10	10.2	35
14	Failure of topical antibiotics to prevent disseminated Borrelia burgdorferi infection following a tick bite in C3H/HeJ mice. <i>Journal of Infectious Diseases</i> , <b>2012</b> , 205, 991-4	7	7
13	The Role of Culture and Nucleic Acid Amplification in Diagnosis of Lyme Borreliosis <b>2011</b> , 159-183		1
12	Pattern of proinflammatory cytokine induction in RAW264.7 mouse macrophages is identical for virulent and attenuated Borrelia burgdorferi. <i>Journal of Immunology</i> , <b>2008</b> , 180, 8306-15	5.3	19

11	Diagnosis of lyme borreliosis. <i>Clinical Microbiology Reviews</i> , <b>2005</b> , 18, 484-509	34	486
10	Variations in Barbour-Stoenner-Kelly culture medium modulate infectivity and pathogenicity of Borrelia burgdorferi clinical isolates. <i>Infection and Immunity</i> , <b>2004</b> , 72, 6702-6	3.7	37
9	Impaired host defense to infection and Toll-like receptor 2-independent killing of Borrelia burgdorferi clinical isolates in TLR2-deficient C3H/HeJ mice. <i>FEMS Microbiology Letters</i> , <b>2004</b> , 231, 219-	-2 <del>3</del> .9	50
8	Real-time PCR for simultaneous detection and quantification of Borrelia burgdorferi in field-collected Ixodes scapularis ticks from the Northeastern United States. <i>Applied and Environmental Microbiology</i> , <b>2003</b> , 69, 4561-5	4.8	50
7	Quantitative detection of Borrelia burgdorferi in 2-millimeter skin samples of erythema migrans lesions: correlation of results with clinical and laboratory findings. <i>Journal of Clinical Microbiology</i> , <b>2002</b> , 40, 1249-53	9.7	74
6	Disease severity in a murine model of lyme borreliosis is associated with the genotype of the infecting Borrelia burgdorferi sensu stricto strain. <i>Journal of Infectious Diseases</i> , <b>2002</b> , 186, 782-91	7	123
5	Direct detection methods for Lyme Borrelia, including the use of quantitative assays. <i>Vector-Borne and Zoonotic Diseases</i> , <b>2002</b> , 2, 223-31	2.4	10
4	Analysis of a VMP-like sequence (vls) locus in Borrelia garinii and Vls homologues among four Borrelia burgdorferi sensu lato species. <i>FEMS Microbiology Letters</i> , <b>2001</b> , 199, 39-45	2.9	23
3	Impact of genotypic variation of Borrelia burgdorferi sensu stricto on kinetics of dissemination and severity of disease in C3H/HeJ mice. <i>Infection and Immunity</i> , <b>2001</b> , 69, 4303-12	3.7	107
2	Molecular typing of Borrelia burgdorferi sensu lato: taxonomic, epidemiological, and clinical implications. <i>Clinical Microbiology Reviews</i> , <b>1999</b> , 12, 633-53	34	333
1	Phenotypic and genetic characterization of a novel Borrelia burgdorferi sensu lato isolate from a patient with lyme borreliosis. <i>Journal of Clinical Microbiology</i> , <b>1999</b> , 37, 3025-8	9.7	79