

S Wesley Long

List of Publications by Year in descending order

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Version: 2024-02-01

54
papers

2,825
citations

201674

27
h-index

214800

47
g-index

68
all docs

68
docs citations

68
times ranked

5220
citing authors

#	ARTICLE	IF	CITATIONS
1	Treatment of Coronavirus Disease 2019 (COVID-19) Patients with Convalescent Plasma. <i>American Journal of Pathology</i> , 2020, 190, 1680-1690.	3.8	239
2	Evolutionary pathway to increased virulence and epidemic group A <i>Streptococcus</i> disease derived from 3,615 genome sequences. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2014, 111, E1768-76.	7.1	215
3	Using Machine Learning To Predict Antimicrobial MICs and Associated Genomic Features for Nontyphoidal <i>Salmonella</i> . <i>Journal of Clinical Microbiology</i> , 2019, 57, .	3.9	181
4	Convalescent plasma anti-SARS-CoV-2 spike protein ectodomain and receptor-binding domain IgG correlate with virus neutralization. <i>Journal of Clinical Investigation</i> , 2020, 130, 6728-6738.	8.2	172
5	Signals of Significantly Increased Vaccine Breakthrough, Decreased Hospitalization Rates, and Less Severe Disease in Patients with Coronavirus Disease 2019 Caused by the Omicron Variant of Severe Acute Respiratory Syndrome Coronavirus 2 in Houston, Texas. <i>American Journal of Pathology</i> , 2022, 192, 642-652.	3.8	161
6	Whole-Genome Sequencing of Human Clinical <i>Klebsiella pneumoniae</i> Isolates Reveals Misidentification and Misunderstandings of <i>Klebsiella pneumoniae</i> , <i>Klebsiella variicola</i> , and <i>Klebsiella quasipneumoniae</i> . <i>MSphere</i> , 2017, 2, .	2.9	139
7	Developing an in silico minimum inhibitory concentration panel test for <i>Klebsiella pneumoniae</i> . <i>Scientific Reports</i> , 2018, 8, 421.	3.3	136
8	Population Genomic Analysis of 1,777 Extended-Spectrum Beta-Lactamase-Producing <i>Klebsiella pneumoniae</i> Isolates, Houston, Texas: Unexpected Abundance of Clonal Group 307. <i>MBio</i> , 2017, 8, .	4.1	124
9	PBP2a Mutations Causing High-Level Ceftaroline Resistance in Clinical Methicillin-Resistant <i>Staphylococcus aureus</i> Isolates. <i>Antimicrobial Agents and Chemotherapy</i> , 2014, 58, 6668-6674.	3.2	120
10	Molecular Architecture of Early Dissemination and Massive Second Wave of the SARS-CoV-2 Virus in a Major Metropolitan Area. <i>MBio</i> , 2020, 11, .	4.1	99
11	Delta Variants of SARS-CoV-2 Cause Significantly Increased Vaccine Breakthrough COVID-19 Cases in Houston, Texas. <i>American Journal of Pathology</i> , 2022, 192, 320-331.	3.8	90
12	Absence of Patient-to-Patient Intra-hospital Transmission of <i>Staphylococcus aureus</i> as Determined by Whole-Genome Sequencing. <i>MBio</i> , 2014, 5, e01692-14.	4.1	78
13	Rapidly Progressive, Fatal, Inhalation Anthrax-like Infection in a Human: Case Report, Pathogen Genome Sequencing, Pathology, and Coordinated Response. <i>Archives of Pathology and Laboratory Medicine</i> , 2011, 135, 1447-1459.	2.5	64
14	Strategy for Rapid Identification and Antibiotic Susceptibility Testing of Gram-Negative Bacteria Directly Recovered from Positive Blood Cultures Using the Bruker MALDI Biotyper and the BD Phoenix System. <i>Journal of Clinical Microbiology</i> , 2012, 50, 2452-2454.	3.9	64
15	A Genomic Day in the Life of a Clinical Microbiology Laboratory. <i>Journal of Clinical Microbiology</i> , 2013, 51, 1272-1277.	3.9	60
16	Integrated analysis of population genomics, transcriptomics and virulence provides novel insights into <i>Streptococcus pyogenes</i> pathogenesis. <i>Nature Genetics</i> , 2019, 51, 548-559.	21.4	58
17	Identification of Point Mutations in Clinical <i>Staphylococcus aureus</i> Strains That Produce Small-Colony Variants Auxotrophic for Menadione. <i>Infection and Immunity</i> , 2014, 82, 1600-1605.	2.2	57
18	Evaluation of Transovarial Transmission and Transmissibility of <i>Ehrlichia chaffeensis</i> (Rickettsiales: Anaplasmataceae) in <i>Amblyomma americanum</i> (Acari: Ixodidae). <i>Journal of Medical Entomology</i> , 2003, 40, 1000-1004.	1.8	50

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19	A preliminary investigation of Ehrlichia species in ticks, humans, dogs, and capybaras from Brazil. <i>Veterinary Parasitology</i> , 2007, 143, 189-195.	1.8	50
20	Analysis of the ARTIC Version 3 and Version 4 SARS-CoV-2 Primers and Their Impact on the Detection of the G142D Amino Acid Substitution in the Spike Protein. <i>Microbiology Spectrum</i> , 2021, 9, e0180321.	3.0	50
21	Whole-Genome Sequencing of a Human Clinical Isolate of the Novel Species <i>Klebsiella quasivariicola</i> sp. nov. <i>Genome Announcements</i> , 2017, 5, .	0.8	46
22	Sequence Analysis of 20,453 Severe Acute Respiratory Syndrome Coronavirus 2 Genomes from the Houston Metropolitan Area Identifies the Emergence and Widespread Distribution of Multiple Isolates of All Major Variants of Concern. <i>American Journal of Pathology</i> , 2021, 191, 983-992.	3.8	42
23	Experimental Ehrlichia chaffeensis infection in beagles. <i>Journal of Medical Microbiology</i> , 2003, 52, 1021-1026.	1.8	42
24	Antigenic Variation of Ehrlichia chaffeensis Resulting from Differential Expression of the 28-Kilodalton Protein Gene Family. <i>Infection and Immunity</i> , 2002, 70, 1824-1831.	2.2	39
25	The Reemergence of Seasonal Respiratory Viruses in Houston, Texas, after Relaxing COVID-19 Restrictions. <i>Microbiology Spectrum</i> , 2021, 9, e0043021.	3.0	36
26	Bacterial Genomics in Infectious Disease and the Clinical Pathology Laboratory. <i>Archives of Pathology and Laboratory Medicine</i> , 2012, 136, 1414-1422.	2.5	34
27	The Majority of 9,729 Group A Streptococcus Strains Causing Disease Secrete SpeB Cysteine Protease: Pathogenesis Implications. <i>Infection and Immunity</i> , 2015, 83, 4750-4758.	2.2	33
28	Applications of Artificial Intelligence in Clinical Microbiology Diagnostic Testing. <i>Clinical Microbiology Newsletter</i> , 2020, 42, 61-70.	0.7	27
29	Trajectory of Growth of Severe Acute Respiratory Syndrome Coronavirus 2 (SARS-CoV-2) Variants in Houston, Texas, January through May 2021, Based on 12,476 Genome Sequences. <i>American Journal of Pathology</i> , 2021, 191, 1754-1773.	3.8	26
30	Clinical Laboratory Response to a Mock Outbreak of Invasive Bacterial Infections: a Preparedness Study. <i>Journal of Clinical Microbiology</i> , 2014, 52, 4210-4216.	3.9	22
31	Comparative Whole Genome Sequencing of Community-Associated Methicillin-Resistant <i>Staphylococcus aureus</i> Sequence Type 8 from Primary Care Clinics in a Texas Community. <i>Pharmacotherapy</i> , 2015, 35, 220-228.	2.6	14
32	RocA Has Serotype-Specific Gene Regulatory and Pathogenesis Activities in Serotype M28 Group A Streptococcus. <i>Infection and Immunity</i> , 2018, 86, .	2.2	14
33	<i>Ehrlichia</i> Prevalence in <i>Amblyomma americanum</i> , Central Texas. <i>Emerging Infectious Diseases</i> , 2004, 10, 1342-1343.	4.3	14
34	Overcoming Barriers to the Transformation of the Genus Ehrlichia. <i>Annals of the New York Academy of Sciences</i> , 2005, 1063, 403-410.	3.8	11
35	Whole-Genome Sequencing of a Human Clinical Isolate of emm28 Streptococcus pyogenes Causing Necrotizing Fasciitis Acquired Contemporaneously with Hurricane Harvey. <i>Genome Announcements</i> , 2017, 5, .	0.8	11
36	Pathology Trainee Redeployment and Education During the COVID-19 Pandemic: An Institutional Experience. <i>Academic Pathology</i> , 2020, 7, 2374289520953548.	1.1	11

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37	Carbapenems drive the collateral resistance to ceftaroline in cystic fibrosis patients with MRSA. <i>Communications Biology</i> , 2020, 3, 599.	4.4	9
38	Houston Methodist Variant Viewer: An Application to Support Clinical Laboratory Interpretation of Next-generation Sequencing Data for Cancer. <i>Journal of Pathology Informatics</i> , 2017, 8, 44.	1.7	5
39	Draft Genome Sequence of <i>Candida auris</i> Strain LOM, a Human Clinical Isolate from Greater Metropolitan Houston, Texas. <i>Microbiology Resource Announcements</i> , 2019, 8, .	0.6	4
40	Improving Positive Blood Culture Removal Time Significantly Decreases Total Processing Time. <i>Archives of Pathology and Laboratory Medicine</i> , 2015, 139, 199-203.	2.5	3
41	Real-time Communication With Health Care Providers Through an Online Respiratory Pathogen Laboratory Report. <i>Open Forum Infectious Diseases</i> , 2018, 5, ofy322.	0.9	3
42	Predicting β -lactam resistance using whole genome sequencing in <i>Klebsiella pneumoniae</i> : the challenge of β -lactamase inhibitors. <i>Diagnostic Microbiology and Infectious Disease</i> , 2020, 98, 115149.	1.8	3
43	Development and Evaluation of a Novel Protein-Based Assay for Specific Detection of KPC β -Lactamases from <i>Klebsiella pneumoniae</i> Clinical Isolates. <i>MSphere</i> , 2020, 5, .	2.9	3
44	RecutClub.com: An Open Source, Whole Slide Image-based Pathology Education System. <i>Journal of Pathology Informatics</i> , 2017, 8, 10.	1.7	3
45	Chlorhexidine bathing and <i>Clostridium difficile</i> infection in a surgical intensive care unit. <i>Journal of Surgical Research</i> , 2018, 228, 107-111.	1.6	2
46	Failure of Best Practice Alerts to Affect <i>C difficile</i> Test Utilization. <i>American Journal of Clinical Pathology</i> , 2018, 150, S144-S144.	0.7	2
47	The Ongoing Threat of Methicillin-Resistant <i>Staphylococcus aureus</i> . <i>Journal of Infectious Diseases</i> , 2020, 222, 1943-1945.	4.0	1
48	Human Infections Caused by Clonally Related African Clade (Clade III) Strains of <i>Candida auris</i> in the Greater Houston Region. <i>Journal of Clinical Microbiology</i> , 2020, 58, .	3.9	1
49	A Web-Based Respiratory Pathogen Laboratory Report for Summarizing Key Metrics to Stakeholders. <i>American Journal of Clinical Pathology</i> , 2018, 150, S153-S154.	0.7	0
50	686: CHLORHEXIDINE BATHING AND CLOSTRIDIUM DIFFICILE INFECTION IN A SURGICAL INTENSIVE CARE UNIT. <i>Critical Care Medicine</i> , 2018, 46, 329-329.	0.9	0
51	Updates to a Lab-Developed Bioinformatics Pipeline and Application for Interpretation of Clinical Next-Generation Sequencing Panels. <i>American Journal of Clinical Pathology</i> , 2019, 152, S9-S10.	0.7	0
52	Development and validation of Houston Methodist Variant Viewer version 3: updates to our application for interpretation of next-generation sequencing data. <i>JAMIA Open</i> , 2020, 3, 299-305.	2.0	0
53	Whole Genome Sequence Analysis of a <i>B. cereus</i> Strain Causing a Fatal Anthrax-Like Pulmonary Infection. <i>FASEB Journal</i> , 2012, 26, 1034.5.	0.5	0
54	Implementing flowDensity for Automated Analysis of Bone Marrow Lymphocyte Population. <i>Journal of Pathology Informatics</i> , 2021, 12, 49.	1.7	0