

# S Wesley Long

## List of Publications by Year in descending order

Source: <https://exaly.com/author-pdf/8637980/publications.pdf>

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  | 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        |
| 2  | 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       |
| 3  | 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        |
| 4  | The Reemergence of Seasonal Respiratory Viruses in Houston, Texas, after Relaxing COVID-19 Restrictions. <i>Microbiology Spectrum</i> , 2021, 9, e0043021.   | 3.0 | 36        |
| 5  | 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        |
| 6  | 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        |
| 7  | Implementing flowDensity for Automated Analysis of Bone Marrow Lymphocyte Population. <i>Journal of Pathology Informatics</i> , 2021, 12, 49.  | 1.7 | 0         |
| 8  | Pathology Trainee Redeployment and Education During the COVID-19 Pandemic: An Institutional Experience. <i>Academic Pathology</i> , 2020, 7, 2374289520953548.   | 1.1 | 11        |
| 9  | 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         |
| 10 | Predicting $\beta$ -lactam resistance using whole genome sequencing in <i>Klebsiella pneumoniae</i> : the challenge of $\beta$ -lactamase inhibitors. <i>Diagnostic Microbiology and Infectious Disease</i> , 2020, 98, 115149.  | 1.8 | 3         |
| 11 | 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        |
| 12 | Carbapenems drive the collateral resistance to ceftaroline in cystic fibrosis patients with MRSA. <i>Communications Biology</i> , 2020, 3, 599.  | 4.4 | 9         |
| 13 | The Ongoing Threat of Methicillin-Resistant <i>Staphylococcus aureus</i> . <i>Journal of Infectious Diseases</i> , 2020, 222, 1943-1945.   | 4.0 | 1         |
| 14 | Treatment of Coronavirus Disease 2019 (COVID-19) Patients with Convalescent Plasma. <i>American Journal of Pathology</i> , 2020, 190, 1680-1690.   | 3.8 | 239       |
| 15 | Applications of Artificial Intelligence in Clinical Microbiology Diagnostic Testing. <i>Clinical Microbiology Newsletter</i> , 2020, 42, 61-70.  | 0.7 | 27        |
| 16 | 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         |
| 17 | Development and Evaluation of a Novel Protein-Based Assay for Specific Detection of KPC $\beta$ -Lactamases from <i>Klebsiella pneumoniae</i> Clinical Isolates. <i>MSphere</i> , 2020, 5, .   | 2.9 | 3         |
| 18 | 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       |

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|----|---|------|-----------|
| 19 | 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         |
| 20 | 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         |
| 21 | 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        |
| 22 | 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       |
| 23 | 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         |
| 24 | Developing an in silico minimum inhibitory concentration panel test for <i>Klebsiella pneumoniae</i> . <i>Scientific Reports</i> , 2018, 8, 421.  | 3.3  | 136       |
| 25 | 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         |
| 26 | 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         |
| 27 | 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         |
| 28 | 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         |
| 29 | RocA Has Serotype-Specific Gene Regulatory and Pathogenesis Activities in Serotype M28 Group A <i>Streptococcus</i> . <i>Infection and Immunity</i> , 2018, 86, .   | 2.2  | 14        |
| 30 | 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       |
| 31 | 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        |
| 32 | 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       |
| 33 | Whole-Genome Sequencing of a Human Clinical Isolate of emm28 <i>Streptococcus pyogenes</i> Causing Necrotizing Fasciitis Acquired Contemporaneously with Hurricane Harvey. <i>Genome Announcements</i> , 2017, 5, .   | 0.8  | 11        |
| 34 | 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         |
| 35 | RecutClub.com: An Open Source, Whole Slide Image-based Pathology Education System. <i>Journal of Pathology Informatics</i> , 2017, 8, 10.   | 1.7  | 3         |
| 36 | The Majority of 9,729 Group A <i>Streptococcus</i> Strains Causing Disease Secrete SpeB Cysteine Protease: Pathogenesis Implications. <i>Infection and Immunity</i> , 2015, 83, 4750-4758.  | 2.2  | 33        |

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|----|---|-----|-----------|
| 37 | 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        |
| 38 | 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         |
| 39 | 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       |
| 40 | Absence of Patient-to-Patient Intrahospital Transmission of <i>Staphylococcus aureus</i> as Determined by Whole-Genome Sequencing. <i>MBio</i> , 2014, 5, e01692-14.  | 4.1 | 78        |
| 41 | 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        |
| 42 | 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        |
| 43 | 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       |
| 44 | A Genomic Day in the Life of a Clinical Microbiology Laboratory. <i>Journal of Clinical Microbiology</i> , 2013, 51, 1272-1277.   | 3.9 | 60        |
| 45 | 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        |
| 46 | 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        |
| 47 | 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         |
| 48 | 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        |
| 49 | A preliminary investigation of <i>Ehrlichia</i> species in ticks, humans, dogs, and capybaras from Brazil. <i>Veterinary Parasitology</i> , 2007, 143, 189-195.   | 1.8 | 50        |
| 50 | Overcoming Barriers to the Transformation of the Genus <i>Ehrlichia</i> . <i>Annals of the New York Academy of Sciences</i> , 2005, 1063, 403-410.  | 3.8 | 11        |
| 51 | <i>Ehrlichia</i> Prevalence in <i>Amblyomma americanum</i> , Central Texas. <i>Emerging Infectious Diseases</i> , 2004, 10, 1342-1343.  | 4.3 | 14        |
| 52 | 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        |
| 53 | Experimental <i>Ehrlichia chaffeensis</i> infection in beagles. <i>Journal of Medical Microbiology</i> , 2003, 52, 1021-1026.   | 1.8 | 42        |
| 54 | Antigenic Variation of <i>Ehrlichia chaffeensis</i> Resulting from Differential Expression of the 28-Kilodalton Protein Gene Family. <i>Infection and Immunity</i> , 2002, 70, 1824-1831.   | 2.2 | 39        |