

Egon A Ozer

List of Publications by Year in descending order

Source: <https://exaly.com/author-pdf/5808581/publications.pdf>

Version: 2024-02-01

72
papers

2,707
citations

279798

23
h-index

214800

47
g-index

90
all docs

90
docs citations

90
times ranked

3912
citing authors

| # | ARTICLE | IF | CITATIONS |
|----|--|------|-----------|
| 1 | Placental Pathology After SARS-CoV-2 Infection in the Pre-Variant of Concern, Alpha / Gamma, Delta, or Omicron Eras. <i>International Journal of Surgical Pathology</i> , 2023, 31, 387-397. | 0.8 | 17 |
| 2 | Association Between <i>Clostridium innocuum</i> and Antibiotic-Associated Diarrhea in Adults and Children: A Cross-sectional Study and Comparative Genomics Analysis. <i>Clinical Infectious Diseases</i> , 2023, 76, e1244-e1251. | 5.8 | 5 |
| 3 | Viral whole-genome sequencing to assess impact of universal masking on SARS-CoV-2 transmission among pediatric healthcare workers. <i>Infection Control and Hospital Epidemiology</i> , 2022, 43, 1408-1412. | 1.8 | 4 |
| 4 | Highly sensitive and ultra-rapid antigen-based detection of SARS-CoV-2 using nanomechanical sensor platform. <i>Biosensors and Bioelectronics</i> , 2022, 195, 113647. | 10.1 | 34 |
| 5 | Aminoglycoside-resistance gene signatures are predictive of aminoglycoside MICs for carbapenem-resistant <i>Klebsiella pneumoniae</i> . <i>Journal of Antimicrobial Chemotherapy</i> , 2022, 77, 356-363. | 3.0 | 12 |
| 6 | Serological Markers of SARS-CoV-2 Reinfection. <i>MBio</i> , 2022, 13, e0214121. | 4.1 | 8 |
| 7 | Has Omicron Changed the Evolution of the Pandemic?. <i>JMIR Public Health and Surveillance</i> , 2022, 8, e35763. | 2.6 | 38 |
| 8 | Multiple expansions of globally uncommon SARS-CoV-2 lineages in Nigeria. <i>Nature Communications</i> , 2022, 13, 688. | 12.8 | 23 |
| 9 | Assessment of Virological Contributions to COVID-19 Outcomes in a Longitudinal Cohort of Hospitalized Adults. <i>Open Forum Infectious Diseases</i> , 2022, 9, ofac027. | 0.9 | 8 |
| 10 | Antibody escape and global spread of SARS-CoV-2 lineage A.27. <i>Nature Communications</i> , 2022, 13, 1152. | 12.8 | 20 |
| 11 | Low-level SARS-CoV-2 viremia coincident with COVID placentitis and stillbirth. <i>Placenta</i> , 2022, 121, 79-81. | 1.5 | 14 |
| 12 | Effect of omadacycline alone and in combination with meropenem against carbapenem-resistant <i>Acinetobacter baumannii</i> isolates. <i>Journal of Global Antimicrobial Resistance</i> , 2022, 29, 147-149. | 2.2 | 2 |
| 13 | Longitudinal Analysis of SARS-CoV-2 Vaccine Breakthrough Infections Reveals Limited Infectious Virus Shedding and Restricted Tissue Distribution. <i>Open Forum Infectious Diseases</i> , 2022, 9, . | 0.9 | 36 |
| 14 | Overlapping Delta and Omicron Outbreaks During the COVID-19 Pandemic: Dynamic Panel Data Estimates. <i>JMIR Public Health and Surveillance</i> , 2022, 8, e37377. | 2.6 | 2 |
| 15 | Rapid and Sensitive Detection of Antigen from SARS-CoV-2 Variants of Concern by a Multivalent Minibinder-Functionalized Nanomechanical Sensor. <i>Analytical Chemistry</i> , 2022, 94, 8105-8109. | 6.5 | 6 |
| 16 | Genomic surveillance for multidrug-resistant or hypervirulent <i>Klebsiella pneumoniae</i> among United States bloodstream isolates. <i>BMC Infectious Diseases</i> , 2022, 22, . | 2.9 | 23 |
| 17 | Optimizing aminoglycoside selection for KPC-producing <i>Klebsiella pneumoniae</i> with the aminoglycoside-modifying enzyme (AME) gene <i>aac(6â€™)-Ib</i> . <i>Journal of Antimicrobial Chemotherapy</i> , 2021, 76, 671-679. | 3.0 | 9 |
| 18 | Molecular epidemiology in the HIV and SARS-CoV-2 pandemics. <i>Current Opinion in HIV and AIDS</i> , 2021, 16, 11-24. | 3.8 | 5 |

| # | ARTICLE | IF | CITATIONS |
|----|--|-----|-----------|
| 19 | Genetic Evaluation of Nosocomial <i>Candida auris</i> Transmission. <i>Journal of Clinical Microbiology</i> , 2021, 59, . | 3.9 | 8 |
| 20 | First report of <i>Pseudomonas nitroreducens</i> cultured from the lungs of a patient with pneumonia. <i>BMJ Case Reports</i> , 2021, 14, e241327. | 0.5 | 4 |
| 21 | Conversations With the Editors: The Emergence of Variants Amid Population-Wide SARS-CoV-2 Vaccination Efforts: How Much Should We Worry?. <i>Clinical Therapeutics</i> , 2021, 43, 1630-1635. | 2.5 | 1 |
| 22 | Generating Genotype-Specific Aminoglycoside Combinations with Ceftazidime/Avibactam for KPC-Producing <i>Klebsiella pneumoniae</i> . <i>Antimicrobial Agents and Chemotherapy</i> , 2021, 65, e0069221. | 3.2 | 9 |
| 23 | The Future of Bacteriophage Therapy Will Promote Antimicrobial Susceptibility. <i>MSystems</i> , 2021, 6, e0021821. | 3.8 | 5 |
| 24 | Screening Students and Staff for Asymptomatic Coronavirus Disease 2019 in Chicago Schools. <i>Journal of Pediatrics</i> , 2021, 239, 74-80.e1. | 1.8 | 3 |
| 25 | Genomic Features Associated with the Degree of Phenotypic Resistance to Carbapenems in Carbapenem-Resistant <i>Klebsiella pneumoniae</i> . <i>MSystems</i> , 2021, 6, e0019421. | 3.8 | 26 |
| 26 | Long-term Persistence of an Extensively Drug-Resistant Subclade of Globally Distributed <i>Pseudomonas aeruginosa</i> Clonal Complex 446 in an Academic Medical Center. <i>Clinical Infectious Diseases</i> , 2020, 71, 1524-1531. | 5.8 | 20 |
| 27 | Natural <i>Clostridioides difficile</i> Toxin Immunization in Colonized Infants. <i>Clinical Infectious Diseases</i> , 2020, 70, 2095-2102. | 5.8 | 27 |
| 28 | A clade of SARS-CoV-2 viruses associated with lower viral loads in patient upper airways. <i>EBioMedicine</i> , 2020, 62, 103112. | 6.1 | 77 |
| 29 | Complete Genome Sequence of <i>Clostridium innocuum</i> Strain LC-LUMC-CI-001, Isolated from a Patient with Recurrent Antibiotic-Associated Diarrhea. <i>Microbiology Resource Announcements</i> , 2020, 9, . | 0.6 | 11 |
| 30 | A Genome-Based Model to Predict the Virulence of <i>Pseudomonas aeruginosa</i> Isolates. <i>MBio</i> , 2020, 11, . | 4.1 | 12 |
| 31 | Complete Genome Sequence of <i>Clostridium innocuum</i> Strain ATCC 14501. <i>Microbiology Resource Announcements</i> , 2020, 9, . | 0.6 | 10 |
| 32 | A comparative genomics approach identifies contact-dependent growth inhibition as a virulence determinant. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2020, 117, 6811-6821. | 7.1 | 39 |
| 33 | Complete Genome Sequence of <i>Klebsiella pneumoniae</i> Strain TK421, a Conjugative Hypervirulent Isolate. <i>Microbiology Resource Announcements</i> , 2020, 9, . | 0.6 | 6 |
| 34 | Discovery of a New <i>Neisseria gonorrhoeae</i> Type IV Pilus Assembly Factor, TfpC. <i>MBio</i> , 2020, 11, . | 4.1 | 5 |
| 35 | 520. Longitudinal Analysis of SARS-CoV-2 Viruses in Hospitalized Adults. <i>Open Forum Infectious Diseases</i> , 2020, 7, S325-S326. | 0.9 | 0 |
| 36 | <i>Clostridioides difficile</i> Whole-Genome Sequencing Reveals Limited Within-Host Genetic Diversity in a Pediatric Cohort. <i>Journal of Clinical Microbiology</i> , 2019, 57, . | 3.9 | 5 |

| # | ARTICLE | IF | CITATIONS |
|----|---|-----|-----------|
| 37 | The Population Structure of <i>Pseudomonas aeruginosa</i> Is Characterized by Genetic Isolation of <i>exoU</i> ⁺ and <i>exoS</i> ⁺ Lineages. <i>Genome Biology and Evolution</i> , 2019, 11, 1780-1796. | 2.5 | 74 |
| 38 | Transcriptional initiation of a small RNA, not Râ€loop stability, dictates the frequency of pilin antigenic variation in <i>Neisseria gonorrhoeae</i> . <i>Molecular Microbiology</i> , 2019, 112, 1219-1234. | 2.5 | 14 |
| 39 | Draft Genome Sequence of <i>Pseudomonas aeruginosa</i> Strain BWH047, a Sequence Type 235 Multidrug-Resistant Clinical Isolate Expressing High Levels of Colistin Resistance. <i>Microbiology Resource Announcements</i> , 2019, 8, . | 0.6 | 1 |
| 40 | In Vivo Proteome of <i>Pseudomonas aeruginosa</i> in Airways of Cystic Fibrosis Patients. <i>Journal of Proteome Research</i> , 2019, 18, 2601-2612. | 3.7 | 23 |
| 41 | A Genomic Approach To Identify <i>Klebsiella pneumoniae</i> and <i>Acinetobacter baumannii</i> Strains with Enhanced Competitive Fitness in the Lungs during Multistrain Pneumonia. <i>Infection and Immunity</i> , 2019, 87, . | 2.2 | 9 |
| 42 | PacBio Amplicon Sequencing Method To Measure Pilin Antigenic Variation Frequencies of <i>Neisseria gonorrhoeae</i> . <i>MSphere</i> , 2019, 4, . | 2.9 | 5 |
| 43 | 2453. Prolonged Local Epidemic of an XDR <i>P. aeruginosa</i> Subclade of High-Risk Clonal Complex 298. <i>Open Forum Infectious Diseases</i> , 2019, 6, S848-S848. | 0.9 | 0 |
| 44 | Case Report of an Extensively Drug-Resistant <i>Klebsiella pneumoniae</i> Infection With Genomic Characterization of the Strain and Review of Similar Cases in the United States. <i>Open Forum Infectious Diseases</i> , 2018, 5, ofy074. | 0.9 | 34 |
| 45 | Comparative genomics analysis of <i>Clostridium difficile</i> epidemic strain DH/NAP11/106. <i>Microbes and Infection</i> , 2018, 20, 245-253. | 1.9 | 25 |
| 46 | <i>Clostridium difficile</i> Whole Genome Sequencing Reveals Limited Transmission Among Symptomatic Children: A Single-Center Analysis. <i>Clinical Infectious Diseases</i> , 2018, 67, 229-234. | 5.8 | 31 |
| 47 | Whole-genome analysis reveals the evolution and transmission of an MDR DH/NAP11/106 <i>Clostridium difficile</i> clone in a paediatric hospital. <i>Journal of Antimicrobial Chemotherapy</i> , 2018, 73, 1222-1229. | 3.0 | 10 |
| 48 | ClustAGE: a tool for clustering and distribution analysis of bacterial accessory genomic elements. <i>BMC Bioinformatics</i> , 2018, 19, 150. | 2.6 | 40 |
| 49 | Environmental reservoirs for <i>exoS</i> ⁺ and <i>exoU</i> ⁺ strains of <i>Pseudomonas aeruginosa</i> . <i>Environmental Microbiology Reports</i> , 2018, 10, 485-492. | 2.4 | 25 |
| 50 | 976. <i>Clostridium difficile</i> Colonization Molecular Epidemiology and Anti-toxin Serological Responses in Healthy Infants: A Prospective Cohort Study. <i>Open Forum Infectious Diseases</i> , 2018, 5, S39-S40. | 0.9 | 0 |
| 51 | Treating complicated carbapenem-resistant enterobacteriaceae infections with ceftazidime/avibactam: a retrospective study with molecular strain characterisation. <i>International Journal of Antimicrobial Agents</i> , 2017, 49, 770-773. | 2.5 | 40 |
| 52 | Complete Genome Sequence of <i>Clostridioides difficile</i> Epidemic Strain DH/NAP11/106/ST-42, Isolated from Stool from a Pediatric Patient with Diarrhea. <i>Genome Announcements</i> , 2017, 5, . | 0.8 | 3 |
| 53 | Virulence Characteristics of Carbapenem-Resistant <i>Klebsiella pneumoniae</i> Strains from Patients with Necrotizing Skin and Soft Tissue Infections. <i>Scientific Reports</i> , 2017, 7, 13533. | 3.3 | 35 |
| 54 | A Method for Bioinformatic Analysis of Transposon Insertion Sequencing (INSeq) Results for Identification of Microbial Fitness Determinants. <i>Methods in Molecular Biology</i> , 2017, 1498, 243-253. | 0.9 | 0 |

| # | ARTICLE | IF | CITATIONS |
|----|---|------|-----------|
| 55 | Draft Genome Sequence of a Multidrug-Resistant <i>Klebsiella quasipneumoniae</i> subsp. <i>similipneumoniae</i> Isolate from a Clinical Source. <i>Genome Announcements</i> , 2016, 4, . | 0.8 | 10 |
| 56 | Emergence of Carbapenem-Resistant <i>Klebsiella pneumoniae</i> (CR-KP) as a Cause of Necrotizing Skin and Soft Tissue Infections (NSSTI) and Characterization of Associated Virulence Factors. <i>Open Forum Infectious Diseases</i> , 2016, 3, . | 0.9 | 0 |
| 57 | Utility of Whole-Genome Sequencing in Characterizing <i>Acinetobacter</i> Epidemiology and Analyzing Hospital Outbreaks. <i>Journal of Clinical Microbiology</i> , 2016, 54, 593-612. | 3.9 | 103 |
| 58 | Influence of ACB complex genospecies on clinical outcomes in a U.S. hospital with high rates of multidrug resistance. <i>Journal of Infection</i> , 2015, 70, 144-152. | 3.3 | 56 |
| 59 | Shanghai fever: a distinct <i>Pseudomonas aeruginosa</i> enteric disease. <i>Gut</i> , 2014, 63, 736-743. | 12.1 | 78 |
| 60 | Draft Genome Sequence of <i>Acinetobacter baumannii</i> Strain ABBL099, a Multidrug-Resistant Clinical Outbreak Isolate with a Novel Multilocus Sequence Type. <i>Genome Announcements</i> , 2014, 2, . | 0.8 | 5 |
| 61 | Genome-Wide Identification of <i>Acinetobacter baumannii</i> Genes Necessary for Persistence in the Lung. <i>MBio</i> , 2014, 5, e01163-14. | 4.1 | 224 |
| 62 | Different paths to pathogenesis. <i>Trends in Microbiology</i> , 2014, 22, 168-169. | 7.7 | 3 |
| 63 | Erysipelas and Myocarditis. <i>Canadian Journal of Cardiology</i> , 2014, 30, 465.e11-465.e12. | 1.7 | 1 |
| 64 | Characterization of the core and accessory genomes of <i>Pseudomonas aeruginosa</i> using bioinformatic tools Spine and AGEnt. <i>BMC Genomics</i> , 2014, 15, 737. | 2.8 | 184 |
| 65 | Draft Genome Sequence of the <i>Pseudomonas aeruginosa</i> Bloodstream Isolate PABLO56. <i>Journal of Bacteriology</i> , 2012, 194, 5999-5999. | 2.2 | 2 |
| 66 | The Accessory Genome of <i>Pseudomonas aeruginosa</i> . <i>Microbiology and Molecular Biology Reviews</i> , 2010, 74, 621-641. | 6.6 | 267 |
| 67 | A Common Mutation in Paraoxonase-2 Results in Impaired Lactonase Activity. <i>Journal of Biological Chemistry</i> , 2009, 284, 35564-35571. | 3.4 | 51 |
| 68 | <i>Drosophila</i> are protected from <i>Pseudomonas aeruginosa</i> lethality by transgenic expression of paraoxonase-1. <i>Journal of Clinical Investigation</i> , 2008, 118, 3123-3131. | 8.2 | 74 |
| 69 | Paraoxonase-2 deficiency enhances <i>Pseudomonas aeruginosa</i> quorum sensing in murine tracheal epithelia. <i>American Journal of Physiology - Lung Cellular and Molecular Physiology</i> , 2007, 292, L852-L860. | 2.9 | 130 |
| 70 | Human and murine paraoxonase 1 are host modulators of <i>Pseudomonas aeruginosa</i> quorum-sensing. <i>FEMS Microbiology Letters</i> , 2005, 253, 29-37. | 1.8 | 196 |
| 71 | Xylitol Enhances Bacterial Killing in the Rabbit Maxillary Sinus. <i>Laryngoscope</i> , 2004, 114, 2021-2024. | 2.0 | 34 |
| 72 | Inactivation of a <i>Pseudomonas aeruginosa</i> quorum-sensing signal by human airway epithelia. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2004, 101, 3587-3590. | 7.1 | 266 |