

Egon A Ozer

List of Publications by Year in descending order

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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	The Accessory Genome of <i>Pseudomonas aeruginosa</i> . <i>Microbiology and Molecular Biology Reviews</i> , 2010, 74, 621-641.	6.6	267
2	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
3	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
4	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
5	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
6	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
7	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
8	Shanghai fever: a distinct <i>Pseudomonas aeruginosa</i> enteric disease. <i>Gut</i> , 2014, 63, 736-743.	12.1	78
9	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
10	The Population Structure of <i>Pseudomonas aeruginosa</i> Is Characterized by Genetic Isolation of exoU+ and exoS+ Lineages. <i>Genome Biology and Evolution</i> , 2019, 11, 1780-1796.	2.5	74
11	<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
12	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
13	A Common Mutation in Paraoxonase-2 Results in Impaired Lactonase Activity. <i>Journal of Biological Chemistry</i> , 2009, 284, 35564-35571.	3.4	51
14	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
15	ClustAGE: a tool for clustering and distribution analysis of bacterial accessory genomic elements. <i>BMC Bioinformatics</i> , 2018, 19, 150.	2.6	40
16	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
17	Has Omicron Changed the Evolution of the Pandemic?. <i>JMIR Public Health and Surveillance</i> , 2022, 8, e35763.	2.6	38
18	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

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19	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
20	Xylitol Enhances Bacterial Killing in the Rabbit Maxillary Sinus. <i>Laryngoscope</i> , 2004, 114, 2021-2024.	2.0	34
21	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
22	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
23	<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
24	Natural <i>Clostridioides difficile</i> Toxin Immunization in Colonized Infants. <i>Clinical Infectious Diseases</i> , 2020, 70, 2095-2102.	5.8	27
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	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
27	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
28	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
29	Multiple expansions of globally uncommon SARS-CoV-2 lineages in Nigeria. <i>Nature Communications</i> , 2022, 13, 688.	12.8	23
30	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
31	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
32	Antibody escape and global spread of SARS-CoV-2 lineage A.27. <i>Nature Communications</i> , 2022, 13, 1152.	12.8	20
33	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
34	Transcriptional initiation of a small RNA, not σ -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
35	Low-level SARS-CoV-2 viremia coincident with COVID placentitis and stillbirth. <i>Placenta</i> , 2022, 121, 79-81.	1.5	14
36	A Genome-Based Model to Predict the Virulence of <i>Pseudomonas aeruginosa</i> Isolates. <i>MBio</i> , 2020, 11, .	4.1	12

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37	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
38	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
39	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
40	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
41	Complete Genome Sequence of <i>Clostridium innocuum</i> Strain ATCC 14501. <i>Microbiology Resource Announcements</i> , 2020, 9, .	0.6	10
42	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
43	Optimizing aminoglycoside selection for KPC-producing <i>Klebsiella pneumoniae</i> with the aminoglycoside-modifying enzyme (AME) gene <i>aac(6)-Ib</i> . <i>Journal of Antimicrobial Chemotherapy</i> , 2021, 76, 671-679.	3.0	9
44	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
45	Genetic Evaluation of Nosocomial <i>Candida auris</i> Transmission. <i>Journal of Clinical Microbiology</i> , 2021, 59, .	3.9	8
46	Serological Markers of SARS-CoV-2 Reinfection. <i>MBio</i> , 2022, 13, e0214121.	4.1	8
47	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
48	Complete Genome Sequence of <i>Klebsiella pneumoniae</i> Strain TK421, a Conjugative Hypervirulent Isolate. <i>Microbiology Resource Announcements</i> , 2020, 9, .	0.6	6
49	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
50	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
51	<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
52	PacBio Amplicon Sequencing Method To Measure Pilin Antigenic Variation Frequencies of <i>Neisseria gonorrhoeae</i> . <i>MSphere</i> , 2019, 4, .	2.9	5
53	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
54	The Future of Bacteriophage Therapy Will Promote Antimicrobial Susceptibility. <i>MSystems</i> , 2021, 6, e0021821.	3.8	5

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55	Discovery of a New <i>Neisseria gonorrhoeae</i> Type IV Pilus Assembly Factor, TfpC. <i>MBio</i> , 2020, 11, .	4.1	5
56	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
57	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
58	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
59	Different paths to pathogenesis. <i>Trends in Microbiology</i> , 2014, 22, 168-169.	7.7	3
60	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
61	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
62	Draft Genome Sequence of the <i>Pseudomonas aeruginosa</i> Bloodstream Isolate PABLO56. <i>Journal of Bacteriology</i> , 2012, 194, 5999-5999.	2.2	2
63	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
64	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
65	Erysipelas and Myocarditis. <i>Canadian Journal of Cardiology</i> , 2014, 30, 465.e11-465.e12.	1.7	1
66	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
67	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
68	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
69	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
70	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
71	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
72	520. Longitudinal Analysis of SARS-CoV-2 Viruses in Hospitalized Adults. <i>Open Forum Infectious Diseases</i> , 2020, 7, S325-S326.	0.9	0