

Taj Azarian

List of Publications by Year in descending order

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Version: 2024-02-01

38
papers

670
citations

567281

15
h-index

642732

23
g-index

49
all docs

49
docs citations

49
times ranked

1264
citing authors

| # | ARTICLE | IF | CITATIONS |
|----|---|-----|-----------|
| 1 | Early Emergence Phase of SARS-CoV-2 Delta Variant in Florida, US. <i>Viruses</i> , 2022, 14, 766. | 3.3 | 1 |
| 2 | Meaningful Use of Pathogen Genomic Data. <i>MBio</i> , 2022, , e0031122. | 4.1 | 1 |
| 3 | Carriage prevalence and genomic epidemiology of <i>Staphylococcus aureus</i> among Native American children and adults in the Southwestern USA. <i>Microbial Genomics</i> , 2022, 8, . | 2.0 | 5 |
| 4 | Complete Genome Sequences of Nine <i>Streptococcus pneumoniae</i> Serotype 3 Clonal Complex 180 Strains. <i>Microbiology Resource Announcements</i> , 2022, 11, . | 0.6 | 1 |
| 5 | The Importance of Pathogen Whole-Genome Sequencing in Evaluating Interventions to Reduce the Spread of Multidrug-Resistant Organisms in the Healthcare Setting. <i>Clinical Infectious Diseases</i> , 2021, 72, 1888-1890. | 5.8 | 0 |
| 6 | Complete Genome Sequence of Exfoliative Toxin-Producing <i>Staphylococcus aureus</i> Strain MSSA_SSSS_01, Obtained from a Case of Staphylococcal Scalded-Skin Syndrome. <i>Microbiology Resource Announcements</i> , 2021, 10, . | 0.6 | 2 |
| 7 | SARS-CoV-2 shifting transmission dynamics and hidden reservoirs potentially limit efficacy of public health interventions in Italy. <i>Communications Biology</i> , 2021, 4, 489. | 4.4 | 23 |
| 8 | Genomic Epidemiology and Global Population Structure of Exfoliative Toxin A-Producing <i>Staphylococcus aureus</i> Strains Associated With Staphylococcal Scalded Skin Syndrome. <i>Frontiers in Microbiology</i> , 2021, 12, 663831. | 3.5 | 8 |
| 9 | Toxigenic <i>Vibrio cholerae</i> evolution and establishment of reservoirs in aquatic ecosystems. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2020, 117, 7897-7904. | 7.1 | 33 |
| 10 | Structure and Dynamics of Bacterial Populations: Pangenome Ecology. , 2020, , 115-128. | | 15 |
| 11 | Frequency-dependent selection can forecast evolution in <i>Streptococcus pneumoniae</i> . <i>PLoS Biology</i> , 2020, 18, e3000878. | 5.6 | 24 |
| 12 | Draft Genome Sequence of <i>Verrucosipora</i> sp. Strain CWR15, Isolated from a Gulf of Mexico Sponge. <i>Microbiology Resource Announcements</i> , 2020, 9, . | 0.6 | 2 |
| 13 | Frequency-dependent selection can forecast evolution in <i>Streptococcus pneumoniae</i> . , 2020, 18, e3000878. | | 0 |
| 14 | Frequency-dependent selection can forecast evolution in <i>Streptococcus pneumoniae</i> . , 2020, 18, e3000878. | | 0 |
| 15 | Frequency-dependent selection can forecast evolution in <i>Streptococcus pneumoniae</i> . , 2020, 18, e3000878. | | 0 |
| 16 | Frequency-dependent selection can forecast evolution in <i>Streptococcus pneumoniae</i> . , 2020, 18, e3000878. | | 0 |
| 17 | Frequency-dependent selection can forecast evolution in <i>Streptococcus pneumoniae</i> . , 2020, 18, e3000878. | | 0 |
| 18 | Frequency-dependent selection can forecast evolution in <i>Streptococcus pneumoniae</i> . , 2020, 18, e3000878. | | 0 |

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|----|--|-----|-----------|
| 19 | Long-Term Intra-host Evolution of Methicillin Resistant <i>Staphylococcus aureus</i> Among Cystic Fibrosis Patients With Respiratory Carriage. <i>Frontiers in Genetics</i> , 2019, 10, 546. | 2.3 | 24 |
| 20 | Unexpected Predictors of Antibiotic Resistance in Housekeeping Genes of <i>Staphylococcus Aureus</i> . , 2019, 2019, 259-268. | | 8 |
| 21 | Population genomics of pneumococcal carriage in Massachusetts children following introduction of PCV-13. <i>Microbial Genomics</i> , 2019, 5, . | 2.0 | 12 |
| 22 | Global emergence and population dynamics of divergent serotype 3 CC180 pneumococci. <i>PLoS Pathogens</i> , 2018, 14, e1007438. | 4.7 | 74 |
| 23 | The impact of serotype-specific vaccination on phylodynamic parameters of <i>Streptococcus pneumoniae</i> and the pneumococcal pan-genome. <i>PLoS Pathogens</i> , 2018, 14, e1006966. | 4.7 | 25 |
| 24 | Pneumococcal protein antigen serology varies with age and may predict antigenic profile of colonizing isolates. <i>Journal of Infectious Diseases</i> , 2017, 215, jiw628. | 4.0 | 18 |
| 25 | Multi-drug resistant <i>Klebsiella pneumoniae</i> strains circulating in hospital setting: whole-genome sequencing and Bayesian phylogenetic analysis for outbreak investigations. <i>Scientific Reports</i> , 2017, 7, 3534. | 3.3 | 22 |
| 26 | Th17-Mediated Cross Protection against Pneumococcal Carriage by Vaccination with a Variable Antigen. <i>Infection and Immunity</i> , 2017, 85, . | 2.2 | 36 |
| 27 | Population Structure of Pathogenic Bacteria. , 2017, , 51-70. | | 25 |
| 28 | Genomic Epidemiology of Methicillin-Resistant <i>Staphylococcus aureus</i> in a Neonatal Intensive Care Unit. <i>PLoS ONE</i> , 2016, 11, e0164397. | 2.5 | 25 |
| 29 | Non-toxigenic environmental <i>Vibrio cholerae</i> O1 strain from Haiti provides evidence of pre-pandemic cholera in Hispaniola. <i>Scientific Reports</i> , 2016, 6, 36115. | 3.3 | 31 |
| 30 | Intra-host Evolution of Methicillin-Resistant <i>Staphylococcus aureus</i> USA300 Among Individuals With Reoccurring Skin and Soft-Tissue Infections. <i>Journal of Infectious Diseases</i> , 2016, 214, 895-905. | 4.0 | 40 |
| 31 | Whole-Genome Sequencing for Outbreak Investigations of Methicillin-Resistant <i>Staphylococcus aureus</i> in the Neonatal Intensive Care Unit: Time for Routine Practice?. <i>Infection Control and Hospital Epidemiology</i> , 2015, 36, 777-785. | 1.8 | 62 |
| 32 | Whole-Genome Sequencing (WGS) of 19 Methicillin-Resistant <i>Staphylococcus aureus</i> (MRSA) Isolates From Recurrent Infections in 4 Patients: USA300 Strain Replacement. <i>Open Forum Infectious Diseases</i> , 2015, 2, . | 0.9 | 0 |
| 33 | Impact of spatial dispersion, evolution and selection on Ebola Zaire Virus epidemic waves. <i>Scientific Reports</i> , 2015, 5, 10170. | 3.3 | 27 |
| 34 | High-Frequency Rugose Exopolysaccharide Production by <i>Vibrio cholerae</i> Strains Isolated in Haiti. <i>PLoS ONE</i> , 2014, 9, e112853. | 2.5 | 5 |
| 35 | 273Genomic Epidemiology of Methicillin-resistant <i>Staphylococcus aureus</i> in a Neonatal Intensive Care Unit. <i>Open Forum Infectious Diseases</i> , 2014, 1, S115-S116. | 0.9 | 0 |
| 36 | Phylodynamic Analysis of Clinical and Environmental <i>Vibrio cholerae</i> Isolates from Haiti Reveals Diversification Driven by Positive Selection. <i>MBio</i> , 2014, 5, . | 4.1 | 45 |

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|----|--|-----|-----------|
| 37 | Molecular Epidemiology of Community-Associated Methicillin-resistant Staphylococcus aureus in the genomic era: a Cross-Sectional Study. Scientific Reports, 2013, 3, 1902. | 3.3 | 49 |
| 38 | HIV-1 Subtype distribution in morocco based on national sentinel surveillance data 2004-2005. AIDS Research and Therapy, 2012, 9, 5. | 1.7 | 7 |