

Saugat Poudel

List of Publications by Year in descending order

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Version: 2024-02-01

16
papers

545
citations

932766

10
h-index

940134

16
g-index

29
all docs

29
docs citations

29
times ranked

342
citing authors

| # | ARTICLE | IF | CITATIONS |
|----|---|-----|-----------|
| 1 | Machine Learning of All Mycobacterium tuberculosis H37Rv RNA-seq Data Reveals a Structured Interplay between Metabolism, Stress Response, and Infection. <i>MSphere</i> , 2022, 7, e0003322. | 1.3 | 22 |
| 2 | Mathematical models to study the biology of pathogens and the infectious diseases they cause. <i>IScience</i> , 2022, 25, 104079. | 1.9 | 8 |
| 3 | iModulonDB: a knowledgebase of microbial transcriptional regulation derived from machine learning. <i>Nucleic Acids Research</i> , 2021, 49, D112-D120. | 6.5 | 67 |
| 4 | Identifying the effect of vancomycin on health care-associated methicillin-resistant <i>Staphylococcus aureus</i> strains using bacteriological and physiological media. <i>GigaScience</i> , 2021, 10, . | 3.3 | 5 |
| 5 | Pangenome Analytics Reveal Two-Component Systems as Conserved Targets in ESKAPEE Pathogens. <i>MSystems</i> , 2021, 6, . | 1.7 | 24 |
| 6 | Independent component analysis recovers consistent regulatory signals from disparate datasets. <i>PLoS Computational Biology</i> , 2021, 17, e1008647. | 1.5 | 27 |
| 7 | Machine Learning of Bacterial Transcriptomes Reveals Responses Underlying Differential Antibiotic Susceptibility. <i>MSphere</i> , 2021, 6, e0044321. | 1.3 | 12 |
| 8 | RiboRid: A low cost, advanced, and ultra-efficient method to remove ribosomal RNA for bacterial transcriptomics. <i>PLoS Genetics</i> , 2021, 17, e1009821. | 1.5 | 16 |
| 9 | Machine Learning Uncovers a Data-Driven Transcriptional Regulatory Network for the Crenarchaeal Thermoacidophile <i>Sulfolobus acidocaldarius</i> . <i>Frontiers in Microbiology</i> , 2021, 12, 753521. | 1.5 | 20 |
| 10 | Optimal dimensionality selection for independent component analysis of transcriptomic data. <i>BMC Bioinformatics</i> , 2021, 22, 584. | 1.2 | 34 |
| 11 | Revealing 29 sets of independently modulated genes in <i>Staphylococcus aureus</i> , their regulators, and role in key physiological response. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2020, 117, 17228-17239. | 3.3 | 60 |
| 12 | A computational knowledge-base elucidates the response of <i>Staphylococcus aureus</i> to different media types. <i>PLoS Computational Biology</i> , 2019, 15, e1006644. | 1.5 | 41 |
| 13 | Characterization of CA-MRSA TCH1516 exposed to nafcillin in bacteriological and physiological media. <i>Scientific Data</i> , 2019, 6, 43. | 2.4 | 14 |
| 14 | Profiling the effect of nafcillin on HA-MRSA D712 using bacteriological and physiological media. <i>Scientific Data</i> , 2019, 6, 322. | 2.4 | 8 |
| 15 | Adaptive evolution reveals a tradeoff between growth rate and oxidative stress during naphthoquinone-based aerobic respiration. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2019, 116, 25287-25292. | 3.3 | 56 |
| 16 | Updated and standardized genome-scale reconstruction of <i>Mycobacterium tuberculosis</i> H37Rv, iEK1011, simulates flux states indicative of physiological conditions. <i>BMC Systems Biology</i> , 2018, 12, 25. | 3.0 | 63 |