# Saugat Poudel

## List of Publications by Year
## in descending order

| | | | |
|---|---|---|---|
| **16**<br>papers | **545**<br>citations | 932766<br>**10**<br>h-index | 940134<br>**16**<br>g-index |
| **29**<br>all docs | **29**<br>docs citations | **29**<br>times ranked | **342**<br>citing authors |

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