

Gayatri Ramakrishnan

List of Publications by Year in descending order

Source: <https://exaly.com/author-pdf/1534517/publications.pdf>

Version: 2024-02-01

10
papers

107
citations

1477746

6
h-index

1473754

9
g-index

10
all docs

10
docs citations

10
times ranked

162
citing authors

| # | ARTICLE | IF | CITATIONS |
|----|--|-----|-----------|
| 1 | Homology-Based Prediction of Potential Protein-Protein Interactions between Human Erythrocytes and Plasmodium falciparum. <i>Bioinformatics and Biology Insights</i> , 2015, 9, BBI.S31880. | 1.0 | 21 |
| 2 | Recognizing drug targets using evolutionary information: implications for repurposing FDA-approved drugs against <i>Mycobacterium tuberculosis</i> H37Rv. <i>Molecular BioSystems</i> , 2015, 11, 3316-3331. | 2.9 | 20 |
| 3 | Exploring anti-malarial potential of FDA approved drugs: an in silico approach. <i>Malaria Journal</i> , 2017, 16, 290. | 0.8 | 16 |
| 4 | From workstations to workbenches: Towards predicting physicochemically viable protein-protein interactions across a host and a pathogen. <i>IUBMB Life</i> , 2014, 66, 759-774. | 1.5 | 10 |
| 5 | SInCRE structural interactome computational resource for <i>Mycobacterium tuberculosis</i> . Database: the <i>Journal of Biological Databases and Curation</i> , 2015, 2015, bav060. | 1.4 | 10 |
| 6 | Enriching the annotation of <i>Mycobacterium tuberculosis</i> H37Rv proteome using remote homology detection approaches: Insights into structure and function. <i>Tuberculosis</i> , 2015, 95, 14-25. | 0.8 | 9 |
| 7 | In Silico Modeling of FDA-Approved Drugs for Discovery of Anticandida Agents: A Drug-Repurposing Approach. , 2019, , 463-526. | | 8 |
| 8 | Comparison of <i>Leptospira interrogans</i> and <i>Leptospira biflexa</i> genomes: analysis of potential leptospiral-host interactions. <i>Molecular BioSystems</i> , 2017, 13, 883-891. | 2.9 | 6 |
| 9 | Repurposing Drugs Based on Evolutionary Relationships Between Targets of Approved Drugs and Proteins of Interest. <i>Methods in Molecular Biology</i> , 2019, 1903, 45-59. | 0.4 | 4 |
| 10 | Computational recognition and analysis of hitherto uncharacterized nucleotide cyclase-like proteins in bacteria. <i>Biology Direct</i> , 2016, 11, 27. | 1.9 | 3 |