

Pritee Chunarkar Patil

List of Publications by Year in descending order

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Version: 2024-02-01

11
papers

96
citations

1683354

5
h-index

1473754

9
g-index

11
all docs

11
docs citations

11
times ranked

108
citing authors

| # | ARTICLE | IF | CITATIONS |
|----|--|-----|-----------|
| 1 | Identification of bio-active food compounds as potential SARS-CoV-2 PLpro inhibitors-modulators via negative image-based screening and computational simulations. <i>Computers in Biology and Medicine</i> , 2022, 145, 105474. | 3.9 | 4 |
| 2 | Prevalence of Hepatitis B in Blood Groups and Level of Education of Blood Donors in Al-Najaf Governorate. <i>Biosciences, Biotechnology Research Asia</i> , 2021, 17, 735-739. | 0.2 | 0 |
| 3 | Pharmacoinformatics approach based identification of potential Nsp15 endoribonuclease modulators for SARS-CoV-2 inhibition. <i>Archives of Biochemistry and Biophysics</i> , 2021, 700, 108771. | 1.4 | 15 |
| 4 | Multi-step molecular docking and dynamics simulation-based screening of large antiviral specific chemical libraries for identification of Nipah virus glycoprotein inhibitors. <i>Biophysical Chemistry</i> , 2021, 270, 106537. | 1.5 | 18 |
| 5 | Prevalence of Hepatitis B in Blood Groups and Level of Education of Blood Donors in Al-Najaf Governorate. <i>Biosciences, Biotechnology Research Asia</i> , 2021, 17, 839-851. | 0.2 | 0 |
| 6 | Identification of potential cruzain inhibitors using de novo design, molecular docking and dynamics simulations studies. <i>Journal of Biomolecular Structure and Dynamics</i> , 2020, 38, 4005-4015. | 2.0 | 6 |
| 7 | Computational screening of promising beta-secretase 1 inhibitors through multi-step molecular docking and molecular dynamics simulations - Pharmacoinformatics approach. <i>Journal of Molecular Structure</i> , 2020, 1205, 127660. | 1.8 | 22 |
| 8 | Structure-Based Screening of DNA GyraseB Inhibitors for Therapeutic Applications in Tuberculosis: a Pharmacoinformatics Study. <i>Applied Biochemistry and Biotechnology</i> , 2020, 192, 1107-1123. | 1.4 | 3 |
| 9 | De novo design based identification of potential HIV-1 integrase inhibitors: A pharmacoinformatics study. <i>Computational Biology and Chemistry</i> , 2020, 88, 107319. | 1.1 | 8 |
| 10 | An analysis of non-cultivable bacteria using WEKA. <i>Bioinformatics</i> , 2020, 16, 620-624. | 0.2 | 5 |
| 11 | Pharmacoinformatics-based identification of anti-bacterial catalase-peroxidase enzyme inhibitors. <i>Computational Biology and Chemistry</i> , 2019, 83, 107136. | 1.1 | 15 |