

Ziyad Tariq Muhseen

List of Publications by Year in descending order

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Version: 2024-02-01

14
papers

232
citations

1478505

6
h-index

1125743

13
g-index

14
all docs

14
docs citations

14
times ranked

406
citing authors

| # | ARTICLE | IF | CITATIONS |
|----|---|-----|-----------|
| 1 | Sociodemographic and Diabetes-Related Risk Factors in San Diego County, California. <i>Current Diabetes Reviews</i> , 2022, 18, . | 1.3 | 0 |
| 2 | Integrated computer-aided drug design and biophysical simulation approaches to determine natural anti-bacterial compounds for <i>Acinetobacter baumannii</i> . <i>Scientific Reports</i> , 2022, 12, 6590. | 3.3 | 6 |
| 3 | Computational Investigations of Traditional Chinese Medicinal Compounds against the Omicron Variant of SARS-CoV-2 to Rescue the Host Immune System. <i>Pharmaceuticals</i> , 2022, 15, 741. | 3.8 | 3 |
| 4 | Computational Determination of Potential Multiprotein Targeting Natural Compounds for Rational Drug Design Against SARS-COV-2. <i>Molecules</i> , 2021, 26, 674. | 3.8 | 27 |
| 5 | Natural products for treatment of <i>Plasmodium falciparum</i> malaria: An integrated computational approach. <i>Computers in Biology and Medicine</i> , 2021, 134, 104415. | 7.0 | 5 |
| 6 | Structural basis of UDP-N-acetylglucosamine pyrophosphorylase and identification of promising terpenes to control <i>Aedes aegypti</i> . <i>Colloids and Surfaces B: Biointerfaces</i> , 2021, 204, 111820. | 5.0 | 4 |
| 7 | Molecular Insights into Binding Mode and Interactions of Structure-Based Virtually Screened Inhibitors for <i>Pseudomonas aeruginosa</i> Multiple Virulence Factor Regulator (MvfR). <i>Molecules</i> , 2021, 26, 6811. | 3.8 | 2 |
| 8 | Determination of Novel Anti-Cancer Agents by Targeting OGG1 Enzyme Using Integrated Bioinformatics Methods. <i>International Journal of Environmental Research and Public Health</i> , 2021, 18, 13290. | 2.6 | 1 |
| 9 | Insights into the Binding of Receptor-Binding Domain (RBD) of SARS-CoV-2 Wild Type and B.1.620 Variant with hACE2 Using Molecular Docking and Simulation Approaches. <i>Biology</i> , 2021, 10, 1310. | 2.8 | 5 |
| 10 | Promising Terpenes as Natural Antagonists of Cancer: An In-Silico Approach. <i>Molecules</i> , 2020, 25, 155. | 3.8 | 13 |
| 11 | Promising terpenes as SARS-CoV-2 spike receptor-binding domain (RBD) attachment inhibitors to the human ACE2 receptor: Integrated computational approach. <i>Journal of Molecular Liquids</i> , 2020, 320, 114493. | 4.9 | 97 |
| 12 | Proteomics studies on stress responses in diatoms. <i>Proteomics</i> , 2015, 15, 3943-3953. | 2.2 | 30 |
| 13 | The Aromatic Stacking Interactions Between Proteins and their Macromolecular Ligands. <i>Current Protein and Peptide Science</i> , 2015, 16, 502-512. | 1.4 | 26 |
| 14 | Molecular modeling and molecular dynamics simulation study of the human Rab9 and RhoBTB3 C-terminus complex. <i>Bioinformation</i> , 2014, 10, 757-763. | 0.5 | 13 |