

# Abdulrahim A Alzain

## List of Publications by Year in descending order

Source: <https://exaly.com/author-pdf/1770817/publications.pdf>

Version: 2024-02-01

13  
papers

107  
citations

1478505

6  
h-index

1474206

9  
g-index

13  
all docs

13  
docs citations

13  
times ranked

11  
citing authors

#	ARTICLE	IF	CITATIONS
1	Discovery of novel natural products as rhodesain inhibitors for human African trypanosomiasis using in silico techniques. <i>Journal of Biomolecular Structure and Dynamics</i> , 2023, 41, 5672-5684.	3.5	0
2	Discovery of novel TMPRSS2 inhibitors for COVID-19 using in silico fragment-based drug design, molecular docking, molecular dynamics, and quantum mechanics studies. <i>Informatics in Medicine Unlocked</i> , 2022, 29, 100870.	3.4	22
3	Drug repurposing for SARS-CoV-2 main protease: Molecular docking and molecular dynamics investigations. <i>Biochemistry and Biophysics Reports</i> , 2022, 29, 101225.	1.3	16
4	De novo design of novel spike glycoprotein inhibitors using e-pharmacophore modeling, molecular hybridization, ADMET, quantum mechanics and molecular dynamics studies for COVID-19.. <i>Pakistan Journal of Pharmaceutical Sciences</i> , 2022, 35, 313-321.	0.2	1
5	Identification of novel Plasmodium falciparum dihydroorotate dehydrogenase inhibitors for malaria using in silico studies. <i>Scientific African</i> , 2022, 16, e01214.	1.5	6
6	Drug repurposing against main protease and RNA-dependent RNA polymerase of SARS-CoV-2 using molecular docking, MM-GBSA calculations and molecular dynamics. <i>Structural Chemistry</i> , 2022, 33, 1553-1567.	2.0	6
7	Dual targeting inhibitors for HIV-1 capsid and cyclophilin A: molecular docking, molecular dynamics, and quantum mechanics. <i>Molecular Simulation</i> , 2022, 48, 1476-1489.	2.0	6
8	Identification of novel transmembrane Protease Serine Type 2 drug candidates for COVID-19 using computational studies. <i>Informatics in Medicine Unlocked</i> , 2021, 26, 100725.	3.4	20
9	Bioinspired imidazo[1,2-a:4,5-câ€™]dipyridines with dual antiproliferative and anti-migrative properties in human cancer cells: The SAR investigation. <i>European Journal of Medicinal Chemistry</i> , 2021, 218, 113258.	5.5	3
10	Identification of novel TMPRSS2 inhibitors for COVID-19 using e-pharmacophore modelling, molecular docking, molecular dynamics and quantum mechanics studies. <i>Informatics in Medicine Unlocked</i> , 2021, 26, 100758.	3.4	15
11	Design of novel coumarins as potent Mcl-1 inhibitors for cancer treatment guided by 3D-QSAR, molecular docking and molecular dynamics. <i>Informatics in Medicine Unlocked</i> , 2021, 26, 100765.	3.4	10
12	Discovery of 5-Chlorobenzimidazole-based as Promising Inhibitors of Chloroquine-Resistant Plasmodium Strains: Synthesis, Biological Evaluation, Molecular Docking and Computational Studies. <i>Journal of Pharmaceutical Research International</i> , 0, , 136-147.	1.0	1
13	Phthalide derivatives as dihydrofolate reductase inhibitors for malaria: molecular docking and molecular dynamics studies. <i>Journal of Biomolecular Structure and Dynamics</i> , 0, , 1-11.	3.5	1