Mustapha Abdullahi

List of Publications by Year
in descending order

13	199	1163117 8	1199594 12
papers	citations	h-index	g-index

13	13	13	172
all docs	docs citations	times ranked	citing authors

#	Article	IF	Citations
1	Computer-aided modeling of triazole analogues, docking studies of the compounds on DNA gyrase enzyme and design of new hypothetical compounds with efficient activities. Journal of Biomolecular Structure and Dynamics, 2022, 40, 4004-4020.	3.5	14
2	Homology modeling and molecular docking simulation of some novel imidazo[1,2-a]pyridine-3-carboxamide (IPA) series as inhibitors of Mycobacterium tuberculosis. Journal of Genetic Engineering and Biotechnology, 2021, 19, 12.	3.3	14
3	In-silico design and ADMET predictions of some new imidazo[1,2-a]pyridine-3-carboxamides (IPAs) as anti-tubercular agents. Journal of Clinical Tuberculosis and Other Mycobacterial Diseases, 2021, 25, 100276.	1.3	7
4	In-silico modelling studies on some C14-urea-tetrandrine derivatives as potent anti-cancer agents against prostate (PC3) cell line. Journal of King Saud University - Science, 2020, 32, 770-779.	3.5	19
5	In-silico Molecular Docking and ADME/Pharmacokinetic Prediction Studies of Some Novel Carboxamide Derivatives as Anti-tubercular Agents. Chemistry Africa, 2020, 3, 989-1000.	2.4	39
6	Computational study of some cancer drugs as potent inhibitors of GSK3Î². Scientific African, 2020, 10, e00612.	1.5	8
7	In silico QSAR and molecular docking simulation of some novel aryl sulfonamide derivatives as inhibitors of H5N1 influenza A virus subtype. Beni-Suef University Journal of Basic and Applied Sciences, 2020, 9, .	2.0	25
8	Quantum modelling and molecular docking evaluation of some selected quinoline derivatives as anti-tubercular agents. Heliyon, 2020, 6, e03639.	3.2	24
9	Quantitative Structureâ€“Activity Relationship Model, Molecular Docking Simulation and Computational Design of Some Novel Compounds Against DNA Gyrase Receptor. Chemistry Africa, 2020, 3, 391-408.	2.4	20
10	Computational investigation, virtual docking simulation of 1, 2, 4-Triazole analogues and insillico design of new proposed agents against protein target (3IFZ) binding domain. Bulletin of the National Research Centre, 2020, 44, .	1.8	8
11	Virtual molecular docking study of some novel carboxamide series as new anti-tubercular agents. European Journal of Chemistry, 2020, 11, 30-36.	0.6	19
12	INSILICO MODELLING ON SOME C14-UREA TETRANDRINE COMPOUNDS AS POTENT ANTI-CANCER AGAINST HUMAN ERYTHROLEUKEMIA (HEL) CELL LINE. The Journal of Engineering and Exact Sciences, 2019, 5, 0063-0078.	0.1	1
13	Chemometric Study, Homology Modeling of G Protein-Coupled Bile Acids Receptor (GPBAR_HUMAN) of Type-2 Diabetes Mellitus, Virtual Screening Evaluation, Drug-Likeness and ADME Prediction for Newly Designed Compounds. Macromolecular Research, 0, , .	2.4	1