Mahmoud A El Hassab

List of Publications by Year
in descending order

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20 papers	402 citations	758635 12 h-index	794141 19 g-index
20 all docs	20 docs citations	20 times ranked	270 citing authors

#	Article	IF	Citations
1	Multi-stage structure-based virtual screening approach towards identification of potential SARS-CoV-2 NSP13 helicase inhibitorsÂ. Journal of Enzyme Inhibition and Medicinal Chemistry, 2022, 37, 563-572.	2.5	15
2	Development of potent nanosized isatin-isonicotinohydrazide hybrid for management of Mycobacterium tuberculosis. International Journal of Pharmaceutics, 2022, 612, 121369.	2.6	13
3	GC/MS Profiling, Anti-Collagenase, Anti-Elastase, Anti-Tyrosinase and Anti-Hyaluronidase Activities of a Stenocarpus sinuatus Leaves Extract. Plants, 2022, 11, 918.	1.6	43
4	Fenticonazole nitrate loaded trans-novasomes for effective management of tinea corporis: design characterization, in silico study, and exploratory clinical appraisal. Drug Delivery, 2022, 29, 1100-1111.	2.5	12
5	Development of 4-((3-oxo-3-phenylpropyl)amino)benzenesulfonamide derivatives utilizing tail/dual-tail approaches as novel carbonic anhydrase inhibitors. European Journal of Medicinal Chemistry, 2022, 238, 114412.	2.6	16
6	GC/MS analysis and potential synergistic effect of mandarin and marjoram oils on Helicobacter pylori. Journal of Enzyme Inhibition and Medicinal Chemistry, 2022, 37, 1610-1619.	2.5	6
7	LC/MS analysis of Viscum cruciatum Sieber ex Boiss. extract with anti-proliferative activity against MCF-7Âcell line via G0/G1 cell cycle arrest: An in-silico and in-vitro study. Journal of Ethnopharmacology, 2022, 295, 115439.	2.0	9
8	Multi-Step In Silico Discovery of Natural Drugs against COVID-19 Targeting Main Protease. International Journal of Molecular Sciences, 2022, 23, 6912.	1.8	43
9	In silico identification of potential SARS COV-2 2â€²-O-methyltransferase inhibitor: fragment-based screening approach and MM-PBSA calculations. RSC Advances, 2021, 11, 16026-16033.	1.7	15
10	In silico identification of novel SARS-COV-2 2â€²-O-methyltransferase (nsp16) inhibitors: structure-based virtual screening, molecular dynamics simulation and MM-PBSA approaches. Journal of Enzyme Inhibition and Medicinal Chemistry, 2021, 36, 727-736.	2.5	40
11	Development of novel isatinâ€“nicotinohydrazide hybrids with potent activity against susceptible/resistantMycobacterium tuberculosisand bronchitis causingâ€“bacteria. Journal of Enzyme Inhibition and Medicinal Chemistry, 2021, 36, 384-392.	2.5	30
12	Development of isatin-thiazolo[3,2-a]benzimidazole hybrids as novel CDK2 inhibitors with potent in vitro apoptotic anti-proliferative activity: Synthesis, biological and molecular dynamics investigations. Bioorganic Chemistry, 2021, 110, 104748.	2.0	50
13	In Silico Approach Using Free Software to Optimize the Antiproliferative Activity and Predict the Potential Mechanism of Action of Pyrrolizine-Based Schiff Bases. Molecules, 2021, 26, 4002.	1.7	9
14	Toward the Identification of Potential Î±-Ketoamide Covalent Inhibitors for SARS-CoV-2 Main Protease: Fragment-Based Drug Design and MM-PBSA Calculations. Processes, 2021, 9, 1004.	1.3	21
15	Cyclin-Dependent Kinase as a Novel Therapeutic Target: An Endless Story. Current Chemical Biology, 2021, 15, 139-162.	0.2	0
16	Computational prediction of the potential target of SARSâ€CoVâ€2 inhibitor plitidepsin via molecular docking, dynamic simulations and MMâ€PBSA calculations. Chemistry and Biodiversity, 2021, , .	1.0	4
17	Identification of potential inhibitors for HCV NS5b of genotype 4a by combining dynamic simulation, proteinâ€“ligand interaction fingerprint, 3D pharmacophore, docking and 3D QSAR. Journal of Biomolecular Structure and Dynamics, 2020, 38, 4521-4535.	2.0	10
18	Identification of a New Potential SARS-COV-2 RNA-Dependent RNA Polymerase Inhibitor via Combining Fragment-Based Drug Design, Docking, Molecular Dynamics, and MM-PBSA Calculations. Frontiers in Chemistry, 2020, 8, 584894.	1.8	35

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19	Unexpected Synthesis, Single-Crystal X-ray Structure, Anticancer Activity, and Molecular Docking Studies of Certain 2â€“((Imidazole/Benzimidazolâ€“2â€“yl)thio)â€“1â€“arylethanones. Crystals, 2020, 10, 446.	1.0	9
20	Identification of potential inhibitors for HCV NS3 genotype 4a by combining proteinâ€“ligand interaction fingerprint, 3D pharmacophore, docking, and dynamic simulation. Journal of Biomolecular Structure and Dynamics, 2018, 36, 1713-1727.	2.0	22