Mahmoud A El Hassab

List of Publications by Year
in descending order

Source: https://exaly.com/author-pdf/5647891/publications.pdf

Version: 2024-02-01

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	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
2	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
3	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
4	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
5	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
6	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
7	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
8	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
9	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
10	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
11	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
12	Development of potent nanosized isatin-isonicotinohydrazide hybrid for management of Mycobacterium tuberculosis. International Journal of Pharmaceutics, 2022, 612, 121369.	2.6	13
13	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
14	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
15	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
16	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
17	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
18	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

#	Article	IF	Citations
19	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
20	Cyclin-Dependent Kinase as a Novel Therapeutic Target: An Endless Story. Current Chemical Biology, 2021, 15, 139-162.	0.2	0