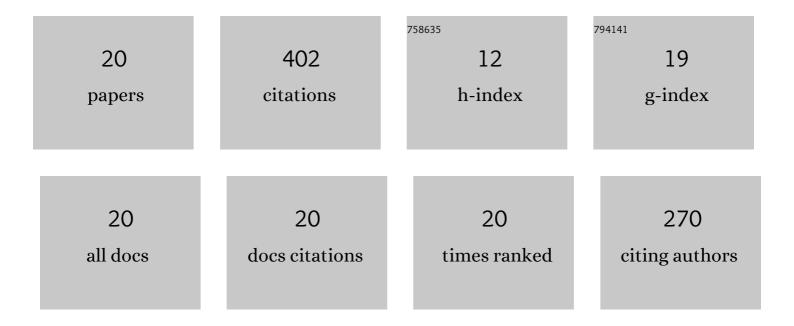
Mahmoud A El Hassab

List of Publications by Year in descending order

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#	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 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 isatin–nicotinohydrazide hybrids with potent activity against susceptible/resistant <i>Mycobacterium tuberculosis</i> and bronchitis causing–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 protein–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 α-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	<i>In silico</i> identification of potential SARS COV-2 2â€2- <i>O</i> -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, <i>in silico</i> 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, protein–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 2–((Imidazole/Benzimidazol–2–yl)thio)–1–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 <i>Helicobacter pylori</i> . 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