Karim M Elsawy

List of Publications by Year
in descending order

23 papers	1,693 citations	840585 11 h-index	839398 18 g-index
23 all docs	23 docs citations	23 times ranked	2970 citing authors

#	Article	IF	Citations
1	Bio3d: an R package for the comparative analysis of protein structures. Bioinformatics, 2006, 22, 2695-2696.	1.8	1,440
2	On the interaction mechanisms of a p53 peptide and nutlin with the MDM2 and MDMX proteins: A Brownian dynamics study. Cell Cycle, 2013, 12, 394-404.	1.3	38
3	The physical determinants of the DNA conformational landscape: an analysis of the potential energy surface of single-strand dinucleotides in the conformational space of duplex DNA. Nucleic Acids Research, 2005, 33, 5749-5762.	6.5	26
4	Blueprints for viral capsids in the family of Polyomaviridae. Journal of Theoretical Biology, 2008, 253, 808-816.	0.8	24
5	The Impact of Viral RNA on the Association Rates of Capsid Protein Assembly: Bacteriophage MS2 as a Case Study. Journal of Molecular Biology, 2010, 400, 935-947.	2.0	23
6	On the origin of the stereoselective affinity of Nutlin-3 geometrical isomers for the MDM2 protein. Cell Cycle, 2013, 12, 3727-3735.	1.3	18
7	Peptide Inhibitors of Viral Assembly: A Novel Route to Broad-Spectrum Antivirals. Journal of Chemical Information and Modeling, 2012, 52, 770-776.	2.5	17
8	Recognition Dynamics of p53 and MDM2: Implications for Peptide Design. Journal of Physical Chemistry B, 2016, 120, 320-328.	1.2	16
9	Characterization of the Ligand Receptor Encounter Complex and Its Potential for in Silico Kinetics-Based Drug Development. Journal of Chemical Theory and Computation, 2012, 8, 314-321.	2.3	15
10	Electronic Structure of Some Adenosine Receptor Antagonists. VQSAR Investigation. Journal of Chemical Information and Computer Sciences, 2002, 42, 386-392.	2.8	13
11	On the Origin of Order in the Genome Organization of ssRNA Viruses. Biophysical Journal, 2011, 101, 774-780.	0.2	12
12	A spatiotemporal characterization of the effect of p53 phosphorylation on its interaction with MDM2. Cell Cycle, 2015, 14, 179-188.	1.3	10
13	Reactivation of mutant p53: Constraints on mechanism highlighted by principal component analysis of the DNA binding domain. Proteins: Structure, Function and Bioinformatics, 2016, 84, 1443-1461.	1.5	10
14	Energy Landscape of Pentapeptides in a Higher-Order <mml:math xmlns:mml="http://www.w3.org/1998/Math/MathML" id="M1"><mml:mo stretchy="false">(</mml:mo><mml:mi>Ï•</mml:mi><mml:mo>,</mml:mo><mml:mi>Ï^</mml:mi><mml:mo) Tj ETQq0 0 0 rgBT /Overlock 2016, 2016, 1-10.	2.0	9
15	Electronic structure of some adenosine receptor antagonists. III. Quantitative investigation of the electronic absorption spectra of alkyl xanthines. Spectrochimica Acta - Part A: Molecular and Biomolecular Spectroscopy, 2002, 58, 2013-2027.	2.0	7
16	Potential Breast Anticancer Drug Targets Revealed by Differential Gene Regulatory Network Analysis and Molecular Docking: Neoadjuvant Docetaxel Drug as a Case Study. Cancer Informatics, 2018, 17, 117693511875535.	0.9	7
17	Dynamical implications of Viral Tiling Theory. Journal of Theoretical Biology, 2008, 252, 357-369.	0.8	4
18	Polyomaviridae Assembly Polymorphism from an Energy Landscape Perspective. Computational and Mathematical Methods in Medicine, 2008, 9, 245-256.	0.7	2

#	Article	IF	Citations
19	Disruption of 3CLpro protease self-association by short peptides as a potential route to broad spectrum coronavirus. Journal of Biomolecular Structure and Dynamics, 2021, , 1-11.	2.0	2
20	Electronic structure of some adenosine receptor antagonists: I. Equilibrium geometries, charge density distributions, and substituent effects. International Journal of Quantum Chemistry, 2002, 87, 389-399.	1.0	0
21	The impact of viral RNA on the association free energies of capsid protein assembly: bacteriophage MS2 as a case study. Journal of Molecular Modeling, 2017, 23, 47.	0.8	0
22	Activating the p53 anti-cancer pathway by targeting the MDM2/MDMX dimer interface with short peptide segments: a computational peptide design experiment. Molecular Systems Design and Engineering, 0, , .	1.7	0
23	Design of peptide-based coronavirus inhibitors that target disruption of 3CLpro protease self-association. Molecular Systems Design and Engineering, 0, , .	1.7	0