Wei Yang

List of Publications by Year
in descending order

Source: https://exaly.com/author-pdf/6891395/publications.pdf

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19	542	933447	794594
papers	citations	10	19
		h-index	g-index

22	22	22	789
all docs	docs citations	times ranked	citing authors

#	Article	IF	Citations
1	Recombining the structures of HIV integrase, RuvC and RNase H. Structure, 1995, 3, 131-134.	3.3	243
2	Mechanism of MicroRNA-Target Interaction: Molecular Dynamics Simulations and Thermodynamics Analysis. PLoS Computational Biology, 2010, 6, e1000866.	3.2	76
3	M1 aminopeptidases as drug targets: broad applications or therapeutic niche?. FEBS Journal, 2017, 284, 1473-1488.	4.7	53
4	Discovery of High Affinity Receptors for Dityrosine through Inverse Virtual Screening and Docking and Molecular Dynamics. International Journal of Molecular Sciences, 2019, 20, 115.	4.1	24
5	Dynamic communication between androgen and coactivator: Mutually induced conformational perturbations in androgen receptor ligandâ€binding domain. Proteins: Structure, Function and Bioinformatics, 2011, 79, 1154-1171.	2.6	22
6	3D-QSAR, molecular docking and molecular dynamics studies of a series of RORÎ³t inhibitors. Journal of Biomolecular Structure and Dynamics, 2015, 33, 1929-1940.	3.5	20
7	Novel Human Aminopeptidase N Inhibitors: Discovery and Optimization of Subsite Binding Interactions. Journal of Medicinal Chemistry, 2019, 62, 7185-7209.	6.4	17
8	Discovery of estrogen receptor modulators: a review of virtual screening and SAR efforts. Expert Opinion on Drug Discovery, 2010, 5, 21-31.	5.0	15
9	Structural analysis of selective agonists of thyroid hormone receptor Î² using 3D-QSAR and molecular docking. Journal of the Taiwan Institute of Chemical Engineers, 2015, 49, 1-18.	5.3	15
10	Generation of AMBER force field parameters for zinc centres of M1 and M17 family aminopeptidases. Journal of Biomolecular Structure and Dynamics, 2018, 36, 2595-2604.	3.5	13
11	Molecular determinants of thyroid hormone receptor selectivity in a series of phosphonic acid derivatives: 3D-QSAR analysis and molecular docking. Chemico-Biological Interactions, 2015, 240, 324-335.	4.0	9
12	Mapping the Pathway and Dynamics of Bestatin Inhibition of the Plasmodium falciparum M1 Aminopeptidase PfAâ€M1. ChemMedChem, 2018, 13, 2504-2513.	3.2	9
13	In silico study on Î²-aminoketone derivatives as thyroid hormone receptor inhibitors: a combined 3D-QSAR and molecular docking study. Journal of Biomolecular Structure and Dynamics, 2016, 34, 1-13.	3.5	4
14	Identification of the structural features of quinazoline derivatives as EGFR inhibitors using 3D-QSAR modeling, molecular docking, molecular dynamics simulations and free energy calculations. Journal of Biomolecular Structure and Dynamics, 2022, 40, 11125-11140.	3.5	4
15	Microscopic Observation of Preferential Capillary Pumping in Hollow Nanowire Bundles. Langmuir, 2021, , .	3.5	3
16	Probing the structural requirements for thyroid hormone receptor inhibitory activity of sulfonylnitrophenylthiazoles (SNPTs) using 2D-QSAR and 3D-QSAR approaches. Medicinal Chemistry Research, 2017, 26, 344-360.	2.4	2
17	Molecular-level understanding of the hTAS2R1 receptor-bitter tasting tetra-peptide binding: a structural biology study based on computational approaches. New Journal of Chemistry, 2021, 45, 21369-21381.	2.8	1
18	A metal ionâ€“dependent conformational switch modulates activity of the Plasmodium M17 aminopeptidase. Journal of Biological Chemistry, 2022, 298, 102119.	3.4	1

#	Article	IF	Citations
19	A feasible synthetic strategy for three-armed star poly(ester amine) via Michael addition polymerization. E-Polymers, 2009, 9, .	3.0	0