

Ting Ran

List of Publications by Year in descending order

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Version: 2024-02-01

25
papers

4,384
citations

687363

13
h-index

580821

25
g-index

27
all docs

27
docs citations

27
times ranked

6288
citing authors

#	ARTICLE	IF	CITATIONS
1	CHARMM36m: an improved force field for folded and intrinsically disordered proteins. <i>Nature Methods</i> , 2017, 14, 71-73.	19.0	3,959
2	Targeting epigenetic reader and eraser: Rational design, synthesis and in vitro evaluation of dimethylisoxazoles derivatives as BRD4/HDAC dual inhibitors. <i>Bioorganic and Medicinal Chemistry Letters</i> , 2016, 26, 2931-2935.	2.2	56
3	An Integrated Virtual Screening Approach for VEGFR-2 Inhibitors. <i>Journal of Chemical Information and Modeling</i> , 2013, 53, 3163-3177.	5.4	48
4	De Novo Molecule Design Through the Molecular Generative Model Conditioned by 3D Information of Protein Binding Sites. <i>Journal of Chemical Information and Modeling</i> , 2021, 61, 3240-3254.	5.4	38
5	A hypermethylation strategy utilized by enhancer-bound CARM1 to promote estrogen receptor β -dependent transcriptional activation and breast carcinogenesis. <i>Theranostics</i> , 2020, 10, 3451-3473.	10.0	31
6	Identification of Covalent Binding Sites Targeting Cysteines Based on Computational Approaches. <i>Molecular Pharmaceutics</i> , 2016, 13, 3106-3118.	4.6	22
7	Structure of Mycobacterium tuberculosis cytochrome bcc in complex with Q203 and TB47, two anti-TB drug candidates. <i>ELife</i> , 2021, 10, .	6.0	22
8	Novel Strategy for Three-Dimensional Fragment-Based Lead Discovery. <i>Journal of Chemical Information and Modeling</i> , 2011, 51, 959-974.	5.4	20
9	Structure-based and shape-complemented pharmacophore modeling for the discovery of novel checkpoint kinase 1 inhibitors. <i>Journal of Molecular Modeling</i> , 2010, 16, 1195-1204.	1.8	18
10	Insight into the key interactions of bromodomain inhibitors based on molecular docking, interaction fingerprinting, molecular dynamics and binding free energy calculation. <i>Molecular BioSystems</i> , 2015, 11, 1295-1304.	2.9	18
11	Fragment virtual screening based on Bayesian categorization for discovering novel VEGFR-2 scaffolds. <i>Molecular Diversity</i> , 2015, 19, 895-913.	3.9	15
12	A selectivity study of sodium-dependent glucose cotransporter 2/sodium-dependent glucose cotransporter 1 inhibitors by molecular modeling. <i>Journal of Molecular Recognition</i> , 2015, 28, 467-479.	2.1	15
13	Discovery of a highly selective FLT3 inhibitor with specific proliferation inhibition against AML cells harboring FLT3-ITD mutation. <i>European Journal of Medicinal Chemistry</i> , 2019, 163, 195-206.	5.5	14
14	A selectivity study on mTOR/PI3K β inhibitors by homology modeling and 3D-QSAR. <i>Journal of Molecular Modeling</i> , 2012, 18, 171-186.	1.8	13
15	3D-QSAR and molecular fragment replacement study on diaminopyrimidine and pyrrolotriazine ALK inhibitors. <i>Journal of Molecular Structure</i> , 2014, 1067, 127-137.	3.6	13
16	In Silico Discovery of JMJD6 Inhibitors for Cancer Treatment. <i>ACS Medicinal Chemistry Letters</i> , 2019, 10, 1609-1613.	2.8	12
17	Discovery of 1-(5-(1H-benzo[d]imidazole-2-yl)-2,4-dimethyl-1H-pyrrol-3-yl)ethan-1-one derivatives as novel and potent bromodomain and extra-terminal (BET) inhibitors with anticancer efficacy. <i>European Journal of Medicinal Chemistry</i> , 2022, 227, 113953.	5.5	12
18	Synthesis and Biological Evaluation of 1-(2-Aminophenyl)-3-aryurea Derivatives as Potential EphA2 and HDAC Dual Inhibitors. <i>Chemical and Pharmaceutical Bulletin</i> , 2016, 64, 1136-1141.	1.3	11

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19	Kinase Inhibitor Scaffold Hopping with Deep Learning Approaches. <i>Journal of Chemical Information and Modeling</i> , 2021, 61, 4900-4912.	5.4	11
20	An efficient multistep ligand-based virtual screening approach for GPR40 agonists. <i>Molecular Diversity</i> , 2014, 18, 183-193.	3.9	10
21	Studies on [5,6]-Fused Bicyclic Scaffolds Derivatives as Potent Dual B-RafV600E/KDR Inhibitors Using Docking and 3D-QSAR Approaches. <i>International Journal of Molecular Sciences</i> , 2015, 16, 24451-24474.	4.1	9
22	Virtual Screening with a Structure-Based Pharmacophore Model to Identify Small-Molecule Inhibitors of CARM1. <i>Journal of Chemical Information and Modeling</i> , 2019, 59, 522-534.	5.4	8
23	Protein flexibility oriented virtual screening strategy for JAK2 inhibitors. <i>Journal of Molecular Structure</i> , 2015, 1097, 136-144.	3.6	5
24	De novodesign of quinazoline derivatives as CDK2 inhibitors: 3D-QSAR, molecular fragment replacement and Volsurf predictions. <i>Molecular Simulation</i> , 2011, 37, 824-836.	2.0	2
25	SyntaLinker-Hybrid: A deep learning approach for target specific drug design. <i>Artificial Intelligence in the Life Sciences</i> , 2022, 2, 100035.	2.2	2