Ting Ran

List of Publications by Year
in descending order

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25 papers	4,384 citations	686830 13 h-index	580395 25 g-index
27 all docs	27 docs citations	27 times ranked	6288 citing authors

#	Article	IF	Citations
1	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. European Journal of Medicinal Chemistry, 2022, 227, 113953.	2.6	12
2	SyntaLinker-Hybrid: A deep learning approach for target specific drug design. Artificial Intelligence in the Life Sciences, 2022, 2, 100035.	1.6	2
3	De Novo Molecule Design Through the Molecular Generative Model Conditioned by 3D Information of Protein Binding Sites. Journal of Chemical Information and Modeling, 2021, 61, 3240-3254.	2.5	38
4	Kinase Inhibitor Scaffold Hopping with Deep Learning Approaches. Journal of Chemical Information and Modeling, 2021, 61, 4900-4912.	2.5	11
5	Structure of Mycobacterium tuberculosis cytochrome bcc in complex with Q203 and TB47, two anti-TB drug candidates. ELife, 2021, 10, .	2.8	22
6	A hypermethylation strategy utilized by enhancer-bound CARM1 to promote estrogen receptor Î±-dependent transcriptional activation and breast carcinogenesis. Theranostics, 2020, 10, 3451-3473.	4.6	31
7	In Silico Discovery of JMJD6 Inhibitors for Cancer Treatment. ACS Medicinal Chemistry Letters, 2019, 10, 1609-1613.	1.3	12
8	Virtual Screening with a Structure-Based Pharmacophore Model to Identify Small-Molecule Inhibitors of CARM1. Journal of Chemical Information and Modeling, 2019, 59, 522-534.	2.5	8
9	Discovery of a highly selective FLT3 inhibitor with specific proliferation inhibition against AML cells harboring FLT3-ITD mutation. European Journal of Medicinal Chemistry, 2019, 163, 195-206.	2.6	14
10	CHARMM36m: an improved force field for folded and intrinsically disordered proteins. Nature Methods, 2017, 14, 71-73.	9.0	3,959
11	Targeting epigenetic reader and eraser: Rational design, synthesis and in vitro evaluation of dimethylisoxazoles derivatives as BRD4/HDAC dual inhibitors. Bioorganic and Medicinal Chemistry Letters, 2016, 26, 2931-2935.	1.0	56
12	Identification of Covalent Binding Sites Targeting Cysteines Based on Computational Approaches. Molecular Pharmaceutics, 2016, 13, 3106-3118.	2.3	22
13	Synthesis and Biological Evaluation of 1-(2-Aminophenyl)-3-arylurea Derivatives as Potential EphA2 and HDAC Dual Inhibitors. Chemical and Pharmaceutical Bulletin, 2016, 64, 1136-1141.	0.6	11
14	Studies on [5,6]-Fused Bicyclic Scaffolds Derivatives as Potent Dual B-RafV600E/KDR Inhibitors Using Docking and 3D-QSAR Approaches. International Journal of Molecular Sciences, 2015, 16, 24451-24474.	1.8	9
15	Insight into the key interactions of bromodomain inhibitors based on molecular docking, interaction fingerprinting, molecular dynamics and binding free energy calculation. Molecular BioSystems, 2015, 11, 1295-1304.	2.9	18
16	Fragment virtual screening based on Bayesian categorization for discovering novel VEGFR-2 scaffolds. Molecular Diversity, 2015, 19, 895-913.	2.1	15
17	Protein flexibility oriented virtual screening strategy for JAK2 inhibitors. Journal of Molecular Structure, 2015, 1097, 136-144.	1.8	5
18	A selectivity study of sodium-dependent glucose cotransporter 2/sodium-dependent glucose cotransporter 1 inhibitors by molecular modeling. Journal of Molecular Recognition, 2015, 28, 467-479.	1.1	15

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19	An efficient multistep ligand-based virtual screening approach for GPR40 agonists. Molecular Diversity, 2014, 18, 183-193.	2.1	10
20	3D-QSAR and molecular fragment replacement study on diaminopyrimidine and pyrrolotriazine ALK inhibitors. Journal of Molecular Structure, 2014, 1067, 127-137.	1.8	13
21	An Integrated Virtual Screening Approach for VEGFR-2 Inhibitors. Journal of Chemical Information and Modeling, 2013, 53, 3163-3177.	2.5	48
22	A selectivity study on mTOR/PI3KÎ± inhibitors by homology modeling and 3D-QSAR. Journal of Molecular Modeling, 2012, 18, 171-186.	0.8	13
23	De novodesign of quinazoline derivatives as CDK2 inhibitors: 3D-QSAR, molecular fragment replacement and Volsurf predictions. Molecular Simulation, 2011, 37, 824-836.	0.9	2
24	Novel Strategy for Three-Dimensional Fragment-Based Lead Discovery. Journal of Chemical Information and Modeling, 2011, 51, 959-974.	2.5	20
25	Structure-based and shape-complemented pharmacophore modeling for the discovery of novel checkpoint kinase 1 inhibitors. Journal of Molecular Modeling, 2010, 16, 1195-1204.	0.8	18