Ming Hao

List of Publications by Year
in descending order

23	574	759233 12	642732 23
papers	citations	h-index	g-index

23	23	23	785
all docs	docs citations	times ranked	citing authors

#	Article	IF	Citations
1	Open-source chemogenomic data-driven algorithms for predicting drugâ€“target interactions. Briefings in Bioinformatics, 2019, 20, 1465-1474.	6.5	28
2	A new chemoinformatics approach with improved strategies for effective predictions of potential drugs. Journal of Cheminformatics, 2018, 10, 50.	6.1	10
3	Predicting drug-target interactions by dual-network integrated logistic matrix factorization. Scientific Reports, 2017, 7, 40376.	3.3	71
4	Predicting drugâ€“drug interactions through drug structural similarities and interaction networks incorporating pharmacokinetics and pharmacodynamics knowledge. Journal of Cheminformatics, 2017, 9, 16.	6.1	82
5	Large-Scale Prediction of Drug-Target Interaction: a Data-Centric Review. AAPS Journal, 2017, 19, 1264-1275.	4.4	39
6	Cheminformatics analysis of the AR agonist and antagonist datasets in PubChem. Journal of Cheminformatics, 2016, 8, 37.	6.1	11
7	Improved prediction of drug-target interactions using regularized least squares integrating with kernel fusion technique. Analytica Chimica Acta, 2016, 909, 41-50.	5.4	46
8	PubChem applications in drug discovery: a bibliometric analysis. Drug Discovery Today, 2014, 19, 1751-1756.	6.4	53
9	An efficient algorithm coupled with synthetic minority over-sampling technique to classify imbalanced PubChem BioAssay data. Analytica Chimica Acta, 2014, 806, 117-127.	5.4	50
10	Web search and data mining of natural products and their bioactivities in PubChem. Science China Chemistry, 2013, 56, 1424-1435.	8.2	15
11	A Computational Study on Thiourea Analogs as Potent MK-2 Inhibitors. International Journal of Molecular Sciences, 2012, 13, 7057-7079.	4.1	4
12	Toward the Prediction of FBPase Inhibitory Activity Using Chemoinformatic Methods. International Journal of Molecular Sciences, 2012, 13, 7015-7037.	4.1	4
13	Docking, molecular dynamics and quantitative structure-activity relationship studies for HEPTs and DABOs as HIV-1 reverse transcriptase inhibitors. Journal of Molecular Modeling, 2012, 18, 2185-2198.	1.8	32
14	Exploring the structure requirement for PKCÎ¸ inhibitory activity of pyridinecarbonitrile derivatives: an in silico analysis. Journal of Molecular Graphics and Modelling, 2012, 34, 76-88.	2.4	2
15	Investigation on the binding mode of benzothiophene analogues as potent factor IXa (FIXa) inhibitors in thrombosis by CoMFA, docking and molecular dynamic studies. Journal of Enzyme Inhibition and Medicinal Chemistry, 2011, 26, 792-804.	5.2	9
16	Investigation of the Structure Requirement for 5-HT6 Binding Affinity of Arylsulfonyl Derivatives: A Computational Study. International Journal of Molecular Sciences, 2011, 12, 5011-5030.	4.1	15
17	Combined 3D-QSAR, Molecular Docking, and Molecular Dynamics Study on Piperazinyl-Glutamate-Pyridines/Pyrimidines as Potent P2Y12 Antagonists for Inhibition of Platelet Aggregation. Journal of Chemical Information and Modeling, 2011, 51, 2560-2572.	5.4	38
18	A classification study of human Î² 3-adrenergic receptor agonists using BCUT descriptors. Molecular Diversity, 2011, 15, 877-887.	3.9	9

#	Article	IF	Citations
19	Prediction of P2Y12 antagonists using a novel genetic algorithm-support vector machine coupled approach. Analytica Chimica Acta, 2011, 690, 53-63.	5.4	19
20	Investigation on Quantitative Structure Activity Relationships and Pharmacophore Modeling of a Series of mGluR2 Antagonists. International Journal of Molecular Sciences, 2011, 12, 5999-6023.	4.1	5
21	In Silico Identification of Structure Requirement for Novel Thiazole and Oxazole Derivatives as Potent Fructose 1,6-Bisphosphatase Inhibitors. International Journal of Molecular Sciences, 2011, 12, 8161-8180.	4.1	7
22	A Classification Study of Respiratory Syncytial Virus (RSV) Inhibitors by Variable Selection with Random Forest. International Journal of Molecular Sciences, 2011, 12, 1259-1280.	4.1	10
23	Prediction of PKCÎ¸ Inhibitory Activity Using the Random Forest Algorithm. International Journal of Molecular Sciences, 2010, 11, 3413-3433.	4.1	15