

Jianjun Tan

List of Publications by Year in descending order

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papers

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46
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46
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citing authors

#	ARTICLE	IF	CITATIONS
1	From machine learning to deep learning: progress in machine intelligence for rational drug discovery. <i>Drug Discovery Today</i> , 2017, 22, 1680-1685.	6.4	468
2	Therapeutic strategies underpinning the development of novel techniques for the treatment of HIV infection. <i>Drug Discovery Today</i> , 2010, 15, 186-197.	6.4	61
3	Prediction of the binding mode between BMS-378806 and HIV-1 gp120 by docking and molecular dynamics simulation. <i>Biochimica Et Biophysica Acta - Proteins and Proteomics</i> , 2006, 1764, 766-772.	2.3	39
4	Development of Integrase Inhibitors of Quinolone Acid Derivatives for Treatment of AIDS: An Overview. <i>Mini-Reviews in Medicinal Chemistry</i> , 2010, 10, 1046-1057.	2.4	28
5	Investigating interactions between HIV-1 gp41 and inhibitors by molecular dynamics simulation and MM-PBSA/GBSA calculations. <i>Computational and Theoretical Chemistry</i> , 2006, 766, 77-82.	1.5	25
6	Molecular dynamics simulations of the bacterial periplasmic heme binding proteins ShuT and PhuT. <i>Biophysical Chemistry</i> , 2008, 138, 42-49.	2.8	21
7	Design, Synthesis and Anti-HIV Integrase Evaluation of N-(5-Chloro-8-Hydroxy-2-Styrylquinolin-7-yl)Benzenesulfonamide Derivatives. <i>Molecules</i> , 2010, 15, 1903-1917.	3.8	20
8	Study on the inhibitory mechanism and binding mode of the hydroxycoumarin compound NSC158393 to HIV-1 integrase by molecular modeling. <i>Biopolymers</i> , 2009, 91, 700-709.	2.4	18
9	Cation-pi interactions at non-redundant protein-RNA interfaces. <i>Biochemistry (Moscow)</i> , 2014, 79, 643-652.	1.5	18
10	EDLMFC: an ensemble deep learning framework with multi-scale features combination for ncRNA-protein interaction prediction. <i>BMC Bioinformatics</i> , 2021, 22, 133.	2.6	18
11	DM-RPIs: Predicting ncRNA-protein interactions using stacked ensembling strategy. <i>Computational Biology and Chemistry</i> , 2019, 83, 107088.	2.3	17
12	Development of HIV-1 integrase inhibitors: recent molecular modeling perspectives. <i>Drug Discovery Today</i> , 2015, 20, 1337-1348.	6.4	14
13	The Current Status and Challenges in the Development of Fusion Inhibitors as Therapeutics for HIV-1 Infection. <i>Current Pharmaceutical Design</i> , 2013, 19, 1810-1817.	1.9	14
14	Allosteric transitions of ATP-binding cassette transporter MsbA studied by the adaptive anisotropic network model. <i>Proteins: Structure, Function and Bioinformatics</i> , 2015, 83, 1643-1653.	2.6	12
15	Molecular dynamics simulation on the complexes of N-terminal region of HIV-1 gp41 and its C-peptide inhibitors. <i>Computational and Theoretical Chemistry</i> , 2004, 682, 9-15.	1.5	11
16	Allosteric transitions of the maltose transporter studied by an elastic network model. <i>Biopolymers</i> , 2014, 101, 758-768.	2.4	8
17	Structure-activity relationship and binding mode studies for a series of diketo-acids as HIV integrase inhibitors by 3D-QSAR, molecular docking and molecular dynamics simulations. <i>RSC Advances</i> , 2016, 6, 27594-27606.	3.6	8
18	Studies on binding free energies and the binding mode by docking and MM-PBSA in gp41-ligand complex. <i>Molecular Simulation</i> , 2005, 31, 1051-1056.	2.0	7

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19	3D-QSAR studies of quinoline ring derivatives as HIV-1 integrase inhibitors. SAR and QSAR in Environmental Research, 2012, 23, 683-703.	2.2	7
20	Design, synthesis and activity evaluation of novel peptide fusion inhibitors targeting HIV-1 gp41. Bioorganic and Medicinal Chemistry, 2016, 24, 201-206.	3.0	7
21	Computational identification and analysis of early diagnostic biomarkers for kidney cancer. Journal of Human Genetics, 2019, 64, 1015-1022.	2.3	7
22	Computational Study of Binding Mode for N-substituted Pyrrole Derivatives to HIV-1 gp41*. Progress in Biochemistry and Biophysics, 2010, 37, 904-915.	0.3	7
23	The Identification and Analysis of MicroRNAs Combined Biomarkers for Hepatocellular Carcinoma Diagnosis. Medicinal Chemistry, 2022, 18, 1073-1085.	1.5	7
24	Constructing a Mobility and Acceleration Computing Platform with NVIDIA Jetson TK1. , 2015, , .		6
25	LPI-CSFFR: Combining serial fusion with feature reuse for predicting LncRNA-protein interactions. Computational Biology and Chemistry, 2022, 99, 107718.	2.3	6
26	Peptide HIV fusion inhibitors: modifications and conjugations. MedChemComm, 2014, 5, 1472-1482.	3.4	5
27	Molecular Dynamics Studies of the Inhibitor C34 Binding to the Wild-Type and Mutant HIV-1 gp41: Inhibitory and Drug Resistant Mechanism. PLoS ONE, 2014, 9, e111923.	2.5	4
28	Constructing a Bioinformatics Platform with Web and Mobile Services Based on NVIDIA Jetson TK1. International Journal of Grid and High Performance Computing, 2015, 7, 57-73.	0.9	4
29	Quantitative Structure Activity/Pharmacokinetics Relationship Studies of HIV-1 Protease Inhibitors Using Three Modelling Methods. Medicinal Chemistry, 2021, 17, 396-406.	1.5	4
30	An efficient perturbation method to predict the functionally key sites of glutamine binding protein. Computational Biology and Chemistry, 2017, 67, 62-68.	2.3	3
31	Combined topomer CoMFA and hologram QSAR studies of a series of pyrrole derivatives as potential HIV fusion inhibitors. Medicinal Chemistry Research, 2018, 27, 1770-1781.	2.4	3
32	Reverse Virtual Screening on Persistent Organic Pollutants 4,4'-DDE and CB-153. Wuli Huaxue Xuebao/ Acta Physico - Chimica Sinica, 2013, 29, 2276-2285.	4.9	2
33	Pharmacophore and docking-based 3D-QSAR studies on HIV-1 integrase inhibitors. Chemical Research in Chinese Universities, 2014, 30, 297-305.	2.6	2
34	Insights into the Functions of M-T Hook Structure in HIV Fusion Inhibitor Using Molecular Modeling. Computational Biology and Chemistry, 2016, 61, 202-209.	2.3	2
35	A novel peptide shows excellent anti-HIV-1 potency as a gp41 fusion inhibitor. Bioorganic and Medicinal Chemistry Letters, 2018, 28, 910-914.	2.2	2
36	An integrated GIS-based data model for multimodal urban public transportation analysis and management. , 2008, , .		1

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37	Identification of functionally key residues in maltose transporter with an elastic network model-based thermodynamic method. <i>Molecular Physics</i> , 2016, 114, 3407-3417.	1.7	1
38	Recent Advances in Predicting ncRNA-Protein Interactions Based on Machine Learning. <i>Current Chinese Science</i> , 2021, 1, 513-522.	0.5	1
39	Novel Nanotechnology Strategies for the Treatment and Prevention of HIV Infection. , 2012, , 467-489.		1
40	Estimation of soil moisture conditions with Landsat TM in Guangzhou. <i>Proceedings of SPIE</i> , 2008, , .	0.8	0
41	Analysis of the Interactions between the N-Terminal Peptide of gp41 and T20 Using Molecular Dynamics and Free Energy Calculations. , 2009, , .		0
42	Study on the Resistance and the Binding Mode of HIV-1 Integrase to NSC158393. , 2009, , .		0
43	Advances in Data Repositories for ncRNA-Protein Interaction Predictions Based on Machine Learning: A Mini-Review. <i>Current Chinese Science</i> , 2022, 2, 354-371.	0.5	0