Hua Wan

List of Publications by Year
in descending order

17 papers	265 citations	1040056 9 h-index	940533 16 g-index
17 all docs	17 docs citations	17 times ranked	370 citing authors

#	Article	IF	Citations
1	Classification and Design of HIV-1 Integrase Inhibitors Based on Machine Learning. Computational and Mathematical Methods in Medicine, 2021, 2021, 1-11.	1.3	6
2	Automatic Detection and Segmentation for Group-Housed Pigs Based on PigMS R-CNN. Sensors, 2021, 21, 3251.	3.8	15
3	Passion fruit detection and counting based on multiple scale faster R-CNN using RGB-D images. Precision Agriculture, 2020, 21, 1072-1091.	6.0	82
4	BP[dG]-induced distortions to DNA polymerase and DNA duplex: A detailed mechanism of BP adducts blocking replication. Food and Chemical Toxicology, 2020, 140, 111325.	3.6	8
5	An Overview of Computational Tools of Nucleic Acid Binding Site Prediction for Site-specific Proteins and Nucleases. Protein and Peptide Letters, 2020, 27, 370-384.	0.9	2
6	The Advances of the Structure and Function of Indoleamine 2, 3- dioxygenase 1 and Its Inhibitors. Current Protein and Peptide Science, 2020, 21, 1027-1039.	1.4	4
7	Probing the Behaviour of Cas1-Cas2 upon Protospacer Binding in CRISPR-Cas Systems using Molecular Dynamics Simulations. Scientific Reports, 2019, 9, 3188.	3.3	10
8	Inhibition Mechanism of Indoleamine 2, 3-Dioxygenase 1 (IDO1) by Amidoxime Derivatives and Its Revelation in Drug Design: Comparative Molecular Dynamics Simulations. Frontiers in Molecular Biosciences, 2019, 6, 164.	3.5	5
9	Applications of Molecular Simulation in the Discovery of Antituberculosis Drugs: A Review. Protein and Peptide Letters, 2019, 26, 648-663.	0.9	9
10	Single image deraining using deep convolutional networks. Multimedia Tools and Applications, 2018, 77, 25905-25918.	3.9	6
11	PD-L1 Nanobody Competitively Inhibits the Formation of the PD-1/PD-L1 Complex: Comparative Molecular Dynamics Simulations. International Journal of Molecular Sciences, 2018, 19, 1984.	4.1	31
12	Molecular Simulation Studies on the Binding Selectivity of Type-I Inhibitors in the Complexes with ROS1 versus ALK. Journal of Chemical Information and Modeling, 2017, 57, 977-987.	5.4	14
13	An effective HIV-1 integrase inhibitor screening platform: Rationality validation of drug screening, conformational mobility and molecular recognition analysis for PFV integrase complex with viral DNA. Journal of Molecular Graphics and Modelling, 2017, 78, 96-109.	2.4	3
14	3D-QSAR, Molecular Docking and Molecular Dynamics Simulation of Pseudomonas aeruginosa LpxC Inhibitors. International Journal of Molecular Sciences, 2017, 18, 761.	4.1	15
15	Potential Role of the Last Half Repeat in TAL Effectors Revealed by a Molecular Simulation Study. BioMed Research International, 2016, 2016, 1-11.	1.9	1
16	Exploring the molecular basis of RNA recognition by the dimeric RNA-binding protein via molecular simulation methods. RNA Biology, 2016, 13, 1133-1143.	3.1	18
17	Molecular Dynamics Simulations of DNA-Free and DNA-Bound TAL Effectors. PLoS ONE, 2013, 8, e76045.	2.5	36