

# Hua Wan

## List of Publications by Year in descending order

Source: <https://exaly.com/author-pdf/4390074/publications.pdf>

Version: 2024-02-01

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	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
2	Molecular Dynamics Simulations of DNA-Free and DNA-Bound TAL Effectors. PLoS ONE, 2013, 8, e76045.	2.5	36
3	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
4	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
5	3D-QSAR, Molecular Docking and Molecular Dynamics Simulation of Pseudomonas aeruginosa LpxC Inhibitors. International Journal of Molecular Sciences, 2017, 18, 761.	4.1	15
6	Automatic Detection and Segmentation for Group-Housed Pigs Based on PigMS R-CNN. Sensors, 2021, 21, 3251.	3.8	15
7	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
8	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
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	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
11	Single image deraining using deep convolutional networks. Multimedia Tools and Applications, 2018, 77, 25905-25918.	3.9	6
12	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
13	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
14	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
15	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
16	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
17	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