Yanjing Wang

List of Publications by Year
in descending order

25	627	687363 13	610901 24
papers	citations	h-index	g-index

26	26	26	585
all docs	docs citations	times ranked	citing authors

#	Article	IF	Citations
1	In silico and in vitro evaluation of kaempferol as a potential inhibitor of the <scp>SARSâ€CoV</scp>â€2 main protease (<scp>3CLpro</scp>). Phytotherapy Research, 2021, 35, 2841-2845.	5.8	80
2	MDF-SA-DDI: predicting drugâ€“drug interaction events based on multi-source drug fusion, multi-source feature fusion and transformer self-attention mechanism. Briefings in Bioinformatics, 2022, 23, .	6.5	59
3	A transformer-based model to predict peptideâ€“HLA class I binding and optimize mutated peptides for vaccine design. Nature Machine Intelligence, 2022, 4, 300-311.	16.0	55
4	DTI-MLCD: predicting drug-target interactions using multi-label learning with community detection method. Briefings in Bioinformatics, 2021, 22, .	6.5	52
5	SARS-CoV-2 new variants: Characteristic features and impact on the efficacy of different vaccines. Biomedicine and Pharmacotherapy, 2021, 143, 112176.	5.6	51
6	MDA-GCNFTG: identifying miRNA-disease associations based on graph convolutional networks via graph sampling through the feature and topology graph. Briefings in Bioinformatics, 2021, 22, .	6.5	43
7	Design, synthesis and structure-activity relationships of novel 4-phenoxyquinoline derivatives containing 1,2,4-triazolone moiety as c-Met kinase inhibitors. European Journal of Medicinal Chemistry, 2016, 123, 431-446.	5.5	38
8	ATC-NLSP: Prediction of the Classes of Anatomical Therapeutic Chemicals Using a Network-Based Label Space Partition Method. Frontiers in Pharmacology, 2019, 10, 971.	3.5	30
9	T4SE-XGB: Interpretable Sequence-Based Prediction of Type IV Secreted Effectors Using eXtreme Gradient Boosting Algorithm. Frontiers in Microbiology, 2020, 11, 580382.	3.5	23
10	NeuroPpred-Fuse: an interpretable stacking model for prediction of neuropeptides by fusing sequence information and feature selection methods. Briefings in Bioinformatics, 2021, 22, .	6.5	23
11	Bioinformatics analysis of the differences in the binding profile of the wild-type and mutants of the SARS-CoV-2 spike protein variants with the ACE2 receptor. Computers in Biology and Medicine, 2021, 138, 104936.	7.0	23
12	MDA-CF: Predicting MiRNA-Disease associations based on a cascade forest model by fusing multi-source information. Computers in Biology and Medicine, 2021, 136, 104706.	7.0	21
13	Blocking key mutated hotspot residues in the RBD of the omicron variant (B.1.1.529) with medicinal compounds to disrupt the RBD-hACE2 complex using molecular screening and simulation approaches. RSC Advances, 2022, 12, 7318-7327.	3.6	20
14	STS-NLSP: A Network-Based Label Space Partition Method for Predicting the Specificity of Membrane Transporter Substrates Using a Hybrid Feature of Structural and Semantic Similarity. Frontiers in Bioengineering and Biotechnology, 2019, 7, 306.	4.1	17
15	An Integrated Pan-Cancer Analysis and Structure-Based Virtual Screening of GPR15. International Journal of Molecular Sciences, 2019, 20, 6226.	4.1	15
16	An in-silico approach to identify the potential hot spots in SARS-CoV-2 spike RBD to block the interaction with ACE2 receptor. Journal of Biomolecular Structure and Dynamics, 2021, , 1-16.	3.5	14
17	New strategy for identifying potential natural HIV-1 non-nucleoside reverse transcriptase inhibitors against drug-resistance: an in silico study. Journal of Biomolecular Structure and Dynamics, 2020, 38, 3327-3341.	3.5	13
18	Discovering potent inhibitors against the Mpro of the SARS-CoV-2. A medicinal chemistry approach. Computers in Biology and Medicine, 2022, 143, 105235.	7.0	11

#	Article	IF	Citations
19	Subtractive proteomics assisted therapeutic targets mining and designing ensemble vaccine against Candida auris for immune response induction. Computers in Biology and Medicine, 2022, 145, 105462.	7.0	10
20	Towards an Ensemble Vaccine against the Pegivirus Using Computational Modelling Approaches and Its Validation through In Silico Cloning and Immune Simulation. Vaccines, 2021, 9, 818.	4.4	9
21	A protein coupling and molecular simulation analysis of the clinical mutants of androgen receptor revealed a higher binding for Leupaxin, to increase the prostate cancer invasion and motility. Computers in Biology and Medicine, 2022, 146, 105537.	7.0	6
22	Copper(<scp>ii</scp>)-mediated formation of oxazole-4-carbonitrile from acetophenone and coordinated cyanide anion via a radical coupling. RSC Advances, 2017, 7, 24643-24646.	3.6	5
23	Evaluation and identification of essential therapeutic proteins and vaccinomics approach towards multi-epitopes vaccine designing against Legionella pneumophila for immune response instigation. Computers in Biology and Medicine, 2022, 143, 105291.	7.0	3
24	Preharvest Hydrogen Peroxide Treatment Delays Leaf Senescence of Chinese Flowering Cabbage During Storage by Reducing Water Loss and Activating Antioxidant Defense System. Frontiers in Plant Science, 2022, 13, 856646.	3.6	3
25	Repositioning of experimentally validated anti-breast cancer peptides to target FAK-PAX complex to halt the breast cancer progression: a biomolecular simulation approach. Molecular Diversity, 0, , .	3.9	1