

# yanyi Chu

## List of Publications by Year in descending order

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13  
papers

595  
citations

759233

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times ranked

380  
citing authors

#	ARTICLE	IF	CITATIONS
1	MDF-SA-DDI: predicting drug-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
2	A transformer-based model to predict peptide-HLA class I binding and optimize mutated peptides for vaccine design. Nature Machine Intelligence, 2022, 4, 300-311.	16.0	55
3	De novo molecular design with deep molecular generative models for PPI inhibitors. Briefings in Bioinformatics, 2022, 23, .	6.5	27
4	DTI-MLCD: predicting drug-target interactions using multi-label learning with community detection method. Briefings in Bioinformatics, 2021, 22, .	6.5	52
5	DTI-CDF: a cascade deep forest model towards the prediction of drug-target interactions based on hybrid features. Briefings in Bioinformatics, 2021, 22, 451-462.	6.5	142
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	NeuroPred-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
8	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
9	Prediction of Blood-Brain Barrier Permeability of Compounds by Fusing Resampling Strategies and eXtreme Gradient Boosting. IEEE Access, 2021, 9, 9557-9566.	4.2	11
10	Accelerated Blood Clearance of Nanoemulsions Modified with PEG-Cholesterol and PEG-Phospholipid Derivatives in Rats: The Effect of PEG-Lipid Linkages and PEG Molecular Weights. Molecular Pharmaceutics, 2020, 17, 1059-1070.	4.6	24
11	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
12	Prediction of CYP450 Enzyme Substrate Selectivity Based on the Network-Based Label Space Division Method. Journal of Chemical Information and Modeling, 2019, 59, 4577-4586.	5.4	55
13	SPVec: A Word2vec-Inspired Feature Representation Method for Drug-Target Interaction Prediction. Frontiers in Chemistry, 2019, 7, 895.	3.6	52