Min Liu

List of Publications by Citations

17 papers	**225** citations
8 h-index	**15** g-index
17 ext. papers	**424** ext. citations
3.8 avg, IF	**3.75** L-index

#	Paper	IF	Citations
17	Identification of synthetic lethality based on a functional network by using machine learning algorithms. *Journal of Cellular Biochemistry*, **2019**, 120, 405-416	4.7	42
16	iATC-FRAKEL: a simple multi-label web server for recognizing anatomical therapeutic chemical classes of drugs with their fingerprints only. *Bioinformatics*, **2020**, 36, 3568-3569	7.2	40
15	Tissue Expression Difference between mRNAs and lncRNAs. *International Journal of Molecular Sciences*, **2018**, 19,	6.3	35
14	Identification of leukemia stem cell expression signatures through Monte Carlo feature selection strategy and support vector machine. *Cancer Gene Therapy*, **2020**, 27, 56-69	5.4	27
13	Classification of Widely and Rarely Expressed Genes with Recurrent Neural Network. *Computational and Structural Biotechnology Journal*, **2019**, 17, 49-60	6.8	26
12	Identification of genes related to proliferative diabetic retinopathy through RWR algorithm based on protein-protein interaction network. *Biochimica Et Biophysica Acta - Molecular Basis of Disease*, **2018**, 1864, 2369-2375	6.9	18
11	bSiteFinder, an improved protein-binding sites prediction server based on structural alignment: more accurate and less time-consuming. *Journal of Cheminformatics*, **2016**, 8, 38	8.6	10
10	DNN-m6A: A Cross-Species Method for Identifying RNA N6-Methyladenosine Sites Based on Deep Neural Network with Multi-Information Fusion. *Genes*, **2021**, 12,	4.2	8
9	Succinylation Site Prediction Based on Protein Sequences Using the IFS-LightGBM (BO) Model. *Computational and Mathematical Methods in Medicine*, **2020**, 2020, 8858489	2.8	6
8	Predicting Protein Ligand Binding Sites with Structure Alignment Method on Hadoop. *Current Proteomics*, **2016**, 13, 113-121	0.7	4
7	Structural protein fold recognition based on secondary structure and evolutionary information using machine learning algorithms. *Computational Biology and Chemistry*, **2021**, 91, 107456	3.6	3
6	iMPT-FRAKEL: A Simple Multi-label Web-server that Only Uses Fingerprints to Identify which Metabolic Pathway Types Compounds can Participate In. *Open Bioinformatics Journal*, **2020**, 13, 83-91	0.8	2
5	The research of routing algorithm based on density control for underwater acoustic sensor networks **2011**,		1
4	Prediction of Citrullination Sites on the Basis of mRMR Method and SNN. *Combinatorial Chemistry and High Throughput Screening*, **2019**, 22, 705-715	1.3	1
3	Prediction of Nitration Sites Based on FCBF Method and Stacking Ensemble Model. *Current Proteomics*, **2021**, 18,	0.7	1
2	BERT-m7G: A Transformer Architecture Based on BERT and Stacking Ensemble to Identify RNA N7-Methylguanosine Sites from Sequence Information. *Computational and Mathematical Methods in Medicine*, **2021**, 2021, 7764764	2.8	1
1	Relating Substructures and Side Effects of Drugs with Chemical-chemical Interactions. *Combinatorial Chemistry and High Throughput Screening*, **2020**, 23, 285-294	1.3	0