

# Min Liu

## List of Publications by Year in Descending Order

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**Version:** 2024-04-28

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The third column is the impact factor (IF) of the journal, and the fourth column is the number of citations of the article.

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

