Hui Liu

List of Publications by Year
in descending order

33	1,291	471371	434063
papers	citations	17 h-index	31 g-index

39	39	39	1734
all docs	docs citations	times ranked	citing authors

#	Article	IF	Citations
1	Cassava genome from a wild ancestor to cultivated varieties. Nature Communications, 2014, 5, 5110.	5.8	230
2	Improving compoundâ€“protein interaction prediction by building up highly credible negative samples. Bioinformatics, 2015, 31, i221-i229.	1.8	201
3	SynLethDB: synthetic lethality database toward discovery of selective and sensitive anticancer drug targets. Nucleic Acids Research, 2016, 44, D1011-D1017.	6.5	115
4	DrugCombDB: a comprehensive database of drug combinations toward the discovery of combinatorial therapy. Nucleic Acids Research, 2020, 48, D871-D881.	6.5	99
5	Inferring new indications for approved drugs via random walk on drug-disease heterogenous networks. BMC Bioinformatics, 2016, 17, 539.	1.2	72
6	DeepDDS: deep graph neural network with attention mechanism to predict synergistic drug combinations. Briefings in Bioinformatics, 2022, 23, .	3.2	59
7	Anti-aging effect of polysaccharide from Bletilla striata on nematode Caenorhabditis elegans. Pharmacognosy Magazine, 2015, 11, 449.	0.3	54
8	Beneficial Effects of Wheat Gluten Hydrolysate to Extend Lifespan and Induce Stress Resistance in Nematode Caenorhabditis elegans. PLoS ONE, 2013, 8, e74553.	1.1	40
9	PDRLGB: precise DNA-binding residue prediction using a light gradient boosting machine. BMC Bioinformatics, 2018, 19, 522.	1.2	33
10	Predicting effective drug combinations using gradient tree boosting based on features extracted from drug-protein heterogeneous network. BMC Bioinformatics, 2019, 20, 645.	1.2	33
11	Accurate prediction of protein-lncRNA interactions by diffusion and HeteSim features across heterogeneous network. BMC Bioinformatics, 2018, 19, 370.	1.2	32
12	Pathway-Guided Deep Neural Network toward Interpretable and Predictive Modeling of Drug Sensitivity. Journal of Chemical Information and Modeling, 2020, 60, 4497-4505.	2.5	31
13	miRFANs: an integrated database for Arabidopsis thalianamicroRNA function annotations. BMC Plant Biology, 2012, 12, 68.	1.6	30
14	Graph2MDA: a multi-modal variational graph embedding model for predicting microbeâ€“drug associations. Bioinformatics, 2022, 38, 1118-1125.	1.8	26
15	A comparative evaluation on prediction methods of nucleosome positioning. Briefings in Bioinformatics, 2014, 15, 1014-1027.	3.2	23
16	Effectively Identifying Compound-Protein Interactions by Learning from Positive and Unlabeled Examples. IEEE/ACM Transactions on Computational Biology and Bioinformatics, 2018, 15, 1832-1843.	1.9	21
17	MADOKA: an ultra-fast approach for large-scale protein structure similarity searching. BMC Bioinformatics, 2019, 20, 662.	1.2	21
18	HNet-DNN: Inferring New Drugâ€“Disease Associations with Deep Neural Network Based on Heterogeneous Network Features. Journal of Chemical Information and Modeling, 2020, 60, 2367-2376.	2.5	19

#	Article	IF	Citations
19	PredCSO: an ensemble method for the prediction of S-sulfenylation sites in proteins. Molecular Omics, 2018, 14, 257-265.	1.4	16
20	SynLethDB 2.0: a web-based knowledge graph database on synthetic lethality for novel anticancer drug discovery. Database: the Journal of Biological Databases and Curation, 2022, 2022, .	1.4	16
21	Protein function prediction by collective classification with explicit and implicit edges in protein-protein interaction networks. BMC Bioinformatics, 2013, 14, S4.	1.2	15
22	The Lifespan-Extending Effects of Nymphaea hybrid Root Extract in the Nematode Caenorhabditis elegans. Plant Foods for Human Nutrition, 2014, 69, 304-309.	1.4	15
23	Screening lifespan-extending drugs in Caenorhabditis elegans via label propagation on drug-protein networks. BMC Systems Biology, 2016, 10, 131.	3.0	15
24	Deep neural networks for inferring binding sites of RNA-binding proteins by using distributed representations of RNA primary sequence and secondary structure. BMC Genomics, 2020, 21, 866.	1.2	15
25	Histone modifications involved in cassette exon inclusions: a quantitative and interpretable analysis. BMC Genomics, 2014, 15, 1148.	1.2	13
26	Knowledge-guided fuzzy logic modeling to infer cellular signaling networks from proteomic data. Scientific Reports, 2016, 6, 35652.	1.6	12
27	The centrality of cancer proteins in human protein-protein interaction network: a revisit. International Journal of Computational Biology and Drug Design, 2014, 7, 146.	0.3	10
28	Identifying Mammalian MicroRNA Targets Based on Supervised Distance Metric Learning. IEEE Journal of Biomedical and Health Informatics, 2013, 17, 427-435.	3.9	7
29	Detecting microarray data supported microRNA-mRNA interactions. International Journal of Data Mining and Bioinformatics, 2010, 4, 639.	0.1	6
30	Generalized logical model based on network topology to capture the dynamical trends of cellular signaling pathways. BMC Systems Biology, 2016, 10, 7.	3.0	2
31	Quantifying transcriptional regulatory networks by integrating sequence features and microarray data. Bioprocess and Biosystems Engineering, 2010, 33, 495-505.	1.7	1
32	Inferring Minimal Feasible Metabolic Networks of Escherichia coli. Applied Biochemistry and Biotechnology, 2010, 160, 222-231.	1.4	1
33	Effectively predicting protein functions by collective classification — An extended abstract. , 2012, , .		1