Hui Liu

List of Publications by Year
in descending order

33 papers	1,291 citations	471371 17 h-index	434063 31 g-index
39 all docs	39 docs citations	39 times ranked	1734 citing authors

#	ARTICLE	IF	CITATIONS
1	DeepDDS: deep graph neural network with attention mechanism to predict synergistic drug combinations. Briefings in Bioinformatics, 2022, 23, .	3.2	59
2	Graph2MDA: a multi-modal variational graph embedding model for predicting microbe–drug associations. Bioinformatics, 2022, 38, 1118-1125.	1.8	26
3	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
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	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
6	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
7	HNet-DNN: Inferring New Drug–Disease Associations with Deep Neural Network Based on Heterogeneous Network Features. Journal of Chemical Information and Modeling, 2020, 60, 2367-2376.	2.5	19
8	MADOKA: an ultra-fast approach for large-scale protein structure similarity searching. BMC Bioinformatics, 2019, 20, 662.	1.2	21
9	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
10	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
11	PDRLGB: precise DNA-binding residue prediction using a light gradient boosting machine. BMC Bioinformatics, 2018, 19, 522.	1.2	33
12	Accurate prediction of protein-lncRNA interactions by diffusion and HeteSim features across heterogeneous network. BMC Bioinformatics, 2018, 19, 370.	1.2	32
13	PredCSO: an ensemble method for the prediction of S-sulfenylation sites in proteins. Molecular Omics, 2018, 14, 257-265.	1.4	16
14	Screening lifespan-extending drugs in Caenorhabditis elegans via label propagation on drug-protein networks. BMC Systems Biology, 2016, 10, 131.	3.0	15
15	Knowledge-guided fuzzy logic modeling to infer cellular signaling networks from proteomic data. Scientific Reports, 2016, 6, 35652.	1.6	12
16	Inferring new indications for approved drugs via random walk on drug-disease heterogenous networks. BMC Bioinformatics, 2016, 17, 539.	1.2	72
17	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
18	SynLethDB: synthetic lethality database toward discovery of selective and sensitive anticancer drug targets. Nucleic Acids Research, 2016, 44, D1011-D1017.	6.5	115

#	ARTICLE	IF	CITATIONS
19	Improving compound–protein interaction prediction by building up highly credible negative samples. Bioinformatics, 2015, 31, i221-i229.	1.8	201
20	Anti-aging effect of polysaccharide from Bletilla striata on nematode Caenorhabditis elegans. Pharmacognosy Magazine, 2015, 11, 449.	0.3	54
21	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
22	Histone modifications involved in cassette exon inclusions: a quantitative and interpretable analysis. BMC Genomics, 2014, 15, 1148.	1.2	13
23	Cassava genome from a wild ancestor to cultivated varieties. Nature Communications, 2014, 5, 5110.	5.8	230
24	A comparative evaluation on prediction methods of nucleosome positioning. Briefings in Bioinformatics, 2014, 15, 1014-1027.	3.2	23
25	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
26	Protein function prediction by collective classification with explicit and implicit edges in protein-protein interaction networks. BMC Bioinformatics, 2013, 14, S4.	1.2	15
27	Identifying Mammalian MicroRNA Targets Based on Supervised Distance Metric Learning. IEEE Journal of Biomedical and Health Informatics, 2013, 17, 427-435.	3.9	7
28	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
29	Effectively predicting protein functions by collective classification — An extended abstract. , 2012, , .		1
30	miRFANs: an integrated database for Arabidopsis thalianamicroRNA function annotations. BMC Plant Biology, 2012, 12, 68.	1.6	30
31	Detecting microarray data supported microRNA-mRNA interactions. International Journal of Data Mining and Bioinformatics, 2010, 4, 639.	0.1	6
32	Quantifying transcriptional regulatory networks by integrating sequence features and microarray data. Bioprocess and Biosystems Engineering, 2010, 33, 495-505.	1.7	1
33	Inferring Minimal Feasible Metabolic Networks of Escherichia coli. Applied Biochemistry and Biotechnology, 2010, 160, 222-231.	1.4	1