Zaynab

List of Publications by Year in Descending Order

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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.

16	304	8	17
papers	citations	h-index	g-index
21	429	5	3.69
ext. papers	ext. citations	avg, IF	L-index

#	Paper	IF	Citations
16	StrongestPath: a Cytoscape application for protein-protein interaction analysis. *BMC Bioinformatics*, **2021**, 22, 352	3.6	3
15	A propagation-based seed-centric local community detection for multilayer environment: The case study of colon adenocarcinoma. *PLoS ONE*, **2021**, 16, e0255718	3.7	0
14	Identification of Key Components in Colon Adenocarcinoma Using Transcriptome to Interactome Multilayer Framework. *Scientific Reports*, **2020**, 10, 4991	4.9	4
13	FRnet-DTI: Deep convolutional neural network for drug-target interaction prediction. *Heliyon*, **2020**, 6, e03444	3.6	16
12	Differential network analysis and protein-protein interaction study reveals active protein modules in glucocorticoid resistance for infant acute lymphoblastic leukemia. *Molecular Medicine*, **2019**, 25, 36	6.2	7
11	Comparison of gene co-expression networks in Pseudomonas aeruginosa and Staphylococcus aureus reveals conservation in some aspects of virulence. *Gene*, **2018**, 639, 1-10	3.8	7
10	Reconstruction of the genome-scale co-expression network for the Hippo signaling pathway in colorectal cancer. *Computers in Biology and Medicine*, **2018**, 99, 76-84	7	5
9	Network-based expression analysis reveals key genes related to glucocorticoid resistance in infant acute lymphoblastic leukemia. *Cellular Oncology (Dordrecht)*, **2017**, 40, 33-45	7.2	16
8	iDTI-ESBoost: Identification of Drug Target Interaction Using Evolutionary and Structural Features with Boosting. *Scientific Reports*, **2017**, 7, 17731	4.9	58
7	Information theory in systems biology. Part II: protein-protein interaction and signaling networks. *Seminars in Cell and Developmental Biology*, **2016**, 51, 14-23	7.5	22
6	Drug-target interaction prediction from PSSM based evolutionary information. *Journal of Pharmacological and Toxicological Methods*, **2016**, 78, 42-51	1.7	45
5	Information theory in systems biology. Part I: Gene regulatory and metabolic networks. *Seminars in Cell and Developmental Biology*, **2016**, 51, 3-13	7.5	22
4	CeFunMO: A centrality based method for discovering functional motifs with application in biological networks. *Computers in Biology and Medicine*, **2016**, 76, 154-9	7	1
3	Drug-target interaction prediction via chemogenomic space: learning-based methods. *Expert Opinion on Drug Metabolism and Toxicology*, **2014**, 10, 1273-87	5.5	60
2	Drug-target and disease networks: polypharmacology in the post-genomic era. *In Silico Pharmacology*, **2013**, 1, 17	4.3	31
1	Scalable graph analyzing approach for software fault-localization **2011**,		5