

Zaynab

List of Publications by Year in descending order

Source: <https://exaly.com/author-pdf/2165273/publications.pdf>

Version: 2024-02-01

19
papers

491
citations

933447

10
h-index

996975

15
g-index

21
all docs

21
docs citations

21
times ranked

549
citing authors

#	ARTICLE	IF	CITATIONS
1	iDTI-ESBoost: Identification of Drug Target Interaction Using Evolutionary and Structural Features with Boosting. Scientific Reports, 2017, 7, 17731.	3.3	99
2	Drug–target interaction prediction via chemogenomic space: learning-based methods. Expert Opinion on Drug Metabolism and Toxicology, 2014, 10, 1273-1287.	3.3	83
3	Drug–target interaction prediction from PSSM based evolutionary information. Journal of Pharmacological and Toxicological Methods, 2016, 78, 42-51.	0.7	68
4	Drug-target and disease networks: polypharmacology in the post-genomic era. In Silico Pharmacology, 2013, 1, 17.	3.3	47
5	FRnet-DTI: Deep convolutional neural network for drug-target interaction prediction. Heliyon, 2020, 6, e03444.	3.2	35
6	Information theory in systems biology. Part II: protein–protein interaction and signaling networks. Seminars in Cell and Developmental Biology, 2016, 51, 14-23.	5.0	34
7	Information theory in systems biology. Part I: Gene regulatory and metabolic networks. Seminars in Cell and Developmental Biology, 2016, 51, 3-13.	5.0	31
8	Network-based expression analysis reveals key genes related to glucocorticoid resistance in infant acute lymphoblastic leukemia. Cellular Oncology (Dordrecht), 2017, 40, 33-45.	4.4	21
9	StrongestPath: a Cytoscape application for protein–protein interaction analysis. BMC Bioinformatics, 2021, 22, 352.	2.6	19
10	Comparison of gene co-expression networks in Pseudomonas aeruginosa and Staphylococcus aureus reveals conservation in some aspects of virulence. Gene, 2018, 639, 1-10.	2.2	17
11	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.	7.0	8
12	Identification of Key Components in Colon Adenocarcinoma Using Transcriptome to Interactome Multilayer Framework. Scientific Reports, 2020, 10, 4991.	3.3	8
13	Scalable graph analyzing approach for software fault-localization. , 2011, , .		7
14	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.	4.4	7
15	CeFunMO: A centrality based method for discovering functional motifs with application in biological networks. Computers in Biology and Medicine, 2016, 76, 154-159.	7.0	4
16	Analyzing program dynamic graphs for software fault localization. , 2010, , .		1
17	Finding software fault relevant subgraphs a new graph mining approach for software debugging. , 2011, , .		1
18	A propagation-based seed-centric local community detection for multilayer environment: The case study of colon adenocarcinoma. PLoS ONE, 2021, 16, e0255718.	2.5	1

#	ARTICLE	IF	CITATIONS
19	New algorithms for online unit clustering. , 2008, , .		0