

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

932766

10
h-index

996533

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. <i>Scientific Reports</i> , 2017, 7, 17731.	1.6	99
2	Drugâ€target interaction prediction via chemogenomic space: learning-based methods. <i>Expert Opinion on Drug Metabolism and Toxicology</i> , 2014, 10, 1273-1287.	1.5	83
3	Drugâ€target interaction prediction from PSSM based evolutionary information. <i>Journal of Pharmacological and Toxicological Methods</i> , 2016, 78, 42-51.	0.3	68
4	Drug-target and disease networks: polypharmacology in the post-genomic era. <i>In Silico Pharmacology</i> , 2013, 1, 17.	1.8	47
5	FRnet-DTI: Deep convolutional neural network for drug-target interaction prediction. <i>Heliyon</i> , 2020, 6, e03444.	1.4	35
6	Information theory in systems biology. Part II: proteinâ€protein interaction and signaling networks. <i>Seminars in Cell and Developmental Biology</i> , 2016, 51, 14-23.	2.3	34
7	Information theory in systems biology. Part I: Gene regulatory and metabolic networks. <i>Seminars in Cell and Developmental Biology</i> , 2016, 51, 3-13.	2.3	31
8	Network-based expression analysis reveals key genes related to glucocorticoid resistance in infant acute lymphoblastic leukemia. <i>Cellular Oncology (Dordrecht)</i> , 2017, 40, 33-45.	2.1	21
9	StrongestPath: a Cytoscape application for proteinâ€protein interaction analysis. <i>BMC Bioinformatics</i> , 2021, 22, 352.	1.2	19
10	Comparison of gene co-expression networks in <i>Pseudomonas aeruginosa</i> and <i>Staphylococcus aureus</i> reveals conservation in some aspects of virulence. <i>Gene</i> , 2018, 639, 1-10.	1.0	17
11	Reconstruction of the genome-scale co-expression network for the Hippo signaling pathway in colorectal cancer. <i>Computers in Biology and Medicine</i> , 2018, 99, 76-84.	3.9	8
12	Identification of Key Components in Colon Adenocarcinoma Using Transcriptome to Interactome Multilayer Framework. <i>Scientific Reports</i> , 2020, 10, 4991.	1.6	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. <i>Molecular Medicine</i> , 2019, 25, 36.	1.9	7
15	CeFunMO: A centrality based method for discovering functional motifs with application in biological networks. <i>Computers in Biology and Medicine</i> , 2016, 76, 154-159.	3.9	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. <i>PLoS ONE</i> , 2021, 16, e0255718.	1.1	1

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