Young-Rae Cho

List of Publications by Year
in descending order

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Version: 2024-02-01

		858243	799663
52	644	12	21
papers	citations	h-index	g-index

53	53	53	707
all docs	docs citations	times ranked	citing authors

#	Article	IF	Citations
1	Comparative analysis of network-based approaches and machine learning algorithms for predicting drug-target interactions. Methods, 2022, 198, 19-31.	1.9	14
2	Network-Based Approaches for Disease-Gene Association Prediction Using Protein-Protein Interaction Networks. International Journal of Molecular Sciences, 2022, 23, 7411.	1.8	12
3	Entropy-Based Graph Clustering of PPI Networks for Predicting Overlapping Functional Modules of Proteins. Entropy, 2021, 23, 1271.	1.1	1
4	Integrative analysis of breast cancer profiles in TCGA by TNBC subgrouping reveals novel microRNA-specific clusters, including miR-17-92a, distinguishing basal-like 1 and basal-like 2 TNBC subtypes. BMC Cancer, 2020, 20, 141.	1.1	18
5	Survey of biological network alignment: cross-species analysis of conserved systems. , 2019, , .		2
6	LePrimAlign: local entropy-based alignment of PPI networks to predict conserved modules. BMC Genomics, 2019, 20, 964.	1.2	4
7	PrimAlign: PageRank-inspired Markovian alignment for large biological networks. Bioinformatics, 2018, 34, i537-i546.	1.8	25
8	Mining cross-ontology weighted association rules between GO and HPO. , 2017, , .		0
9	Alignment of PPI Networks Using Semantic Similarity for Conserved Protein Complex Prediction. IEEE Transactions on Nanobioscience, 2016, 15, 380-389.	2.2	5
10	Filtering association rules in Gene Ontology based on term specificity. , 2016, , .		0
11	An integrative measure of graph- and vector-based semantic similarity using information content distance. , 2015, , .		3
12	Semantic mapping to align PPI networks and predict conserved protein complexes. , 2015, , .		0
13	P-Finder: Reconstruction of Signaling Networks from Protein-Protein Interactions and GO Annotations. IEEE/ACM Transactions on Computational Biology and Bioinformatics, 2015, 12, 309-321.	1.9	6
14	DISTANCE-WISE PATHWAY DISCOVERY FROM PROTEINâ€“PROTEIN INTERACTION NETWORKS WEIGHTED BY SEMANTIC SIMILARITY. Journal of Bioinformatics and Computational Biology, 2014, 12, 1450004.	0.3	4
15	Survey: Enhancing protein complex prediction in PPI networks with GO similarity weighting. Interdisciplinary Sciences, Computational Life Sciences, 2013, 5, 196-210.	2.2	17
16	Editorial: special issue on computational approaches for extracting knowledge from biological networks. Interdisciplinary Sciences, Computational Life Sciences, 2013, 5, 165-166.	2.2	0
17	Prediction of signaling networks by information propagation on protein-protein interaction networks integrated with GO annotations. , 2013, , .		1
18	M-Finder: Uncovering functionally associated proteins from interactome data integrated with GO annotations. Proteome Science, 2013, 11, S3.	0.7	34

#	ARTICLE	IF	CITATIONS
19	Signaling pathway prediction by path frequency in protein-protein interaction networks. , 2013, , .		1
20	Improvements of graph entropy approach to detect protein complexes by ontological analysis of PPIs. , 2012, , .		0
21	M-Finder: Functional association mining from protein interaction networks weighted by semantic similarity. , 2012, , .		2
22	Assessing reliability of protein-protein interactions by gene ontology integration. , 2012, , .		3
23	Accuracy improvement in protein complex prediction from protein interaction networks by refining cluster overlaps. Proteome Science, 2012, 10, S3.	0.7	5
24	Entropy-Based Graph Clustering: Application to Biological and Social Networks. , 2011, , .		24
25	Detecting protein complexes and functional modules from protein interaction networks: A graph entropy approach. Proteomics, 2011, 11, 3835-3844.	1.3	42
26	Assessment of Cluster Overlaps to Improve Accuracy of Module Detection from PPI Networks. , 2011, , .		0
27	Predicting Protein Function by Frequent Functional Association Pattern Mining in Protein Interaction Networks. IEEE Transactions on Information Technology in Biomedicine, 2010, 14, 30-36.	3.6	42
28	Identification of functional hubs and modules by converting interactome networks into hierarchical ordering of proteins. BMC Bioinformatics, 2010, 11, S3.	1.2	16
29	Mining Protein Interactome Networks to Measure Interaction Reliability and Select Hub Proteins. International Journal of Knowledge Discovery in Bioinformatics, 2010, 1, 20-35.	0.8	0
30	Decomposing protein interactome networks by graph entropy. , 2010, , .		6
31	Functional Flow Simulation Based Analysis of Protein Interaction Network. , 2010, , .		1
32	Functional Influence-Based Approach to Identify Overlapping Modules in Biological Networks. , 2010, , 535-556.		0
33	flowNet: Flow-Based Approach for Efficient Analysis of Complex Biological Networks. , 2009, , .		9
34	ANN Based Protein Function Prediction Using Integrated Protein-Protein Interaction Data. , 2009, , .		7
35	Mining of Attribute Interactions Using Information Theoretic Metrics. , 2009, , .		11
36	Restructuring Protein Interaction Networks to Reveal Structural Hubs and Functional Organizations. , 2009, , .		2

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37	Semantic similarity based feature extraction from microarray expression data. International Journal of Data Mining and Bioinformatics, 2009, 3, 333.	0.1	12
38	A probabilistic framework to predict protein function from interaction data integrated with semantic knowledge. BMC Bioinformatics, 2008, 9, 382.	1.2	19
39	CASCADE: a novel quasi all paths-based network analysis algorithm for clustering biological interactions. BMC Bioinformatics, 2008, 9, 64.	1.2	22
40	Functional module detection by functional flow pattern mining in protein interaction networks. BMC Bioinformatics, 2008, 9, .	1.2	9
41	Discovering Frequent Patterns of Functional Associations in Protein Interaction Networks for Function Prediction. , 2008, , .		1
42	Modularization of Protein Interaction Networks by Incorporating Gene Ontology Annotations. , 2007, , .		0
43	SIGN: reliable protein interaction identification by integrating the Similarity In GO and the similarity in protein interaction Networks. , 2007, , .		4
44	Optimizing Flow-based Modularization by Iterative Centroid Search in Protein Interaction Networks. , 2007, , .		3
45	Assessing Reliability of Protein-Protein Interactions by Semantic Data Integration. , 2007, , .		0
46	Feature Extraction from Microarray Expression Data by Integration of Semantic Knowledge. , 2007, , .		1
47	Semantic integration to identify overlapping functional modules in protein interaction networks. BMC Bioinformatics, 2007, 8, 265.	1.2	138
48	A novel functional module detection algorithm for protein-protein interaction networks. Algorithms for Molecular Biology, 2006, 1, 24.	0.3	76
49	Efficient Modularization of Weighted Protein Interaction Networks using k-Hop Graph Reduction. , 2006, , .		10
50	Identification of Overlapping Functional Modules in Protein Interaction Networks: Information Flow-based Approach. , 2006, , .		12
51	Clustering Methods in a Proteinâ€“Protein Interaction Network. , 0, , 319-355.		19
52	Mining Protein Interactome Networks to Measure Interaction Reliability and Select Hub Proteins. , 0, , 222-238.		0