Norberto Diaz-Diaz

List of Publications by Year
in descending order

25 papers	203 citations	933264 10 h-index	1058333 14 g-index
26 all docs	26 docs citations	26 times ranked	222 citing authors

#	Article	IF	Citations
1	Enhancement of COPD biological networks using a web-based collaboration interface. F1000Research, 2015, 4, 32.	0.8	29
2	Identifying livestock behavior patterns based on accelerometer dataset. Journal of Computational Science, 2020, 41, 101076.	1.5	23
3	Enhancement of COPD biological networks using a web-based collaboration interface. F1000Research, 2015, 4, 32.	0.8	22
4	GO-based Functional Dissimilarity of Gene Sets. BMC Bioinformatics, 2011, 12, 360.	1.2	17
5	GNC–app: A new Cytoscape app to rate gene networks biological coherence using gene–gene indirect relationships. BioSystems, 2018, 166, 61-65.	0.9	14
6	Gene network coherence based on prior knowledge using direct and indirect relationships. Computational Biology and Chemistry, 2015, 56, 142-151.	1.1	11
7	Development and use of the Cytoscape app GFD-Net for measuring semantic dissimilarity of gene networks. F1000Research, 2014, 3, 142.	0.8	11
8	Dynamics of the Ethanolamine Glycerophospholipid Remodeling Network. PLoS ONE, 2012, 7, e50858.	1.1	10
9	Community-Reviewed Biological Network Models for Toxicology and Drug Discovery Applications. Gene Regulation and Systems Biology, 2016, 10, GRSB.S39076.	2.3	10
10	Incorporating biological knowledge for construction of fuzzy networks of gene associations. Applied Soft Computing Journal, 2016, 42, 144-155.	4.1	10
11	GFD-Net: A novel semantic similarity methodology for the analysis of gene networks. Journal of Biomedical Informatics, 2017, 68, 71-82.	2.5	7
12	OCEAN: An Algorithm to Predict the Separation of Biogas Using Zeolites. Industrial & Engineering Chemistry Research, 2020, 59, 7212-7223.	1.8	7
13	CarGene: Characterisation of sets of genes based on metabolic pathways analysis. International Journal of Data Mining and Bioinformatics, 2011, 5, 558.	0.1	6
14	Gene Network Biological Validity Based on Gene-Gene Interaction Relevance. Scientific World Journal, The, 2014, 2014, 1-11.	0.8	6
15	A Computational Intelligence Approach to Predict Energy Demand Using Random Forest in a Cloudera Cluster. Applied Sciences (Switzerland), 2021, 11, 8635.	1.3	6
16	Pattern Recognition in Biological Time Series. Lecture Notes in Computer Science, 2011, , 164-172.	1.0	4
17	An Approach to Reduce the Cost of Evaluation in Evolutionary Learning. Lecture Notes in Computer Science, 2005, , 804-811.	1.0	2
18	Development and use of a Cytoscape app for GRNCOP2. Computer Methods and Programs in Biomedicine, 2019, 177, 211-218.	2.6	2

#	Article	IF	Citations
19	Web-based Gene Pathogenicity Analysis (WGPA): a web platform to interpret gene pathogenicity from personal genome data. Bioinformatics, 2016, 32, 635-637.	1.8	1
20	BIGO: A web application to analyse gene enrichment analysis results. Computational Biology and Chemistry, 2018, 76, 169-178.	1.1	1
21	Gene Regulatory Networks Validation Framework Based in KEGG. Lecture Notes in Computer Science, 2011, , 279-286.	1.0	1
22	Using graph theory to analyze gene network coherence. EMBnet Journal, 2012, 18, 32.	0.2	1
23	Gene Networks Validation based on Metabolic Pathways. , 2011, , .		0
24	Gene-gene interaction based clustering method for microarray data. , 2011, , .		0
25	Genes functional coherence based on actual biological knowledge. AI Communications, 2013, 26, 247-249.	0.8	0