Giovanni Micale

List of Publications by Year
in descending order

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23
papers

158
citations

1306789
7
h-index

1281420
11
g-index

23
all docs

23
docs citations

23
times ranked

181
citing authors

#	ARTICLE	IF	CITATIONS
1	Next generation sequencing in a cohort of patients with rare sarcoma histotypes: A single institution experience. Pathology Research and Practice, 2022, 232, 153820.	1.0	4
2	Mechanistic Translation of Melanoma Genetic Landscape in Enriched Pathways and Oncogenic Protein-Protein Interactions. Cancer Genomics and Proteomics, 2022, 19, 350-361.	1.0	2
3	TemporalRI: subgraph isomorphism in temporal networks with multiple contacts. Applied Network Science, 2021, 6, .	0.8	2
4	TemporalRI: A Subgraph Isomorphism Algorithm for Temporal Networks. Studies in Computational Intelligence, 2021, , 675-687.	0.7	4
5	MODIT: MOtif DIscovery in Temporal Networks. Frontiers in Big Data, 2021, 4, 806014.	1.8	3
6	Establish the expected number of induced motifs on unlabeled graphs through analytical models. Applied Network Science, 2020, 5, .	0.8	2
7	Establish the Expected Number of Injective Motifs on Unlabeled Graphs Through Analytical Models. Studies in Computational Intelligence, 2020, , 255-267.	0.7	1
8	Fast Subgraph Matching Strategies Based on Pattern-Only Heuristics. Interdisciplinary Sciences, Computational Life Sciences, 2019, 11, 21-32.	2.2	3
9	Fast methods for finding significant motifs on labelled multi-relational networks. Journal of Complex Networks, 2019, 7, 817-837.	1.1	1
10	Computational Methods to Investigate the Impact of miRNAs on Pathways. Methods in Molecular Biology, 2019, 1970, 183-209.	0.4	5
11	Simple Pattern-only Heuristics Lead to Fast Subgraph Matching Strategies on Very Large Networks. Advances in Intelligent Systems and Computing, 2019, , 131-138.	0.5	2
12	Fast analytical methods for finding significant labeled graph motifs. Data Mining and Knowledge Discovery, 2018, 32, 504-531.	2.4	18
13	gLabTrie: A Data Structure for Motif Discovery with Constraints. Data-centric Systems and Applications, 2018, , 71-95.	0.2	3
14	INBIA: a boosting methodology for proteomic network inference. BMC Bioinformatics, 2018, 19, 188.	1.2	2
15	Mining and ranking of generalized multi-dimensional frequent subgraphs. , 2017, , .		6
16	APPAGATO: an APproximate PArallel and stochastic GrAph querying TOol for biological networks. Bioinformatics, 2016, 32, 2159-2166.	1.8	10
17	SPECTRA: An Integrated Knowledge Base for Comparing Tissue and Tumor-Specific PPI Networks in Human. Frontiers in Bioengineering and Biotechnology, 2015, 3, 58.	2.0	13
18	NetMatchStar: an enhanced Cytoscape network queryingÂapp. F1000Research, 2015, 4, 479.	0.8	17

#	Article	IF	Citations
19	NetMatchStar: an enhanced Cytoscape network queryingÂapp. F1000Research, 2015, 4, 479.	0.8	11
20	Proteins comparison through probabilistic optimal structure local alignment. Frontiers in Genetics, 2014, 5, 302.	1.1	4
21	GASOLINE: a Cytoscape app for multiple local alignment of PPI networks. F1000Research, 2014, 3, 140.	0.8	7
22	GASOLINE: a Cytoscape app for multiple local alignment of PPI networks. F1000Research, 2014, 3, 140.	0.8	10
23	GASOLINE: a Greedy And Stochastic algorithm for Optimal Local multiple alignment of Interaction NEtworks. PLoS ONE, 2014, 9, e98750.	1.1	28