

Vincenzo Bonnici

List of Publications by Year in descending order

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Version: 2024-02-01

34
papers

507
citations

840585

11
h-index

677027

22
g-index

40
all docs

40
docs citations

40
times ranked

620
citing authors

#	ARTICLE	IF	CITATIONS
1	A subgraph isomorphism algorithm and its application to biochemical data. BMC Bioinformatics, 2013, 14, S13.	1.2	125
2	miRandola 2017: a curated knowledge base of non-invasive biomarkers. Nucleic Acids Research, 2018, 46, D354-D359.	6.5	61
3	DT-Web: a web-based application for drug-target interaction and drug combination prediction through domain-tuned network-based inference. BMC Systems Biology, 2015, 9, S4.	3.0	38
4	GRAPES: A Software for Parallel Searching on Biological Graphs Targeting Multi-Core Architectures. PLoS ONE, 2013, 8, e76911.	1.1	33
5	On the Variable Ordering in Subgraph Isomorphism Algorithms. IEEE/ACM Transactions on Computational Biology and Bioinformatics, 2017, 14, 193-203.	1.9	32
6	Enhancing Graph Database Indexing by Suffix Tree Structure. Lecture Notes in Computer Science, 2010, , 195-203.	1.0	27
7	Informational laws of genome structures. Scientific Reports, 2016, 6, 28840.	1.6	26
8	Comprehensive Reconstruction and Visualization of Non-Coding Regulatory Networks in Human. Frontiers in Bioengineering and Biotechnology, 2014, 2, 69.	2.0	25
9	A knowledge base for the discovery of function, diagnostic potential and drug effects on cellular and extracellular miRNAs. BMC Genomics, 2014, 15, S4.	1.2	25
10	Arena-Idb: a platform to build human non-coding RNA interaction networks. BMC Bioinformatics, 2018, 19, 350.	1.2	17
11	NetMatchStar: an enhanced Cytoscape network querying App. F1000Research, 2015, 4, 479.	0.8	17
12	PanDelos: a dictionary-based method for pan-genome content discovery. BMC Bioinformatics, 2018, 19, 437.	1.2	13
13	NetMatchStar: an enhanced Cytoscape network querying App. F1000Research, 2015, 4, 479.	0.8	11
14	APPAGATO: an APPROXIMATE PARALLEL and stochastic GRAPH querying TOOL for biological networks. Bioinformatics, 2016, 32, 2159-2166.	1.8	10
15	Challenges in gene-oriented approaches for pangenome content discovery. Briefings in Bioinformatics, 2021, 22, .	3.2	8
16	An Informational Test for Random Finite Strings. Entropy, 2018, 20, 934.	1.1	5
17	Spectral concepts in genome informational analysis. Theoretical Computer Science, 2021, 894, 23-30.	0.5	5
18	GRAFIMO: Variant and haplotype aware motif scanning on pangenome graphs. PLoS Computational Biology, 2021, 17, e1009444.	1.5	5

#	ARTICLE	IF	CITATIONS
19	cuRnet: an R package for graph traversing on GPU. BMC Bioinformatics, 2018, 19, 356.	1.2	4
20	Fast Subgraph Matching Strategies Based on Pattern-Only Heuristics. Interdisciplinary Sciences, Computational Life Sciences, 2019, 11, 21-32.	2.2	3
21	GRAPES-DD: exploiting decision diagrams for index-driven search in biological graph databases. BMC Bioinformatics, 2021, 22, 209.	1.2	3
22	Recurrence Distance Distributions in Computational Genomics. American Journal of Bioinformatics and Computational Biology, 0, , .	0.0	3
23	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
24	TEDAR: Temporal dynamic signal detection of adverse reactions. Artificial Intelligence in Medicine, 2021, 122, 102212.	3.8	2
25	An Efficient Implementation of a Subgraph Isomorphism Algorithm for GPUs.. , 2018, , .		1
26	Parallel Searching on Biological Networks. , 2019, , .		1
27	PANPROVA: pangenomic prokaryotic evolution of full assemblies. Bioinformatics, 2022, 38, 2631-2632.	1.8	1
28	Covid19/IT the digital side of Covid19: A picture from Italy with clustering and taxonomy. PLoS ONE, 2022, 17, e0269687.	1.1	1
29	Genetic Alteration of MicroRNA Affecting Cancer Pathways. , 2018, , 269-287.		0
30	LErNet: characterization of lncRNAs via context-aware network expansion and enrichment analysis. , 2019, , .		0
31	Construction and Analysis of miRNA Regulatory Networks. Methods in Molecular Biology, 2019, 1970, 121-167.	0.4	0
32	An integrated system for mining relations among microRNAs, drugs and phenotypes. EMBnet Journal, 2012, 18, 75.	0.2	0
33	Core algorithms to search in biological structured data. EMBnet Journal, 2012, 18, 65.	0.2	0
34	Centrality Speeds the Subgraph Isomorphism Search Up in Target Aware Contexts. Lecture Notes in Computer Science, 2020, , 19-26.	1.0	0