

Filippo Geraci

List of Publications by Year in descending order

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Version: 2024-02-01

36
papers

922
citations

840776

11
h-index

580821

25
g-index

42
all docs

42
docs citations

42
times ranked

831
citing authors

#	ARTICLE	IF	CITATIONS
1	STIMO: STILL and MOving video storyboard for the web scenario. Multimedia Tools and Applications, 2010, 46, 47-69.	3.9	214
2	Extraction and classification of dense communities in the web. , 2007, , .		143
3	A comparison of several algorithms for the single individual SNP haplotyping reconstruction problem. Bioinformatics, 2010, 26, 2217-2225.	4.1	64
4	miRandola 2017: a curated knowledge base of non-invasive biomarkers. Nucleic Acids Research, 2018, 46, D354-D359.	14.5	61
5	Extraction and classification of dense implicit communities in the Web graph. ACM Transactions on the Web, 2009, 3, 1-36.	2.5	45
6	Protein complex prediction for large protein protein interaction networks with the Core&Peel method. BMC Bioinformatics, 2016, 17, 372.	2.6	38
7	AI applications in functional genomics. Computational and Structural Biotechnology Journal, 2021, 19, 5762-5790.	4.1	34
8	Fast Exact Computation of betweenness Centrality in Social Networks. , 2012, , .		33
9	SpeedHap: An Accurate Heuristic for the Single Individual SNP Haplotyping Problem with Many Gaps, High Reading Error Rate and Low Coverage. IEEE/ACM Transactions on Computational Biology and Bioinformatics, 2008, 5, 492-502.	3.0	28
10	VISTO. , 2007, , .		27
11	Cluster Generation and Labeling for Web Snippets: A Fast, Accurate Hierarchical Solution. Internet Mathematics, 2006, 3, 413-443.	0.7	23
12	A scalable algorithm for high-quality clustering of web snippets. , 2006, , .		18
13	Editorial: RNA-Seq Analysis: Methods, Applications and Challenges. Frontiers in Genetics, 2020, 11, 220.	2.3	16
14	On Using Clustering Algorithms to Produce Video Abstracts for the Web Scenario. , 2008, , .		15
15	K-Boost: A Scalable Algorithm for High-Quality Clustering of Microarray Gene Expression Data. Journal of Computational Biology, 2009, 16, 859-873.	1.6	15
16	<i>Dot2dot</i>: accurate whole-genome tandem repeats discovery. Bioinformatics, 2019, 35, 914-922.	4.1	13
17	Genome-wide analysis of NGS data to compile cancer-specific panels of miRNA biomarkers. PLoS ONE, 2018, 13, e0200353.	2.5	12
18	A New Method for Discovering Disease-Specific MiRNA-Target Regulatory Networks. PLoS ONE, 2015, 10, e0122473.	2.5	9

#	ARTICLE	IF	CITATIONS
19	A Census of Tandemly Repeated Polymorphic Loci in Genic Regions Through the Comparative Integration of Human Genome Assemblies. <i>Frontiers in Genetics</i> , 2018, 9, 155.	2.3	9
20	AMIC@: All Microarray Clusterings @ once. <i>Nucleic Acids Research</i> , 2008, 36, W315-W319.	14.5	8
21	Machine Learning and Bioinformatics Framework Integration to Potential Familial DCM-Related Markers Discovery. <i>Genes</i> , 2021, 12, 1946.	2.4	8
22	FPF-SB: A Scalable Algorithm for Microarray Gene Expression Data Clustering. <i>Lecture Notes in Computer Science</i> , 2007, , 606-615.	1.3	6
23	A Fast and Accurate Heuristic for the Single Individual SNP Haplotyping Problem with Many Gaps, High Reading Error Rate and Low Coverage. <i>Lecture Notes in Computer Science</i> , 2007, , 49-60.	1.3	6
24	Identification of Web Spam through Clustering of Website Structures. , 2015, , .		4
25	GFS. , 2017, , .		4
26	EZcount: An all-in-one software for microRNA expression quantification from NGS sequencing data. <i>Computers in Biology and Medicine</i> , 2021, 133, 104352.	7.0	4
27	On the Benefits of Keyword Spreading in Sponsored Search Auctions: An Experimental Analysis. <i>Lecture Notes in Business Information Processing</i> , 2010, , 158-171.	1.0	4
28	MicroRNA signature for interpretable breast cancer classification with subtype clue. <i>Journal of Computational Mathematics and Data Science</i> , 2022, 3, 100042.	2.3	4
29	Medium sized crawling made fast and easy through Lumbricus webis. , 2011, , .		2
30	Fast Exact and Approximate Computation of Betweenness Centrality in Social Networks. <i>Lecture Notes in Social Networks</i> , 2014, , 53-73.	0.1	2
31	From Literature to Knowledge: Exploiting PubMed to Answer Biomedical Questions in Natural Language. <i>Lecture Notes in Computer Science</i> , 2015, , 3-15.	1.3	2
32	Graph-Based Integration of Histone Modification Profiles. <i>Mathematics</i> , 2022, 10, 1842.	2.2	2
33	Distilling Router Data Analysis for Faster and Simpler Dynamic IPÂLookup Algorithms. <i>Lecture Notes in Computer Science</i> , 2005, , 580-592.	1.3	1
34	An Efficient Combinatorial Approach for Solving the DNA Motif Finding Problem. , 2009, , .		1
35	Technology and Species Independent Simulation of Sequencing Data and Genomic Variants. , 2019, , .		1
36	Web Crawling and Processing with Limited Resources for Business Intelligence and Analytics Applications. <i>Journal of Software</i> , 2018, 13, 300-316.	0.6	0