

Marco Frasca

List of Publications by Year in descending order

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Version: 2024-02-01

63
papers

1,365
citations

567281

15
h-index

377865

34
g-index

66
all docs

66
docs citations

66
times ranked

1368
citing authors

#	ARTICLE	IF	CITATIONS
1	Identification of key miRNAs in prostate cancer progression based on miRNA-mRNA network construction. Computational and Structural Biotechnology Journal, 2022, 20, 864-873.	4.1	4
2	Heterogeneous data integration methods for patient similarity networks. Briefings in Bioinformatics, 2022, 23, .	6.5	12
3	Transcriptional Profiling of Hippocampus Identifies Network Alterations in Alzheimer's Disease. Applied Sciences (Switzerland), 2022, 12, 5035.	2.5	2
4	Semi-automatic Column Type Inference for CSV Table Understanding. Lecture Notes in Computer Science, 2021, , 535-549.	1.3	5
5	Compression strategies and space-conscious representations for deep neural networks. , 2021, , .		4
6	Identification of Breast Cancer Subtype-Specific Biomarkers by Integrating Copy Number Alterations and Gene Expression Profiles. Medicina (Lithuania), 2021, 57, 261.	2.0	8
7	Table understanding approaches for extracting knowledge from heterogeneous tables. Wiley Interdisciplinary Reviews: Data Mining and Knowledge Discovery, 2021, 11, e1407.	6.8	8
8	Visual design of dialogue flows for conversational interfaces. Behaviour and Information Technology, 2021, 40, 1008-1023.	4.0	5
9	Reproducing the Sparse Huffman Address Map Compression for Deep Neural Networks. Lecture Notes in Computer Science, 2021, , 161-166.	1.3	1
10	Protein function prediction as a graph-transduction game. Pattern Recognition Letters, 2020, 134, 96-105.	4.2	8
11	parSMURF, a high-performance computing tool for the genome-wide detection of pathogenic variants. GigaScience, 2020, 9, .	6.4	11
12	Explainable Machine Learning for Early Assessment of COVID-19 Risk Prediction in Emergency Departments. IEEE Access, 2020, 8, 196299-196325.	4.2	55
13	Network modeling of patients' biomolecular profiles for clinical phenotype/outcome prediction. Scientific Reports, 2020, 10, 3612.	3.3	11
14	Multitask Hopfield Networks. Lecture Notes in Computer Science, 2020, , 349-365.	1.3	0
15	Multi-resolution visualization and analysis of biomolecular networks through hierarchical community detection and web-based graphical tools. PLoS ONE, 2020, 15, e0244241.	2.5	5
16	A Graphical Tool for the Exploration and Visual Analysis of Biomolecular Networks. Lecture Notes in Computer Science, 2020, , 88-98.	1.3	0
17	Committee-Based Active Learning to Select Negative Examples for Predicting Protein Functions. Lecture Notes in Computer Science, 2020, , 80-87.	1.3	0
18	UNIPred-Web: a web tool for the integration and visualization of biomolecular networks for protein function prediction. BMC Bioinformatics, 2019, 20, 422.	2.6	9

#	ARTICLE	IF	CITATIONS
19	Diseaseâ€“Genes Must Guide Data Source Integration in the Gene Prioritization Process. Lecture Notes in Computer Science, 2019, , 60-69.	1.3	0
20	Ensembling Descendant Term Classifiers to Improve Gene - Abnormal Phenotype Predictions. Lecture Notes in Computer Science, 2019, , 70-80.	1.3	2
21	The CAFA challenge reports improved protein function prediction and new functional annotations for hundreds of genes through experimental screens. Genome Biology, 2019, 20, 244.	8.8	261
22	Ontology-Based Consistent Specification of Sensor Data Acquisition Plans in Cross-Domain IoT Platforms. IEEE Access, 2019, 7, 176141-176169.	4.2	10
23	Multitask Protein Function Prediction through Task Dissimilarity. IEEE/ACM Transactions on Computational Biology and Bioinformatics, 2019, 16, 1550-1560.	3.0	15
24	Analysis of Novel Annotations in the Gene Ontology for Boosting the Selection of Negative Examples. , 2019, , .		0
25	Web accessibility legislation in Italy: a survey 10Âyears after the Stanca Act. Universal Access in the Information Society, 2018, 17, 211-222.	3.0	13
26	Protection and composition of crossmedia content in collaborative environments. Multimedia Tools and Applications, 2018, 77, 2083-2114.	3.9	3
27	Evaluating the impact of topological protein features on the negative examples selection. BMC Bioinformatics, 2018, 19, 417.	2.6	2
28	A GPU-based algorithm for fast node label learning in large and unbalanced biomolecular networks. BMC Bioinformatics, 2018, 19, 353.	2.6	2
29	A novel computational method for automatic segmentation, quantification and comparative analysis of immunohistochemically labeled tissue sections. BMC Bioinformatics, 2018, 19, 357.	2.6	17
30	COSNet: An R package for label prediction in unbalanced biological networks. Neurocomputing, 2017, 237, 397-400.	5.9	8
31	Analysis of Informative Features for Negative Selection in Protein Function Prediction. Lecture Notes in Computer Science, 2017, , 267-276.	1.3	2
32	Gene2DisCo: Gene to disease using disease commonalities. Artificial Intelligence in Medicine, 2017, 82, 34-46.	6.5	6
33	Exploiting Negative Sample Selection for Prioritizing Candidate Disease Genes. Genomics and Computational Biology, 2017, 3, 47.	0.7	5
34	â€œThere's no Reason whyâ€ A Campaign to Raise Cancer Awareness among Adolescents. Tumori, 2016, 102, 270-275.	1.1	8
35	Gene-Disease Prioritization Through Cost-Sensitive Graph-Based Methodologies. Lecture Notes in Computer Science, 2016, , 739-751.	1.3	2
36	An expanded evaluation of protein function prediction methods shows an improvement in accuracy. Genome Biology, 2016, 17, 184.	8.8	308

#	ARTICLE	IF	CITATIONS
37	End-User Development for Lifelogging and eWellness. , 2016, , .		1
38	Multi-species protein function prediction. , 2016, , .		2
39	Learning node labels with multi-category Hopfield networks. Neural Computing and Applications, 2016, 27, 1677-1692.	5.6	5
40	<i>RANKS</i> : a flexible tool for node label ranking and classification in biological networks. Bioinformatics, 2016, 32, 2872-2874.	4.1	30
41	MergeGraphs. , 2015, , .		2
42	An editable live ETL system for Ambient Intelligence environments. , 2015, , .		4
43	UNIPred: Unbalance-Aware Network Integration and Prediction of Protein Functions. Journal of Computational Biology, 2015, 22, 1057-1074.	1.6	17
44	Automated gene function prediction through gene multifunctionality in biological networks. Neurocomputing, 2015, 162, 48-56.	5.9	14
45	Making the Analysis of the Italian Legislative System Easy: The ILMA Web Portal. Journal of Information Technology and Politics, 2015, 12, 88-102.	2.9	0
46	A Hierarchical Ensemble Method for DAG-Structured Taxonomies. Lecture Notes in Computer Science, 2015, , 15-26.	1.3	8
47	GOsTo: a stand-alone application and a web tool for calculating semantic similarities on the Gene Ontology. Bioinformatics, 2014, 30, 2235-2236.	4.1	44
48	Think globally and solve locally: secondary memory-based network learning for automated multi-species function prediction. GigaScience, 2014, 3, 5.	6.4	12
49	A neural network algorithm for semi-supervised node label learning from unbalanced data. Neural Networks, 2013, 43, 84-98.	5.9	43
50	A neural network based algorithm for gene expression prediction from chromatin structure. , 2013, , .		13
51	A Neural Procedure for Gene Function Prediction. Smart Innovation, Systems and Technologies, 2013, , 179-188.	0.6	1
52	Participatory knowledge-management design: A semiotic approach. Journal of Visual Languages and Computing, 2012, 23, 103-115.	1.8	24
53	A Mathematical Model for the Validation of Gene Selection Methods. IEEE/ACM Transactions on Computational Biology and Bioinformatics, 2011, 8, 1385-1392.	3.0	4
54	COSNet: A Cost Sensitive Neural Network for Semi-supervised Learning in Graphs. Lecture Notes in Computer Science, 2011, , 219-234.	1.3	21

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55	Report on the EDBT/ICDT 2010 workshop on updates in XML. SIGMOD Record, 2010, 39, 54-57.	1.2	2
56	XML-based approaches for the integration of heterogeneous bio-molecular data. BMC Bioinformatics, 2009, 10, S7.	2.6	21
57	Measuring the structural similarity among XML documents and DTDs. Journal of Intelligent Information Systems, 2008, 30, 55-92.	3.9	20
58	DESIGN OF KNOWLEDGE DRIVEN INTERFACES IN CULTURAL CONTEXTS. International Journal of Semantic Computing, 2008, 02, 525-553.	0.5	9
59	A matching algorithm for measuring the structural similarity between an XML document and a DTD and its applications. Information Systems, 2004, 29, 23-46.	3.6	79
60	REPORT on the EDBT'04 workshop on database technologies for handling XML information on the web. SIGMOD Record, 2004, 33, 132-134.	1.2	1
61	Protection and administration of XML data sources. Data and Knowledge Engineering, 2002, 43, 237-260.	3.4	33
62	Specifying and enforcing access control policies for XML document sources. World Wide Web, 2000, 3, 139-151.	4.0	135
63	Artificial Intelligence in Predicting Clinical Outcome in COVID-19 Patients from Clinical, Biochemical and a Qualitative Chest X-Ray Scoring System. Reports in Medical Imaging, 0, Volume 14, 27-39.	0.8	4