

Marco Notaro

List of Publications by Year in descending order

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Version: 2024-02-01

13
papers

334
citations

1478505

6
h-index

1281871

11
g-index

14
all docs

14
docs citations

14
times ranked

477
citing authors

#	ARTICLE	IF	CITATIONS
1	The CAFA challenge reports improved protein function prediction and new functional annotations for hundreds of genes through experimental screens. <i>Genome Biology</i> , 2019, 20, 244.	8.8	261
2	Prediction of Human Phenotype Ontology terms by means of hierarchical ensemble methods. <i>BMC Bioinformatics</i> , 2017, 18, 449.	2.6	22
3	Heterogeneous data integration methods for patient similarity networks. <i>Briefings in Bioinformatics</i> , 2022, 23, .	6.5	12
4	UNIPred-Web: a web tool for the integration and visualization of biomolecular networks for protein function prediction. <i>BMC Bioinformatics</i> , 2019, 20, 422.	2.6	9
5	FZD6 triggers Wnt signalling driven by WNT10B^{IVS1} expression and highlights new targets in T cell acute lymphoblastic leukemia. <i>Hematological Oncology</i> , 2021, 39, 364-379.	1.7	8
6	A Hierarchical Ensemble Method for DAG-Structured Taxonomies. <i>Lecture Notes in Computer Science</i> , 2015, , 15-26.	1.3	8
7	Multi-resolution visualization and analysis of biomolecular networks through hierarchical community detection and web-based graphical tools. <i>PLoS ONE</i> , 2020, 15, e0244241.	2.5	5
8	Prediction of Human Gene - Phenotype Associations by Exploiting the Hierarchical Structure of the Human Phenotype Ontology. <i>Lecture Notes in Computer Science</i> , 2015, , 66-77.	1.3	3
9	A GPU-based algorithm for fast node label learning in large and unbalanced biomolecular networks. <i>BMC Bioinformatics</i> , 2018, 19, 353.	2.6	2
10	Ensembling Descendant Term Classifiers to Improve Gene - Abnormal Phenotype Predictions. <i>Lecture Notes in Computer Science</i> , 2019, , 70-80.	1.3	2
11	HEMDAG: a family of modular and scalable hierarchical ensemble methods to improve Gene Ontology term prediction. <i>Bioinformatics</i> , 2021, 37, 4526-4533.	4.1	2
12	Disease Genes Must Guide Data Source Integration in the Gene Prioritization Process. <i>Lecture Notes in Computer Science</i> , 2019, , 60-69.	1.3	0
13	A Graphical Tool for the Exploration and Visual Analysis of Biomolecular Networks. <i>Lecture Notes in Computer Science</i> , 2020, , 88-98.	1.3	0