

Marinka Zitnik

List of Publications by Year in descending order

Source: <https://exaly.com/author-pdf/1691726/publications.pdf>

Version: 2024-02-01

16
papers

2,264
citations

759233

12
h-index

1058476

14
g-index

18
all docs

18
docs citations

18
times ranked

2441
citing authors

#	ARTICLE	IF	CITATIONS
1	Modeling polypharmacy side effects with graph convolutional networks. <i>Bioinformatics</i> , 2018, 34, i457-i466.	4.1	741
2	Machine learning for integrating data in biology and medicine: Principles, practice, and opportunities. <i>Information Fusion</i> , 2019, 50, 71-91.	19.1	340
3	Predicting multicellular function through multi-layer tissue networks. <i>Bioinformatics</i> , 2017, 33, i190-i198.	4.1	304
4	Learning Structural Node Embeddings via Diffusion Wavelets. , 2018, , .		200
5	Cross-type biomedical named entity recognition with deep multi-task learning. <i>Bioinformatics</i> , 2019, 35, 1745-1752.	4.1	182
6	To Embed or Not: Network Embedding as a Paradigm in Computational Biology. <i>Frontiers in Genetics</i> , 2019, 10, 381.	2.3	123
7	Network enhancement as a general method to denoise weighted biological networks. <i>Nature Communications</i> , 2018, 9, 3108.	12.8	82
8	Evolution of resilience in protein interactomes across the tree of life. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2019, 116, 4426-4433.	7.1	75
9	GNNExplainer: Generating Explanations for Graph Neural Networks. <i>Advances in Neural Information Processing Systems</i> , 2019, 32, 9240-9251.	2.8	53
10	Large-scale analysis of disease pathways in the human interactome. , 2018, , .		40
11	Prioritizing network communities. <i>Nature Communications</i> , 2018, 9, 2544.	12.8	37
12	Jumping across biomedical contexts using compressive data fusion. <i>Bioinformatics</i> , 2016, 32, i90-i100.	4.1	24
13	Leveraging the Cell Ontology to classify unseen cell types. <i>Nature Communications</i> , 2021, 12, 5556.	12.8	21
14	Sparse dictionary learning recovers pleiotropy from human cell fitness screens. <i>Cell Systems</i> , 2022, 13, 286-303.e10.	6.2	18
15	Co-evolution based machine-learning for predicting functional interactions between human genes. <i>Nature Communications</i> , 2021, 12, 6454.	12.8	12
16	Population-scale identification of differential adverse events before and during a pandemic. <i>Nature Computational Science</i> , 2021, 1, 666-677.	8.0	4