Giulia Fiscon

List of Publications by Year
in descending order

50 papers	1,551 citations	331538 21 h-index	330025 37 g-index
54 all docs	54 docs citations	54 times ranked	1816 citing authors

#	Article	IF	Citations
1	MIENTURNET: an interactive web tool for microRNA-target enrichment and network-based analysis. BMC Bioinformatics, 2019, 20, 545.	1.2	228
2	Molecular networks in Network Medicine: Development and applications. Wiley Interdisciplinary Reviews: Systems Biology and Medicine, 2020, 12, e1489.	6.6	128
3	Role of the long non-coding RNA PVT1 in the dysregulation of the ceRNA-ceRNA network in human breast cancer. PLoS ONE, 2017, 12, e0171661.	1.1	92
4	Combining EEG signal processing with supervised methods for Alzheimer's patients classification. BMC Medical Informatics and Decision Making, 2018, 18, 35.	1.5	91
5	SAveRUNNER: A network-based algorithm for drug repurposing and its application to COVID-19. PLoS Computational Biology, 2021, 17, e1008686.	1.5	72
6	Supervised DNA Barcodes species classification: analysis, comparisons and results. BioData Mining, 2014, 7, 4.	2.2	71
7	Gene co-expression in the interactome: moving from correlation toward causation via an integrated approach to disease module discovery. Npj Systems Biology and Applications, 2021, 7, 3.	1.4	64
8	A paradigm shift in medicine: A comprehensive review of network-based approaches. Biochimica Et Biophysica Acta - Gene Regulatory Mechanisms, 2020, 1863, 194416.	0.9	60
9	Network-Based Approaches to Explore Complex Biological Systems towards Network Medicine. Genes, 2018, 9, 437.	1.0	59
10	SWIM: a computational tool to unveiling crucial nodes in complex biological networks. Scientific Reports, 2017, 7, 44797.	1.6	50
11	Integer programming models for feature selection: New extensions and a randomized solution algorithm. European Journal of Operational Research, 2016, 250, 389-399.	3.5	49
12	Computational identification of specific genes for glioblastoma stem-like cells identity. Scientific Reports, 2018, 8, 7769.	1.6	48
13	SAveRUNNER: an R-based tool for drug repurposing. BMC Bioinformatics, 2021, 22, 150.	1.2	42
14	Integrated transcriptomic correlation network analysis identifies COPD molecular determinants. Scientific Reports, 2020, 10, 3361.	1.6	35
15	Interplay Between Long Noncoding RNAs and MicroRNAs in Cancer. Methods in Molecular Biology, 2018, 1819, 75-92.	0.4	34
16	TCGA2BED: extracting, extending, integrating, and querying The Cancer Genome Atlas. BMC Bioinformatics, 2017, 18, 6.	1.2	33
17	CAMUR: Knowledge extraction from RNA-seq cancer data through equivalent classification rules. Bioinformatics, 2016, 32, 697-704.	1.8	31
18	BRAFV600E-mutant cancers display a variety of networks by SWIM analysis: prediction of vemurafenib clinical response. Endocrine, 2019, 64, 406-413.	1.1	28

#	Article	IF	Citations
19	Alzheimer's disease patients classification through EEG signals processing. , 2014, , .		27
20	SWIM tool application to expression data of glioblastoma stem-like cell lines, corresponding primary tumors and conventional glioma cell lines. BMC Bioinformatics, 2018, 19, 436.	1.2	26
21	Drug Repurposing: A Network-based Approach to Amyotrophic Lateral Sclerosis. Neurotherapeutics, 2021, 18, 1678-1691.	2.1	24
22	An Overview of the Computational Models Dealing with the Regulatory ceRNA Mechanism and ceRNA Deregulation in Cancer. Methods in Molecular Biology, 2021, 2324, 149-164.	0.4	22
23	The New Paradigm of Network Medicine to Analyze Breast Cancer Phenotypes. International Journal of Molecular Sciences, 2020, 21, 6690.	1.8	21
24	Next generation sequencing reads comparison with an alignment-free distance. BMC Research Notes, 2014, 7, 869.	0.6	17
25	Prostate cancer screening research can benefit from network medicine: an emerging awareness. Npj Systems Biology and Applications, 2020, 6, 13.	1.4	17
26	In silico drug repurposing in COVID-19: A network-based analysis. Biomedicine and Pharmacotherapy, 2021, 142, 111954.	2.5	17
27	MONSTER v1.1: a tool to extract and search for RNA non-branching structures. BMC Genomics, 2015, 16, S1.	1.2	15
28	MISSEL: a method to identify a large number of small species-specific genomic subsequences and its application to viruses classification. BioData Mining, 2016, 9, 38.	2.2	15
29	The role of FOSL1 in stem-like cell reprogramming processes. Scientific Reports, 2021, 11, 14677.	1.6	13
30	Polymorphonuclear Myeloid-Derived Suppressor Cells Are Abundant in Peripheral Blood of Cancer Patients and Suppress Natural Killer Cell Anti-Tumor Activity. Frontiers in Immunology, 2021, 12, 803014.	2.2	13
31	Gene network analysis using SWIM reveals interplay between the transcription factorâ€encoding genes HMGA1, FOXM1, and MYBL2 in tripleâ€negative breast cancer. FEBS Letters, 2021, 595, 1569-1586.	1.3	12
32	Disruption of redox homeostasis for combinatorial drug efficacy in K-Ras tumors as revealed by metabolic connectivity profiling. Cancer & Metabolism, 2020, 8, 22.	2.4	10
33	Transcriptomics and Metabolomics Integration Reveals Redox-Dependent Metabolic Rewiring in Breast Cancer Cells. Cancers, 2021, 13, 5058.	1.7	10
34	SWIMmeR: an R-based software to unveiling crucial nodes in complex biological networks. Bioinformatics, 2022, 38, 586-588.	1.8	9
35	Comprehensive network medicine-based drug repositioning via integration of therapeutic efficacy and side effects. Npj Systems Biology and Applications, 2022, 8, 12.	1.4	9
36	An integrated approach based on EEG signals processing combined with supervised methods to classify Alzheimerâ€™s disease patients. , 2018, , .		8

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37	Assessing the impact of data-driven limitations on tracing and forecasting the outbreak dynamics of COVID-19. Computers in Biology and Medicine, 2021, 135, 104657.	3.9	8
38	Identification of Disease–miRNA Networks Across Different Cancer Types Using SWIM. Methods in Molecular Biology, 2019, 1970, 169-181.	0.4	5
39	Integro-differential approach for modeling the COVID-19 dynamics - Impact of confinement measures in Italy. Computers in Biology and Medicine, 2021, 139, 105013.	3.9	5
40	Repurposing Histaminergic Drugs in Multiple Sclerosis. International Journal of Molecular Sciences, 2022, 23, 6347.	1.8	5
41	An ontology-based approach to improve data querying and organization of Alzheimer's Disease data. , 2018, , .		3
42	A New Procedure to Analyze RNA Non-Branching Structures. Current Bioinformatics, 2015, 10, 242-258.	0.7	3
43	A Perspective on the Algorithms Predicting and Evaluating the RNA Secondary Structure. Journal of Genetics and Genome Research, 2016, 3, .	0.3	3
44	A Comparison of Network-Based Methods for Drug Repurposing along with an Application to Human Complex Diseases. International Journal of Molecular Sciences, 2022, 23, 3703.	1.8	3
45	GELA: A Software Tool for the Analysis of Gene Expression Data. , 2015, , .		2
46	Mining clinical and laboratory data of neurodegenerative diseases by Machine Learning: transcriptomic biomarkers. , 2018, , .		2
47	SPINNAKER: an R-based tool to highlight key RNA interactions in complex biological networks. BMC Bioinformatics, 2022, 23, 166.	1.2	2
48	String-Matching and Alignment Algorithms for Finding Motifs in NGS Data. , 2017, , 235-264.		0
49	Adjuvant epidermal growth factor receptor (EGFR) tyrosine kinase inhibitors (TKIs) for the treatment of people with resected stage I to III non-small-cell lung cancer and EGFR mutation. The Cochrane Library, 2022, 2022, .	1.5	0
50	Network analysis to determine association between immuno-related toxicities and immune soluble profile in patients treated with anti–PD-1.. Journal of Clinical Oncology, 2022, 40, 2553-2553.	0.8	0