

Giulia Fiscon

List of Publications by Year in descending order

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Version: 2024-02-01

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	SWIMmeR: an R-based software to unveiling crucial nodes in complex biological networks. <i>Bioinformatics</i> , 2022, 38, 586-588.	1.8	9
2	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. <i>The Cochrane Library</i> , 2022, 2022, .	1.5	0
3	A Comparison of Network-Based Methods for Drug Repurposing along with an Application to Human Complex Diseases. <i>International Journal of Molecular Sciences</i> , 2022, 23, 3703.	1.8	3
4	Comprehensive network medicine-based drug repositioning via integration of therapeutic efficacy and side effects. <i>Npj Systems Biology and Applications</i> , 2022, 8, 12.	1.4	9
5	SPINNAKER: an R-based tool to highlight key RNA interactions in complex biological networks. <i>BMC Bioinformatics</i> , 2022, 23, 166.	1.2	2
6	Repurposing Histaminergic Drugs in Multiple Sclerosis. <i>International Journal of Molecular Sciences</i> , 2022, 23, 6347.	1.8	5
7	Network analysis to determine association between immuno-related toxicities and immune soluble profile in patients treated with anti-PD-1. <i>Journal of Clinical Oncology</i> , 2022, 40, 2553-2553.	0.8	0
8	Gene co-expression in the interactome: moving from correlation toward causation via an integrated approach to disease module discovery. <i>Npj Systems Biology and Applications</i> , 2021, 7, 3.	1.4	64
9	An Overview of the Computational Models Dealing with the Regulatory ceRNA Mechanism and ceRNA Deregulation in Cancer. <i>Methods in Molecular Biology</i> , 2021, 2324, 149-164.	0.4	22
10	SAveRUNNER: A network-based algorithm for drug repurposing and its application to COVID-19. <i>PLoS Computational Biology</i> , 2021, 17, e1008686.	1.5	72
11	SAveRUNNER: an R-based tool for drug repurposing. <i>BMC Bioinformatics</i> , 2021, 22, 150.	1.2	42
12	Gene network analysis using SWIM reveals interplay between the transcription factor encoding genes HMGA1, FOXM1, and MYBL2 in triple-negative breast cancer. <i>FEBS Letters</i> , 2021, 595, 1569-1586.	1.3	12
13	Drug Repurposing: A Network-based Approach to Amyotrophic Lateral Sclerosis. <i>Neurotherapeutics</i> , 2021, 18, 1678-1691.	2.1	24
14	The role of FOSL1 in stem-like cell reprogramming processes. <i>Scientific Reports</i> , 2021, 11, 14677.	1.6	13
15	Assessing the impact of data-driven limitations on tracing and forecasting the outbreak dynamics of COVID-19. <i>Computers in Biology and Medicine</i> , 2021, 135, 104657.	3.9	8
16	In silico drug repurposing in COVID-19: A network-based analysis. <i>Biomedicine and Pharmacotherapy</i> , 2021, 142, 111954.	2.5	17
17	Transcriptomics and Metabolomics Integration Reveals Redox-Dependent Metabolic Rewiring in Breast Cancer Cells. <i>Cancers</i> , 2021, 13, 5058.	1.7	10
18	Integro-differential approach for modeling the COVID-19 dynamics - Impact of confinement measures in Italy. <i>Computers in Biology and Medicine</i> , 2021, 139, 105013.	3.9	5

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19	Polymorphonuclear Myeloid-Derived Suppressor Cells Are Abundant in Peripheral Blood of Cancer Patients and Suppress Natural Killer Cell Anti-Tumor Activity. <i>Frontiers in Immunology</i> , 2021, 12, 803014.	2.2	13
20	A paradigm shift in medicine: A comprehensive review of network-based approaches. <i>Biochimica Et Biophysica Acta - Gene Regulatory Mechanisms</i> , 2020, 1863, 194416.	0.9	60
21	Disruption of redox homeostasis for combinatorial drug efficacy in K-Ras tumors as revealed by metabolic connectivity profiling. <i>Cancer & Metabolism</i> , 2020, 8, 22.	2.4	10
22	The New Paradigm of Network Medicine to Analyze Breast Cancer Phenotypes. <i>International Journal of Molecular Sciences</i> , 2020, 21, 6690.	1.8	21
23	Prostate cancer screening research can benefit from network medicine: an emerging awareness. <i>Npj Systems Biology and Applications</i> , 2020, 6, 13.	1.4	17
24	Integrated transcriptomic correlation network analysis identifies COPD molecular determinants. <i>Scientific Reports</i> , 2020, 10, 3361.	1.6	35
25	Molecular networks in Network Medicine: Development and applications. <i>Wiley Interdisciplinary Reviews: Systems Biology and Medicine</i> , 2020, 12, e1489.	6.6	128
26	MIENTURNET: an interactive web tool for microRNA-target enrichment and network-based analysis. <i>BMC Bioinformatics</i> , 2019, 20, 545.	1.2	228
27	BRAFV600E-mutant cancers display a variety of networks by SWIM analysis: prediction of vemurafenib clinical response. <i>Endocrine</i> , 2019, 64, 406-413.	1.1	28
28	Identification of Disease-specific miRNA Networks Across Different Cancer Types Using SWIM. <i>Methods in Molecular Biology</i> , 2019, 1970, 169-181.	0.4	5
29	An ontology-based approach to improve data querying and organization of Alzheimer's Disease data. , 2018, , .		3
30	An integrated approach based on EEG signals processing combined with supervised methods to classify Alzheimer's disease patients. , 2018, , .		8
31	Mining clinical and laboratory data of neurodegenerative diseases by Machine Learning: transcriptomic biomarkers. , 2018, , .		2
32	Interplay Between Long Noncoding RNAs and MicroRNAs in Cancer. <i>Methods in Molecular Biology</i> , 2018, 1819, 75-92.	0.4	34
33	SWIM tool application to expression data of glioblastoma stem-like cell lines, corresponding primary tumors and conventional glioma cell lines. <i>BMC Bioinformatics</i> , 2018, 19, 436.	1.2	26
34	Network-Based Approaches to Explore Complex Biological Systems towards Network Medicine. <i>Genes</i> , 2018, 9, 437.	1.0	59
35	Computational identification of specific genes for glioblastoma stem-like cells identity. <i>Scientific Reports</i> , 2018, 8, 7769.	1.6	48
36	Combining EEG signal processing with supervised methods for Alzheimer's patients classification. <i>BMC Medical Informatics and Decision Making</i> , 2018, 18, 35.	1.5	91

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37	TCGA2BED: extracting, extending, integrating, and querying The Cancer Genome Atlas. BMC Bioinformatics, 2017, 18, 6.	1.2	33
38	SWIM: a computational tool to unveiling crucial nodes in complex biological networks. Scientific Reports, 2017, 7, 44797.	1.6	50
39	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
40	String-Matching and Alignment Algorithms for Finding Motifs in NGS Data. , 2017, , 235-264.		0
41	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
42	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
43	CAMUR: Knowledge extraction from RNA-seq cancer data through equivalent classification rules. Bioinformatics, 2016, 32, 697-704.	1.8	31
44	A Perspective on the Algorithms Predicting and Evaluating the RNA Secondary Structure. Journal of Genetics and Genome Research, 2016, 3, .	0.3	3
45	MONSTER v1.1: a tool to extract and search for RNA non-branching structures. BMC Genomics, 2015, 16, S1.	1.2	15
46	GELA: A Software Tool for the Analysis of Gene Expression Data. , 2015, , .		2
47	A New Procedure to Analyze RNA Non-Branching Structures. Current Bioinformatics, 2015, 10, 242-258.	0.7	3
48	Next generation sequencing reads comparison with an alignment-free distance. BMC Research Notes, 2014, 7, 869.	0.6	17
49	Alzheimer's disease patients classification through EEG signals processing. , 2014, , .		27
50	Supervised DNA Barcodes species classification: analysis, comparisons and results. BioData Mining, 2014, 7, 4.	2.2	71