Federica Conte

List of Publications by Year in descending order

28 papers	1,137 citations	471371 17 h-index	501076 28 g-index
28 all docs	28 docs citations	28 times ranked	1399 citing authors

#	Article	IF	Citations
1	In silico recognition of a prognostic signature in basal-like breast cancer patients. PLoS ONE, 2022, 17, e0264024.	1.1	5
2	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
3	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
4	Repurposing Histaminergic Drugs in Multiple Sclerosis. International Journal of Molecular Sciences, 2022, 23, 6347.	1.8	5
5	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
6	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
7	SAveRUNNER: A network-based algorithm for drug repurposing and its application to COVID-19. PLoS Computational Biology, 2021, 17, e1008686.	1.5	72
8	Gene network analysis using SWIM reveals interplay between the transcription factor–encoding genes HMGA1, FOXM1, and MYBL2 in triple–negative breast cancer. FEBS Letters, 2021, 595, 1569-1586.	1.3	12
9	Drug Repurposing: A Network-based Approach to Amyotrophic Lateral Sclerosis. Neurotherapeutics, 2021, 18, 1678-1691.	2.1	24
10	The role of FOSL1 in stem-like cell reprogramming processes. Scientific Reports, 2021, 11, 14677.	1.6	13
11	In silico drug repurposing in COVID-19: A network-based analysis. Biomedicine and Pharmacotherapy, 2021, 142, 111954.	2.5	17
12	Network Analysis Integrating microRNA Expression Profiling with MRI Biomarkers and Clinical Data for Prostate Cancer Early Detection: A Proof of Concept Study. Biomedicines, 2021, 9, 1470.	1.4	5
13	Transcriptomics and Metabolomics Integration Reveals Redox-Dependent Metabolic Rewiring in Breast Cancer Cells. Cancers, 2021, 13, 5058.	1.7	10
14	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
15	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
16	Network Analysis of Gut Microbiome and Metabolome to Discover Microbiota-Linked Biomarkers in Patients Affected by Non-Small Cell Lung Cancer. International Journal of Molecular Sciences, 2020, 21, 8730.	1.8	75
17	The New Paradigm of Network Medicine to Analyze Breast Cancer Phenotypes. International Journal of Molecular Sciences, 2020, 21, 6690.	1.8	21
18	Applications of Nonlinear Programming to the Optimization of Fractionated Protocols in Cancer Radiotherapy. Information (Switzerland), 2020, 11, 313.	1.7	3

#	Article	IF	Citations
19	Integrated transcriptomic correlation network analysis identifies COPD molecular determinants. Scientific Reports, 2020, 10, 3361.	1.6	35
20	Molecular networks in Network Medicine: Development and applications. Wiley Interdisciplinary Reviews: Systems Biology and Medicine, 2020, 12, e1489.	6.6	128
21	MIENTURNET: an interactive web tool for microRNA-target enrichment and network-based analysis. BMC Bioinformatics, 2019, 20, 545.	1.2	228
22	BRAFV600E-mutant cancers display a variety of networks by SWIM analysis: prediction of vemurafenib clinical response. Endocrine, 2019, 64, 406-413.	1.1	28
23	Interplay Between Long Noncoding RNAs and MicroRNAs in Cancer. Methods in Molecular Biology, 2018, 1819, 75-92.	0.4	34
24	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
25	Network-Based Approaches to Explore Complex Biological Systems towards Network Medicine. Genes, 2018, 9, 437.	1.0	59
26	Computational identification of specific genes for glioblastoma stem-like cells identity. Scientific Reports, 2018, 8, 7769.	1.6	48
27	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
28	Insulin Signaling in Insulin Resistance States and Cancer: A Modeling Analysis. PLoS ONE, 2016, 11, e0154415.	1.1	29