# Federica Conte

## List of Publications by Year
in descending order

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|---|---|
| 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 | 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 | 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 |
| 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 | 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 |
| 7 | 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 |
| 8 | Network-Based Approaches to Explore Complex Biological Systems towards Network Medicine. Genes, 2018, 9, 437. | 1.0 | 59 |
| 9 | Computational identification of specific genes for glioblastoma stem-like cells identity. Scientific Reports, 2018, 8, 7769. | 1.6 | 48 |
| 10 | Integrated transcriptomic correlation network analysis identifies COPD molecular determinants. Scientific Reports, 2020, 10, 3361. | 1.6 | 35 |
| 11 | Interplay Between Long Noncoding RNAs and MicroRNAs in Cancer. Methods in Molecular Biology, 2018, 1819, 75-92. | 0.4 | 34 |
| 12 | Insulin Signaling in Insulin Resistance States and Cancer: A Modeling Analysis. PLoS ONE, 2016, 11, e0154415. | 1.1 | 29 |
| 13 | BRAFV600E-mutant cancers display a variety of networks by SWIM analysis: prediction of vemurafenib clinical response. Endocrine, 2019, 64, 406-413. | 1.1 | 28 |
| 14 | 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 |
| 15 | Drug Repurposing: A Network-based Approach to Amyotrophic Lateral Sclerosis. Neurotherapeutics, 2021, 18, 1678-1691. | 2.1 | 24 |
| 16 | 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 |
| 17 | The New Paradigm of Network Medicine to Analyze Breast Cancer Phenotypes. International Journal of Molecular Sciences, 2020, 21, 6690. | 1.8 | 21 |
| 18 | In silico drug repurposing in COVID-19: A network-based analysis. Biomedicine and Pharmacotherapy, 2021, 142, 111954. | 2.5 | 17 |

| # | Article | IF | Citations |
|---|---------|----|-----------|
| 19 | The role of FOSL1 in stem-like cell reprogramming processes. Scientific Reports, 2021, 11, 14677. | 1.6 | 13 |
| 20 | 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 |
| 21 | 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 |
| 22 | Transcriptomics and Metabolomics Integration Reveals Redox-Dependent Metabolic Rewiring in Breast Cancer Cells. Cancers, 2021, 13, 5058. | 1.7 | 10 |
| 23 | 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 |
| 24 | 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 |
| 25 | In silico recognition of a prognostic signature in basal-like breast cancer patients. PLoS ONE, 2022, 17, e0264024. | 1.1 | 5 |
| 26 | Repurposing Histaminergic Drugs in Multiple Sclerosis. International Journal of Molecular Sciences, 2022, 23, 6347. | 1.8 | 5 |
| 27 | Applications of Nonlinear Programming to the Optimization of Fractionated Protocols in Cancer Radiotherapy. Information (Switzerland), 2020, 11, 313. | 1.7 | 3 |
| 28 | 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 |