

# Paola Paci

## List of Publications by Year in descending order

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Version: 2024-02-01

71  
papers

3,129  
citations

218381

26  
h-index

168136

53  
g-index

74  
all docs

74  
docs citations

74  
times ranked

4840  
citing authors

#	ARTICLE	IF	CITATIONS
1	Gut microbiota profiling of pediatric nonalcoholic fatty liver disease and obese patients unveiled by an integrated meta-omics-based approach. <i>Hepatology</i> , 2017, 65, 451-464.	3.6	572
2	Computational analysis identifies a sponge interaction network between long non-coding RNAs and messenger RNAs in human breast cancer. <i>BMC Systems Biology</i> , 2014, 8, 83.	3.0	233
3	MIENTURNET: an interactive web tool for microRNA-target enrichment and network-based analysis. <i>BMC Bioinformatics</i> , 2019, 20, 545.	1.2	228
4	PVT1: A Rising Star among Oncogenic Long Noncoding RNAs. <i>BioMed Research International</i> , 2015, 2015, 1-10.	0.9	191
5	Molecular networks in Network Medicine: Development and applications. <i>Wiley Interdisciplinary Reviews: Systems Biology and Medicine</i> , 2020, 12, e1489.	6.6	128
6	Ripening Transcriptomic Program in Red and White Grapevine Varieties Correlates with Berry Skin Anthocyanin Accumulation. <i>Plant Physiology</i> , 2017, 174, 2376-2396.	2.3	121
7	Integrated Network Analysis Identifies Fight-Club Nodes as a Class of Hubs Encompassing Key Putative Switch Genes That Induce Major Transcriptome Reprogramming during Grapevine Development. <i>Plant Cell</i> , 2015, 26, 4617-4635.	3.1	110
8	Gut microbiota signatures in cystic fibrosis: Loss of host CFTR function drives the microbiota enterophenotype. <i>PLoS ONE</i> , 2018, 13, e0208171.	1.1	107
9	Role of the long non-coding RNA PVT1 in the dysregulation of the ceRNA-ceRNA network in human breast cancer. <i>PLoS ONE</i> , 2017, 12, e0171661.	1.1	92
10	Phylogenetic and Metabolic Tracking of Gut Microbiota during Perinatal Development. <i>PLoS ONE</i> , 2015, 10, e0137347.	1.1	84
11	Network Analysis of Gut Microbiome and Metabolome to Discover Microbiota-Linked Biomarkers in Patients Affected by Non-Small Cell Lung Cancer. <i>International Journal of Molecular Sciences</i> , 2020, 21, 8730.	1.8	75
12	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
13	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
14	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
15	Network-Based Approaches to Explore Complex Biological Systems towards Network Medicine. <i>Genes</i> , 2018, 9, 437.	1.0	59
16	SWIM: a computational tool to unveiling crucial nodes in complex biological networks. <i>Scientific Reports</i> , 2017, 7, 44797.	1.6	50
17	Distinct transcriptome responses to water limitation in isohydric and anisohydric grapevine cultivars. <i>BMC Genomics</i> , 2016, 17, 815.	1.2	49
18	Computational identification of specific genes for glioblastoma stem-like cells identity. <i>Scientific Reports</i> , 2018, 8, 7769.	1.6	48

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19	SAveRUNNER: an R-based tool for drug repurposing. BMC Bioinformatics, 2021, 22, 150.	1.2	42
20	GIANT: A Cytoscape Plugin for Modular Networks. PLoS ONE, 2014, 9, e105001.	1.1	39
21	Modules Identification in Protein Structures: The Topological and Geometrical Solutions. Journal of Chemical Information and Modeling, 2014, 54, 159-168.	2.5	38
22	ImmunoGrid, an integrative environment for large-scale simulation of the immune system for vaccine discovery, design and optimization. Briefings in Bioinformatics, 2008, 10, 330-340.	3.2	36
23	Clinical epigenetics settings for cancer and cardiovascular diseases: real-life applications of network medicine at the bedside. Clinical Epigenetics, 2021, 13, 66.	1.8	36
24	Integrated transcriptomic correlation network analysis identifies COPD molecular determinants. Scientific Reports, 2020, 10, 3361.	1.6	35
25	Interplay Between Long Noncoding RNAs and MicroRNAs in Cancer. Methods in Molecular Biology, 2018, 1819, 75-92.	0.4	34
26	Proteins as Sponges: A Statistical Journey along Protein Structure Organization Principles. Journal of Chemical Information and Modeling, 2012, 52, 474-482.	2.5	29
27	BRAFV600E-mutant cancers display a variety of networks by SWIM analysis: prediction of vemurafenib clinical response. Endocrine, 2019, 64, 406-413.	1.1	28
28	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
29	<scp>JARID</scp> 1B expression and its function in <scp>DNA</scp> damage repair are tightly regulated by mi<scp>RNA</scp>s in breast cancer. Cancer Science, 2019, 110, 1232-1243.	1.7	25
30	Drug Repurposing: A Network-based Approach to Amyotrophic Lateral Sclerosis. Neurotherapeutics, 2021, 18, 1678-1691.	2.1	24
31	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
32	The New Paradigm of Network Medicine to Analyze Breast Cancer Phenotypes. International Journal of Molecular Sciences, 2020, 21, 6690.	1.8	21
33	Kinetics effects and modeling of <scp>mRNA</scp> turnover. Wiley Interdisciplinary Reviews RNA, 2015, 6, 327-336.	3.2	20
34	Inverse Problems in Systems Biology: A Critical Review. Methods in Molecular Biology, 2018, 1702, 69-94.	0.4	19
35	Genetic, epigenetic and genomic effects on variation of gene expression among grape varieties. Plant Journal, 2019, 99, 895-909.	2.8	19
36	Prostate cancer screening research can benefit from network medicine: an emerging awareness. Npj Systems Biology and Applications, 2020, 6, 13.	1.4	17

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37	Convolutional Neural Networks for Automated Classification of Prostate Multiparametric Magnetic Resonance Imaging Based on Image Quality. <i>Journal of Magnetic Resonance Imaging</i> , 2022, 55, 480-490.	1.9	17
38	In silico drug repurposing in COVID-19: A network-based analysis. <i>Biomedicine and Pharmacotherapy</i> , 2021, 142, 111954.	2.5	17
39	MONSTER v1.1: a tool to extract and search for RNA non-branching structures. <i>BMC Genomics</i> , 2015, 16, S1.	1.2	15
40	A Simplified Genomic Profiling Approach Predicts Outcome in Metastatic Colorectal Cancer. <i>Cancers</i> , 2019, 11, 147.	1.7	15
41	Identifying Correlations between Chromosomal Proximity of Genes and Distance of Their Products in Protein-Protein Interaction Networks of Yeast. <i>PLoS ONE</i> , 2013, 8, e57707.	1.1	13
42	The role of FOSL1 in stem-like cell reprogramming processes. <i>Scientific Reports</i> , 2021, 11, 14677.	1.6	13
43	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
44	Stochastic Modeling of Expression Kinetics Identifies Messenger Half-Lives and Reveals Sequential Waves of Co-ordinated Transcription and Decay. <i>PLoS Computational Biology</i> , 2012, 8, e1002772.	1.5	12
45	Structural and Functional Analysis of Hemoglobin and Serum Albumin Through Protein Long-Range Interaction Networks. <i>Current Proteomics</i> , 2012, 9, 160-166.	0.1	12
46	The clinical significance of HCV core antigen detection during Telaprevir/Peg-Interferon/Ribavirin therapy in patients with HCV 1 genotype infection. <i>Journal of Clinical Virology</i> , 2015, 69, 68-73.	1.6	12
47	Clinical Multigene Panel Sequencing Identifies Distinct Mutational Association Patterns in Metastatic Colorectal Cancer. <i>Frontiers in Oncology</i> , 2020, 10, 560.	1.3	12
48	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
49	Disruption of redox homeostasis for combinatorial drug efficacy in K-Ras tumors as revealed by metabolic connectivity profiling. <i>Cancer &amp; Metabolism</i> , 2020, 8, 22.	2.4	10
50	Transcriptomics and Metabolomics Integration Reveals Redox-Dependent Metabolic Rewiring in Breast Cancer Cells. <i>Cancers</i> , 2021, 13, 5058.	1.7	10
51	SWIMmeR: an R-based software to unveiling crucial nodes in complex biological networks. <i>Bioinformatics</i> , 2022, 38, 586-588.	1.8	9
52	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
53	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
54	Are Proteins Just Coiled Cords? Local and Global Analysis of Contact Maps Reveals the Backbone-Dependent Nature of Proteins. <i>Current Protein and Peptide Science</i> , 2015, 17, 26-29.	0.7	6

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55	s- AND d-WAVE SYMMETRIES IN NONADIABATIC THEORY OF SUPERCONDUCTIVITY. International Journal of Modern Physics B, 2000, 14, 2982-2987.	1.0	5
56	Ultrasensitive HCV RNA Quantification in Antiviral Triple Therapy: New Insight on Viral Clearance Dynamics and Treatment Outcome Predictors. PLoS ONE, 2016, 11, e0158989.	1.1	5
57	Identification of Disease-Related miRNA Networks Across Different Cancer Types Using SWIM. Methods in Molecular Biology, 2019, 1970, 169-181.	0.4	5
58	Network Analysis Integrating microRNA Expression Profiling with MRI Biomarkers and Clinical Data for Prostate Cancer Early Detection: A Proof of Concept Study. Biomedicine, 2021, 9, 1470.	1.4	5
59	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
60	In silico recognition of a prognostic signature in basal-like breast cancer patients. PLoS ONE, 2022, 17, e0264024.	1.1	5
61	Repurposing Histaminergic Drugs in Multiple Sclerosis. International Journal of Molecular Sciences, 2022, 23, 6347.	1.8	5
62	Human Papillomavirus Infections in Cervical Samples From HIV-Positive Women: Evaluation of the Presence of the Nonavalent HPV Genotypes and Genetic Diversity. Frontiers in Microbiology, 2020, 11, 603657.	1.5	4
63	SEaCorAl: Identifying and contrasting the regulation-correlation bias in RNA-Seq paired expression data of patient groups. Computers in Biology and Medicine, 2021, 135, 104567.	3.9	4
64	Criticality of Timing for Anti-HIV Therapy Initiation. PLoS ONE, 2010, 5, e15294.	1.1	3
65	A New Procedure to Analyze RNA Non-Branching Structures. Current Bioinformatics, 2015, 10, 242-258.	0.7	3
66	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
67	SPINNAKER: an R-based tool to highlight key RNA interactions in complex biological networks. BMC Bioinformatics, 2022, 23, 166.	1.2	2
68	A feature-based integrated scoring scheme for cell cycle-regulated genes prioritization. Journal of Theoretical Biology, 2018, 459, 130-141.	0.8	0
69	Mining sponge phenomena in RNA expression data. Journal of Bioinformatics and Computational Biology, 2021, , 2150022.	0.3	0
70	An integrative in-silico analysis discloses a novel molecular subset of colorectal cancer possibly eligible for immune checkpoint immunotherapy. Biology Direct, 2022, 17, 10.	1.9	0
71	StaRTrEK: in silico estimation of RNA half-lives from genome-wide time-course experiments without transcriptional inhibition. BMC Bioinformatics, 2022, 23, .	1.2	0