Paola Paci

List of Publications by Year
in descending order

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	Convolutional Neural Networks for Automated Classification of Prostate Multiparametric Magnetic Resonance Imaging Based on Image Quality. Journal of Magnetic Resonance Imaging, 2022, 55, 480-490.	1.9	17
2	SWIMmeR: an R-based software to unveiling crucial nodes in complex biological networks. Bioinformatics, 2022, 38, 586-588.	1.8	9
3	In silico recognition of a prognostic signature in basal-like breast cancer patients. PLoS ONE, 2022, 17, e0264024.	1.1	5
4	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
5	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
6	SPINNAKER: an R-based tool to highlight key RNA interactions in complex biological networks. BMC Bioinformatics, 2022, 23, 166.	1.2	2
7	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
8	StaRTrEK:in silico estimation of RNA half-lives from genome-wide time-course experiments without transcriptional inhibition. BMC Bioinformatics, 2022, 23, .	1.2	0
9	Repurposing Histaminergic Drugs in Multiple Sclerosis. International Journal of Molecular Sciences, 2022, 23, 6347.	1.8	5
10	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
11	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
12	SAveRUNNER: A network-based algorithm for drug repurposing and its application to COVID-19. PLoS Computational Biology, 2021, 17, e1008686.	1.5	72
13	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
14	SAveRUNNER: an R-based tool for drug repurposing. BMC Bioinformatics, 2021, 22, 150.	1.2	42
15	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
16	Drug Repurposing: A Network-based Approach to Amyotrophic Lateral Sclerosis. Neurotherapeutics, 2021, 18, 1678-1691.	2.1	24
17	The role of FOSL1 in stem-like cell reprogramming processes. Scientific Reports, 2021, 11, 14677.	1.6	13
18	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

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19	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
20	In silico drug repurposing in COVID-19: A network-based analysis. Biomedicine and Pharmacotherapy, 2021, 142, 111954.	2.5	17
21	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
22	Transcriptomics and Metabolomics Integration Reveals Redox-Dependent Metabolic Rewiring in Breast Cancer Cells. Cancers, 2021, 13, 5058.	1.7	10
23	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
24	Mining sponge phenomena in RNA expression data. Journal of Bioinformatics and Computational Biology, 2021, , 2150022.	0.3	0
25	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
26	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
27	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
28	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
29	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
30	The New Paradigm of Network Medicine to Analyze Breast Cancer Phenotypes. International Journal of Molecular Sciences, 2020, 21, 6690.	1.8	21
31	Prostate cancer screening research can benefit from network medicine: an emerging awareness. Npj Systems Biology and Applications, 2020, 6, 13.	1.4	17
32	Clinical Multigene Panel Sequencing Identifies Distinct Mutational Association Patterns in Metastatic Colorectal Cancer. Frontiers in Oncology, 2020, 10, 560.	1.3	12
33	Integrated transcriptomic correlation network analysis identifies COPD molecular determinants. Scientific Reports, 2020, 10, 3361.	1.6	35
34	Molecular networks in Network Medicine: Development and applications. Wiley Interdisciplinary Reviews: Systems Biology and Medicine, 2020, 12, e1489.	6.6	128
35	MIENTURNET: an interactive web tool for microRNA-target enrichment and network-based analysis. BMC Bioinformatics, 2019, 20, 545.	1.2	228
36	A Simplified Genomic Profiling Approach Predicts Outcome in Metastatic Colorectal Cancer. Cancers, 2019, 11, 147.	1.7	15

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37	Genetic, epigenetic and genomic effects on variation of gene expression among grape varieties. Plant Journal, 2019, 99, 895-909.	2.8	19
38	<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
39	BRAFV600E-mutant cancers display a variety of networks by SWIM analysis: prediction of vemurafenib clinical response. Endocrine, 2019, 64, 406-413.	1.1	28
40	Identification of Disease–miRNA Networks Across Different Cancer Types Using SWIM. Methods in Molecular Biology, 2019, 1970, 169-181.	0.4	5
41	Inverse Problems in Systems Biology: A Critical Review. Methods in Molecular Biology, 2018, 1702, 69-94.	0.4	19
42	Interplay Between Long Noncoding RNAs and MicroRNAs in Cancer. Methods in Molecular Biology, 2018, 1819, 75-92.	0.4	34
43	Gut microbiota signatures in cystic fibrosis: Loss of host CFTR function drives the microbiota enterophenotype. PLoS ONE, 2018, 13, e0208171.	1.1	107
44	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
45	A feature-based integrated scoring scheme for cell cycle-regulated genes prioritization. Journal of Theoretical Biology, 2018, 459, 130-141.	0.8	0
46	Network-Based Approaches to Explore Complex Biological Systems towards Network Medicine. Genes, 2018, 9, 437.	1.0	59
47	Computational identification of specific genes for glioblastoma stem-like cells identity. Scientific Reports, 2018, 8, 7769.	1.6	48
48	Gut microbiota profiling of pediatric nonalcoholic fatty liver disease and obese patients unveiled by an integrated meta–omics–based approach. Hepatology, 2017, 65, 451-464.	3.6	572
49	SWIM: a computational tool to unveiling crucial nodes in complex biological networks. Scientific Reports, 2017, 7, 44797.	1.6	50
50	Ripening Transcriptomic Program in Red and White Grapevine Varieties Correlates with Berry Skin Anthocyanin Accumulation. Plant Physiology, 2017, 174, 2376-2396.	2.3	121
51	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
52	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
53	Distinct transcriptome responses to water limitation in isohydric and anisohydric grapevine cultivars. BMC Genomics, 2016, 17, 815.	1.2	49
54	MONSTER v1.1: a tool to extract and search for RNA non-branching structures. BMC Genomics, 2015, 16, S1.	1.2	15

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55	Are Proteins Just Coiled Cords? Local and Global Analysis of Contact Maps Reveals the Backbone-Dependent Nature of Proteins. Current Protein and Peptide Science, 2015, 17, 26-29.	0.7	6
56	Phylogenetic and Metabolic Tracking of Gut Microbiota during Perinatal Development. PLoS ONE, 2015, 10, e0137347.	1.1	84
57	PVT1: A Rising Star among Oncogenic Long Noncoding RNAs. BioMed Research International, 2015, 2015, 1-10.	0.9	191
58	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 Â. Plant Cell, 2015, 26, 4617-4635.	3.1	110
59	The clinical significance of HCV core antigen detection during Telaprevir/Peg-Interferon/Ribavirin therapy in patients with HCV 1 genotype infection. Journal of Clinical Virology, 2015, 69, 68-73.	1.6	12
60	Kinetics effects and modeling of <scp>mRNA</scp> turnover. Wiley Interdisciplinary Reviews RNA, 2015, 6, 327-336.	3.2	20
61	A New Procedure to Analyze RNA Non-Branching Structures. Current Bioinformatics, 2015, 10, 242-258.	0.7	3
62	Computational analysis identifies a sponge interaction network between long non-coding RNAs and messenger RNAs in human breast cancer. BMC Systems Biology, 2014, 8, 83.	3.0	233
63	Modules Identification in Protein Structures: The Topological and Geometrical Solutions. Journal of Chemical Information and Modeling, 2014, 54, 159-168.	2.5	38
64	GIANT: A Cytoscape Plugin for Modular Networks. PLoS ONE, 2014, 9, e105001.	1.1	39
65	Identifying Correlations between Chromosomal Proximity of Genes and Distance of Their Products in Protein-Protein Interaction Networks of Yeast. PLoS ONE, 2013, 8, e57707.	1.1	13
66	Stochastic Modeling of Expression Kinetics Identifies Messenger Half-Lives and Reveals Sequential Waves of Co-ordinated Transcription and Decay. PLoS Computational Biology, 2012, 8, e1002772.	1.5	12
67	Structural and Functional Analysis of Hemoglobin and Serum Albumin Through Protein Long-Range Interaction Networks. Current Proteomics, 2012, 9, 160-166.	0.1	12
68	Proteins as Sponges: A Statistical Journey along Protein Structure Organization Principles. Journal of Chemical Information and Modeling, 2012, 52, 474-482.	2.5	29
69	Criticality of Timing for Anti-HIV Therapy Initiation. PLoS ONE, 2010, 5, e15294.	1.1	3
70	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
71	s- AND d-WAVE SYMMETRIES IN NONADIABATIC THEORY OF SUPERCONDUCTIVITY. International Journal of Modern Physics B, 2000, 14, 2982-2987.	1.0	5