

Christine Nardini

List of Publications by Year in descending order

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Version: 2024-02-01

63
papers

1,710
citations

394421

19
h-index

302126

39
g-index

68
all docs

68
docs citations

68
times ranked

3391
citing authors

#	ARTICLE	IF	CITATIONS
1	Identification of noninvasive imaging surrogates for brain tumor gene-expression modules. Proceedings of the National Academy of Sciences of the United States of America, 2008, 105, 5213-5218.	7.1	408
2	Vaccination in the elderly: The challenge of immune changes with aging. Seminars in Immunology, 2018, 40, 83-94.	5.6	286
3	Acceleration of leukocytesâ€™ epigenetic age as an early tumor and sex-specific marker of breast and colorectal cancer. Oncotarget, 2017, 8, 23237-23245.	1.8	90
4	Enhanced modularity-based community detection by random walk network preprocessing. Physical Review E, 2010, 81, 066118.	2.1	56
5	TOM: a web-based integrated approach for identification of candidate disease genes. Nucleic Acids Research, 2006, 34, W285-W292.	14.5	55
6	Multilevel omic data integration in cancer cell lines: advanced annotation and emergent properties. BMC Systems Biology, 2013, 7, 14.	3.0	55
7	A Comprehensive Molecular Interaction Map for Rheumatoid Arthritis. PLoS ONE, 2010, 5, e10137.	2.5	51
8	Discovering Coherent Biclusters from Gene Expression Data Using Zero-Suppressed Binary Decision Diagrams. IEEE/ACM Transactions on Computational Biology and Bioinformatics, 2005, 2, 339-354.	3.0	50
9	The emerging role of ECM crosslinking in T cell mobility as a hallmark of immunosenescence in humans. Ageing Research Reviews, 2017, 35, 322-335.	10.9	45
10	Missing value estimation methods for DNA methylation data. Bioinformatics, 2019, 35, 3786-3793.	4.1	39
11	The methylation of nuclear and mitochondrial DNA in ageing phenotypes and longevity. Mechanisms of Ageing and Development, 2017, 165, 156-161.	4.6	36
12	Finding communities in directed networks by PageRank random walk induced network embedding. Physica A: Statistical Mechanics and Its Applications, 2010, 389, 2443-2454.	2.6	34
13	The evolution of personalized healthcare and the pivotal role of European regions in its implementation. Personalized Medicine, 2021, 18, 283-294.	1.5	32
14	The epigenetics of inflammaging: The contribution of age-related heterochromatin loss and locus-specific remodelling and the modulation by environmental stimuli. Seminars in Immunology, 2018, 40, 49-60.	5.6	29
15	The greater inflammatory pathwayâ€™high clinical potential by innovative predictive, preventive, and personalized medical approach. EPMA Journal, 2020, 11, 1-16.	6.1	24
16	Molecular Aging of Human Liver: An Epigenetic/Transcriptomic Signature. Journals of Gerontology - Series A Biological Sciences and Medical Sciences, 2019, 74, 1-8.	3.6	23
17	Exploring the molecular causes of hepatitis B virus vaccination response: an approach with epigenomic and transcriptomic data. BMC Medical Genomics, 2014, 7, 12.	1.5	21
18	Partitioning networks into communities by message passing. Physical Review E, 2011, 83, 016115.	2.1	19

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19	TOM: enhancement and extension of a tool suite for in silico approaches to multigenic hereditary disorders. <i>Bioinformatics</i> , 2008, 24, 428-429.	4.1	18
20	An S-System Parameter Estimation Method (SPEM) for Biological Networks. <i>Journal of Computational Biology</i> , 2012, 19, 175-187.	1.6	18
21	MIMO: an efficient tool for molecular interaction maps overlap. <i>BMC Bioinformatics</i> , 2013, 14, 159.	2.6	16
22	Multi-omic landscape of rheumatoid arthritis: re-evaluation of drug adverse effects. <i>Frontiers in Cell and Developmental Biology</i> , 2014, 2, 59.	3.7	16
23	Methylation data imputation performances under different representations and missingness patterns. <i>BMC Bioinformatics</i> , 2020, 21, 268.	2.6	15
24	Aberrant methylation patterns in colorectal cancer: a meta-analysis. <i>Oncotarget</i> , 2017, 8, 12820-12830.	1.8	15
25	A geroscience approach for Parkinson's disease: Conceptual framework and design of PROPAG-AGEING project. <i>Mechanisms of Ageing and Development</i> , 2021, 194, 111426.	4.6	14
26	Early downregulation of hsa-miR-144-3p in serum from drug-naïve Parkinson's disease patients. <i>Scientific Reports</i> , 2022, 12, 1330.	3.3	14
27	Systemic Wound Healing Associated with local sub-Cutaneous Mechanical Stimulation. <i>Scientific Reports</i> , 2016, 6, 39043.	3.3	13
28	Editorial: Multi-omic data integration. <i>Frontiers in Cell and Developmental Biology</i> , 2015, 3, 46.	3.7	12
29	Evaluation of pre-processing on the meta-analysis of DNA methylation data from the Illumina HumanMethylation450 BeadChip platform. <i>PLoS ONE</i> , 2020, 15, e0229763.	2.5	12
30	Extracting weights from edge directions to find communities in directed networks. <i>Journal of Statistical Mechanics: Theory and Experiment</i> , 2010, 2010, P06003.	2.3	11
31	LEARNING OVERLAPPING COMMUNITIES IN COMPLEX NETWORKS VIA NON-NEGATIVE MATRIX FACTORIZATION. <i>International Journal of Modern Physics C</i> , 2011, 22, 1173-1190.	1.7	11
32	Signalling pathway database usability: lessons learned. <i>Molecular BioSystems</i> , 2013, 9, 2401.	2.9	11
33	Metabolite and lipoprotein profiles reveal sex-related oxidative stress imbalance in de novo drug-naïve Parkinson's disease patients. <i>Npj Parkinson's Disease</i> , 2022, 8, 14.	5.3	11
34	From desk to bed: Computational simulations provide indication for rheumatoid arthritis clinical trials. <i>BMC Systems Biology</i> , 2013, 7, 10.	3.0	10
35	A method for automated pathogenic content estimation with application to rheumatoid arthritis. <i>BMC Systems Biology</i> , 2016, 10, 107.	3.0	9
36	Estimage: a webserver hub for the computation of methylation age. <i>Nucleic Acids Research</i> , 2021, 49, W199-W206.	14.5	9

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37	Joint analysis of transcriptional and post-transcriptional brain tumor data: searching for emergent properties of cellular systems. BMC Bioinformatics, 2011, 12, 86.	2.6	8
38	A corrected normalized mutual information for performance evaluation of community detection. Journal of Statistical Mechanics: Theory and Experiment, 2016, 2016, 093403.	2.3	8
39	Enhanced pClustering and its applications to gene expression data. , 0, , .		7
40	Adapting functional genomic tools to metagenomic analyses: investigating the role of gut bacteria in relation to obesity. Briefings in Functional Genomics, 2010, 9, 355-361.	2.7	6
41	Inference of gene networksâ€™ application to Bifidobacterium. Bioinformatics, 2011, 27, 232-237.	4.1	6
42	Mechanotransduction map: simulation model, molecular pathway, gene set. Bioinformatics, 2015, 31, 1053-1059.	4.1	6
43	Correlation enhanced modularity-based belief propagation method for community detection in networks. Journal of Statistical Mechanics: Theory and Experiment, 2016, 2016, 053301.	2.3	6
44	Dissection of the module network implementation â€œLemonTreeâ€• enhancements towards applications in metagenomics and translation in autoimmune maladies. Molecular BioSystems, 2017, 13, 2083-2091.	2.9	6
45	Host-Microbiome Synergistic Control on Sphingolipid Metabolism by Mechanotransduction in Model Arthritis. Biomolecules, 2019, 9, 144.	4.0	6
46	Feature - Circuits and systems for high-throughput biology. IEEE Circuits and Systems Magazine, 2006, 6, 10-20.	2.3	4
47	High parallelism, portability, and broad accessibility. ACM Journal on Emerging Technologies in Computing Systems, 2008, 4, 1-39.	2.3	4
48	Systemic evaluation of cellular reprogramming processes exploiting a novel R-tool: <i>eegc</i> . Bioinformatics, 2017, 33, 2532-2538.	4.1	4
49	Link prediction in complex networks via modularity-based belief propagation. Chinese Physics B, 2017, 26, 038902.	1.4	4
50	Evaluation of different computational methods for DNA methylation-based biological age. Briefings in Bioinformatics, 2022, 23, .	6.5	4
51	Understanding human diseases with high-throughput quantitative measurement and analysis of molecular signatures. Science China Life Sciences, 2013, 56, 213-219.	4.9	3
52	Task-oriented attributed network embedding by multi-view features. Knowledge-Based Systems, 2021, 232, 107448.	7.1	3
53	Biochips for Regenerative Medicine: Real-time Stem Cell Continuous Monitoring as Inferred by High-Throughput Gene Analysis. BioNanoScience, 2011, 1, 183-191.	3.5	2
54	Brain cancer prognosis: independent validation of a clinical bioinformatics approach. Journal of Clinical Bioinformatics, 2012, 2, 2.	1.2	2

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55	Electrostimulation of a 3D <i>in vitro</i> skin model to activate wound healing. <i>Biomedical Science and Engineering</i> , 2021, 4, .	0.0	2
56	Heterogeneity of prodromal Parkinson symptoms in siblings of Parkinson disease patients. <i>Npj Parkinson's Disease</i> , 2021, 7, 78.	5.3	2
57	SPNConverter: a new link between static and dynamic complex network analysis. <i>Bioinformatics</i> , 2013, 29, 2507-2508.	4.1	1
58	MM-Correction: Meta-analysis-Based Multiple Hypotheses Correction in Omic Studies. <i>Communications in Computer and Information Science</i> , 2008, , 242-255.	0.5	1
59	Mining Gene Sets for Measuring Similarities. , 2006, , .		0
60	MANIA: A GENE NETWORK REVERSE ALGORITHM FOR COMPOUNDS MODE-OF-ACTION AND GENES INTERACTIONS INFERENCE. <i>International Journal of Modeling, Simulation, and Scientific Computing</i> , 2010, 13, 83-94.	1.4	0
61	STATISTICAL SIGNIFICANCE IN OMIC DATA ANALYSES - Alternative/Complementary Method for Efficient Automatic Identification of Statistically Significant Tests in High Throughput Biological Studies. , 2008, , .		0
62	MANIA: A Gene Network Reverse Algorithm for Compounds Mode-of-Action and Genes Interactions Inference. <i>Lecture Notes of the Institute for Computer Sciences, Social-Informatics and Telecommunications Engineering</i> , 2009, , 389-399.	0.3	0
63	Explainable Drug Repurposing Approach From Biased Random Walks. <i>IEEE/ACM Transactions on Computational Biology and Bioinformatics</i> , 2023, 20, 1009-1019.	3.0	0