Christine Nardini

List of Publications by Year
in descending order

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	Explainable Drug Repurposing Approach From Biased Random Walks. IEEE/ACM Transactions on Computational Biology and Bioinformatics, 2023, 20, 1009-1019.	3.0	0
2	Early downregulation of hsa-miR-144-3p in serum from drug-naïve Parkinson's disease patients. Scientific Reports, 2022, 12, 1330.	3.3	14
3	Metabolite and lipoprotein profiles reveal sex-related oxidative stress imbalance in de novo drug-naive Parkinson's disease patients. Npj Parkinson's Disease, 2022, 8, 14.	5.3	11
4	Evaluation of different computational methods for DNA methylation-based biological age. Briefings in Bioinformatics, 2022, 23, .	6.5	4
5	A geroscience approach for Parkinson's disease: Conceptual framework and design of PROPAG-AGEING project. Mechanisms of Ageing and Development, 2021, 194, 111426.	4.6	14
6	The evolution of personalized healthcare and the pivotal role of European regions in its implementation. Personalized Medicine, 2021, 18, 283-294.	1.5	32
7	Estimage: a webserver hub for the computation of methylation age. Nucleic Acids Research, 2021, 49, W199-W206.	14.5	9
8	Electrostimulation of a 3D in vitro skin model to activate wound healing. Biomedical Science and Engineering, 2021, 4, .	0.0	2
9	Heterogeneity of prodromal Parkinson symptoms in siblings of Parkinson disease patients. Npj Parkinson's Disease, 2021, 7, 78.	5.3	2
10	Task-oriented attributed network embedding by multi-view features. Knowledge-Based Systems, 2021, 232, 107448.	7.1	3
11	The greater inflammatory pathway—high clinical potential by innovative predictive, preventive, and personalized medical approach. EPMA Journal, 2020, 11, 1-16.	6.1	24
12	Evaluation of pre-processing on the meta-analysis of DNA methylation data from the Illumina HumanMethylation450 BeadChip platform. PLoS ONE, 2020, 15, e0229763.	2.5	12
13	Methylation data imputation performances under different representations and missingness patterns. BMC Bioinformatics, 2020, 21, 268.	2.6	15
14	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
15	Host-Microbiome Synergistic Control on Sphingolipid Metabolism by Mechanotransduction in Model Arthritis. Biomolecules, 2019, 9, 144.	4.0	6
16	Missing value estimation methods for DNA methylation data. Bioinformatics, 2019, 35, 3786-3793.	4.1	39
17	Vaccination in the elderly: The challenge of immune changes with aging. Seminars in Immunology, 2018, 40, 83-94.	5.6	286
18	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

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19	The methylation of nuclear and mitochondrial DNA in ageing phenotypes and longevity. Mechanisms of Ageing and Development, 2017, 165, 156-161.	4.6	36
20	Systemic evaluation of cellular reprogramming processes exploiting a novel R-tool: *eegc*. Bioinformatics, 2017, 33, 2532-2538.	4.1	4
21	Link prediction in complex networks via modularity-based belief propagation. Chinese Physics B, 2017, 26, 038902.	1.4	4
22	Dissection of the module network implementation "LemonTree" enhancements towards applications in metagenomics and translation in autoimmune maladies. Molecular BioSystems, 2017, 13, 2083-2091.	2.9	6
23	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
24	Aberrant methylation patterns in colorectal cancer: a meta-analysis. Oncotarget, 2017, 8, 12820-12830.	1.8	15
25	Acceleration of leukocytes' epigenetic age as an early tumor and sex-specific marker of breast and colorectal cancer. Oncotarget, 2017, 8, 23237-23245.	1.8	90
26	Systemic Wound Healing Associated with local sub-Cutaneous Mechanical Stimulation. Scientific Reports, 2016, 6, 39043.	3.3	13
27	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
28	A corrected normalized mutual information for performance evaluation of community detection. Journal of Statistical Mechanics: Theory and Experiment, 2016, 2016, 093403.	2.3	8
29	A method for automated pathogenic content estimation with application to rheumatoid arthritis. BMC Systems Biology, 2016, 10, 107.	3.0	9
30	Editorial: Multi-omic data integration. Frontiers in Cell and Developmental Biology, 2015, 3, 46.	3.7	12
31	Mechanotransduction map: simulation model, molecular pathway, gene set. Bioinformatics, 2015, 31, 1053-1059.	4.1	6
32	Multi-omic landscape of rheumatoid arthritis: re-evaluation of drug adverse effects. Frontiers in Cell and Developmental Biology, 2014, 2, 59.	3.7	16
33	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
34	Multilevel omic data integration in cancer cell lines: advanced annotation and emergent properties. BMC Systems Biology, 2013, 7, 14.	3.0	55
35	From desk to bed: Computational simulations provide indication for rheumatoid arthritis clinical trials. BMC Systems Biology, 2013, 7, 10.	3.0	10
36	Understanding human diseases with high-throughput quantitative measurement and analysis of molecular signatures. Science China Life Sciences, 2013, 56, 213-219.	4.9	3

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37	SPNConverter: a new link between static and dynamic complex network analysis. Bioinformatics, 2013, 29, 2507-2508.	4.1	1
38	Signalling pathway database usability: lessons learned. Molecular BioSystems, 2013, 9, 2401.	2.9	11
39	MIMO: an efficient tool for molecular interaction maps overlap. BMC Bioinformatics, 2013, 14, 159.	2.6	16
40	An S-System Parameter Estimation Method (SPEM) for Biological Networks. Journal of Computational Biology, 2012, 19, 175-187.	1.6	18
41	Brain cancer prognosis: independent validation of a clinical bioinformatics approach. Journal of Clinical Bioinformatics, 2012, 2, 2.	1.2	2
42	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
43	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
44	Inference of gene networks—application to Bifidobacterium. Bioinformatics, 2011, 27, 232-237.	4.1	6
45	Partitioning networks into communities by message passing. Physical Review E, 2011, 83, 016115.	2.1	19
46	LEARNING OVERLAPPING COMMUNITIES IN COMPLEX NETWORKS VIA NON-NEGATIVE MATRIX FACTORIZATION. International Journal of Modern Physics C, 2011, 22, 1173-1190.	1.7	11
47	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
48	A Comprehensive Molecular Interaction Map for Rheumatoid Arthritis. PLoS ONE, 2010, 5, e10137.	2.5	51
49	Enhanced modularity-based community detection by random walk network preprocessing. Physical Review E, 2010, 81, 066118.	2.1	56
50	MANIA: A GENE NETWORK REVERSE ALGORITHM FOR COMPOUNDS MODE-OF-ACTION AND GENES INTERACTIONS INFERENCE. International Journal of Modeling, Simulation, and Scientific Computing, 2010, 13, 83-94.	1.4	0
51	Extracting weights from edge directions to find communities in directed networks. Journal of Statistical Mechanics: Theory and Experiment, 2010, 2010, P06003.	2.3	11
52	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
53	MANIA: A Gene Network Reverse Algorithm for Compounds Mode-of-Action and Genes Interactions Inference. Lecture Notes of the Institute for Computer Sciences, Social-Informatics and Telecommunications Engineering, 2009, , 389-399.	0.3	0
54	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

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55	High parallelism, portability, and broad accessibility. ACM Journal on Emerging Technologies in Computing Systems, 2008, 4, 1-39.	2.3	4
56	TOM: enhancement and extension of a tool suite for in silico approaches to multigenic hereditary disorders. Bioinformatics, 2008, 24, 428-429.	4.1	18
57	MM-Correction: Meta-analysis-Based Multiple Hypotheses Correction in Omic Studies. Communications in Computer and Information Science, 2008, , 242-255.	0.5	1
58	STATISTICAL SIGNIFICANCE IN OMIC DATA ANALYSES - Alternative/Complementary Method for Efficient Automatic Identification of Statistically Significant Tests in High Throughput Biological Studies. , 2008, , .		0
59	Mining Gene Sets for Measuring Similarities. , 2006, , .		0
60	Feature - Circuits and systems for high-throughput biology. IEEE Circuits and Systems Magazine, 2006, 6, 10-20.	2.3	4
61	TOM: a web-based integrated approach for identification of candidate disease genes. Nucleic Acids Research, 2006, 34, W285-W292.	14.5	55
62	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
63	Enhanced pClustering and its applications to gene expression data. , 0, , .		7