

Mario Lauria

List of Publications by Year in descending order

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Version: 2024-02-01

48
papers

1,215
citations

516710

16
h-index

477307

29
g-index

49
all docs

49
docs citations

49
times ranked

1754
citing authors

#	ARTICLE	IF	CITATIONS
1	High performance messaging on workstations. , 1995, , .		241
2	Id proteins synchronize stemness and anchorage to the niche of neural stem cells. Nature Cell Biology, 2012, 14, 477-487.	10.3	120
3	Strengths and limitations of microarray-based phenotype prediction: lessons learned from the IMPROVER Diagnostic Signature Challenge. Bioinformatics, 2013, 29, 2892-2899.	4.1	108
4	The Organic Grid: Self-Organizing Computation on a Peer-to-Peer Network. IEEE Transactions on Systems, Man and Cybernetics, Part A: Systems and Humans, 2005, 35, 373-384.	2.9	90
5	MPI-FM: High Performance MPI on Workstation Clusters. Journal of Parallel and Distributed Computing, 1997, 40, 4-18.	4.1	81
6	Crowdsourced estimation of cognitive decline and resilience in Alzheimer's disease. Alzheimer's and Dementia, 2016, 12, 645-653.	0.8	72
7	Cross-disease analysis of Alzheimer's disease and type-2 Diabetes highlights the role of autophagy in the pathophysiology of two highly comorbid diseases. Scientific Reports, 2019, 9, 3965.	3.3	66
8	The Central Role of AMP-Kinase and Energy Homeostasis Impairment in Alzheimer's Disease: A Multifactor Network Analysis. PLoS ONE, 2013, 8, e78919.	2.5	40
9	Diversity of key players in the microbial ecosystems of the human body. Scientific Reports, 2015, 5, 15920.	3.3	30
10	Cross-species evidence from human and rat brain transcriptome for growth factor signaling pathway dysregulation in major depression. Neuropsychopharmacology, 2018, 43, 2134-2145.	5.4	25
11	Reverse engineering a mouse embryonic stem cell-specific transcriptional network reveals a new modulator of neuronal differentiation. Nucleic Acids Research, 2013, 41, 711-726.	14.5	24
12	Self-Organizing Scheduling on the Organic Grid. International Journal of High Performance Computing Applications, 2006, 20, 115-130.	3.7	23
13	Combined use of protein biomarkers and network analysis unveils deregulated regulatory circuits in Duchenne muscular dystrophy. PLoS ONE, 2018, 13, e0194225.	2.5	23
14	Design and Evaluation of an HPVM-Based Windows NT Supercomputer. International Journal of High Performance Computing Applications, 1999, 13, 201-219.	3.7	21
15	Integration of transcriptomic and genomic data suggests candidate mechanisms for APOE4-mediated pathogenic action in Alzheimer's disease. Scientific Reports, 2016, 6, 32583.	3.3	19
16	A Community Challenge for Inferring Genetic Predictors of Gene Essentialities through Analysis of a Functional Screen of Cancer Cell Lines. Cell Systems, 2017, 5, 485-497.e3.	6.2	19
17	Systems biology approaches to study the molecular effects of caloric restriction and polyphenols on aging processes. Genes and Nutrition, 2015, 10, 58.	2.5	18
18	Systems biology meets -omic technologies: novel approaches to biomarker discovery and companion diagnostic development. Expert Review of Molecular Diagnostics, 2015, 15, 255-265.	3.1	18

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19	Systems view of adipogenesis via novel omics-driven and tissue-specific activity scoring of network functional modules. <i>Scientific Reports</i> , 2016, 6, 28851.	3.3	17
20	A mouse embryonic stem cell bank for inducible overexpression of human chromosome 21 genes. <i>Genome Biology</i> , 2010, 11, R64.	9.6	16
21	Depression-Associated Gene Negr1-Fgfr2 Pathway Is Altered by Antidepressant Treatment. <i>Cells</i> , 2020, 9, 1818.	4.1	16
22	SCUDO: a tool for signature-based clustering of expression profiles. <i>Nucleic Acids Research</i> , 2015, 43, W188-W192.	14.5	15
23	A performance enhanced PSI-BLAST based on hybrid alignment. <i>Bioinformatics</i> , 2011, 27, 31-37.	4.1	12
24	Efficient implementation of reduce-scatter in MPI. <i>Journal of Systems Architecture</i> , 2003, 49, 89-108.	4.3	10
25	Consensus Clustering of temporal profiles for the identification of metabolic markers of pre-diabetes in childhood (EarlyBird 73). <i>Scientific Reports</i> , 2018, 8, 1393.	3.3	10
26	The Organic Grid: Self-organizing Computational Biology on Desktop Grids. , 2005, , 671-703.		9
27	Rank-based transcriptional signatures. <i>Systems Biomedicine (Austin, Tex)</i> , 2013, 1, 228-239.	0.7	9
28	Gene expression signature of antidepressant treatment response/non-response in Flinders Sensitive Line rats subjected to maternal separation. <i>European Neuropsychopharmacology</i> , 2020, 31, 69-85.	0.7	9
29	Improving the Throughput of Remote Storage Access through Pipelining. <i>Lecture Notes in Computer Science</i> , 2002, , 305-316.	1.3	9
30	NIRest: A Tool for Gene Network and Mode of Action Inference. <i>Annals of the New York Academy of Sciences</i> , 2009, 1158, 257-264.	3.8	8
31	Experimental results about MPI collective communication operations. <i>Lecture Notes in Computer Science</i> , 1999, , 774-783.	1.3	7
32	Efficient layering for high speed communication: the MPI over Fast Messages (FM) experience. <i>Cluster Computing</i> , 1999, 2, 107-116.	5.0	6
33	Cross-platform analysis of fast messages for Myrinet. <i>Lecture Notes in Computer Science</i> , 1998, , 217-231.	1.3	5
34	A high performance redundancy scheme for cluster file systems. <i>International Journal of High Performance Computing and Networking</i> , 2004, 2, 90.	0.4	4
35	Rank-Based miRNA Signatures for Early Cancer Detection. <i>BioMed Research International</i> , 2014, 2014, 1-7.	1.9	3
36	MOUSSE: Multi-Omics Using Subject-Specific SignaturEs. <i>Cancers</i> , 2021, 13, 3423.	3.7	3

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37	A combinatorial model for self-organizing networks. , 2007, , .		2
38	Exploring the Limitations of Peripheral Blood Transcriptional Biomarkers in Predicting Influenza Vaccine Responsiveness. Complexity, 2017, 2017, 1-9.	1.6	2
39	Using hybrid alignment for iterative sequence database searches. Concurrency Computation Practice and Experience, 2004, 16, 841-853.	2.2	1
40	Rank-based miRNA signatures for blood-based diagnosis of tuberculosis. , 2015, 2015, 4462-5.		1
41	Sequential forward-inverse design for genetic network modeling. Journal of Industrial and Production Engineering, 2017, 34, 520-528.	3.1	1
42	Design of experiments for steady-state system identification with applications in genetic and business network modelinG. Journal of Industrial and Production Engineering, 2020, 37, 259-274.	3.1	1
43	Self-Organizing Scheduling on the Organic Grid. , 2006, , 389-411.		1
44	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
45	rScudo: an R package for classification of molecular profiles using rank-based signatures. Bioinformatics, 2020, 36, 4095-4096.	4.1	0
46	DiST: A Scalable, Efficient P2P Lookup Protocol. Lecture Notes in Computer Science, 2005, , 40-53.	1.3	0
47	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
48	A Stochastic Model for Layered Self-organizing Complex Systems. Lecture Notes of the Institute for Computer Sciences, Social-Informatics and Telecommunications Engineering, 2009, , 1495-1503.	0.3	0