Mario Lauria

List of Publications by Year
in descending order

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	MOUSSE: Multi-Omics Using Subject-Specific SignaturEs. Cancers, 2021, 13, 3423.	3.7	3
2	Gene expression signature of antidepressant treatment response/non-response in Flinders Sensitive Line rats subjected to maternal separation. European Neuropsychopharmacology, 2020, 31, 69-85.	0.7	9
3	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
4	Depression-Associated Gene Negr1-Fgfr2 Pathway Is Altered by Antidepressant Treatment. Cells, 2020, 9, 1818.	4.1	16
5	rScudo: an R package for classification of molecular profiles using rank-based signatures. Bioinformatics, 2020, 36, 4095-4096.	4.1	0
6	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
7	Consensus Clustering of temporal profiles for the identification of metabolic markers of pre-diabetes in childhood (EarlyBird 73). Scientific Reports, 2018, 8, 1393.	3.3	10
8	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
9	Combined use of protein biomarkers and network analysis unveils deregulated regulatory circuits in Duchenne muscular dystrophy. PLoS ONE, 2018, 13, e0194225.	2.5	23
10	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
11	Sequential forward-inverse design for genetic network modeling. Journal of Industrial and Production Engineering, 2017, 34, 520-528.	3.1	1
12	Exploring the Limitations of Peripheral Blood Transcriptional Biomarkers in Predicting Influenza Vaccine Responsiveness. Complexity, 2017, 2017, 1-9.	1.6	2
13	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
14	Systems view of adipogenesis via novel omics-driven and tissue-specific activity scoring of network functional modules. Scientific Reports, 2016, 6, 28851.	3.3	17
15	Crowdsourced estimation of cognitive decline and resilience in Alzheimer's disease. Alzheimer's and Dementia, 2016, 12, 645-653.	0.8	72
16	Diversity of key players in the microbial ecosystems of the human body. Scientific Reports, 2015, 5, 15920.	3.3	30
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	SCUDO: a tool for signature-based clustering of expression profiles. Nucleic Acids Research, 2015, 43, W188-W192.	14.5	15

#	Article	IF	Citations
19	Rank-based miRNA signatures for blood-based diagnosis of tuberculosis. , 2015, 2015, 4462-5.		1
20	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
21	Rank-Based miRNA Signatures for Early Cancer Detection. BioMed Research International, 2014, 2014, 1-7.	1.9	3
22	Strengths and limitations of microarray-based phenotype prediction: lessons learned from the IMPROVER Diagnostic Signature Challenge. Bioinformatics, 2013, 29, 2892-2899.	4.1	108
23	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
24	Rank-based transcriptional signatures. Systems Biomedicine (Austin, Tex), 2013, 1, 228-239.	0.7	9
25	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
26	Id proteins synchronize stemness and anchorage to the niche of neural stem cells. Nature Cell Biology, 2012, 14, 477-487.	10.3	120
27	A performance enhanced PSI-BLAST based on hybrid alignment. Bioinformatics, 2011, 27, 31-37.	4.1	12
28	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
29	A mouse embryonic stem cell bank for inducible overexpression of human chromosome 21 genes. Genome Biology, 2010, 11, R64.	9.6	16
30	NIRest: A Tool for Gene Network and Mode of Action Inference. Annals of the New York Academy of Sciences, 2009, 1158, 257-264.	3.8	8
31	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
32	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
33	A combinatorial model for self-organizing networks. , 2007, , .		2
34	Self-Organizing Scheduling on the Organic Grid. International Journal of High Performance Computing Applications, 2006, 20, 115-130.	3.7	23
35	Self-Organizing Scheduling on the Organic Grid. , 2006, , 389-411.		1
36	The Organic Grid: Self-organizing Computational Biology on Desktop Grids. , 2005, , 671-703.		9

#	Article	IF	Citations
37	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
38	DiST: A Scalable, Efficient P2P Lookup Protocol. Lecture Notes in Computer Science, 2005, , 40-53.	1.3	0
39	A high performance redundancy scheme for cluster file systems. International Journal of High Performance Computing and Networking, 2004, 2, 90.	0.4	4
40	Using hybrid alignment for iterative sequence database searches. Concurrency Computation Practice and Experience, 2004, 16, 841-853.	2.2	1
41	Efficient implementation of reduce-scatter in MPI. Journal of Systems Architecture, 2003, 49, 89-108.	4.3	10
42	Improving the Throughput of Remote Storage Access through Pipelining. Lecture Notes in Computer Science, 2002, , 305-316.	1.3	9
43	Design and Evaluation of an HPVM-Based Windows NT Supercomputer. International Journal of High Performance Computing Applications, 1999, 13, 201-219.	3.7	21
44	Efficient layering for high speed communication: the MPI over Fast Messages (FM) experience. Cluster Computing, 1999, 2, 107-116.	5.0	6
45	Experimental results about MPI collective communication operations. Lecture Notes in Computer Science, 1999, , 774-783.	1.3	7
46	Cross-platform analysis of fast messages for Myrinet. Lecture Notes in Computer Science, 1998, , 217-231.	1.3	5
47	MPI-FM: High Performance MPI on Workstation Clusters. Journal of Parallel and Distributed Computing, 1997, 40, 4-18.	4.1	81
48	High performance messaging on workstations. , 1995, , .		241