Alfredo Benso

List of Publications by Year
in descending order

85 papers	1,282 citations	623734 14 h-index	454955 30 g-index

90 all docs	90 docs citations	90 times ranked	1429 citing authors

#	Article	IF	Citations
1	Gene Ontology GAN (GOGAN): a novel architecture for protein function prediction. Soft Computing, 2022, 26, 7653-7667.	3.6	7
2	The integration of clinical data in the assessment of multiple sclerosisâ€"Â review. Computer Methods and Programs in Biomedicine, 2022, 221, 106900.	4.7	3
3	Severe and moderate seasonal influenza epidemics among Italian healthcare workers: A comparison of the excess of absenteeism. Influenza and Other Respiratory Viruses, 2021, 15, 81-90.	3.4	7
4	Engineering Minds for Biologists. , 2021, , 79-90.		0
5	Nets-within-nets for modeling emergent patterns in ontogenetic processes. Computational and Structural Biotechnology Journal, 2021, 19, 5701-5721.	4.1	5
6	IL6-mediated HCoV-host interactome regulatory network and GO/Pathway enrichment analysis. PLoS Computational Biology, 2020, 16, e1008238.	3.2	3
7	Determinants Associated With the Risk of Emergency Department Visits Among Patients Receiving Integrated Home Care Services: A 6-Year Retrospective Observational Study in a Large Italian Region. International Journal of Health Policy and Management, 2020, 10, 605-612.	0.9	2
8	IL6-mediated HCoV-host interactome regulatory network and GO/Pathway enrichment analysis. , 2020, 16, e1008238.		0
9	IL6-mediated HCoV-host interactome regulatory network and GO/Pathway enrichment analysis. , 2020, 16, e1008238.		0
10	IL6-mediated HCoV-host interactome regulatory network and GO/Pathway enrichment analysis. , 2020, 16, e1008238.		0
11	IL6-mediated HCoV-host interactome regulatory network and GO/Pathway enrichment analysis. , 2020, 16, e1008238.		0
12	Beyond Homology Transfer: Deep Learning for Automated Annotation of Proteins. Journal of Grid Computing, 2019, 17, 225-237.	3.9	29
13	Cost of Sickness Absenteeism during Seasonal Influenza Outbreaks of Medium Intensity among Health Care Workers. International Journal of Environmental Research and Public Health, 2019, 16, 747.	2.6	29
14	â€˜One DB to rule them allâ€™â€"the RING: a Regulatory INteraction Graph combining TFs, genes/proteins, SNPs, diseases and drugs. Database: the Journal of Biological Databases and Curation, 2019, 2019, .	3.0	5
15	The CAFA challenge reports improved protein function prediction and new functional annotations for hundreds of genes through experimental screens. Genome Biology, 2019, 20, 244.	8.8	261
16	Modeling antibiotic resistance in the microbiota using multi-level Petri Nets. BMC Systems Biology, 2018, 12, 108.	3.0	8
17	Computational Tools for Applying Multi-level Models to Synthetic Biology. , 2018, , 95-112.		3
18	DNA Pool Analysis-based Forgery-Detection of Dairy Products. International Journal of Electrical and Computer Engineering, 2018, 8, 3913.	0.7	1

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19	Multi-level and hybrid modelling approaches for systems biology. Computational and Structural Biotechnology Journal, 2017, 15, 396-402.	4.1	51
20	Estimation of sickness absenteeism among Italian healthcare workers during seasonal influenza epidemics. PLoS ONE, 2017, 12, e0182510.	2.5	46
21	Prioritizing single-nucleotide polymorphisms and variants associated with clinical mastitis. Advances and Applications in Bioinformatics and Chemistry, 2017, Volume 10, 57-64.	2.6	16
22	A three-way approach for protein function classification. PLoS ONE, 2017, 12, e0171702.	2.5	11
23	An expanded evaluation of protein function prediction methods shows an improvement in accuracy. Genome Biology, 2016, 17, 184.	8.8	308
24	CyTRANSFINDER: a Cytoscape 3.3 plugin for three-component (TF, gene, miRNA) signal transduction pathway construction. BMC Bioinformatics, 2016, 17, 157.	2.6	14
25	A Graph Based Framework to Model Virus Integration Sites. Computational and Structural Biotechnology Journal, 2016, 14, 69-77.	4.1	5
26	Implementing a Cloud-Based Service Supporting Biological Network Simulations. , 2016, , .		0
27	FishAPP: A mobile App to detect fish falsification through image processing and machine learning techniques. , 2016, , .		18
28	Using Nets-Within-Nets for Modeling Differentiating Cells in the Epigenetic Landscape. Lecture Notes in Computer Science, 2016, , 315-321.	1.3	6
29	Identification of miRNAs Potentially Involved in Bronchiolitis Obliterans Syndrome: A Computational Study. PLoS ONE, 2016, 11, e0161771.	2.5	6
30	A Structure based Approach for Accurate Prediction of Protein Interactions Networks. , 2016, , .		7
31	LSC Abstract â€" Identification of pathogenic micro RNA (miR) in BOS: A system biology approach. , 2016, , .		0
32	Editorial: Annotation and curation of uncharacterized proteins: systems biology approaches. Frontiers in Genetics, 2015, 6, 224.	2.3	2
33	Evaluating Scalability of a Cloud Based Platform for Biological Networks Analysis. , 2015, , .		1
34	A cloud-based approach for Gene Regulatory Networks dynamics simulations. , 2015, , .		2
35	A 3D Voxel Neighborhood Classification Approach within a Multiparametric MRI Classifier for Prostate Cancer Detection. Lecture Notes in Computer Science, 2015, , 231-239.	1.3	1
36	A Computational Pipeline to Identify New Potential Regulatory Motifs in Melanoma Progression. Communications in Computer and Information Science, 2015, , 181-194.	0.5	0

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37	System biology (SB) allows the identification of pathogenic micro RNA (miR) in BOS. , 2015, , .		0
38	Breathomics can discriminate between anti IgE-treated and non-treated severe asthma adults. , 2015, , .		0
39	ReNE: A Cytoscape Plugin for Regulatory Network Enhancement. PLoS ONE, 2014, 9, e115585.	2.5	15
40	FunMod: A Cytoscape Plugin for Identifying Functional Modules in Undirected Protein–Protein Networks. Genomics, Proteomics and Bioinformatics, 2014, 12, 178-186.	6.9	6
41	Using Boolean networks to model post-transcriptional regulation in gene regulatory networks. Journal of Computational Science, 2014, 5, 332-344.	2.9	22
42	Augmented Reading: The Present and Future of Electronic Scientific Publications. Computer, 2014, 47, 64-74.	1.1	6
43	An extended gene protein/products boolean network model including post-transcriptional regulation. Theoretical Biology and Medical Modelling, 2014, 11, S5.	2.1	9
44	A systematic analysis of a mi-RNA inter-pathway regulatory motif. Journal of Clinical Bioinformatics, 2013, 3, 20.	1.2	11
45	A combined approach for genome wide protein function annotation/prediction. Proteome Science, 2013, 11, S1.	1.7	22
46	Reducing the Complexity of Complex Gene Coexpression Networks by Coupling Multiweighted Labeling with Topological Analysis. BioMed Research International, 2013, 2013, 1-9.	1.9	2
47	Combining homolog and motif similarity data with Gene Ontology relationships for protein function prediction. , 2012, , .		9
48	Using gnome wide data for protein function prediction by exploiting gene ontology relationships. , 2012, , .		5
49	Statistical Reliability Estimation of Microprocessor-Based Systems. IEEE Transactions on Computers, 2012, 61, 1521-1534.	3.4	36
50	Software-Based Self-Test for Reliable Applications in Railway Systems. , 2012, , 198-220.		4
51	A cDNA Microarray Gene Expression Data Classifier for Clinical Diagnostics Based on Graph Theory. IEEE/ACM Transactions on Computational Biology and Bioinformatics, 2011, 8, 577-591.	3.0	12
52	Guest Editors' Introduction: Special Section on Chips and Architectures for Emerging Technologies and Applications. IEEE Transactions on Computers, 2011, 60, 450-451.	3.4	0
53	Building gene expression profile classifiers with a simple and efficient rejection option in R. BMC Bioinformatics, 2011, 12, S3.	2.6	8
54	GPU acceleration for statistical gene classification. , 2010, , .		9

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55	Gene expression reliability estimation through cluster-based analysis. , 2009, , .		0
56	</title> </titles> <publication_date> <month>05</month> <year>2009</year> </publication_date> <pages> <first_page>3</first_page> <last_page>3</last_page> </pages> <publisher_item> <item_number item_number_type='sequence-number'>5167501</item_number> </publisher_item> <doi_data> <doi>10.1109/MDT.2009.45</doi> <resource>http://ieeexplore.ieee.org/lp	1.0	2
57	Gene expression classifiers and out-of-class samples detection. , 2009, , .		0
58	March Test Generation Revealed. IEEE Transactions on Computers, 2008, 57, 1704-1713.	3.4	17
59	IEEE Standard 1500 Compliance Verification for Embedded Cores. IEEE Transactions on Very Large Scale Integration (VLSI) Systems, 2008, 16, 397-407.	3.1	14
60	Using ER models for microprocessor functional test coverage evaluation. , 2008, , .		0
61	Differential gene expression graphs: A data structure for classification in DNA microarrays. , 2008, , .		3
62	Analysis of System-Failure Rate Caused by Soft-Errors using a UML-Based Systematic Methodology in an SoC. , 2007, , .		2
63	Automating the IEEE std. 1500 compliance verification for embedded cores. , 2007, , .		1
64	ATPG for Dynamic Burn-In Test in Full-Scan Circuits. Proceedings of the Asian Test Symposium, 2006, , .	0.0	18
65	A Dependable Autonomic Computing Environment for Self-Testing of Complex Heterogeneous Systems. Electronic Notes in Theoretical Computer Science, 2005, 116, 45-57.	0.9	3
66	System-level functional testing from UML specifications in end-of-production industrial environments. International Journal on Software Tools for Technology Transfer, 2005, 7, 326-340.	1.9	3
67	An on-line BIST RAM architecture with self-repair capabilities. IEEE Transactions on Reliability, 2002, 51, 123-128.	4.6	41
68	A self-repairing execution unit for microprogrammed processors. IEEE Micro, 2001, 21, 16-22.	1.8	6
69	Online and offline BIST in IP-core design. IEEE Design and Test of Computers, 2001, 18, 92-99.	1.0	6
70	A High-Level EDA Environment for the Automatic Insertion of HD-BIST Structures. Journal of Electronic Testing: Theory and Applications (JETTA), 2000, 16, 179-184.	1.2	4
71	Testing embedded memories in telecommunication systems. , 1999, 37, 84-89.		2
72	FlexFi: A Flexible Fault Injection Environment for Microprocessor-Based Systems. Lecture Notes in Computer Science, 1999, , 323-335.	1.3	4

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73	Fault behavior observation of a microprocessor system through a VHDL simulation-based fault injection experiment. , 0, , .		17
74	Exploiting high-level descriptions for circuits fault tolerance assessments. , 0, , .		1
75	A new approach to build a low-level malicious fault list starting from high-level description and alternative graphs. , 0, , .		4
76	A programmable BIST architecture for clusters of multiple-port SRAMs. , 0, , .		20
77	Self-repairing in a micro-programmed processor for dependable applications. , 0, , .		1
78	On integrating a proprietary and a commercial architecture for optimal BIST performances in SoCs. , 0, , .		0
79	Memory read faults: taxonomy and automatic test generation. , 0, , .		1
80	Control-flow checking via regular expressions. , 0, , .		31
81	Towards a unified test process: from UML to end-of-line functional test. , 0, , .		5
82	Software dependability techniques validated via fault injection experiments. , 0, , .		1
83	Efficient design of system test: a layered architecture. , 0, , .		3
84	Automatic March Tests Generation for Static and Dynamic Faults in SRAMs. , 0, , .		21
85	Single-Event Upset Analysis and Protection in High Speed Circuits. , 0, , .		7