

Alfredo Benso

List of Publications by Year in descending order

Source: <https://exaly.com/author-pdf/8824661/publications.pdf>

Version: 2024-02-01

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 | An expanded evaluation of protein function prediction methods shows an improvement in accuracy. <i>Genome Biology</i> , 2016, 17, 184. | 8.8 | 308 |
| 2 | The CAFA challenge reports improved protein function prediction and new functional annotations for hundreds of genes through experimental screens. <i>Genome Biology</i> , 2019, 20, 244. | 8.8 | 261 |
| 3 | Multi-level and hybrid modelling approaches for systems biology. <i>Computational and Structural Biotechnology Journal</i> , 2017, 15, 396-402. | 4.1 | 51 |
| 4 | Estimation of sickness absenteeism among Italian healthcare workers during seasonal influenza epidemics. <i>PLoS ONE</i> , 2017, 12, e0182510. | 2.5 | 46 |
| 5 | An on-line BIST RAM architecture with self-repair capabilities. <i>IEEE Transactions on Reliability</i> , 2002, 51, 123-128. | 4.6 | 41 |
| 6 | Statistical Reliability Estimation of Microprocessor-Based Systems. <i>IEEE Transactions on Computers</i> , 2012, 61, 1521-1534. | 3.4 | 36 |
| 7 | Control-flow checking via regular expressions. , 0, , . | | 31 |
| 8 | Beyond Homology Transfer: Deep Learning for Automated Annotation of Proteins. <i>Journal of Grid Computing</i> , 2019, 17, 225-237. | 3.9 | 29 |
| 9 | Cost of Sickness Absenteeism during Seasonal Influenza Outbreaks of Medium Intensity among Health Care Workers. <i>International Journal of Environmental Research and Public Health</i> , 2019, 16, 747. | 2.6 | 29 |
| 10 | A combined approach for genome wide protein function annotation/prediction. <i>Proteome Science</i> , 2013, 11, S1. | 1.7 | 22 |
| 11 | Using Boolean networks to model post-transcriptional regulation in gene regulatory networks. <i>Journal of Computational Science</i> , 2014, 5, 332-344. | 2.9 | 22 |
| 12 | Automatic March Tests Generation for Static and Dynamic Faults in SRAMs. , 0, , . | | 21 |
| 13 | A programmable BIST architecture for clusters of multiple-port SRAMs. , 0, , . | | 20 |
| 14 | ATPG for Dynamic Burn-In Test in Full-Scan Circuits. <i>Proceedings of the Asian Test Symposium</i> , 2006, , . | 0.0 | 18 |
| 15 | FishAPP: A mobile App to detect fish falsification through image processing and machine learning techniques. , 2016, , . | | 18 |
| 16 | Fault behavior observation of a microprocessor system through a VHDL simulation-based fault injection experiment. , 0, , . | | 17 |
| 17 | March Test Generation Revealed. <i>IEEE Transactions on Computers</i> , 2008, 57, 1704-1713. | 3.4 | 17 |
| 18 | Prioritizing single-nucleotide polymorphisms and variants associated with clinical mastitis. <i>Advances and Applications in Bioinformatics and Chemistry</i> , 2017, Volume 10, 57-64. | 2.6 | 16 |

| # | ARTICLE | IF | CITATIONS |
|----|---|-----|-----------|
| 19 | ReNE: A Cytoscape Plugin for Regulatory Network Enhancement. PLoS ONE, 2014, 9, e115585. | 2.5 | 15 |
| 20 | IEEE Standard 1500 Compliance Verification for Embedded Cores. IEEE Transactions on Very Large Scale Integration (VLSI) Systems, 2008, 16, 397-407. | 3.1 | 14 |
| 21 | CyTRANSFINDER: a Cytoscape 3.3 plugin for three-component (TF, gene, miRNA) signal transduction pathway construction. BMC Bioinformatics, 2016, 17, 157. | 2.6 | 14 |
| 22 | 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 |
| 23 | A systematic analysis of a mi-RNA inter-pathway regulatory motif. Journal of Clinical Bioinformatics, 2013, 3, 20. | 1.2 | 11 |
| 24 | A three-way approach for protein function classification. PLoS ONE, 2017, 12, e0171702. | 2.5 | 11 |
| 25 | GPU acceleration for statistical gene classification. , 2010, , . | | 9 |
| 26 | Combining homolog and motif similarity data with Gene Ontology relationships for protein function prediction. , 2012, , . | | 9 |
| 27 | An extended gene protein/products boolean network model including post-transcriptional regulation. Theoretical Biology and Medical Modelling, 2014, 11, S5. | 2.1 | 9 |
| 28 | Building gene expression profile classifiers with a simple and efficient rejection option in R. BMC Bioinformatics, 2011, 12, S3. | 2.6 | 8 |
| 29 | Modeling antibiotic resistance in the microbiota using multi-level Petri Nets. BMC Systems Biology, 2018, 12, 108. | 3.0 | 8 |
| 30 | Single-Event Upset Analysis and Protection in High Speed Circuits. , 0, , . | | 7 |
| 31 | 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 |
| 32 | A Structure based Approach for Accurate Prediction of Protein Interactions Networks. , 2016, , . | | 7 |
| 33 | Gene Ontology GAN (GOGAN): a novel architecture for protein function prediction. Soft Computing, 2022, 26, 7653-7667. | 3.6 | 7 |
| 34 | A self-repairing execution unit for microprogrammed processors. IEEE Micro, 2001, 21, 16-22. | 1.8 | 6 |
| 35 | Online and offline BIST in IP-core design. IEEE Design and Test of Computers, 2001, 18, 92-99. | 1.0 | 6 |
| 36 | FunMod: A Cytoscape Plugin for Identifying Functional Modules in Undirected Protein-Protein Networks. Genomics, Proteomics and Bioinformatics, 2014, 12, 178-186. | 6.9 | 6 |

| # | ARTICLE | IF | CITATIONS |
|----|---|-----|-----------|
| 37 | Augmented Reading: The Present and Future of Electronic Scientific Publications. <i>Computer</i> , 2014, 47, 64-74. | 1.1 | 6 |
| 38 | Using Nets-Within-Nets for Modeling Differentiating Cells in the Epigenetic Landscape. <i>Lecture Notes in Computer Science</i> , 2016, , 315-321. | 1.3 | 6 |
| 39 | Identification of miRNAs Potentially Involved in Bronchiolitis Obliterans Syndrome: A Computational Study. <i>PLoS ONE</i> , 2016, 11, e0161771. | 2.5 | 6 |
| 40 | Towards a unified test process: from UML to end-of-line functional test. , 0, , . | | 5 |
| 41 | Using genome wide data for protein function prediction by exploiting gene ontology relationships. , 2012, , . | | 5 |
| 42 | A Graph Based Framework to Model Virus Integration Sites. <i>Computational and Structural Biotechnology Journal</i> , 2016, 14, 69-77. | 4.1 | 5 |
| 43 | “One DB to rule them all” the RING: a Regulatory INteraction Graph combining TFs, genes/proteins, SNPs, diseases and drugs. <i>Database: the Journal of Biological Databases and Curation</i> , 2019, 2019, . | 3.0 | 5 |
| 44 | Nets-within-nets for modeling emergent patterns in ontogenetic processes. <i>Computational and Structural Biotechnology Journal</i> , 2021, 19, 5701-5721. | 4.1 | 5 |
| 45 | A new approach to build a low-level malicious fault list starting from high-level description and alternative graphs. , 0, , . | | 4 |
| 46 | A High-Level EDA Environment for the Automatic Insertion of HD-BIST Structures. <i>Journal of Electronic Testing: Theory and Applications (JETTA)</i> , 2000, 16, 179-184. | 1.2 | 4 |
| 47 | FlexFi: A Flexible Fault Injection Environment for Microprocessor-Based Systems. <i>Lecture Notes in Computer Science</i> , 1999, , 323-335. | 1.3 | 4 |
| 48 | Software-Based Self-Test for Reliable Applications in Railway Systems. , 2012, , 198-220. | | 4 |
| 49 | Efficient design of system test: a layered architecture. , 0, , . | | 3 |
| 50 | A Dependable Autonomic Computing Environment for Self-Testing of Complex Heterogeneous Systems. <i>Electronic Notes in Theoretical Computer Science</i> , 2005, 116, 45-57. | 0.9 | 3 |
| 51 | System-level functional testing from UML specifications in end-of-production industrial environments. <i>International Journal on Software Tools for Technology Transfer</i> , 2005, 7, 326-340. | 1.9 | 3 |
| 52 | Differential gene expression graphs: A data structure for classification in DNA microarrays. , 2008, , . | | 3 |
| 53 | Computational Tools for Applying Multi-level Models to Synthetic Biology. , 2018, , 95-112. | | 3 |
| 54 | IL6-mediated HCoV-host interactome regulatory network and GO/Pathway enrichment analysis. <i>PLoS Computational Biology</i> , 2020, 16, e1008238. | 3.2 | 3 |

| # | ARTICLE | IF | CITATIONS |
|----|---|-----|-----------|
| 55 | The integration of clinical data in the assessment of multiple sclerosis—A review. Computer Methods and Programs in Biomedicine, 2022, 221, 106900. | 4.7 | 3 |
| 56 | Testing embedded memories in telecommunication systems. , 1999, 37, 84-89. | | 2 |
| 57 | Analysis of System-Failure Rate Caused by Soft-Errors using a UML-Based Systematic Methodology in an SoC, 2007 | | 2 |
| 58 | </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' </item_number> </publisher_item> </doi_data> </doi>10.1109/MDT.2009.45</doi> </resource>http://ieeexplore.ieee.org/lp | 1.0 | 2 |
| 59 | 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 |
| 60 | Editorial: Annotation and curation of uncharacterized proteins: systems biology approaches. Frontiers in Genetics, 2015, 6, 224. | 2.3 | 2 |
| 61 | A cloud-based approach for Gene Regulatory Networks dynamics simulations. , 2015, , . | | 2 |
| 62 | 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 |
| 63 | Exploiting high-level descriptions for circuits fault tolerance assessments. , 0, , . | | 1 |
| 64 | Self-repairing in a micro-programmed processor for dependable applications. , 0, , . | | 1 |
| 65 | Memory read faults: taxonomy and automatic test generation. , 0, , . | | 1 |
| 66 | Software dependability techniques validated via fault injection experiments. , 0, , . | | 1 |
| 67 | Automating the IEEE std. 1500 compliance verification for embedded cores. , 2007, , . | | 1 |
| 68 | Evaluating Scalability of a Cloud Based Platform for Biological Networks Analysis. , 2015, , . | | 1 |
| 69 | 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 |
| 70 | DNA Pool Analysis-based Forgery-Detection of Dairy Products. International Journal of Electrical and Computer Engineering, 2018, 8, 3913. | 0.7 | 1 |
| 71 | On integrating a proprietary and a commercial architecture for optimal BIST performances in SoCs. , 0, , . | | 0 |
| 72 | Using ER models for microprocessor functional test coverage evaluation. , 2008, , . | | 0 |

| # | ARTICLE | IF | CITATIONS |
|----|--|-----|-----------|
| 73 | Gene expression reliability estimation through cluster-based analysis. , 2009, , . | | 0 |
| 74 | Gene expression classifiers and out-of-class samples detection. , 2009, , . | | 0 |
| 75 | 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 |
| 76 | Implementing a Cloud-Based Service Supporting Biological Network Simulations. , 2016, , . | | 0 |
| 77 | Engineering Minds for Biologists. , 2021, , 79-90. | | 0 |
| 78 | A Computational Pipeline to Identify New Potential Regulatory Motifs in Melanoma Progression. Communications in Computer and Information Science, 2015, , 181-194. | 0.5 | 0 |
| 79 | System biology (SB) allows the identification of pathogenic micro RNA (miR) in BOS. , 2015, , . | | 0 |
| 80 | Breathomics can discriminate between anti IgE-treated and non-treated severe asthma adults. , 2015, , . | | 0 |
| 81 | LSC Abstract " Identification of pathogenic micro RNA (miR) in BOS: A system biology approach. , 2016, , . | | 0 |
| 82 | IL6-mediated HCoV-host interactome regulatory network and GO/Pathway enrichment analysis. , 2020, 16, e1008238. | | 0 |
| 83 | IL6-mediated HCoV-host interactome regulatory network and GO/Pathway enrichment analysis. , 2020, 16, e1008238. | | 0 |
| 84 | IL6-mediated HCoV-host interactome regulatory network and GO/Pathway enrichment analysis. , 2020, 16, e1008238. | | 0 |
| 85 | IL6-mediated HCoV-host interactome regulatory network and GO/Pathway enrichment analysis. , 2020, 16, e1008238. | | 0 |