

Alfredo Pulvirenti

List of Publications by Citations

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The third column is the impact factor (IF) of the journal, and the fourth column is the number of citations of the article.

133
papers

2,879
citations

29
h-index

49
g-index

148
ext. papers

3,443
ext. citations

5.4
avg, IF

5.06
L-index

#	Paper	IF	Citations
133	Introduction of gluten, HLA status, and the risk of celiac disease in children. <i>New England Journal of Medicine</i> , 2014 , 371, 1295-303	59.2	301
132	Integrated microRNA and mRNA signatures associated with survival in triple negative breast cancer. <i>PLoS ONE</i> , 2013 , 8, e55910	3.7	132
131	miRandola: extracellular circulating microRNAs database. <i>PLoS ONE</i> , 2012 , 7, e47786	3.7	129
130	Drug-target interaction prediction through domain-tuned network-based inference. <i>Bioinformatics</i> , 2013 , 29, 2004-8	7.2	124
129	Celiac disease from a global perspective. <i>Baillieres Best Practice and Research in Clinical Gastroenterology</i> , 2015 , 29, 365-79	2.5	108
128	Neutrophil-To-Lymphocyte Ratio: An Emerging Marker Predicting Prognosis in Elderly Adults with Community-Acquired Pneumonia. <i>Journal of the American Geriatrics Society</i> , 2017 , 65, 1796-1801	5.6	83
127	The neurology of coeliac disease in childhood: what is the evidence? A systematic review and meta-analysis. <i>Developmental Medicine and Child Neurology</i> , 2010 , 52, 700-7	3.3	80
126	A subgraph isomorphism algorithm and its application to biochemical data. <i>BMC Bioinformatics</i> , 2013 , 14 Suppl 7, S13	3.6	77
125	miRĀa miRNA knowledge base. <i>Database: the Journal of Biological Databases and Curation</i> , 2009 , 2009, bap008	5	77
124	Prediction of human population responses to toxic compounds by a collaborative competition. <i>Nature Biotechnology</i> , 2015 , 33, 933-40	44.5	70
123	Cellular and molecular effects of protons: apoptosis induction and potential implications for cancer therapy. <i>Apoptosis: an International Journal on Programmed Cell Death</i> , 2006 , 11, 57-66	5.4	66
122	Enhancing density-based clustering: Parameter reduction and outlier detection. <i>Information Systems</i> , 2013 , 38, 317-330	2.7	63
121	NetMatch: a Cytoscape plugin for searching biological networks. <i>Bioinformatics</i> , 2007 , 23, 910-2	7.2	62
120	Acute disseminated encephalomyelitis: a long-term prospective study and meta-analysis. <i>Neuropediatrics</i> , 2010 , 41, 246-55	1.6	59
119	SIGMA: a set-cover-based inexact graph matching algorithm. <i>Journal of Bioinformatics and Computational Biology</i> , 2010 , 8, 199-218	1	49
118	Tools and collaborative environments for bioinformatics research. <i>Briefings in Bioinformatics</i> , 2011 , 12, 549-61	13.4	46
117	Neutrophil-to-Lymphocyte Ratio is a strong predictor of atherosclerotic carotid plaques in older adults. <i>Nutrition, Metabolism and Cardiovascular Diseases</i> , 2018 , 28, 23-27	4.5	45

116	miRandola 2017: a curated knowledge base of non-invasive biomarkers. <i>Nucleic Acids Research</i> , 2018 , 46, D354-D359	20.1	44
115	Prevalence and natural history of potential celiac disease in at-family-risk infants prospectively investigated from birth. <i>Journal of Pediatrics</i> , 2012 , 161, 908-14	3.6	44
114	Variability in the incidence of miRNAs and genes in fragile sites and the role of repeats and CpG islands in the distribution of genetic material. <i>PLoS ONE</i> , 2010 , 5, e11166	3.7	43
113	GSK-3 β Induced Tau pathology drives hippocampal neuronal cell death in Huntington's disease: involvement of astrocyte-neuron interactions. <i>Cell Death and Disease</i> , 2016 , 7, e2206	9.8	40
112	ncPred: ncRNA-Disease Association Prediction through Tripartite Network-Based Inference. <i>Frontiers in Bioengineering and Biotechnology</i> , 2014 , 2, 71	5.8	39
111	. <i>IEEE Transactions on Knowledge and Data Engineering</i> , 2005 , 17, 535-550	4.2	36
110	SING: subgraph search in non-homogeneous graphs. <i>BMC Bioinformatics</i> , 2010 , 11, 96	3.6	34
109	Clustering and classification of infrasonic events at Mount Etna using pattern recognition techniques. <i>Geophysical Journal International</i> , 2011 , 185, 253-264	2.6	33
108	Extracellular circulating viral microRNAs: current knowledge and perspectives. <i>Frontiers in Genetics</i> , 2013 , 4, 120	4.5	32
107	Re-challenge Studies in Non-celiac Gluten Sensitivity: A Systematic Review and Meta-Analysis. <i>Frontiers in Physiology</i> , 2017 , 8, 621	4.6	31
106	A novel computational method for inferring competing endogenous interactions. <i>Briefings in Bioinformatics</i> , 2017 , 18, 1071-1081	13.4	31
105	DT-Web: a web-based application for drug-target interaction and drug combination prediction through domain-tuned network-based inference. <i>BMC Systems Biology</i> , 2015 , 9 Suppl 3, S4	3.5	30
104	Geo-Epidemiology of Age-Related Macular Degeneration: New Clues Into the Pathogenesis. <i>American Journal of Ophthalmology</i> , 2016 , 161, 78-93.e1-2	4.9	29
103	POOLED ESTIMATES OF INCIDENCE OF ENDOPHTHALMITIS AFTER INTRAVITREAL INJECTION OF ANTI-VASCULAR ENDOTHELIAL GROWTH FACTOR AGENTS WITH AND WITHOUT TOPICAL ANTIBIOTIC PROPHYLAXIS. <i>Retina</i> , 2018 , 38, 1-11	3.6	29
102	miR-Synth: a computational resource for the design of multi-site multi-target synthetic miRNAs. <i>Nucleic Acids Research</i> , 2014 , 42, 5416-25	20.1	28
101	Risk of acute stroke in patients with retinal artery occlusion: a systematic review and meta-analysis. <i>Eye</i> , 2020 , 34, 683-689	4.4	26
100	Internal limiting membrane peeling versus no peeling during primary vitrectomy for rhegmatogenous retinal detachment: A systematic review and meta-analysis. <i>PLoS ONE</i> , 2018 , 13, e0201010	3.7	25
99	Recommendation Techniques for Drug-Target Interaction Prediction and Drug Repositioning. <i>Methods in Molecular Biology</i> , 2016 , 1415, 441-62	1.4	24

98	Network-Based Drug Repositioning: Approaches, Resources, and Research Directions. <i>Methods in Molecular Biology</i> , 2019 , 1903, 97-113	1.4	24
97	Intracellular and extracellular miRNome deregulation in cellular models of NAFLD or NASH: Clinical implications. <i>Nutrition, Metabolism and Cardiovascular Diseases</i> , 2016 , 26, 1129-1139	4.5	23
96	miR-EdiTar: a database of predicted A-to-I edited miRNA target sites. <i>Bioinformatics</i> , 2012 , 28, 3166-8	7.2	23
95	Post-transcriptional knowledge in pathway analysis increases the accuracy of phenotypes classification. <i>Oncotarget</i> , 2016 , 7, 54572-54582	3.3	23
94	A Subset of Patients With Autism Spectrum Disorders Show a Distinctive Metabolic Profile by Dried Blood Spot Analyses. <i>Frontiers in Psychiatry</i> , 2018 , 9, 636	5	23
93	A knowledge base for the discovery of function, diagnostic potential and drug effects on cellular and extracellular miRNAs. <i>BMC Genomics</i> , 2014 , 15 Suppl 3, S4	4.5	21
92	GASOLINE: a Greedy And Stochastic algorithm for optimal Local multiple alignment of Interaction NETworks. <i>PLoS ONE</i> , 2014 , 9, e98750	3.7	21
91	Comprehensive reconstruction and visualization of non-coding regulatory networks in human. <i>Frontiers in Bioengineering and Biotechnology</i> , 2014 , 2, 69	5.8	20
90	Helicobacter pylori infection and atopic diseases: is there a relationship? A systematic review and meta-analysis. <i>World Journal of Gastroenterology</i> , 2014 , 20, 17635-47	5.6	20
89	Identification of tRNA-derived ncRNAs in TCGA and NCI-60 panel cell lines and development of the public database tRFexplorer. <i>Database: the Journal of Biological Databases and Curation</i> , 2019 , 2019,	5	20
88	Detecting Disease Specific Pathway Substructures through an Integrated Systems Biology Approach. <i>Non-coding RNA</i> , 2017 , 3,	7.1	18
87	GRAPES: a software for parallel searching on biological graphs targeting multi-core architectures. <i>PLoS ONE</i> , 2013 , 8, e76911	3.7	18
86	Prediction of human targets for viral-encoded microRNAs by thermodynamics and empirical constraints. <i>Journal of Rnai and Gene Silencing</i> , 2010 , 6, 379-85		18
85	Mode of Delivery and Risk of Celiac Disease: Risk of Celiac Disease and Age at Gluten Introduction Cohort Study. <i>Journal of Pediatrics</i> , 2017 , 184, 81-86.e2	3.6	17
84	Diathermy of leaking sclerotomies after 23-gauge transconjunctival pars plana vitrectomy: a prospective study. <i>Retina</i> , 2013 , 33, 939-45	3.6	17
83	Computational design of artificial RNA molecules for gene regulation. <i>Methods in Molecular Biology</i> , 2015 , 1269, 393-412	1.4	16
82	OCDB: a database collecting genes, miRNAs and drugs for obsessive-compulsive disorder. <i>Database: the Journal of Biological Databases and Curation</i> , 2015 , 2015, bav069	5	15
81	Enhancing Graph Database Indexing by Suffix Tree Structure. <i>Lecture Notes in Computer Science</i> , 2010 , 195-203	0.9	14

80	Long-Term Outcome of Potential Celiac Disease in Genetically at-Risk Children: The Prospective CELIPREV Cohort Study. <i>Journal of Clinical Medicine</i> , 2019 , 8,	5.1	13
79	A knowledge base for <i>Vitis vinifera</i> functional analysis. <i>BMC Systems Biology</i> , 2015 , 9 Suppl 3, S5	3.5	13
78	NetMatchStar: an enhanced Cytoscape network querying app. <i>F1000Research</i> , 2015 , 4, 479	3.6	13
77	MIDClass: microarray data classification by association rules and gene expression intervals. <i>PLoS ONE</i> , 2013 , 8, e69873	3.7	13
76	Risk of Death Associated With Intravitreal Anti-Vascular Endothelial Growth Factor Therapy: A Systematic Review and Meta-analysis. <i>JAMA Ophthalmology</i> , 2020 , 138, 50-57	3.9	13
75	Fast analytical methods for finding significant labeled graph motifs. <i>Data Mining and Knowledge Discovery</i> , 2018 , 32, 504-531	5.6	12
74	Knowledge in the Investigation of A-to-I RNA Editing Signals. <i>Frontiers in Bioengineering and Biotechnology</i> , 2015 , 3, 18	5.8	12
73	GraphFind: enhancing graph searching by low support data mining techniques. <i>BMC Bioinformatics</i> , 2008 , 9 Suppl 4, S10	3.6	12
72	Intravitreal anti-vascular endothelial growth factors, panretinal photocoagulation and combined treatment for proliferative diabetic retinopathy: a systematic review and network meta-analysis. <i>Acta Ophthalmologica</i> , 2021 , 99, e795-e805	3.7	12
71	Motif Discovery on Seismic Amplitude Time Series: The Case Study of Mt Etna 2011 Eruptive Activity. <i>Pure and Applied Geophysics</i> , 2013 , 170, 529-545	2.2	11
70	SPECTRA: An Integrated Knowledge Base for Comparing Tissue and Tumor-Specific PPI Networks in Human. <i>Frontiers in Bioengineering and Biotechnology</i> , 2015 , 3, 58	5.8	11
69	Current Knowledge and Computational Techniques for Grapevine Meta-Omics Analysis. <i>Frontiers in Plant Science</i> , 2017 , 8, 2241	6.2	10
68	VIRGO: visualization of A-to-I RNA editing sites in genomic sequences. <i>BMC Bioinformatics</i> , 2013 , 14 Suppl 7, S5	3.6	9
67	Disentangling Restrictive and Repetitive Behaviors and Social Impairments in Children and Adolescents with Gilles de la Tourette Syndrome and Autism Spectrum Disorder. <i>Brain Sciences</i> , 2020 , 10,	3.4	8
66	An Efficient Approximate Algorithm for the 1-Median Problem in Metric Spaces. <i>SIAM Journal on Optimization</i> , 2005 , 16, 434-451	2	8
65	GASOLINE: a Cytoscape app for multiple local alignment of PPI networks. <i>F1000Research</i> , 2014 , 3, 140	3.6	8
64	NetMatchStar: an enhanced Cytoscape network querying app. <i>F1000Research</i> , 2015 , 4, 479	3.6	8
63	APPAGATO: an APproximate PARallel and stochastic GrAph querying TOol for biological networks. <i>Bioinformatics</i> , 2016 , 32, 2159-66	7.2	8

62	Multilocus sequence typing analysis of Italian <i>Xanthomonas campestris</i> pv. <i>campestris</i> strains suggests the evolution of local endemic populations of the pathogen and does not correlate with race distribution. <i>Plant Pathology</i> , 2019 , 68, 278-287	2.8	8
61	GASOLINE: a Cytoscape app for multiple local alignment of PPI networks. <i>F1000Research</i> , 2014 , 3, 140	3.6	7
60	Ex Machina: Analytical platforms, Law and the Challenges of Computational Legal Science. <i>Future Internet</i> , 2018 , 10, 37	3.3	6
59	Exploring the role of interdisciplinarity in physics: Success, talent and luck. <i>PLoS ONE</i> , 2019 , 14, e0218793	3.7	6
58	Elucidating the role of microRNAs in cancer through data mining techniques. <i>Advances in Experimental Medicine and Biology</i> , 2013 , 774, 291-315	3.6	6
57	In vitro and in silico cloning of <i>Xenopus laevis</i> SOD2 cDNA and its phylogenetic analysis. <i>DNA and Cell Biology</i> , 2005 , 24, 111-6	3.6	6
56	BitCube: A Bottom-Up Cubing Engineering. <i>Lecture Notes in Computer Science</i> , 2009 , 189-203	0.9	6
55	A benchmarking of pipelines for detecting ncRNAs from RNA-Seq data. <i>Briefings in Bioinformatics</i> , 2020 , 21, 1987-1998	13.4	6
54	B-type natriuretic peptide may predict prognosis in older adults admitted with a diagnosis other than heart failure. <i>Nutrition, Metabolism and Cardiovascular Diseases</i> , 2018 , 28, 636-642	4.5	5
53	Best-match retrieval for structured images. <i>IEEE Transactions on Pattern Analysis and Machine Intelligence</i> , 2001 , 23, 707-718	13.3	5
52	An Efficient Duplicate Record Detection Using q-Grams Array Inverted Index. <i>Lecture Notes in Computer Science</i> , 2010 , 309-323	0.9	5
51	Computational Methods to Investigate the Impact of miRNAs on Pathways. <i>Methods in Molecular Biology</i> , 2019 , 1970, 183-209	1.4	4
50	Electrocardiographic Evaluation in Patients With Spinal Muscular Atrophy: A Case-Control Study. <i>Journal of Child Neurology</i> , 2018 , 33, 487-492	2.5	4
49	Mining and ranking of generalized multi-dimensional frequent subgraphs 2017 ,		4
48	A pilot study on neurological manifestations and antibodies against antigens in children with hematological and other cancers. <i>European Journal of Paediatric Neurology</i> , 2013 , 17, 97-101	3.8	4
47	Obstacles constrained group mobility models in event-driven wireless networks with movable base stations. <i>Ad Hoc Networks</i> , 2011 , 9, 400-417	4.8	4
46	Involvement of GTA protein NC2beta in neuroblastoma pathogenesis suggests that it physiologically participates in the regulation of cell proliferation. <i>Molecular Cancer</i> , 2008 , 7, 52	42.1	4
45	Sequence similarity is more relevant than species specificity in probabilistic backtranslation. <i>BMC Bioinformatics</i> , 2007 , 8, 58	3.6	4

44	Genomics, evolution, and expression of TBPL2, a member of the TBP family. <i>DNA and Cell Biology</i> , 2007 , 26, 369-85	3.6	4
43	FAST CLUSTERING AND MINIMUM WEIGHT MATCHING ALGORITHMS FOR VERY LARGE MOBILE BACKBONE WIRELESS NETWORKS. <i>International Journal of Foundations of Computer Science</i> , 2003 , 14, 223-236	0.6	4
42	VECTOR: An Integrated Correlation Network Database for the Identification of CeRNA Axes in Uveal Melanoma. <i>Genes</i> , 2021 , 12,	4.2	4
41	PHENSIM: Phenotype Simulator. <i>PLoS Computational Biology</i> , 2021 , 17, e1009069	5	4
40	Clinical characteristics and predictors of death among hospitalized patients infected with SARS-CoV-2 in Sicily, Italy: A retrospective observational study.. <i>Biomedical Reports</i> , 2022 , 16, 34	1.8	4
39	Treat and extend versus fixed regimen in neovascular age related macular degeneration: A systematic review and meta-analysis. <i>European Journal of Ophthalmology</i> , 2021 , 31, 2496-2504	1.9	3
38	Endogenous and artificial miRNAs explore a rich variety of conformations: a potential relationship between secondary structure and biological functionality. <i>Scientific Reports</i> , 2020 , 10, 453	4.9	3
37	Proteins comparison through probabilistic optimal structure local alignment. <i>Frontiers in Genetics</i> , 2014 , 5, 302	4.5	3
36	New approaches in hepatitis B vaccination for celiac disease. <i>Immunotherapy</i> , 2014 , 6, 945-52	3.8	3
35	Circulating Noncoding RNAs as Clinical Biomarkers 2016 , 239-258		3
34	TemporalRI: A Subgraph Isomorphism Algorithm for Temporal Networks. <i>Studies in Computational Intelligence</i> , 2021 , 675-687	0.8	3
33	Fast Subgraph Matching Strategies Based on Pattern-Only Heuristics. <i>Interdisciplinary Sciences, Computational Life Sciences</i> , 2019 , 11, 21-32	3.5	2
32	Infant feeding pattern, HLA status, and prevalence of celiac disease. <i>Digestive and Liver Disease</i> , 2014 , 46, e75-e76	3.3	2
31	Multiple-Winners Randomized Tournaments with Consensus for Optimization Problems in Generic Metric Spaces. <i>Lecture Notes in Computer Science</i> , 2005 , 265-276	0.9	2
30	NETME: on-the-fly knowledge network construction from biomedical literature.. <i>Applied Network Science</i> , 2022 , 7, 1	2.9	2
29	Novel Mechanisms of Tumor Promotion by the Insulin Receptor Isoform A in Triple-Negative Breast Cancer Cells. <i>Cells</i> , 2021 , 10,	7.9	2
28	Bioinformatics Approach to Mitigate Mislabeling in EU Seafood Market and Protect Consumer Health. <i>International Journal of Environmental Research and Public Health</i> , 2021 , 18,	4.6	2
27	INBIA: a boosting methodology for proteomic network inference. <i>BMC Bioinformatics</i> , 2018 , 19, 188	3.6	2

26	Fast methods for finding significant motifs on labelled multi-relational networks. <i>Journal of Complex Networks</i> , 2019 , 7, 817-837	1.7	1
25	Bioinformatics in Italy: BITS 2012, the ninth annual meeting of the Italian Society of Bioinformatics. <i>BMC Bioinformatics</i> , 2013 , 14 Suppl 7, S1	3.6	1
24	Involvement of GTA protein NC2beta in Neuroblastoma pathogenesis suggests that it physiologically participates in the regulation of cell proliferation. <i>Molecular Cancer</i> , 2008 , 7, 59	42.1	1
23	Distributed antipole clustering for efficient data search and management in Euclidean and metric spaces 2006 ,		1
22	Locally sensitive backtranslation based on multiple sequence alignment		1
21	Simple Pattern-only Heuristics Lead to Fast Subgraph Matching Strategies on Very Large Networks. <i>Advances in Intelligent Systems and Computing</i> , 2019 , 131-138	0.4	1
20	PHENSIM: Phenotype Simulator		1
19	Establish the Expected Number of Injective Motifs on Unlabeled Graphs Through Analytical Models. <i>Studies in Computational Intelligence</i> , 2020 , 255-267	0.8	1
18	Establish the expected number of induced motifs on unlabeled graphs through analytical models. <i>Applied Network Science</i> , 2020 , 5,	2.9	1
17	Rapid Identification of Druggable Targets and the Power of the PHENotype SIMulator for Effective Drug Repurposing in COVID-19 2021 ,		1
16	"Diagnosis on the Dock" project: A proactive screening program for diagnosing pulmonary tuberculosis in disembarking refugees and new SEI model. <i>International Journal of Infectious Diseases</i> , 2021 , 106, 98-104	10.5	1
15	RNAdetector: a free user-friendly stand-alone and cloud-based system for RNA-Seq data analysis. <i>BMC Bioinformatics</i> , 2021 , 22, 298	3.6	1
14	TACITuS: transcriptomic data collector, integrator, and selector on big data platform. <i>BMC Bioinformatics</i> , 2019 , 20, 366	3.6	1
13	Computational Resources for the Interpretation of Variations in Cancer.. <i>Advances in Experimental Medicine and Biology</i> , 2022 , 1361, 177-198	3.6	1
12	Computational Methods for Drug Repurposing.. <i>Advances in Experimental Medicine and Biology</i> , 2022 , 1361, 119-141	3.6	1
11	KAOS: a new automated computational method for the identification of overexpressed genes. <i>BMC Bioinformatics</i> , 2016 , 17, 340	3.6	0
10	Efficient Techniques for Graph Searching and Biological Network Mining. <i>Advances in Data Mining and Database Management Book Series</i> , 89-111	0.6	
9	Efficient Boundary Values Generation in General Metric Spaces for Software Component Testing. <i>Lecture Notes in Computer Science</i> , 2003 , 318-331	0.9	

8	Clustered Trie Structures for Approximate Search in Hierarchical Objects Collections. <i>Lecture Notes in Computer Science</i> , 2005 , 63-70	0.9
7	MySQL Data Mining: Extending MySQL to Support Data Mining Primitives (Demo). <i>Lecture Notes in Computer Science</i> , 2010 , 438-444	0.9
6	Reply To: Neutrophil to Lymphocyte Ratio As a Risk Stratification Tool for Older Adults with Pneumonia. <i>Journal of the American Geriatrics Society</i> , 2018 , 66, 418-420	5.6
5	Genetic Alteration of MicroRNA Affecting Cancer Pathways 2018 , 269-287	
4	Psychopathological outcomes and defence mechanisms in clinically healed adults with a paediatric cancer history: an exploratory study. <i>Annals of General Psychiatry</i> , 2021 , 34, e100307	5.3
3	Pathway Analysis for Cancer Research and Precision Oncology Applications.. <i>Advances in Experimental Medicine and Biology</i> , 2022 , 1361, 143-161	3.6
2	MODIT: MOTif Discovery in Temporal Networks.. <i>Frontiers in Big Data</i> , 2021 , 4, 806014	2.8
1	BioTAGME: A Comprehensive Platform for Biological Knowledge Network Analysis.. <i>Frontiers in Genetics</i> , 2022 , 13, 855739	4.5