Alfredo Pulvirenti

List of Publications by Year
in descending order

142 papers	3,984 citations	134610 34 h-index	156644 58 g-index
148 all docs	148 docs citations	148 times ranked	6611 citing authors

#	Article	IF	Citations
1	aEEG vs cEEG's sensivity for seizure detection in the setting of neonatal intensive care units: a systematic review and meta‑analysis. Acta Paediatrica, International Journal of Paediatrics, 2022, , .	0.7	5
2	NETME: on-the-fly knowledge network construction from biomedical literature. Applied Network Science, 2022, 7, 1.	0.8	12
3	Diagnostic Accuracy of IgA Anti-Transglutaminase and IgG Anti-Deamidated Gliadin for Diagnosis of Celiac Disease in Children under Two Years of Age: A Systematic Review and Meta-Analysis. Nutrients, 2022, 14, 7.	1.7	12
4	Psychological well‑being and family distress of Italian caregivers during the COVID‑19 outbreak. Journal of Community Psychology, 2022, 50, 2243-2259.	1.0	7
5	Pathway Analysis for Cancer Research and Precision Oncology Applications. Advances in Experimental Medicine and Biology, 2022, 1361, 143-161.	0.8	2
6	Computational Resources for the Interpretation of Variations in Cancer. Advances in Experimental Medicine and Biology, 2022, 1361, 177-198.	0.8	2
7	Computational Methods for Drug Repurposing. Advances in Experimental Medicine and Biology, 2022, 1361, 119-141.	0.8	8
8	Clinical characteristics and predictors of death among hospitalized patients infected with SARS‑CoV‑2 in Sicily, Italy: A retrospective observational study. Biomedical Reports, 2022, 16, 34.	0.9	16
9	BioTAGME: A Comprehensive Platform for Biological Knowledge Network Analysis. Frontiers in Genetics, 2022, 13, 855739.	1.1	0
10	Dysregulation of microRNAs and tRNA-derived ncRNAs in mesothelial and mesothelioma cell lines after asbestiform fiber exposure. Scientific Reports, 2022, 12, .	1.6	5
11	Virus finding tools: current solutions and limitations. Briefings in Bioinformatics, 2022, 23, .	3.2	2
12	Network analysis of synovial RNA sequencing identifies gene-gene interactions predictive of response in rheumatoid arthritis. Arthritis Research and Therapy, 2022, 24, .	1.6	6
13	Treat and extend versus fixed regimen in neovascular age related macular degeneration: A systematic review and meta-analysis. European Journal of Ophthalmology, 2021, 31, 2496-2504.	0.7	10
14	"Diagnosis on the Dock" project: A proactive screening program for diagnosing pulmonary tuberculosis in disembarking refugees and new SEI model. International Journal of Infectious Diseases, 2021, 106, 98-104.	1.5	1
15	RNAdetector: a free user-friendly stand-alone and cloud-based system for RNA-Seq data analysis. BMC Bioinformatics, 2021, 22, 298.	1.2	7
16	VECTOR: An Integrated Correlation Network Database for the Identification of CeRNA Axes in Uveal Melanoma. Genes, 2021, 12, 1004.	1.0	10
17	PHENSIM: Phenotype Simulator. PLoS Computational Biology, 2021, 17, e1009069.	1.5	9
18	Bioinformatics Approach to Mitigate Mislabeling in EU Seafood Market and Protect Consumer Health. International Journal of Environmental Research and Public Health, 2021, 18, 7497.	1.2	4

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19	Psychopathological outcomes and defence mechanisms in clinically healed adults with a paediatric cancer history: an exploratory study. Annals of General Psychiatry, 2021, 34, e100307.	1.1	2
20	TemporalRI: A Subgraph Isomorphism Algorithm for Temporal Networks. Studies in Computational Intelligence, 2021, , 675-687.	0.7	4
21	Intravitreal antiâ€vascular endothelial growth factors, panretinal photocoagulation and combined treatment for proliferative diabetic retinopathy: a systematic review and network metaâ€analysis. Acta Ophthalmologica, 2021, 99, e795-e805.	0.6	25
22	Novel Mechanisms of Tumor Promotion by the Insulin Receptor Isoform A in Triple-Negative Breast Cancer Cells. Cells, 2021, 10, 3145.	1.8	14
23	MODIT: MOtif DIscovery in Temporal Networks. Frontiers in Big Data, 2021, 4, 806014.	1.8	3
24	Risk of acute stroke in patients with retinal artery occlusion: a systematic review and meta-analysis. Eye, 2020, 34, 683-689.	1.1	53
25	A benchmarking of pipelines for detecting ncRNAs from RNA-Seq data. Briefings in Bioinformatics, 2020, 21, 1987-1998.	3.2	16
26	Risk of Death Associated With Intravitreal Antiâ€"Vascular Endothelial Growth Factor Therapy. JAMA Ophthalmology, 2020, 138, 50.	1.4	20
27	P22â€ƒMicro-RNA enriched pathway impact analysis applied to synovial RNA-seq in early rheumatoid arthritis identifies response prediction pathways. Rheumatology, 2020, 59, .	0.9	0
28	Establish the expected number of induced motifs on unlabeled graphs through analytical models. Applied Network Science, 2020, 5, .	0.8	2
29	Disentangling Restrictive and Repetitive Behaviors and Social Impairments in Children and Adolescents with Gilles de la Tourette Syndrome and Autism Spectrum Disorder. Brain Sciences, 2020, 10, 308.	1.1	11
30	Endogenous and artificial miRNAs explore a rich variety of conformations: a potential relationship between secondary structure and biological functionality. Scientific Reports, 2020, 10, 453.	1.6	7
31	Establish the Expected Number of Injective Motifs on Unlabeled Graphs Through Analytical Models. Studies in Computational Intelligence, 2020, , 255-267.	0.7	1
32	Exploring the role of interdisciplinarity in physics: Success, talent and luck. PLoS ONE, 2019, 14, e0218793.	1.1	20
33	Fast Subgraph Matching Strategies Based on Pattern-Only Heuristics. Interdisciplinary Sciences, Computational Life Sciences, 2019, 11, 21-32.	2.2	3
34	Fast methods for finding significant motifs on labelled multi-relational networks. Journal of Complex Networks, 2019, 7, 817-837.	1.1	1
35	Computational Methods to Investigate the Impact of miRNAs on Pathways. Methods in Molecular Biology, 2019, 1970, 183-209.	0.4	5
36	Long-Term Outcome of Potential Celiac Disease in Genetically at-Risk Children: The Prospective CELIPREV Cohort Study. Journal of Clinical Medicine, 2019, 8, 186.	1.0	23

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37	Identification of tRNA-derived ncRNAs in TCGA and NCI-60 panel cell lines and development of the public database tRFexplorer. Database: the Journal of Biological Databases and Curation, 2019, 2019, .	1.4	36
38	TACITuS: transcriptomic data collector, integrator, and selector on big data platform. BMC Bioinformatics, 2019, 20, 366.	1.2	3
39	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. Plant Pathology, 2019, 68, 278-287.	1.2	14
40	Network-Based Drug Repositioning: Approaches, Resources, and Research Directions. Methods in Molecular Biology, 2019, 1903, 97-113.	0.4	40
41	Simple Pattern-only Heuristics Lead to Fast Subgraph Matching Strategies on Very Large Networks. Advances in Intelligent Systems and Computing, 2019, , 131-138.	0.5	2
42	B-type natriuretic peptide may predict prognosis in older adults admitted with a diagnosis other than heart failure. Nutrition, Metabolism and Cardiovascular Diseases, 2018, 28, 636-642.	1.1	8
43	Electrocardiographic Evaluation in Patients With Spinal Muscular Atrophy: A Case-Control Study. Journal of Child Neurology, 2018, 33, 487-492.	0.7	4
44	POOLED ESTIMATES OF INCIDENCE OF ENDOPHTHALMITIS AFTER INTRAVITREAL INJECTION OF ANTI–VASCULAR ENDOTHELIAL GROWTH FACTOR AGENTS WITH AND WITHOUT TOPICAL ANTIBIOTIC PROPHYLAXIS. Retina, 2018, 38, 01-11.	1.0	37
45	miRandola 2017: a curated knowledge base of non-invasive biomarkers. Nucleic Acids Research, 2018, 46, D354-D359.	6.5	61
46	Fast analytical methods for finding significant labeled graph motifs. Data Mining and Knowledge Discovery, 2018, 32, 504-531.	2.4	18
47	Neutrophil-to-Lymphocyte Ratio is a strong predictor of atherosclerotic carotid plaques in older adults. Nutrition, Metabolism and Cardiovascular Diseases, 2018, 28, 23-27.	1.1	78
48	Reply To: Neutrophil to Lymphocyte Ratio As a Risk Stratification Tool for Older Adults with Pneumonia. Journal of the American Geriatrics Society, 2018, 66, 418-420.	1.3	0
49	A Subset of Patients With Autism Spectrum Disorders Show a Distinctive Metabolic Profile by Dried Blood Spot Analyses. Frontiers in Psychiatry, 2018, 9, 636.	1.3	41
50	INBIA: a boosting methodology for proteomic network inference. BMC Bioinformatics, 2018, 19, 188.	1.2	2
51	Genetic Alteration of MicroRNA Affecting Cancer Pathways. , 2018, , 269-287.		0
52	Ex Machina: Analytical platforms, Law and the Challenges of Computational Legal Science. Future Internet, 2018, 10, 37.	2.4	10
53	Internal limiting membrane peeling versus no peeling during primary vitrectomy for rhegmatogenous retinal detachment: A systematic review and meta-analysis. PLoS ONE, 2018, 13, e0201010.	1.1	34
54	Mode of Delivery and Risk of Celiac Disease: Risk of Celiac Disease and Age at Gluten Introduction Cohort Study. Journal of Pediatrics, 2017, 184, 81-86.e2.	0.9	27

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55	Neutrophilâ€Toâ€Lymphocyte Ratio: An Emerging Marker Predicting Prognosis in Elderly Adults with Communityâ€Acquired Pneumonia. Journal of the American Geriatrics Society, 2017, 65, 1796-1801.	1.3	133
56	Mining and ranking of generalized multi-dimensional frequent subgraphs. , 2017, , .		6
57	Re-challenge Studies in Non-celiac Gluten Sensitivity: A Systematic Review and Meta-Analysis. Frontiers in Physiology, 2017, 8, 621.	1.3	40
58	Detecting Disease Specific Pathway Substructures through an Integrated Systems Biology Approach. Non-coding RNA, 2017, 3, 20.	1.3	25
59	Current Knowledge and Computational Techniques for Grapevine Meta-Omics Analysis. Frontiers in Plant Science, 2017, 8, 2241.	1.7	24
60	Circulating Noncoding RNAs as Clinical Biomarkers. , 2016, , 239-258.		4
61	Recommendation Techniques for Drugâ€"Target Interaction Prediction and Drug Repositioning. Methods in Molecular Biology, 2016, 1415, 441-462.	0.4	33
62	GSK-3Î²-induced Tau pathology drives hippocampal neuronal cell death in Huntingtonâ€™s disease: involvement of astrocyteâ€"neuron interactions. Cell Death and Disease, 2016, 7, e2206-e2206.	2.7	67
63	APPAGATO: an APproximate PArallel and stochastic GrAph querying TOol for biological networks. Bioinformatics, 2016, 32, 2159-2166.	1.8	10
64	A novel computational method for inferring competing endogenous interactions. Briefings in Bioinformatics, 2016, 18, bbw084.	3.2	37
65	Intracellular and extracellular miRNome deregulation in cellular models of NAFLD or NASH: Clinical implications. Nutrition, Metabolism and Cardiovascular Diseases, 2016, 26, 1129-1139.	1.1	31
66	KAOS: a new automated computational method for the identification of overexpressed genes. BMC Bioinformatics, 2016, 17, 340.	1.2	2
67	Geo-Epidemiology of Age-Related Macular Degeneration: New Clues Into the Pathogenesis. American Journal of Ophthalmology, 2016, 161, 78-93.e2.	1.7	38
68	Post-transcriptional knowledge in pathway analysis increases the accuracy of phenotypes classification. Oncotarget, 2016, 7, 54572-54582.	0.8	43
69	A knowledge base for Vitis vinifera functional analysis. BMC Systems Biology, 2015, 9, S5.	3.0	24
70	OCDB: a database collecting genes, miRNAs and drugs for obsessive-compulsive disorder. Database: the Journal of Biological Databases and Curation, 2015, 2015, bav069.	1.4	18
71	DT-Web: a web-based application for drug-target interaction and drug combination prediction through domain-tuned network-based inference. BMC Systems Biology, 2015, 9, S4.	3.0	38
72	Knowledge in the Investigation of A-to-I RNA Editing Signals. Frontiers in Bioengineering and Biotechnology, 2015, 3, 18.	2.0	17

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73	SPECTRA: An Integrated Knowledge Base for Comparing Tissue and Tumor-Specific PPI Networks in Human. Frontiers in Bioengineering and Biotechnology, 2015, 3, 58.	2.0	13
74	Prediction of human population responses to toxic compounds by a collaborative competition. Nature Biotechnology, 2015, 33, 933-940.	9.4	88
75	Celiac disease from a global perspective. Bailliere's Best Practice and Research in Clinical Gastroenterology, 2015, 29, 365-379.	1.0	127
76	Mode of delivery and risk of celiac disease. Digestive and Liver Disease, 2015, 47, e271.	0.4	0
77	Computational Design of Artificial RNA Molecules for Gene Regulation. Methods in Molecular Biology, 2015, 1269, 393-412.	0.4	28
78	NetMatchStar: an enhanced Cytoscape network queryingÂapp. F1000Research, 2015, 4, 479.	0.8	17
79	NetMatchStar: an enhanced Cytoscape network queryingÂapp. F1000Research, 2015, 4, 479.	0.8	11
80	Comprehensive Reconstruction and Visualization of Non-Coding Regulatory Networks in Human. Frontiers in Bioengineering and Biotechnology, 2014, 2, 69.	2.0	25
81	ncPred: ncRNA-Disease Association Prediction through Tripartite Network-Based Inference. Frontiers in Bioengineering and Biotechnology, 2014, 2, 71.	2.0	56
82	Proteins comparison through probabilistic optimal structure local alignment. Frontiers in Genetics, 2014, 5, 302.	1.1	4
83	<i>Helicobacter pylori</i>infection and atopic diseases: Is there a relationship? A systematic review and meta-analysis. World Journal of Gastroenterology, 2014, 20, 17635.	1.4	29
84	New approaches in hepatitis B vaccination for celiac disease. Immunotherapy, 2014, 6, 945-952.	1.0	5
85	miR-Synth: a computational resource for the design of multi-site multi-target synthetic miRNAs. Nucleic Acids Research, 2014, 42, 5416-5425.	6.5	36
86	Introduction of Gluten, HLA Status, and the Risk of Celiac Disease in Children. New England Journal of Medicine, 2014, 371, 1295-1303.	13.9	410
87	A knowledge base for the discovery of function, diagnostic potential and drug effects on cellular and extracellular miRNAs. BMC Genomics, 2014, 15, S4.	1.2	25
88	Infant feeding pattern, HLA status, and prevalence of celiac disease. Digestive and Liver Disease, 2014, 46, e75-e76.	0.4	2
89	GASOLINE: a Cytoscape app for multiple local alignment of PPI networks. F1000Research, 2014, 3, 140.	0.8	7
90	GASOLINE: a Cytoscape app for multiple local alignment of PPI networks. F1000Research, 2014, 3, 140.	0.8	10

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91	GASOLINE: a Greedy And Stochastic algorithm for Optimal Local multiple alignment of Interaction NEtworks. PLoS ONE, 2014, 9, e98750.	1.1	28
92	Motif Discovery on Seismic Amplitude Time Series: The Case Study of Mt Etna 2011 Eruptive Activity. Pure and Applied Geophysics, 2013, 170, 529-545.	0.8	18
93	Bioinformatics in Italy: BITS2012, the ninth annual meeting of the Italian Society of Bioinformatics. BMC Bioinformatics, 2013, 14, S1.	1.2	1
94	VIRGO: visualization of A-to-I RNA editing sites in genomic sequences. BMC Bioinformatics, 2013, 14, S5.	1.2	10
95	A subgraph isomorphism algorithm and its application to biochemical data. BMC Bioinformatics, 2013, 14, S13.	1.2	125
96	Enhancing density-based clustering: Parameter reduction and outlier detection. Information Systems, 2013, 38, 317-330.	2.4	97
97	Elucidating the Role of microRNAs in Cancer Through Data Mining Techniques. Advances in Experimental Medicine and Biology, 2013, 774, 291-315.	0.8	6
98	A pilot study on neurological manifestations and antibodies against antigens in children with hematological and other cancers. European Journal of Paediatric Neurology, 2013, 17, 97-101.	0.7	4
99	Drugâ€"target interaction prediction through domain-tuned network-based inference. Bioinformatics, 2013, 29, 2004-2008.	1.8	146
100	DIATHERMY OF LEAKING SCLEROTOMIES AFTER 23-GAUGE TRANSCONJUNCTIVAL PARS PLANA VITRECTOMY. Retina, 2013, 33, 939-945.	1.0	18
101	GRAPES: A Software for Parallel Searching on Biological Graphs Targeting Multi-Core Architectures. PLoS ONE, 2013, 8, e76911.	1.1	33
102	Extracellular circulating viral microRNAs: current knowledge and perspectives. Frontiers in Genetics, 2013, 4, 120.	1.1	33
103	Integrated MicroRNA and mRNA Signatures Associated with Survival in Triple Negative Breast Cancer. PLoS ONE, 2013, 8, e55910.	1.1	158
104	MIDClass: Microarray Data Classification by Association Rules and Gene Expression Intervals. PLoS ONE, 2013, 8, e69873.	1.1	17
105	Prevalence and Natural History of Potential Celiac Disease in At-Family-Risk Infants Prospectively Investigated from Birth. Journal of Pediatrics, 2012, 161, 908-914.e2.	0.9	55
106	miR-EdiTar: a database of predicted A-to-I edited miRNA target sites. Bioinformatics, 2012, 28, 3166-3168.	1.8	28
107	miRandola: Extracellular Circulating MicroRNAs Database. PLoS ONE, 2012, 7, e47786.	1.1	142
108	DBStrata. , 2011, , .		2

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109	Clustering and classification of infrasonic events at Mount Etna using pattern recognition techniques. Geophysical Journal International, 2011, 185, 253-264.	1.0	38
110	Obstacles constrained group mobility models in event-driven wireless networks with movable base stations. Ad Hoc Networks, 2011, 9, 400-417.	3.4	6
111	Editorial. Briefings in Bioinformatics, 2011, 12, 547-548.	3.2	2
112	Tools and collaborative environments for bioinformatics research. Briefings in Bioinformatics, 2011, 12, 549-561.	3.2	58
113	SING: Subgraph search In Non-homogeneous Graphs. BMC Bioinformatics, 2010, 11, 96.	1.2	47
114	The neurology of coeliac disease in childhood: what is the evidence? A systematic review and metaâ€analysis. Developmental Medicine and Child Neurology, 2010, 52, 700-707.	1.1	92
115	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. PLoS ONE, 2010, 5, e11166.	1.1	51
116	SIGMA: A SET-COVER-BASED INEXACT GRAPH MATCHING ALGORITHM. Journal of Bioinformatics and Computational Biology, 2010, 08, 199-218.	0.3	61
117	Acute Disseminated Encephalomyelitis: A Long-Term Prospective Study and Meta-Analysis. Neuropediatrics, 2010, 41, 246-255.	0.3	75
118	PA13 THE NEUROLOGY OF COELIAC DISEASE IN CHILDHOOD: WHAT IS THE EVIDENCE? A SYSTEMATIC REVIEW AND META-ANALYSIS. Digestive and Liver Disease, 2010, 42, S347.	0.4	1
119	An Efficient Duplicate Record Detection Using q-Grams Array Inverted Index. Lecture Notes in Computer Science, 2010, , 309-323.	1.0	6
120	Enhancing Graph Database Indexing by Suffix Tree Structure. Lecture Notes in Computer Science, 2010, , 195-203.	1.0	27
121	MySQL Data Mining: Extending MySQL to Support Data Mining Primitives (Demo). Lecture Notes in Computer Science, 2010, , 438-444.	1.0	1
122	Prediction of human targets for viral-encoded microRNAs by thermodynamics and empirical constraints. Journal of Rnai and Gene Silencing, 2010, 6, 379-85.	1.2	18
123	miRo: a miRNA knowledge base. Database: the Journal of Biological Databases and Curation, 2009, 2009, bap008-bap008.	1.4	84
124	Distributed randomized algorithms for low-support data mining. , 2009, , .		0
125	BitCube: A Bottom-Up Cubing Engineering. Lecture Notes in Computer Science, 2009, , 189-203.	1.0	10
126	GraphFind: enhancing graph searching by low support data mining techniques. BMC Bioinformatics, 2008, 9, S10.	1.2	15

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127	Involvement of GTA protein NC2$\hat{I}^2$ in Neuroblastoma pathogenesis suggests that it physiologically participates in the regulation of cell proliferation. Molecular Cancer, 2008, 7, 52.	7.9	5
128	Genomics, Evolution, and Expression of TBPL2, a Member of the TBP Family. DNA and Cell Biology, 2007, 26, 369-385.	0.9	5
129	NetMatch: a Cytoscape plugin for searching biological networks. Bioinformatics, 2007, 23, 910-912.	1.8	75
130	Sequence similarity is more relevant than species specificity in probabilistic backtranslation. BMC Bioinformatics, 2007, 8, 58.	1.2	6
131	Cellular and molecular effects of protons: Apoptosis induction and potential implications for cancer therapy. Apoptosis: an International Journal on Programmed Cell Death, 2006, 11, 57-66.	2.2	73
132	Distributed antipole clustering for efficient data search and management in Euclidean and metric spaces. , 2006, , .		1
133	Antipole tree indexing to support range search and k-nearest neighbor search in metric spaces. IEEE Transactions on Knowledge and Data Engineering, 2005, 17, 535-550.	4.0	47
134	An Efficient Approximate Algorithm for the 1-Median Problem in Metric Spaces. SIAM Journal on Optimization, 2005, 16, 434-451.	1.2	8
135	In Vitro and In Silico Cloning of Xenopus laevis SOD2 cDNA and Its Phylogenetic Analysis. DNA and Cell Biology, 2005, 24, 111-116.	0.9	7
136	Clustered Trie Structures for Approximate Search in Hierarchical Objects Collections. Lecture Notes in Computer Science, 2005, , 63-70.	1.0	0
137	FAST CLUSTERING AND MINIMUM WEIGHT MATCHING ALGORITHMS FOR VERY LARGE MOBILE BACKBONE WIRELESS NETWORKS. International Journal of Foundations of Computer Science, 2003, 14, 223-236.	0.8	6
138	Efficient Boundary Values Generation in General Metric Spaces for Software Component Testing. Lecture Notes in Computer Science, 2003, , 318-331.	1.0	0
139	Best-match retrieval for structured images. IEEE Transactions on Pattern Analysis and Machine Intelligence, 2001, 23, 707-718.	9.7	5
140	Remote sensed images segmentation through shape refinement. , 0, , .		0
141	Locally sensitive backtranslation based on multiple sequence alignment. , 0, , .		1
142	Efficient Techniques for Graph Searching and Biological Network Mining. Advances in Data Mining and Database Management Book Series, 0, , 89-111.	0.4	0