

Alfredo Ferro

List of Publications by Year in descending order

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Version: 2024-02-01

39
papers

692
citations

623734

14
h-index

580821

25
g-index

40
all docs

40
docs citations

40
times ranked

948
citing authors

#	ARTICLE	IF	CITATIONS
1	A subgraph isomorphism algorithm and its application to biochemical data. BMC Bioinformatics, 2013, 14, S13.	2.6	125
2	miRandola 2017: a curated knowledge base of non-invasive biomarkers. Nucleic Acids Research, 2018, 46, D354-D359.	14.5	61
3	Colistin Resistant <i>A. baumannii</i> : Genomic and Transcriptomic Traits Acquired Under Colistin Therapy. Frontiers in Microbiology, 2018, 9, 3195.	3.5	53
4	Post-transcriptional knowledge in pathway analysis increases the accuracy of phenotypes classification. Oncotarget, 2016, 7, 54572-54582.	1.8	43
5	A Subset of Patients With Autism Spectrum Disorders Show a Distinctive Metabolic Profile by Dried Blood Spot Analyses. Frontiers in Psychiatry, 2018, 9, 636.	2.6	41
6	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, .	3.0	36
7	GASOLINE: a Greedy And Stochastic algorithm for Optimal Local multiple alignment of Interaction NETworks. PLoS ONE, 2014, 9, e98750.	2.5	28
8	Detecting Disease Specific Pathway Substructures through an Integrated Systems Biology Approach. Non-coding RNA, 2017, 3, 20.	2.6	25
9	Current Knowledge and Computational Techniques for Grapevine Meta-Omics Analysis. Frontiers in Plant Science, 2017, 8, 2241.	3.6	24
10	Exploring the role of interdisciplinarity in physics: Success, talent and luck. PLoS ONE, 2019, 14, e0218793.	2.5	20
11	OCDB: a database collecting genes, miRNAs and drugs for obsessive-compulsive disorder. Database: the Journal of Biological Databases and Curation, 2015, 2015, bav069.	3.0	18
12	Fast analytical methods for finding significant labeled graph motifs. Data Mining and Knowledge Discovery, 2018, 32, 504-531.	3.7	18
13	MiREDiBase, a manually curated database of validated and putative editing events in microRNAs. Scientific Data, 2021, 8, 199.	5.3	18
14	Knowledge in the Investigation of A-to-I RNA Editing Signals. Frontiers in Bioengineering and Biotechnology, 2015, 3, 18.	4.1	17
15	NetMatchStar: an enhanced Cytoscape network querying app. F1000Research, 2015, 4, 479.	1.6	17
16	A benchmarking of pipelines for detecting ncRNAs from RNA-Seq data. Briefings in Bioinformatics, 2020, 21, 1987-1998.	6.5	16
17	Novel Mechanisms of Tumor Promotion by the Insulin Receptor Isoform A in Triple-Negative Breast Cancer Cells. Cells, 2021, 10, 3145.	4.1	14
18	NETME: on-the-fly knowledge network construction from biomedical literature. Applied Network Science, 2022, 7, 1.	1.5	12

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19	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, 308.	2.3	11
20	NetMatchStar: an enhanced Cytoscape network querying app. <i>F1000Research</i> , 2015, 4, 479.	1.6	11
21	VECTOR: An Integrated Correlation Network Database for the Identification of CeRNA Axes in Uveal Melanoma. <i>Genes</i> , 2021, 12, 1004.	2.4	10
22	GASOLINE: a Cytoscape app for multiple local alignment of PPI networks. <i>F1000Research</i> , 2014, 3, 140.	1.6	10
23	Prevalence and Clinical Characteristics of Children and Adolescents with Metabolically Healthy Obesity: Role of Insulin Sensitivity. <i>Life</i> , 2020, 10, 127.	2.4	9
24	PHENSIM: Phenotype Simulator. <i>PLoS Computational Biology</i> , 2021, 17, e1009069.	3.2	9
25	Computational Methods for Drug Repurposing. <i>Advances in Experimental Medicine and Biology</i> , 2022, 1361, 119-141.	1.6	8
26	RNAdetector: a free user-friendly stand-alone and cloud-based system for RNA-Seq data analysis. <i>BMC Bioinformatics</i> , 2021, 22, 298.	2.6	7
27	GASOLINE: a Cytoscape app for multiple local alignment of PPI networks. <i>F1000Research</i> , 2014, 3, 140.	1.6	7
28	Computational Methods to Investigate the Impact of miRNAs on Pathways. <i>Methods in Molecular Biology</i> , 2019, 1970, 183-209.	0.9	5
29	Fast Subgraph Matching Strategies Based on Pattern-Only Heuristics. <i>Interdisciplinary Sciences, Computational Life Sciences</i> , 2019, 11, 21-32.	3.6	3
30	TACITuS: transcriptomic data collector, integrator, and selector on big data platform. <i>BMC Bioinformatics</i> , 2019, 20, 366.	2.6	3
31	MODIT: MOtif Discovery in Temporal Networks. <i>Frontiers in Big Data</i> , 2021, 4, 806014.	2.9	3
32	INBIA: a boosting methodology for proteomic network inference. <i>BMC Bioinformatics</i> , 2018, 19, 188.	2.6	2
33	Pathway Analysis for Cancer Research and Precision Oncology Applications. <i>Advances in Experimental Medicine and Biology</i> , 2022, 1361, 143-161.	1.6	2
34	Computational Resources for the Interpretation of Variations in Cancer. <i>Advances in Experimental Medicine and Biology</i> , 2022, 1361, 177-198.	1.6	2
35	Virus finding tools: current solutions and limitations. <i>Briefings in Bioinformatics</i> , 2022, 23, .	6.5	2
36	Fast methods for finding significant motifs on labelled multi-relational networks. <i>Journal of Complex Networks</i> , 2019, 7, 817-837.	1.8	1

#	ARTICLE	IF	CITATIONS
37	ANERGY TO SYNERGY-THE ENERGY FUELING THE RXCOVEA FRAMEWORK. International Journal for Multiscale Computational Engineering, 2020, 18, 329-333.	1.2	1
38	P22 Micro-RNA enriched pathway impact analysis applied to synovial RNA-seq in early rheumatoid arthritis identifies response prediction pathways. Rheumatology, 2020, 59, .	1.9	0
39	BioTAGME: A Comprehensive Platform for Biological Knowledge Network Analysis. Frontiers in Genetics, 2022, 13, 855739.	2.3	0