

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	NETME: on-the-fly knowledge network construction from biomedical literature. <i>Applied Network Science</i> , 2022, 7, 1.	1.5	12
2	Pathway Analysis for Cancer Research and Precision Oncology Applications. <i>Advances in Experimental Medicine and Biology</i> , 2022, 1361, 143-161.	1.6	2
3	Computational Resources for the Interpretation of Variations in Cancer. <i>Advances in Experimental Medicine and Biology</i> , 2022, 1361, 177-198.	1.6	2
4	Computational Methods for Drug Repurposing. <i>Advances in Experimental Medicine and Biology</i> , 2022, 1361, 119-141.	1.6	8
5	BioTAGME: A Comprehensive Platform for Biological Knowledge Network Analysis. <i>Frontiers in Genetics</i> , 2022, 13, 855739.	2.3	0
6	Virus finding tools: current solutions and limitations. <i>Briefings in Bioinformatics</i> , 2022, 23, .	6.5	2
7	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
8	VECTOR: An Integrated Correlation Network Database for the Identification of CeRNA Axes in Uveal Melanoma. <i>Genes</i> , 2021, 12, 1004.	2.4	10
9	PHENSIM: Phenotype Simulator. <i>PLoS Computational Biology</i> , 2021, 17, e1009069.	3.2	9
10	MiREDiBase, a manually curated database of validated and putative editing events in microRNAs. <i>Scientific Data</i> , 2021, 8, 199.	5.3	18
11	Novel Mechanisms of Tumor Promotion by the Insulin Receptor Isoform A in Triple-Negative Breast Cancer Cells. <i>Cells</i> , 2021, 10, 3145.	4.1	14
12	MODIT: MOtif Discovery in Temporal Networks. <i>Frontiers in Big Data</i> , 2021, 4, 806014.	2.9	3
13	A benchmarking of pipelines for detecting ncRNAs from RNA-Seq data. <i>Briefings in Bioinformatics</i> , 2020, 21, 1987-1998.	6.5	16
14	P22 Micro-RNA enriched pathway impact analysis applied to synovial RNA-seq in early rheumatoid arthritis identifies response prediction pathways. <i>Rheumatology</i> , 2020, 59, .	1.9	0
15	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
16	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
17	ANERGY TO SYNERGY-THE ENERGY FUELING THE RXCOVEA FRAMEWORK. <i>International Journal for Multiscale Computational Engineering</i> , 2020, 18, 329-333.	1.2	1
18	Exploring the role of interdisciplinarity in physics: Success, talent and luck. <i>PLoS ONE</i> , 2019, 14, e0218793.	2.5	20

#	ARTICLE	IF	CITATIONS
19	Fast Subgraph Matching Strategies Based on Pattern-Only Heuristics. <i>Interdisciplinary Sciences, Computational Life Sciences</i> , 2019, 11, 21-32.	3.6	3
20	Fast methods for finding significant motifs on labelled multi-relational networks. <i>Journal of Complex Networks</i> , 2019, 7, 817-837.	1.8	1
21	Computational Methods to Investigate the Impact of miRNAs on Pathways. <i>Methods in Molecular Biology</i> , 2019, 1970, 183-209.	0.9	5
22	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, .	3.0	36
23	TACITuS: transcriptomic data collector, integrator, and selector on big data platform. <i>BMC Bioinformatics</i> , 2019, 20, 366.	2.6	3
24	miRandola 2017: a curated knowledge base of non-invasive biomarkers. <i>Nucleic Acids Research</i> , 2018, 46, D354-D359.	14.5	61
25	Fast analytical methods for finding significant labeled graph motifs. <i>Data Mining and Knowledge Discovery</i> , 2018, 32, 504-531.	3.7	18
26	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.	2.6	41
27	INBIA: a boosting methodology for proteomic network inference. <i>BMC Bioinformatics</i> , 2018, 19, 188.	2.6	2
28	Colistin Resistant <i>A. baumannii</i> : Genomic and Transcriptomic Traits Acquired Under Colistin Therapy. <i>Frontiers in Microbiology</i> , 2018, 9, 3195.	3.5	53
29	Detecting Disease Specific Pathway Substructures through an Integrated Systems Biology Approach. <i>Non-coding RNA</i> , 2017, 3, 20.	2.6	25
30	Current Knowledge and Computational Techniques for Grapevine Meta-Omics Analysis. <i>Frontiers in Plant Science</i> , 2017, 8, 2241.	3.6	24
31	Post-transcriptional knowledge in pathway analysis increases the accuracy of phenotypes classification. <i>Oncotarget</i> , 2016, 7, 54572-54582.	1.8	43
32	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.	3.0	18
33	Knowledge in the Investigation of A-to-I RNA Editing Signals. <i>Frontiers in Bioengineering and Biotechnology</i> , 2015, 3, 18.	4.1	17
34	NetMatchStar: an enhanced Cytoscape network querying App. <i>F1000Research</i> , 2015, 4, 479.	1.6	17
35	NetMatchStar: an enhanced Cytoscape network querying App. <i>F1000Research</i> , 2015, 4, 479.	1.6	11
36	GASOLINE: a Cytoscape app for multiple local alignment of PPI networks. <i>F1000Research</i> , 2014, 3, 140.	1.6	7

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37	GASOLINE: a Cytoscape app for multiple local alignment of PPI networks. F1000Research, 2014, 3, 140.	1.6	10
38	GASOLINE: a Greedy And Stochastic algorithm for Optimal Local multiple alignment of Interaction NEtworks. PLoS ONE, 2014, 9, e98750.	2.5	28
39	A subgraph isomorphism algorithm and its application to biochemical data. BMC Bioinformatics, 2013, 14, S13.	2.6	125