

Rosalba Giugno

List of Publications by Year in descending order

Source: [//exaly.com/author-pdf/2319564/publications.pdf](https://exaly.com/author-pdf/2319564/publications.pdf)

Version: 2025-02-01

116
papers

2,729
citations

178948

27
h-index

211087

45
g-index

132
all docs

132
docs citations

132
times ranked

4161
citing authors

#	ARTICLE	IF	CITATIONS
1	Identifying the joint signature of brain atrophy and gene variant scores in Alzheimer's Disease. Journal of Biomedical Informatics, 2024, 149, 104569.	4.8	5
2	Motif Finding Algorithms: A Performance Comparison. Lecture Notes in Computer Science, 2024, , 250-267.	0.0	1
3	GateMeClass: Gate Mining and Classification of cytometry data. Bioinformatics, 2024, 40, .	5.0	1
4	GPU-Accelerated BFS for Dynamic Networks. Lecture Notes in Computer Science, 2024, , 74-87.	0.0	1
5	Esearch3D: propagating gene expression in chromatin networks to illuminate active enhancers. Nucleic Acids Research, 2023, 51, e55-e55.	16.2	3
6	APDB: a database on air pollutant characterization and similarity prediction. Database: the Journal of Biological Databases and Curation, 2023, 2023, .	3.0	1
7	MODIMO: Workshop on Multi-Omics Data Integration for Modelling Biological Systems. , 2023, , 5259-5262.		0
8	PanDelos-frags: A methodology for discovering pangenomic content of incomplete microbial assemblies. Journal of Biomedical Informatics, 2023, 148, 104552.	4.8	2
9	Interrupting the nitrosative stress fuels tumor-specific cytotoxic T lymphocytes in pancreatic cancer. , 2022, 10, e003549.		28
10	Single-Cell RNA-Seq Analysis of Olfactory Mucosal Cells of Alzheimer's Disease Patients. Cells, 2022, 11, 676.	4.8	26
11	PANPROVA: pangenomic prokaryotic evolution of full assemblies. Bioinformatics, 2022, 38, 2631-2632.	5.0	2
12	Biometal Dyshomeostasis in Olfactory Mucosa of Alzheimer's Disease Patients. International Journal of Molecular Sciences, 2022, 23, 4123.	4.5	6
13	TUBE Project: Transport-Derived Ultrafines and the Brain Effects. International Journal of Environmental Research and Public Health, 2022, 19, 311.	3.1	4
14	<i>Stardust</i>: improving spatial transcriptomics data analysis through space-aware modularity optimization-based clustering. GigaScience, 2022, 11, .	3.4	6
15	Combined Large Cell Neuroendocrine Carcinomas of the Lung: Integrative Molecular Analysis Identifies Subtypes with Potential Therapeutic Implications. Cancers, 2022, 14, 4653.	4.0	5
16	Human genetic diversity alters off-target outcomes of therapeutic gene editing. Nature Genetics, 2022, 55, 34-43.	16.3	54
17	Challenges in gene-oriented approaches for pangenome content discovery. Briefings in Bioinformatics, 2021, 22, .	7.1	12
18	netDx: Software for building interpretable patient classifiers by multi-'omic data integration using patient similarity networks. F1000Research, 2021, 9, 1239.	0.6	3

#	ARTICLE	IF	CITATIONS
19	Exonâ€“Intron Differential Analysis Reveals the Role of Competing Endogenous RNAs in Post-Transcriptional Regulation of Translation. <i>Non-coding RNA</i> , 2021, 7, 26.	2.3	3
20	GRAPES-DD: exploiting decision diagrams for index-driven search in biological graph databases. <i>BMC Bioinformatics</i> , 2021, 22, .	3.3	5
21	SystemC Implementation of Stochastic Petri Nets for Simulation and Parameterization of Biological Networks. <i>Transactions on Embedded Computing Systems</i> , 2021, 20, 1-20.	2.9	0
22	GRAFIMO: Variant and haplotype aware motif scanning on pangenome graphs. <i>PLoS Computational Biology</i> , 2021, 17, e1009444.	3.3	5
23	Peripheral inflammation preceding ischemia impairs neuronal survival through mechanisms involving miRâ€“127 in aged animals. <i>Aging Cell</i> , 2021, 20, .	7.0	10
24	TEDAR: Temporal dynamic signal detection of adverse reactions. <i>Artificial Intelligence in Medicine</i> , 2021, 122, 102212.	7.3	2
25	CRISPRitz: rapid, high-throughput and variant-aware <i>in silico</i> off-target site identification for CRISPR genome editing. <i>Bioinformatics</i> , 2020, 36, 2001-2008.	5.0	37
26	Telemedicine and Virtual Reality for Cognitive Rehabilitation: A Roadmap for the COVID-19 Pandemic. <i>Frontiers in Neurology</i> , 2020, 11, .	2.5	118
27	Intracerebral overexpression of miR-669c is protective in mouse ischemic stroke model by targeting MyD88 and inducing alternative microglial/macrophage activation. <i>Journal of Neuroinflammation</i> , 2020, 17, .	9.2	23
28	Integrated analysis of transcriptome, methylome and copy number aberrations data of marginal zone lymphoma and follicular lymphoma in dog. <i>Veterinary and Comparative Oncology</i> , 2020, 18, 645-655.	2.0	10
29	Centrality Speeds the Subgraph Isomorphism Search Up in Target Aware Contexts. <i>Lecture Notes in Computer Science</i> , 2020, , 19-26.	0.0	0
30	LErNet: characterization of lncRNAs via context-aware network expansion and enrichment analysis. , 2019, 17, 1-8.		0
31	Parallel Searching on Biological Networks. , 2019, 15, 307-314.		2
32	Immunosuppression by monocytic myeloid-derived suppressor cells in patients with pancreatic ductal carcinoma is orchestrated by STAT3. , 2019, 7, .		137
33	PSEN1 ^{Î”E9} , APP ^{swe} , and APOE4 Confer Disparate Phenotypes in Human iPSC-Derived Microglia. <i>Stem Cell Reports</i> , 2019, 13, 669-683.	4.7	123
34	Long Non-Coding RNAs as Molecular Signatures for Canine B-Cell Lymphoma Characterization. <i>Non-coding RNA</i> , 2019, 5, 47.	2.3	10
35	¹⁸ Fâ€“Florbetaben PET/CT to Assess Alzheimer's Disease: A new Analysis Method for Regional Amyloid Quantification. <i>Journal of Neuroimaging</i> , 2019, 29, 383-393.	2.5	19
36	The 2017 Network Tools and Applications in Biology (NETTAB) workshop: aims, topics and outcomes. <i>BMC Bioinformatics</i> , 2019, 20, .	3.3	2

#	ARTICLE	IF	CITATIONS
37	Construction and Analysis of miRNA Regulatory Networks. <i>Methods in Molecular Biology</i> , 2019, , 121-167.	0.0	0
38	Fast Subgraph Matching Strategies Based on Pattern-Only Heuristics. <i>Interdisciplinary Sciences, Computational Life Sciences</i> , 2019, 11, 21-32.	3.4	4
39	Extracellular Vesicles Mediate Mesenchymal Stromal Cell-Dependent Regulation of B Cell PI3K-AKT Signaling Pathway and Actin Cytoskeleton. <i>Frontiers in Immunology</i> , 2019, 10, .	5.0	70
40	Fast methods for finding significant motifs on labelled multi-relational networks. <i>Journal of Complex Networks</i> , 2019, 7, 817-837.	1.3	1
41	Efficient Simulation and Parametrization of Stochastic Petri Nets in SystemC: A Case study from Systems Biology. , 2019, 17, 1-7.		1
42	miRandola 2017: a curated knowledge base of non-invasive biomarkers. <i>Nucleic Acids Research</i> , 2018, 46, D354-D359.	16.2	62
43	An Efficient Implementation of a Subgraph Isomorphism Algorithm for GPUs. , 2018, 7, 2674-2681.		1
44	Arena-Idb: a platform to build human non-coding RNA interaction networks. <i>BMC Bioinformatics</i> , 2018, 19, .	3.3	17
45	cuRnet: an R package for graph traversing on GPU. <i>BMC Bioinformatics</i> , 2018, 19, .	3.3	3
46	PanDelos: a dictionary-based method for pan-genome content discovery. <i>BMC Bioinformatics</i> , 2018, 19, .	3.3	11
47	Editorial: New Trends on Genome and Transcriptome Characterizations. <i>Frontiers in Genetics</i> , 2018, 9, .	2.4	0
48	INBIA: a boosting methodology for proteomic network inference. <i>BMC Bioinformatics</i> , 2018, 19, .	3.3	2
49	Genetic Alteration of MicroRNA Affecting Cancer Pathways. , 2018, , 269-287.		0
50	Current Knowledge and Computational Techniques for Grapevine Meta-Omics Analysis. <i>Frontiers in Plant Science</i> , 2018, 8, .	4.2	15
51	Ex Machina: Analytical platforms, Law and the Challenges of Computational Legal Science. <i>Future Internet</i> , 2018, 10, 37.	4.9	12
52	Simple Pattern-only Heuristics Lead to Fast Subgraph Matching Strategies on Very Large Networks. <i>Advances in Intelligent Systems and Computing</i> , 2018, , 131-138.	0.0	2
53	On the Variable Ordering in Subgraph Isomorphism Algorithms. <i>IEEE/ACM Transactions on Computational Biology and Bioinformatics</i> , 2017, 14, 193-203.	3.7	39
54	Fast analytical methods for finding significant labeled graph motifs. <i>Data Mining and Knowledge Discovery</i> , 2017, 32, 504-531.	4.2	18

#	ARTICLE	IF	CITATIONS
55	Circulating Noncoding RNAs as Clinical Biomarkers. , 2016, , 239-258.		5
56	A SystemC-based platform for assertion-based verification and mutation analysis in systems biology. , 2016, , 159-164.		1
57	Recommendation Techniques for Drug-Target Interaction Prediction and Drug Repositioning. Methods in Molecular Biology, 2016, , 441-462.	0.0	34
58	APPAGATO: an APproximate PARallel and stochastic GrAph querying TOol for biological networks. Bioinformatics, 2016, 32, 2159-2166.	5.0	10
59	SyQUAL: a platform for qualitative modelling and simulation of biological systems. , 2016, , 155-161.		0
60	Post-transcriptional knowledge in pathway analysis increases the accuracy of phenotypes classification. Oncotarget, 2016, 7, 54572-54582.	1.7	36
61	A knowledge base for Vitis vinifera functional analysis. BMC Systems Biology, 2015, 9, S5.	3.5	13
62	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	15
63	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, .	3.5	34
64	Knowledge in the Investigation of A-to-I RNA Editing Signals. Frontiers in Bioengineering and Biotechnology, 2015, 3, .	4.1	14
65	SPECTRA: An Integrated Knowledge Base for Comparing Tissue and Tumor-Specific PPI Networks in Human. Frontiers in Bioengineering and Biotechnology, 2015, 3, .	4.1	15
66	A SystemC Platform for Signal Transduction Modelling and Simulation in Systems Biology. , 2015, , 233-236.		2
67	Computational Design of Artificial RNA Molecules for Gene Regulation. Methods in Molecular Biology, 2015, , 393-412.	0.0	30
68	NetMatchStar: an enhanced Cytoscape network querying App. F1000Research, 2015, 4, 479.	0.6	11
69	NetMatchStar: an enhanced Cytoscape network querying App. F1000Research, 2015, 4, 479.	0.6	10
70	Comprehensive Reconstruction and Visualization of Non-Coding Regulatory Networks in Human. Frontiers in Bioengineering and Biotechnology, 2014, 2, .	4.1	22
71	ncPred: ncRNA-Disease Association Prediction through Tripartite Network-Based Inference. Frontiers in Bioengineering and Biotechnology, 2014, 2, .	4.1	45
72	Proteins comparison through probabilistic optimal structure local alignment. Frontiers in Genetics, 2014, 5, .	2.4	4

#	ARTICLE	IF	CITATIONS
73	miR-Synth: a computational resource for the design of multi-site multi-target synthetic miRNAs. Nucleic Acids Research, 2014, 42, 5416-5425.	16.2	32
74	A knowledge base for the discovery of function, diagnostic potential and drug effects on cellular and extracellular miRNAs. BMC Genomics, 2014, 15, .	3.2	24
75	Dynamic Modeling and Simulation of Leukocyte Integrin Activation through an Electronic Design Automation Framework. Lecture Notes in Computer Science, 2014, , 143-154.	0.0	6
76	GASOLINE: a Cytoscape app for multiple local alignment of PPI networks. F1000Research, 2014, 3, 140.	0.6	5
77	GASOLINE: a Cytoscape app for multiple local alignment of PPI networks. F1000Research, 2014, 3, 140.	0.6	8
78	GASOLINE: a Greedy And Stochastic algorithm for Optimal Local multiple alignment of Interaction NEtworks. PLoS ONE, 2014, 9, e98750.	2.5	27
79	Bioinformatics in Italy: BITS2012, the ninth annual meeting of the Italian Society of Bioinformatics. BMC Bioinformatics, 2013, 14, .	3.3	1
80	VIRGO: visualization of A-to-I RNA editing sites in genomic sequences. BMC Bioinformatics, 2013, 14, S5.	3.3	10
81	A subgraph isomorphism algorithm and its application to biochemical data. BMC Bioinformatics, 2013, 14, .	3.3	149
82	Enhancing density-based clustering: Parameter reduction and outlier detection. Information Systems, 2013, 38, 317-330.	4.0	105
83	Computational Approaches to RNAi and Gene Silencing. , 2013, , 169-194.		0
84	Elucidating the Role of microRNAs in Cancer Through Data Mining Techniques. Advances in Experimental Medicine and Biology, 2013, , 291-315.	0.0	4
85	Drugâ€target interaction prediction through domain-tuned network-based inference. Bioinformatics, 2013, 29, 2004-2008.	5.0	137
86	Microarray Data Analysis: From Preparation To Classification. , 2013, , 657-674.		0
87	GRAPES: A Software for Parallel Searching on Biological Graphs Targeting Multi-Core Architectures. PLoS ONE, 2013, 8, e76911.	2.5	36
88	Extracellular circulating viral microRNAs: current knowledge and perspectives. Frontiers in Genetics, 2013, 4, .	2.4	31
89	MIDClass: Microarray Data Classification by Association Rules and Gene Expression Intervals. PLoS ONE, 2013, 8, e69873.	2.5	17
90	miR-EdiTAr: a database of predicted A-to-I edited miRNA target sites. Bioinformatics, 2012, 28, 3166-3168.	5.0	26

#	ARTICLE	IF	CITATIONS
91	miRandola: Extracellular Circulating MicroRNAs Database. PLoS ONE, 2012, 7, e47786.	2.5	132
92	Preface - BITS 2012: Ninth Annual Meeting of the Bioinformatics Italian Society. EMBnet Journal, 2012, 18, 4.	0.6	0
93	DBStrata. , 2011, 96, 107-108.		2
94	Editorial. Briefings in Bioinformatics, 2011, 12, 547-548.	7.1	2
95	Tools and collaborative environments for bioinformatics research. Briefings in Bioinformatics, 2011, 12, 549-561.	7.1	56
96	Business Process Model Retrieval Based on Graph Indexing Method. Lecture Notes in Business Information Processing, 2011, , 238-250.	0.0	1
97	SING: Subgraph search In Non-homogeneous Graphs. BMC Bioinformatics, 2010, 11, .	3.3	48
98	The neurology of coeliac disease in childhood: what is the evidence? A systematic review and meta-analysis. Developmental Medicine and Child Neurology, 2010, 52, 700-707.	3.9	84
99	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.	2.5	49
100	SIGMA: A SET-COVER-BASED INEXACT GRAPH MATCHING ALGORITHM. Journal of Bioinformatics and Computational Biology, 2010, 08, 199-218.	1.1	58
101	An Efficient Duplicate Record Detection Using q-Grams Array Inverted Index. Lecture Notes in Computer Science, 2010, , 309-323.	0.0	6
102	Enhancing Graph Database Indexing by Suffix Tree Structure. Lecture Notes in Computer Science, 2010, , 195-203.	0.0	34
103	MySQL Data Mining: Extending MySQL to Support Data Mining Primitives (Demo). Lecture Notes in Computer Science, 2010, , 438-444.	0.0	1
104	Distributed randomized algorithms for low-support data mining. , 2009, , .		0
105	BitCube: A Bottom-Up Cubing Engineering. Lecture Notes in Computer Science, 2009, , 189-203.	0.0	10
106	GraphFind: enhancing graph searching by low support data mining techniques. BMC Bioinformatics, 2008, 9, .	3.3	15
107	Involvement of GTA protein NC2Î² in Neuroblastoma pathogenesis suggests that it physiologically participates in the regulation of cell proliferation. Molecular Cancer, 2008, 7, .	29.8	4
108	Genomics, Evolution, and Expression of TBPL2, a Member of the TBP Family. DNA and Cell Biology, 2007, 26, 369-385.	2.2	5

#	ARTICLE	IF	CITATIONS
109	Multiple-Winners Randomized Tournaments with Consensus for Optimization Problems in Generic Metric Spaces. Lecture Notes in Computer Science, 2005, , 265-276.	0.0	2
110	In Vitro and In Silico Cloning of Xenopus laevis SOD2 cDNA and Its Phylogenetic Analysis. DNA and Cell Biology, 2005, 24, 111-116.	2.2	6
111	Efficient Boundary Values Generation in General Metric Spaces for Software Component Testing. Lecture Notes in Computer Science, 2003, , 318-331.	0.0	0
112	Algorithmics and applications of tree and graph searching. , 2002, , .		240
113	P- $\mathcal{S}\mathcal{H}\mathcal{O}\mathcal{Q}$ \mathcal{D} : A Probabilistic Extension of $\mathcal{S}\mathcal{H}\mathcal{O}\mathcal{Q}$ \mathcal{D} for Probabilistic Ontologies in the Semantic Web. Lecture Notes in Computer Science, 2002, , 86-97.	0.0	71
114	<title>Approximate search in image database</title>. , 1999, , .		0
115	A novel computational method for inferring competing endogenous interactions. Briefings in Bioinformatics, 0, , bbw084.	7.1	35
116	Efficient Techniques for Graph Searching and Biological Network Mining. Advances in Data Mining and Database Management Book Series, 0, , 89-111.	0.0	0