Rosalba Giugno

List of Publications by Year
in descending order

150 papers	6,355 citations	126708 33 h-index	88477 70 g-index
162 all docs	162 docs citations	162 times ranked	9317 citing authors

#	Article	IF	Citations
1	Eleven grand challenges in single-cell data science. Genome Biology, 2020, 21, 31.	3.8	742
2	Engineered CRISPR–Cas12a variants with increased activities and improved targeting ranges for gene, epigenetic and base editing. Nature Biotechnology, 2019, 37, 276-282.	9.4	439
3	Highly efficient therapeutic gene editing of human hematopoietic stem cells. Nature Medicine, 2019, 25, 776-783.	15.2	344
4	An APOBEC3A-Cas9 base editor with minimized bystander and off-target activities. Nature Biotechnology, 2018, 36, 977-982.	9.4	328
5	In vivo CRISPR editing with no detectable genome-wide off-target mutations. Nature, 2018, 561, 416-419.	13.7	274
6	Algorithmics and applications of tree and graph searching. , 2002, , .		240
7	Assessment of computational methods for the analysis of single-cell ATAC-seq data. Genome Biology, 2019, 20, 241.	3.8	225
8	Therapeutic base editing of human hematopoietic stem cells. Nature Medicine, 2020, 26, 535-541.	15.2	196
9	Dissecting hematopoietic and renal cell heterogeneity in adult zebrafish at single-cell resolution using RNA sequencing. Journal of Experimental Medicine, 2017, 214, 2875-2887.	4.2	168
10	Drug–target interaction prediction through domain-tuned network-based inference. Bioinformatics, 2013, 29, 2004-2008.	1.8	146
11	miRandola: Extracellular Circulating MicroRNAs Database. PLoS ONE, 2012, 7, e47786.	1.1	142
12	PSEN1Î"E9, APPswe, and APOE4 Confer Disparate Phenotypes in Human iPSC-Derived Microglia. Stem Cell Reports, 2019, 13, 669-683.	2.3	132
13	A subgraph isomorphism algorithm and its application to biochemical data. BMC Bioinformatics, 2013, 14, S13.	1.2	125
14	Immunosuppression by monocytic myeloid-derived suppressor cells in patients with pancreatic ductal carcinoma is orchestrated by STAT3. , 2019, 7, 255.		123
15	CRISPR prime editing with ribonucleoprotein complexes in zebrafish and primary human cells. Nature Biotechnology, 2022, 40, 189-193.	9.4	118
16	Three subtypes of lung cancer fibroblasts define distinct therapeutic paradigms. Cancer Cell, 2021, 39, 1531-1547.e10.	7.7	106
17	PrimeDesign software for rapid and simplified design of prime editing guide RNAs. Nature Communications, 2021, 12, 1034.	5.8	105
18	Telemedicine and Virtual Reality for Cognitive Rehabilitation: A Roadmap for the COVID-19 Pandemic. Frontiers in Neurology, 2020, 11, 926.	1.1	102

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19	Enhancing density-based clustering: Parameter reduction and outlier detection. Information Systems, 2013, 38, 317-330.	2.4	97
20	Variant-aware saturating mutagenesis using multiple Cas9 nucleases identifies regulatory elements at trait-associated loci. Nature Genetics, 2017, 49, 625-634.	9.4	96
21	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
22	P-$$ mathcal{S}mathcal{H}mathcal{O}mathcal{Q} $$(D): A Probabilistic Extension of $$ mathcal{S}mathcal{H}mathcal{O}mathcal{Q} $$(D) for Probabilistic Ontologies in the Semantic Web. Lecture Notes in Computer Science, 2002, , 86-97.	1.0	75
23	Aging-Associated Alterations in Mammary Epithelia and Stroma Revealed by Single-Cell RNA Sequencing. Cell Reports, 2020, 33, 108566.	2.9	75
24	Extracellular Vesicles Mediate Mesenchymal Stromal Cell-Dependent Regulation of B Cell PI3K-AKT Signaling Pathway and Actin Cytoskeleton. Frontiers in Immunology, 2019, 10, 446.	2.2	73
25	Integrated design, execution, and analysis of arrayed and pooled CRISPR genome-editing experiments. Nature Protocols, 2018, 13, 946-986.	5.5	70
26	SIGMA: A SET-COVER-BASED INEXACT GRAPH MATCHING ALGORITHM. Journal of Bioinformatics and Computational Biology, 2010, 08, 199-218.	0.3	61
27	miRandola 2017: a curated knowledge base of non-invasive biomarkers. Nucleic Acids Research, 2018, 46, D354-D359.	6.5	61
28	Tools and collaborative environments for bioinformatics research. Briefings in Bioinformatics, 2011, 12, 549-561.	3.2	58
29	ncPred: ncRNA-Disease Association Prediction through Tripartite Network-Based Inference. Frontiers in Bioengineering and Biotechnology, 2014, 2, 71.	2.0	56
30	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
31	SING: Subgraph search In Non-homogeneous Graphs. BMC Bioinformatics, 2010, 11, 96.	1.2	47
32	Transcription factor competition at the Î³-globin promoters controls hemoglobin switching. Nature Genetics, 2021, 53, 511-520.	9.4	43
33	Post-transcriptional knowledge in pathway analysis increases the accuracy of phenotypes classification. Oncotarget, 2016, 7, 54572-54582.	0.8	43
34	CRISPRitz: rapid, high-throughput and variant-aware <i>in silico</i> off-target site identification for CRISPR genome editing. Bioinformatics, 2020, 36, 2001-2008.	1.8	41
35	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
36	A novel computational method for inferring competing endogenous interactions. Briefings in Bioinformatics, 2016, 18, bbw084.	3.2	37

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37	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
38	ZNF410 represses fetal globin by singular control of CHD4. Nature Genetics, 2021, 53, 719-728.	9.4	35
39	GRAPES: A Software for Parallel Searching on Biological Graphs Targeting Multi-Core Architectures. PLoS ONE, 2013, 8, e76911.	1.1	33
40	Extracellular circulating viral microRNAs: current knowledge and perspectives. Frontiers in Genetics, 2013, 4, 120.	1.1	33
41	Recommendation Techniques for Drugâ€"Target Interaction Prediction and Drug Repositioning. Methods in Molecular Biology, 2016, 1415, 441-462.	0.4	33
42	CRISPR-SURF: discovering regulatory elements by deconvolution of CRISPR tiling screen data. Nature Methods, 2018, 15, 992-993.	9.0	33
43	On the Variable Ordering in Subgraph Isomorphism Algorithms. IEEE/ACM Transactions on Computational Biology and Bioinformatics, 2017, 14, 193-203.	1.9	32
44	miR-EdiTar: a database of predicted A-to-I edited miRNA target sites. Bioinformatics, 2012, 28, 3166-3168.	1.8	28
45	AmpUMI: design and analysis of unique molecular identifiers for deep amplicon sequencing. Bioinformatics, 2018, 34, i202-i210.	1.8	28
46	Technologies and Computational Analysis Strategies for CRISPR Applications. Molecular Cell, 2020, 79, 11-29.	4.5	28
47	Computational Design of Artificial RNA Molecules for Gene Regulation. Methods in Molecular Biology, 2015, 1269, 393-412.	0.4	28
48	GASOLINE: a Greedy And Stochastic algorithm for Optimal Local multiple alignment of Interaction NEtworks. PLoS ONE, 2014, 9, e98750.	1.1	28
49	Enhancing Graph Database Indexing by Suffix Tree Structure. Lecture Notes in Computer Science, 2010, , 195-203.	1.0	27
50	Comprehensive Reconstruction and Visualization of Non-Coding Regulatory Networks in Human. Frontiers in Bioengineering and Biotechnology, 2014, 2, 69.	2.0	25
51	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
52	Response to â€œUnexpected mutations after CRISPRâ€"Cas9 editing in vivoâ€. Nature Methods, 2018, 15, 238-239.	9.0	25
53	A knowledge base for Vitis vinifera functional analysis. BMC Systems Biology, 2015, 9, S5.	3.0	24
54	Impact of Genetic Variation on CRISPR-Cas Targeting. CRISPR Journal, 2018, 1, 159-170.	1.4	24

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55	Current Knowledge and Computational Techniques for Grapevine Meta-Omics Analysis. Frontiers in Plant Science, 2017, 8, 2241.	1.7	24
56	A Code of Ethics for Gene Drive Research. CRISPR Journal, 2021, 4, 19-24.	1.4	24
57	Dissecting ELANE neutropenia pathogenicity by human HSC gene editing. Cell Stem Cell, 2021, 28, 833-845.e5.	5.2	23
58	Intracerebral overexpression of miR-669c is protective in mouse ischemic stroke model by targeting MyD88 and inducing alternative microglial/macrophage activation. Journal of Neuroinflammation, 2020, 17, 194.	3.1	22
59	Interrupting the nitrosative stress fuels tumor-specific cytotoxic T lymphocytes in pancreatic cancer. , 2022, 10, e003549.		22
60	Single-Cell RNA-Seq Analysis of Olfactory Mucosal Cells of Alzheimerâ€™s Disease Patients. Cells, 2022, 11, 676.	1.8	20
61	18Fâ€Florbetaben PET/CT to Assess Alzheimer's Disease: A new Analysis Method for Regional Amyloid Quantification. Journal of Neuroimaging, 2019, 29, 383-393.	1.0	19
62	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
63	Fast analytical methods for finding significant labeled graph motifs. Data Mining and Knowledge Discovery, 2018, 32, 504-531.	2.4	18
64	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
65	Knowledge in the Investigation of A-to-I RNA Editing Signals. Frontiers in Bioengineering and Biotechnology, 2015, 3, 18.	2.0	17
66	Arena-Idb: a platform to build human non-coding RNA interaction networks. BMC Bioinformatics, 2018, 19, 350.	1.2	17
67	Augmenting and directing long-range CRISPR-mediated activation in human cells. Nature Methods, 2021, 18, 1075-1081.	9.0	17
68	NetMatchStar: an enhanced Cytoscape network queryingÂapp. F1000Research, 2015, 4, 479.	0.8	17
69	MIDClass: Microarray Data Classification by Association Rules and Gene Expression Intervals. PLoS ONE, 2013, 8, e69873.	1.1	17
70	Haystack: systematic analysis of the variation of epigenetic states and cell-type specific regulatory elements. Bioinformatics, 2018, 34, 1930-1933.	1.8	16
71	Parallel Single-Cell RNA-Seq and Genetic Recording Reveals Lineage Decisions in Developing Embryoid Bodies. Cell Reports, 2020, 33, 108222.	2.9	16
72	GraphFind: enhancing graph searching by low support data mining techniques. BMC Bioinformatics, 2008, 9, S10.	1.2	15

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73	singlecellVR: Interactive Visualization of Single-Cell Data in Virtual Reality. Frontiers in Genetics, 2021, 12, 764170.	1.1	14
74	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
75	PanDelos: a dictionary-based method for pan-genome content discovery. BMC Bioinformatics, 2018, 19, 437.	1.2	13
76	Long Non-Coding RNAs as Molecular Signatures for Canine B-Cell Lymphoma Characterization. Non-coding RNA, 2019, 5, 47.	1.3	12
77	Targeting leukemia-specific dependence on the de novo purine synthesis pathway. Leukemia, 2022, 36, 383-393.	3.3	11
78	NetMatchStar: an enhanced Cytoscape network queryingÂapp. F1000Research, 2015, 4, 479.	0.8	11
79	VIRGO: visualization of A-to-I RNA editing sites in genomic sequences. BMC Bioinformatics, 2013, 14, S5.	1.2	10
80	APPAGATO: an APproximate PArallel and stochastic GrAph querying TOol for biological networks. Bioinformatics, 2016, 32, 2159-2166.	1.8	10
81	Ex Machina: Analytical platforms, Law and the Challenges of Computational Legal Science. Future Internet, 2018, 10, 37.	2.4	10
82	BitCube: A Bottom-Up Cubing Engineering. Lecture Notes in Computer Science, 2009, , 189-203.	1.0	10
83	GASOLINE: a Cytoscape app for multiple local alignment of PPI networks. F1000Research, 2014, 3, 140.	0.8	10
84	Integrated analysis of transcriptome, methylome and copy number aberrations data of marginal zone lymphoma and follicular lymphoma in dog. Veterinary and Comparative Oncology, 2020, 18, 645-655.	0.8	9
85	Epigenetic Alterations in Keratinocyte Carcinoma. Journal of Investigative Dermatology, 2021, 141, 1207-1218.	0.3	9
86	Hedgehog interacting proteinâ€"expressing lung fibroblasts suppress lymphocytic inflammation in mice. JCI Insight, 2021, 6, .	2.3	9
87	Challenges in gene-oriented approaches for pangenome content discovery. Briefings in Bioinformatics, 2021, 22, .	3.2	8
88	Current progress and potential opportunities to infer single-cell developmental trajectory and cell fate. Current Opinion in Systems Biology, 2021, 26, 1-11.	1.3	8
89	Gene Editing ELANE in Human Hematopoietic Stem and Progenitor Cells Reveals Disease Mechanisms and Therapeutic Strategies for Severe Congenital Neutropenia. Blood, 2019, 134, 3-3.	0.6	8
90	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

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91	GASOLINE: a Cytoscape app for multiple local alignment of PPI networks. F1000Research, 2014, 3, 140.	0.8	7
92	Peripheral inflammation preceeding ischemia impairs neuronal survival through mechanisms involving miRâ€127 in aged animals. Aging Cell, 2021, 20, e13287.	3.0	7
93	Sequence similarity is more relevant than species specificity in probabilistic backtranslation. BMC Bioinformatics, 2007, 8, 58.	1.2	6
94	Elucidating the Role of microRNAs in Cancer Through Data Mining Techniques. Advances in Experimental Medicine and Biology, 2013, 774, 291-315.	0.8	6
95	Dynamic Modeling and Simulation of Leukocyte Integrin Activation through an Electronic Design Automation Framework. Lecture Notes in Computer Science, 2014, , 143-154.	1.0	6
96	An Efficient Duplicate Record Detection Using q-Grams Array Inverted Index. Lecture Notes in Computer Science, 2010, , 309-323.	1.0	6
97	Genomics, Evolution, and Expression of TBPL2, a Member of the TBP Family. DNA and Cell Biology, 2007, 26, 369-385.	0.9	5
98	Involvement of GTA protein NC2Î² in Neuroblastoma pathogenesis suggests that it physiologically participates in the regulation of cell proliferation. Molecular Cancer, 2008, 7, 52.	7.9	5
99	Motif-Raptor: a cell type-specific and transcription factor centric approach for post-GWAS prioritization of causal regulators. Bioinformatics, 2021, 37, 2103-2111.	1.8	5
100	GRAFIMO: Variant and haplotype aware motif scanning on pangenome graphs. PLoS Computational Biology, 2021, 17, e1009444.	1.5	5
101	Proteins comparison through probabilistic optimal structure local alignment. Frontiers in Genetics, 2014, 5, 302.	1.1	4
102	Circulating Noncoding RNAs as Clinical Biomarkers. , 2016, , 239-258.		4
103	cuRnet: an R package for graph traversing on GPU. BMC Bioinformatics, 2018, 19, 356.	1.2	4
104	Fast Subgraph Matching Strategies Based on Pattern-Only Heuristics. Interdisciplinary Sciences, Computational Life Sciences, 2019, 11, 21-32.	2.2	3
105	DrugThatGene: integrative analysis to streamline the identification of druggable genes, pathways and protein complexes from CRISPR screens. Bioinformatics, 2019, 35, 1981-1984.	1.8	3
106	Exonâ€"Intron Differential Analysis Reveals the Role of Competing Endogenous RNAs in Post-Transcriptional Regulation of Translation. Non-coding RNA, 2021, 7, 26.	1.3	3
107	GRAPES-DD: exploiting decision diagrams for index-driven search in biological graph databases. BMC Bioinformatics, 2021, 22, 209.	1.2	3
108	Biometal Dyshomeostasis in Olfactory Mucosa of Alzheimerâ€™s Disease Patients. International Journal of Molecular Sciences, 2022, 23, 4123.	1.8	3

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109	DBStrata. , 2011, , .		2
110	Editorial. Briefings in Bioinformatics, 2011, 12, 547-548.	3.2	2
111	A SystemC Platform for Signal Transduction Modelling and Simulation in Systems Biology. , 2015, , .		2
112	INBIA: a boosting methodology for proteomic network inference. BMC Bioinformatics, 2018, 19, 188.	1.2	2
113	netDx: Software for building interpretable patient classifiers by multi-'omic data integration using patient similarity networks. F1000Research, 2020, 9, 1239.	0.8	2
114	Highly Efficient Therapeutic Gene Editing of BCL11A enhancer in Human Hematopoietic Stem Cells from AŸ-Hemoglobinopathy Patients for Fetal Hemoglobin Induction. Blood, 2018, 132, 3482-3482.	0.6	2
115	Interrogation of Individual CLL Loss-of-Function Lesions By CRISPR In Vivo Editing Reveals Common and Unique Pathway Alterations. Blood, 2019, 134, 684-684.	0.6	2
116	CRISPR-Cas9 Screen Identifies XPO7 As a Potential Therapeutic Target for TP53-Mutated AML. Blood, 2019, 134, 3784-3784.	0.6	2
117	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
118	TEDAR: Temporal dynamic signal detection of adverse reactions. Artificial Intelligence in Medicine, 2021, 122, 102212.	3.8	2
119	Bioinformatics in Italy: BITS2012, the ninth annual meeting of the Italian Society of Bioinformatics. BMC Bioinformatics, 2013, 14, S1.	1.2	1
120	A SystemC-based platform for assertion-based verification and mutation analysis in systems biology. , 2016, , .		1
121	An Efficient Implementation of a Subgraph Isomorphism Algorithm for GPUs.. , 2018, , .		1
122	Parallel Searching on Biological Networks. , 2019, , .		1
123	Fast methods for finding significant motifs on labelled multi-relational networks. Journal of Complex Networks, 2019, 7, 817-837.	1.1	1
124	Efficient Simulation and Parametrization of Stochastic Petri Nets in SystemC: A Case study from Systems Biology. , 2019, , .		1
125	Business Process Model Retrieval Based on Graph Indexing Method. Lecture Notes in Business Information Processing, 2011, , 238-250.	0.8	1
126	MySQL Data Mining: Extending MySQL to Support Data Mining Primitives (Demo). Lecture Notes in Computer Science, 2010, , 438-444.	1.0	1

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127	Genome-Wide CRISPR/Cas9 Screen Reveals That the Dcps Scavenger Decapping Enzyme Is Essential for AML Cell Survival. Blood, 2017, 130, 782-782.	0.6	1
128	Paics, a De Novo Purine Synthetic Enzyme, Is a Novel Target for AML Therapy. Blood, 2019, 134, 1390-1390.	0.6	1
129	Identification of a Novel Epigenetic Mechanism of MYC Deregulation in Smoldering and Newly Diagnosed Multiple Myeloma Patients. Blood, 2021, 138, 504-504.	0.6	1
130	Multiplexed CRISPR *In Vivo* Editing of CLL Loss-of-Function Lesions Models Transformation of Chronic Lymphocytic Leukemia into Richter's Syndrome. Blood, 2020, 136, 2-3.	0.6	1
131	PANPROVA: pangenomic prokaryotic evolution of full assemblies. Bioinformatics, 2022, 38, 2631-2632.	1.8	1
132	TUBE Project: Transport-Derived Ultrafines and the Brain Effects. International Journal of Environmental Research and Public Health, 2022, 19, 311.	1.2	1
133	<title>Approximate search in image database</title>. , 1999, , .		0
134	Distributed randomized algorithms for low-support data mining. , 2009, , .		0
135	Computational Approaches to RNAi and Gene Silencing. , 2013, , 169-194.		0
136	SyQUAL: a platform for qualitative modelling and simulation of biological systems. , 2016, , .		0
137	Editorial: New Trends on Genome and Transcriptome Characterizations. Frontiers in Genetics, 2018, 9, 322.	1.1	0
138	Genetic Alteration of MicroRNA Affecting Cancer Pathways. , 2018, , 269-287.		0
139	LErNet: characterization of lncRNAs via context-aware network expansion and enrichment analysis. , 2019, , .		0
140	Construction and Analysis of miRNA Regulatory Networks. Methods in Molecular Biology, 2019, 1970, 121-167.	0.4	0
141	SystemC Implementation of Stochastic Petri Nets for Simulation and Parameterization of Biological Networks. Transactions on Embedded Computing Systems, 2021, 20, 1-20.	2.1	0
142	Efficient Boundary Values Generation in General Metric Spaces for Software Component Testing. Lecture Notes in Computer Science, 2003, , 318-331.	1.0	0
143	Preface - BITS 2012: Ninth Annual Meeting of the Bioinformatics Italian Society. EMBnet Journal, 2012, 18, 4.	0.2	0
144	Circular RNAs and Exosomes: The New Frontier of Cancer Diagnosis. Forum on Immunopathological Diseases and Therapeutics, 2015, 6, 181-186.	0.1	0

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145	Comprehensive Integrated Genomic Perturbations Reveal Molecular Mechanisms of Red Blood Cell Trait Associations. Blood, 2018, 132, 532-532.	0.6	0
146	Rational Targeting of a NuRD Sub-Complex for Fetal Hemoglobin Induction Following Comprehensive in Situ Mutagenesis. Blood, 2018, 132, 2342-2342.	0.6	0
147	Centrality Speeds the Subgraph Isomorphism Search Up in Target AwareÂContexts. Lecture Notes in Computer Science, 2020, , 19-26.	1.0	0
148	Characterization of Mammary Cells Coâ€expressing Separate Lineage Markers. FASEB Journal, 2020, 34, 1-1.	0.2	0
149	Efficient Techniques for Graph Searching and Biological Network Mining. Advances in Data Mining and Database Management Book Series, 0, , 89-111.	0.4	0
150	ZNF410 Represses Fetal Globin By Devoted Control of CHD4/NuRD. Blood, 2020, 136, 1-1.	0.6	0