

Rosalba Giugno

List of Publications by Citations

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The third column is the impact factor (IF) of the journal, and the fourth column is the number of citations of the article.

138
papers

3,611
citations

30
h-index

58
g-index

162
ext. papers

5,080
ext. citations

8.7
avg, IF

5.45
L-index

#	Paper	IF	Citations
138	Eleven grand challenges in single-cell data science. <i>Genome Biology</i> , 2020 , 21, 31	18.3	274
137	Engineered CRISPR-Cas12a variants with increased activities and improved targeting ranges for gene, epigenetic and base editing. <i>Nature Biotechnology</i> , 2019 , 37, 276-282	44.5	235
136	An APOBEC3A-Cas9 base editor with minimized bystander and off-target activities. <i>Nature Biotechnology</i> , 2018 , 36, 977-982	44.5	224
135	In vivo CRISPR editing with no detectable genome-wide off-target mutations. <i>Nature</i> , 2018 , 561, 416-419	50.4	202
134	Highly efficient therapeutic gene editing of human hematopoietic stem cells. <i>Nature Medicine</i> , 2019 , 25, 776-783	50.5	197
133	Algorithmics and applications of tree and graph searching 2002 ,		180
132	miRandola: extracellular circulating microRNAs database. <i>PLoS ONE</i> , 2012 , 7, e47786	3.7	129
131	Drug-target interaction prediction through domain-tuned network-based inference. <i>Bioinformatics</i> , 2013 , 29, 2004-8	7.2	124
130	Assessment of computational methods for the analysis of single-cell ATAC-seq data. <i>Genome Biology</i> , 2019 , 20, 241	18.3	97
129	Therapeutic base editing of human hematopoietic stem cells. <i>Nature Medicine</i> , 2020 , 26, 535-541	50.5	84
128	Dissecting hematopoietic and renal cell heterogeneity in adult zebrafish at single-cell resolution using RNA sequencing. <i>Journal of Experimental Medicine</i> , 2017 , 214, 2875-2887	16.6	82
127	Immunosuppression by monocytic myeloid-derived suppressor cells in patients with pancreatic ductal carcinoma is orchestrated by STAT3 2019 , 7, 255		81
126	The neurology of coeliac disease in childhood: what is the evidence? A systematic review and meta-analysis. <i>Developmental Medicine and Child Neurology</i> , 2010 , 52, 700-7	3.3	80
125	A subgraph isomorphism algorithm and its application to biochemical data. <i>BMC Bioinformatics</i> , 2013 , 14 Suppl 7, S13	3.6	77
124	Variant-aware saturating mutagenesis using multiple Cas9 nucleases identifies regulatory elements at trait-associated loci. <i>Nature Genetics</i> , 2017 , 49, 625-634	36.3	73
123	PSEN1 ^{B9} , APP ^{swe} , and APOE4 Confer Disparate Phenotypes in Human iPSC-Derived Microglia. <i>Stem Cell Reports</i> , 2019 , 13, 669-683	8	64
122	Enhancing density-based clustering: Parameter reduction and outlier detection. <i>Information Systems</i> , 2013 , 38, 317-330	2.7	63

121	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. <i>Lecture Notes in Computer Science</i> , 2002 , 86-97	0.9	55
120	SIGMA: a set-cover-based inexact graph matching algorithm. <i>Journal of Bioinformatics and Computational Biology</i> , 2010 , 8, 199-218	1	49
119	Telemedicine and Virtual Reality for Cognitive Rehabilitation: A Roadmap for the COVID-19 Pandemic. <i>Frontiers in Neurology</i> , 2020 , 11, 926	4.1	49
118	Tools and collaborative environments for bioinformatics research. <i>Briefings in Bioinformatics</i> , 2011 , 12, 549-61	13.4	46
117	miRandola 2017: a curated knowledge base of non-invasive biomarkers. <i>Nucleic Acids Research</i> , 2018 , 46, D354-D359	20.1	44
116	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. <i>PLoS ONE</i> , 2010 , 5, e11166	3.7	43
115	Integrated design, execution, and analysis of arrayed and pooled CRISPR genome-editing experiments. <i>Nature Protocols</i> , 2018 , 13, 946-986	18.8	42
114	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, 446	8.4	39
113	ncPred: ncRNA-Disease Association Prediction through Tripartite Network-Based Inference. <i>Frontiers in Bioengineering and Biotechnology</i> , 2014 , 2, 71	5.8	39
112	SING: subgraph search in non-homogeneous graphs. <i>BMC Bioinformatics</i> , 2010 , 11, 96	3.6	34
111	Extracellular circulating viral microRNAs: current knowledge and perspectives. <i>Frontiers in Genetics</i> , 2013 , 4, 120	4.5	32
110	PrimeDesign software for rapid and simplified design of prime editing guide RNAs. <i>Nature Communications</i> , 2021 , 12, 1034	17.4	32
109	A novel computational method for inferring competing endogenous interactions. <i>Briefings in Bioinformatics</i> , 2017 , 18, 1071-1081	13.4	31
108	DT-Web: a web-based application for drug-target interaction and drug combination prediction through domain-tuned network-based inference. <i>BMC Systems Biology</i> , 2015 , 9 Suppl 3, S4	3.5	30
107	CRISPR prime editing with ribonucleoprotein complexes in zebrafish and primary human cells. <i>Nature Biotechnology</i> , 2021 ,	44.5	30
106	miR-Synth: a computational resource for the design of multi-site multi-target synthetic miRNAs. <i>Nucleic Acids Research</i> , 2014 , 42, 5416-25	20.1	28
105	Response to "Unexpected mutations after CRISPR-Cas9 editing in vivo". <i>Nature Methods</i> , 2018 , 15, 238-239	23.6	25
104	Recommendation Techniques for Drug-Target Interaction Prediction and Drug Repositioning. <i>Methods in Molecular Biology</i> , 2016 , 1415, 441-62	1.4	24

103	miR-EdiTar: a database of predicted A-to-I edited miRNA target sites. <i>Bioinformatics</i> , 2012 , 28, 3166-8	7.2	23
102	Post-transcriptional knowledge in pathway analysis increases the accuracy of phenotypes classification. <i>Oncotarget</i> , 2016 , 7, 54572-54582	3.3	23
101	On the Variable Ordering in Subgraph Isomorphism Algorithms. <i>IEEE/ACM Transactions on Computational Biology and Bioinformatics</i> , 2017 , 14, 193-203	3	22
100	A knowledge base for the discovery of function, diagnostic potential and drug effects on cellular and extracellular miRNAs. <i>BMC Genomics</i> , 2014 , 15 Suppl 3, S4	4.5	21
99	GASOLINE: a Greedy And Stochastic algorithm for optimal Local multiple alignment of Interaction NETworks. <i>PLoS ONE</i> , 2014 , 9, e98750	3.7	21
98	Comprehensive reconstruction and visualization of non-coding regulatory networks in human. <i>Frontiers in Bioengineering and Biotechnology</i> , 2014 , 2, 69	5.8	20
97	Aging-Associated Alterations in Mammary Epithelia and Stroma Revealed by Single-Cell RNA Sequencing. <i>Cell Reports</i> , 2020 , 33, 108566	10.6	19
96	GRAPES: a software for parallel searching on biological graphs targeting multi-core architectures. <i>PLoS ONE</i> , 2013 , 8, e76911	3.7	18
95	Prediction of human targets for viral-encoded microRNAs by thermodynamics and empirical constraints. <i>Journal of Rnai and Gene Silencing</i> , 2010 , 6, 379-85		18
94	Transcription factor competition at the β globin promoters controls hemoglobin switching. <i>Nature Genetics</i> , 2021 , 53, 511-520	36.3	18
93	CRISPR-SURF: discovering regulatory elements by deconvolution of CRISPR tiling screen data. <i>Nature Methods</i> , 2018 , 15, 992-993	21.6	17
92	Impact of Genetic Variation on CRISPR-Cas Targeting. <i>CRISPR Journal</i> , 2018 , 1, 159-170	2.5	16
91	Three subtypes of lung cancer fibroblasts define distinct therapeutic paradigms. <i>Cancer Cell</i> , 2021 , 39, 1531-1547.e10	24.3	16
90	Computational design of artificial RNA molecules for gene regulation. <i>Methods in Molecular Biology</i> , 2015 , 1269, 393-412	1.4	16
89	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	5	15
88	CRISPRitz: rapid, high-throughput and variant-aware in silico off-target site identification for CRISPR genome editing. <i>Bioinformatics</i> , 2020 , 36, 2001-2008	7.2	15
87	AmpUMI: design and analysis of unique molecular identifiers for deep amplicon sequencing. <i>Bioinformatics</i> , 2018 , 34, i202-i210	7.2	15
86	Enhancing Graph Database Indexing by Suffix Tree Structure. <i>Lecture Notes in Computer Science</i> , 2010 , 195-203	0.9	14

85	A Code of Ethics for Gene Drive Research. <i>CRISPR Journal</i> , 2021 , 4, 19-24	2.5	14
84	A knowledge base for <i>Vitis vinifera</i> functional analysis. <i>BMC Systems Biology</i> , 2015 , 9 Suppl 3, S5	3.5	13
83	NetMatchStar: an enhanced Cytoscape network querying app. <i>F1000Research</i> , 2015 , 4, 479	3.6	13
82	MIDClass: microarray data classification by association rules and gene expression intervals. <i>PLoS ONE</i> , 2013 , 8, e69873	3.7	13
81	18F-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	2.8	12
80	Fast analytical methods for finding significant labeled graph motifs. <i>Data Mining and Knowledge Discovery</i> , 2018 , 32, 504-531	5.6	12
79	Knowledge in the Investigation of A-to-I RNA Editing Signals. <i>Frontiers in Bioengineering and Biotechnology</i> , 2015 , 3, 18	5.8	12
78	GraphFind: enhancing graph searching by low support data mining techniques. <i>BMC Bioinformatics</i> , 2008 , 9 Suppl 4, S10	3.6	12
77	Arena-Idb: a platform to build human non-coding RNA interaction networks. <i>BMC Bioinformatics</i> , 2018 , 19, 350	3.6	12
76	SPECTRA: An Integrated Knowledge Base for Comparing Tissue and Tumor-Specific PPI Networks in Human. <i>Frontiers in Bioengineering and Biotechnology</i> , 2015 , 3, 58	5.8	11
75	ZNF410 represses fetal globin by singular control of CHD4. <i>Nature Genetics</i> , 2021 , 53, 719-728	36.3	11
74	Dissecting ELANE neutropenia pathogenicity by human HSC gene editing. <i>Cell Stem Cell</i> , 2021 , 28, 833-848.e5	11	11
73	Current Knowledge and Computational Techniques for Grapevine Meta-Omics Analysis. <i>Frontiers in Plant Science</i> , 2017 , 8, 2241	6.2	10
72	PanDelos: a dictionary-based method for pan-genome content discovery. <i>BMC Bioinformatics</i> , 2018 , 19, 437	3.6	10
71	VIRGO: visualization of A-to-I RNA editing sites in genomic sequences. <i>BMC Bioinformatics</i> , 2013 , 14 Suppl 7, S5	3.6	9
70	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, 194	10.1	8
69	Haystack: systematic analysis of the variation of epigenetic states and cell-type specific regulatory elements. <i>Bioinformatics</i> , 2018 , 34, 1930-1933	7.2	8
68	GASOLINE: a Cytoscape app for multiple local alignment of PPI networks. <i>F1000Research</i> , 2014 , 3, 140	3.6	8

67	NetMatchStar: an enhanced Cytoscape network querying app. <i>F1000Research</i> , 2015 , 4, 479	3.6	8
66	APPAGATO: an APproximate PARallel and stochastic GrAph querying TOol for biological networks. <i>Bioinformatics</i> , 2016 , 32, 2159-66	7.2	8
65	Technologies and Computational Analysis Strategies for CRISPR Applications. <i>Molecular Cell</i> , 2020 , 79, 11-29	17.6	7
64	GASOLINE: a Cytoscape app for multiple local alignment of PPI networks. <i>F1000Research</i> , 2014 , 3, 140	3.6	7
63	Ex Machina: Analytical platforms, Law and the Challenges of Computational Legal Science. <i>Future Internet</i> , 2018 , 10, 37	3.3	6
62	Elucidating the role of microRNAs in cancer through data mining techniques. <i>Advances in Experimental Medicine and Biology</i> , 2013 , 774, 291-315	3.6	6
61	In vitro and in silico cloning of <i>Xenopus laevis</i> SOD2 cDNA and its phylogenetic analysis. <i>DNA and Cell Biology</i> , 2005 , 24, 111-6	3.6	6
60	BitCube: A Bottom-Up Cubing Engineering. <i>Lecture Notes in Computer Science</i> , 2009 , 189-203	0.9	6
59	Long Non-Coding RNAs as Molecular Signatures for Canine B-Cell Lymphoma Characterization. <i>Non-coding RNA</i> , 2019 , 5,	7.1	5
58	An Efficient Duplicate Record Detection Using q-Grams Array Inverted Index. <i>Lecture Notes in Computer Science</i> , 2010 , 309-323	0.9	5
57	Parallel Single-Cell RNA-Seq and Genetic Recording Reveals Lineage Decisions in Developing Embryoid Bodies. <i>Cell Reports</i> , 2020 , 33, 108222	10.6	5
56	Involvement of GTA protein NC2beta in neuroblastoma pathogenesis suggests that it physiologically participates in the regulation of cell proliferation. <i>Molecular Cancer</i> , 2008 , 7, 52	42.1	4
55	Sequence similarity is more relevant than species specificity in probabilistic backtranslation. <i>BMC Bioinformatics</i> , 2007 , 8, 58	3.6	4
54	Genomics, evolution, and expression of TBPL2, a member of the TBP family. <i>DNA and Cell Biology</i> , 2007 , 26, 369-85	3.6	4
53	Epigenetic Alterations in Keratinocyte Carcinoma. <i>Journal of Investigative Dermatology</i> , 2021 , 141, 1207-1218	4.3	4
52	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	2.5	3
51	Proteins comparison through probabilistic optimal structure local alignment. <i>Frontiers in Genetics</i> , 2014 , 5, 302	4.5	3
50	Interrupting the nitrosative stress fuels tumor-specific cytotoxic T lymphocytes in pancreatic cancer. 2022 , 10,		3

49	Circulating Noncoding RNAs as Clinical Biomarkers 2016 , 239-258		3
48	DrugThatGene: integrative analysis to streamline the identification of druggable genes, pathways and protein complexes from CRISPR screens. <i>Bioinformatics</i> , 2019 , 35, 1981-1984	7.2	3
47	Targeting leukemia-specific dependence on the de novo purine synthesis pathway. <i>Leukemia</i> , 2021 ,	10.7	3
46	Fast Subgraph Matching Strategies Based on Pattern-Only Heuristics. <i>Interdisciplinary Sciences, Computational Life Sciences</i> , 2019 , 11, 21-32	3.5	2
45	Multiple-Winners Randomized Tournaments with Consensus for Optimization Problems in Generic Metric Spaces. <i>Lecture Notes in Computer Science</i> , 2005 , 265-276	0.9	2
44	Interrogation of Individual CLL Loss-of-Function Lesions By CRISPR In Vivo Editing Reveals Common and Unique Pathway Alterations. <i>Blood</i> , 2019 , 134, 684-684	2.2	2
43	Gene Editing ELANE in Human Hematopoietic Stem and Progenitor Cells Reveals Disease Mechanisms and Therapeutic Strategies for Severe Congenital Neutropenia. <i>Blood</i> , 2019 , 134, 3-3	2.2	2
42	Dynamic Modeling and Simulation of Leukocyte Integrin Activation through an Electronic Design Automation Framework. <i>Lecture Notes in Computer Science</i> , 2014 , 143-154	0.9	2
41	Current progress and potential opportunities to infer single-cell developmental trajectory and cell fate. <i>Current Opinion in Systems Biology</i> , 2021 , 26, 1-11	3.2	2
40	Challenges in gene-oriented approaches for pangenome content discovery. <i>Briefings in Bioinformatics</i> , 2021 , 22,	13.4	2
39	cuRnet: an R package for graph traversing on GPU. <i>BMC Bioinformatics</i> , 2018 , 19, 356	3.6	2
38	INBIA: a boosting methodology for proteomic network inference. <i>BMC Bioinformatics</i> , 2018 , 19, 188	3.6	2
37	Fast methods for finding significant motifs on labelled multi-relational networks. <i>Journal of Complex Networks</i> , 2019 , 7, 817-837	1.7	1
36	Parallel Searching on Biological Networks 2019 ,		1
35	Bioinformatics in Italy: BITS 2012, the ninth annual meeting of the Italian Society of Bioinformatics. <i>BMC Bioinformatics</i> , 2013 , 14 Suppl 7, S1	3.6	1
34	Involvement of GTA protein NC2beta in Neuroblastoma pathogenesis suggests that it physiologically participates in the regulation of cell proliferation. <i>Molecular Cancer</i> , 2008 , 7, 59	42.1	1
33	Multiplexed CRISPR In Vivo Editing of CLL Loss-of-Function Lesions Models Transformation of Chronic Lymphocytic Leukemia into Richter's Syndrome. <i>Blood</i> , 2020 , 136, 2-3	2.2	1
32	Highly Efficient Therapeutic Gene Editing of BCL11A enhancer in Human Hematopoietic Stem Cells from β -Hemoglobinopathy Patients for Fetal Hemoglobin Induction. <i>Blood</i> , 2018 , 132, 3482-3482	2.2	1

31	CRISPR-Cas9 Screen Identifies XPO7 As a Potential Therapeutic Target for TP53-Mutated AML. <i>Blood</i> , 2019 , 134, 3784-3784	2.2	1
30	Simple Pattern-only Heuristics Lead to Fast Subgraph Matching Strategies on Very Large Networks. <i>Advances in Intelligent Systems and Computing</i> , 2019 , 131-138	0.4	1
29	singlecellVR: Interactive Visualization of Single-Cell Data in Virtual Reality. <i>Frontiers in Genetics</i> , 2021 , 12, 764170	4.5	1
28	Peripheral inflammation preceding ischemia impairs neuronal survival through mechanisms involving miR-127 in aged animals. <i>Aging Cell</i> , 2021 , 20, e13287	9.9	1
27	Business Process Model Retrieval Based on Graph Indexing Method. <i>Lecture Notes in Business Information Processing</i> , 2011 , 238-250	0.6	1
26	Efficient Simulation and Parametrization of Stochastic Petri Nets in SystemC: A Case study from Systems Biology 2019 ,		1
25	netDx: Software for building interpretable patient classifiers by multi-omic data integration using patient similarity networks. <i>F1000Research</i> , 2020 , 9, 1239	3.6	1
24	GRAFIMO: variant and haplotype aware motif scanning on pangenome graphs		1
23	An Efficient Implementation of a Subgraph Isomorphism Algorithm for GPUs. 2018 ,		1
22	Augmenting and directing long-range CRISPR-mediated activation in human cells. <i>Nature Methods</i> , 2021 , 18, 1075-1081	21.6	1
21	GRAFIMO: Variant and haplotype aware motif scanning on pangenome graphs. <i>PLoS Computational Biology</i> , 2021 , 17, e1009444	5	1
20	Hedgehog interacting protein-expressing lung fibroblasts suppress lymphocytic inflammation in mice. <i>JCI Insight</i> , 2021 , 6,	9.9	1
19	TUBE Project: Transport-Derived Ultrafines and the Brain Effects.. <i>International Journal of Environmental Research and Public Health</i> , 2021 , 19,	4.6	1
18	Construction and Analysis of miRNA Regulatory Networks. <i>Methods in Molecular Biology</i> , 2019 , 1970, 121-167	1.4	
17	Computational Approaches to RNAi and Gene Silencing 2013 , 169-194		
16	Microarray Data Analysis: From Preparation To Classification 2013 , 657-674		
15	ZNF410 Represses Fetal Globin By Devoted Control of CHD4/NuRD. <i>Blood</i> , 2020 , 136, 1-1	2.2	
14	Characterization of Mammary Cells Co-expressing Separate Lineage Markers. <i>FASEB Journal</i> , 2020 , 34, 1-1	0.9	

- 13 Efficient Techniques for Graph Searching and Biological Network Mining. *Advances in Data Mining and Database Management Book Series*, 89-111 0.6
- 12 Identification of a Novel Epigenetic Mechanism of MYC Deregulation in Smoldering and Newly Diagnosed Multiple Myeloma Patients. *Blood*, **2021**, 138, 504-504 2.2
- 11 TEDAR: Temporal dynamic signal detection of adverse reactions. *Artificial Intelligence in Medicine*, **2021**, 122, 102212 7.4
- 10 Efficient Boundary Values Generation in General Metric Spaces for Software Component Testing. *Lecture Notes in Computer Science*, **2003**, 318-331 0.9
- 9 Genome-Wide CRISPR/Cas9 Screen Reveals That the Dcps Scavenger Decapping Enzyme Is Essential for AML Cell Survival. *Blood*, **2017**, 130, 782-782 2.2
- 8 Comprehensive Integrated Genomic Perturbations Reveal Molecular Mechanisms of Red Blood Cell Trait Associations. *Blood*, **2018**, 132, 532-532 2.2
- 7 Rational Targeting of a NuRD Sub-Complex for Fetal Hemoglobin Induction Following Comprehensive in Situ Mutagenesis. *Blood*, **2018**, 132, 2342-2342 2.2
- 6 Paics, a De Novo Purine Synthetic Enzyme, Is a Novel Target for AML Therapy. *Blood*, **2019**, 134, 1390-1390 2.2
- 5 Centrality Speeds the Subgraph Isomorphism Search Up in Target Aware Contexts. *Lecture Notes in Computer Science*, **2020**, 19-26 0.9
- 4 MySQL Data Mining: Extending MySQL to Support Data Mining Primitives (Demo). *Lecture Notes in Computer Science*, **2010**, 438-444 0.9
- 3 GRAPES-DD: exploiting decision diagrams for index-driven search in biological graph databases. *BMC Bioinformatics*, **2021**, 22, 209 3.6
- 2 SystemC Implementation of Stochastic Petri Nets for Simulation and Parameterization of Biological Networks. *Transactions on Embedded Computing Systems*, **2021**, 20, 1-20 1.8
- 1 Genetic Alteration of MicroRNA Affecting Cancer Pathways **2018**, 269-287