Rosalba Giugno

List of Publications by Year in Descending Order

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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	3,611	30	58
papers	citations	h-index	g-index
162	5,080	8.7	5.45
ext. papers	ext. citations	avg, IF	L-index

#	Paper	IF	Citations
138	Interrupting the nitrosative stress fuels tumor-specific cytotoxic T lymphocytes in pancreatic cancer. **2022**, 10,		3
137	Identification of a Novel Epigenetic Mechanism of MYC Deregulation in Smoldering and Newly Diagnosed Multiple Myeloma Patients. *Blood*, **2021**, 138, 504-504	2.2	
136	TEDAR: Temporal dynamic signal detection of adverse reactions. *Artificial Intelligence in Medicine*, **2021**, 122, 102212	7.4	
135	Three subtypes of lung cancer fibroblasts define distinct therapeutic paradigms. *Cancer Cell*, **2021**, 39, 1531-1547.e10	24.3	16
134	singlecellVR: Interactive Visualization of Single-Cell Data in Virtual Reality. *Frontiers in Genetics*, **2021**, 12, 764170	4.5	1
133	Peripheral inflammation preceeding ischemia impairs neuronal survival through mechanisms involving miR-127 in aged animals. *Aging Cell*, **2021**, 20, e13287	9.9	1
132	Transcription factor competition at the □globin promoters controls hemoglobin switching. *Nature Genetics*, **2021**, 53, 511-520	36.3	18
131	CRISPR prime editing with ribonucleoprotein complexes in zebrafish and primary human cells. *Nature Biotechnology*, **2021**,	44.5	30
130	GRAPES-DD: exploiting decision diagrams for index-driven search in biological graph databases. *BMC Bioinformatics*, **2021**, 22, 209	3.6	
129	ZNF410 represses fetal globin by singular control of CHD4. *Nature Genetics*, **2021**, 53, 719-728	36.3	11
128	Dissecting ELANE neutropenia pathogenicity by human HSC gene editing. *Cell Stem Cell*, **2021**, 28, 833-848.e5	18	11
127	Current progress and potential opportunities to infer single-cell developmental trajectory and cell fate. *Current Opinion in Systems Biology*, **2021**, 26, 1-11	3.2	2
126	SystemC Implementation of Stochastic Petri Nets for Simulation and Parameterization of Biological Networks. *Transactions on Embedded Computing Systems*, **2021**, 20, 1-20	1.8	
125	Epigenetic Alterations in Keratinocyte Carcinoma. *Journal of Investigative Dermatology*, **2021**, 141, 1207-1218	4.3	4
124	Challenges in gene-oriented approaches for pangenome content discovery. *Briefings in Bioinformatics*, **2021**, 22,	13.4	2
123	A Code of Ethics for Gene Drive Research. *CRISPR Journal*, **2021**, 4, 19-24	2.5	14
122	PrimeDesign software for rapid and simplified design of prime editing guide RNAs. *Nature Communications*, **2021**, 12, 1034	17.4	32

121	Targeting leukemia-specific dependence on the de novo purine synthesis pathway. *Leukemia*, **2021**,	10.7	3
120	Augmenting and directing long-range CRISPR-mediated activation in human cells. *Nature Methods*, **2021**, 18, 1075-1081	21.6	1
119	GRAFIMO: Variant and haplotype aware motif scanning on pangenome graphs. *PLoS Computational Biology*, **2021**, 17, e1009444	5	1
118	Hedgehog interacting protein-expressing lung fibroblasts suppress lymphocytic inflammation in mice. *JCI Insight*, **2021**, 6,	9.9	1
117	TUBE Project: Transport-Derived Ultrafines and the Brain Effects.. *International Journal of Environmental Research and Public Health*, **2021**, 19,	4.6	1
116	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	10.1	8
115	Therapeutic base editing of human hematopoietic stem cells. *Nature Medicine*, **2020**, 26, 535-541	50.5	84
114	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	2.5	3
113	Technologies and Computational Analysis Strategies for CRISPR Applications. *Molecular Cell*, **2020**, 79, 11-29	17.6	7
112	Eleven grand challenges in single-cell data science. *Genome Biology*, **2020**, 21, 31	18.3	274
111	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	2.2	1
110	ZNF410 Represses Fetal Globin By Devoted Control of CHD4/NuRD. *Blood*, **2020**, 136, 1-1	2.2	
109	Characterization of Mammary Cells Co-expressing Separate Lineage Markers. *FASEB Journal*, **2020**, 34, 1-1	0.9	
108	Centrality Speeds the Subgraph Isomorphism Search Up in Target Aware Contexts. *Lecture Notes in Computer Science*, **2020**, 19-26	0.9	
107	Aging-Associated Alterations in Mammary Epithelia and Stroma Revealed by Single-Cell RNA Sequencing. *Cell Reports*, **2020**, 33, 108566	10.6	19
106	CRISPRitz: rapid, high-throughput and variant-aware in silico off-target site identification for CRISPR genome editing. *Bioinformatics*, **2020**, 36, 2001-2008	7.2	15
105	Parallel Single-Cell RNA-Seq and Genetic Recording Reveals Lineage Decisions in Developing Embryoid Bodies. *Cell Reports*, **2020**, 33, 108222	10.6	5
104	Telemedicine and Virtual Reality for Cognitive Rehabilitation: A Roadmap for the COVID-19 Pandemic. *Frontiers in Neurology*, **2020**, 11, 926	4.1	49

103	netDx: Software for building interpretable patient classifiers by multi-Somic data integration using patient similarity networks. *F1000Research*, **2020**, 9, 1239	3.6	1
102	Immunosuppression by monocytic myeloid-derived suppressor cells in patients with pancreatic ductal carcinoma is orchestrated by STAT3 **2019**, 7, 255		81
101	PSEN1E9, APPswe, and APOE4 Confer Disparate Phenotypes in Human iPSC-Derived Microglia. *Stem Cell Reports*, **2019**, 13, 669-683	8	64
100	Long Non-Coding RNAs as Molecular Signatures for Canine B-Cell Lymphoma Characterization. *Non-coding RNA*, **2019**, 5,	7.1	5
99	18F-Florbetaben PET/CT to Assess AlzheimerSs Disease: A new Analysis Method for Regional Amyloid Quantification. *Journal of Neuroimaging*, **2019**, 29, 383-393	2.8	12
98	Construction and Analysis of miRNA Regulatory Networks. *Methods in Molecular Biology*, **2019**, 1970, 121-167	1.4	
97	Fast Subgraph Matching Strategies Based on Pattern-Only Heuristics. *Interdisciplinary Sciences, Computational Life Sciences*, **2019**, 11, 21-32	3.5	2
96	Highly efficient therapeutic gene editing of human hematopoietic stem cells. *Nature Medicine*, **2019** , 25, 776-783	50.5	197
95	Extracellular Vesicles Mediate Mesenchymal Stromal Cell-Dependent Regulation of B Cell PI3K-AKT Signaling Pathway and Actin Cytoskeleton. *Frontiers in Immunology*, **2019**, 10, 446	8.4	39
94	Fast methods for finding significant motifs on labelled multi-relational networks. *Journal of Complex Networks*, **2019**, 7, 817-837	1.7	1
93	Engineered CRISPR-Cas12a variants with increased activities and improved targeting ranges for gene, epigenetic and base editing. *Nature Biotechnology*, **2019**, 37, 276-282	44.5	235
92	Parallel Searching on Biological Networks **2019**,		1
91	Interrogation of Individual CLL Loss-of-Function Lesions By CRISPR In Vivo Editing Reveals Common and Unique Pathway Alterations. *Blood*, **2019**, 134, 684-684	2.2	2
90	CRISPR-Cas9 Screen Identifies XPO7 As a Potential Therapeutic Target for TP53-Mutated AML. *Blood*, **2019**, 134, 3784-3784	2.2	1
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	2.2	2
88	Simple Pattern-only Heuristics Lead to Fast Subgraph Matching Strategies on Very Large Networks. *Advances in Intelligent Systems and Computing*, **2019**, 131-138	0.4	1
87	Paics, a De Novo Purine Synthetic Enzyme, Is a Novel Target for AML Therapy. *Blood*, **2019**, 134, 1390-1390	2.2	
86	Assessment of computational methods for the analysis of single-cell ATAC-seq data. *Genome Biology*, **2019**, 20, 241	18.3	97

(2018-2019)

85	Efficient Simulation and Parametrization of Stochastic Petri Nets in SystemC: A Case study from Systems Biology **2019**,		1
84	DrugThatGene: integrative analysis to streamline the identification of druggable genes, pathways and protein complexes from CRISPR screens. *Bioinformatics*, **2019**, 35, 1981-1984	7.2	3
83	Impact of Genetic Variation on CRISPR-Cas Targeting. *CRISPR Journal*, **2018**, 1, 159-170	2.5	16
82	Integrated design, execution, and analysis of arrayed and pooled CRISPR genome-editing experiments. *Nature Protocols*, **2018**, 13, 946-986	18.8	42
81	Haystack: systematic analysis of the variation of epigenetic states and cell-type specific regulatory elements. *Bioinformatics*, **2018**, 34, 1930-1933	7.2	8
80	Response to "Unexpected mutations after CRISPR-Cas9 editing in vivo". *Nature Methods*, **2018**, 15, 238-239	21.6	25
79	miRandola 2017: a curated knowledge base of non-invasive biomarkers. *Nucleic Acids Research*, **2018**, 46, D354-D359	20.1	44
78	Fast analytical methods for finding significant labeled graph motifs. *Data Mining and Knowledge Discovery*, **2018**, 32, 504-531	5.6	12
77	An APOBEC3A-Cas9 base editor with minimized bystander and off-target activities. *Nature Biotechnology*, **2018**, 36, 977-982	44.5	224
76	Ex Machina: Analytical platforms, Law and the Challenges of Computational Legal Science. *Future Internet*, **2018**, 10, 37	3.3	6
75	Highly Efficient Therapeutic Gene Editing of BCL11A enhancer in Human Hematopoietic Stem Cells from Hemoglobinopathy Patients for Fetal Hemoglobin Induction. *Blood*, **2018**, 132, 3482-3482	2.2	1
74	Comprehensive Integrated Genomic Perturbations Reveal Molecular Mechanisms of Red Blood Cell Trait Associations. *Blood*, **2018**, 132, 532-532	2.2	
73	Rational Targeting of a NuRD Sub-Complex for Fetal Hemoglobin Induction Following Comprehensive in Situ Mutagenesis. *Blood*, **2018**, 132, 2342-2342	2.2	
72	An Efficient Implementation of a Subgraph Isomorphism Algorithm for GPUs. **2018**,		1
71	Arena-Idb: a platform to build human non-coding RNA interaction networks. *BMC Bioinformatics*, **2018**, 19, 350	3.6	12
70	cuRnet: an R package for graph traversing on GPU. *BMC Bioinformatics*, **2018**, 19, 356	3.6	2
69	CRISPR-SURF: discovering regulatory elements by deconvolution of CRISPR tiling screen data. *Nature Methods*, **2018**, 15, 992-993	21.6	17
68	PanDelos: a dictionary-based method for pan-genome content discovery. *BMC Bioinformatics*, **2018**, 19, 437	3.6	10

67	In vivo CRISPR editing with no detectable genome-wide off-target mutations. *Nature*, **2018**, 561, 416-419	30.4	202
66	INBIA: a boosting methodology for proteomic network inference. *BMC Bioinformatics*, **2018**, 19, 188	3.6	2
65	Genetic Alteration of MicroRNA Affecting Cancer Pathways **2018**, 269-287		
64	AmpUMI: design and analysis of unique molecular identifiers for deep amplicon sequencing. *Bioinformatics*, **2018**, 34, i202-i210	7.2	15
63	On the Variable Ordering in Subgraph Isomorphism Algorithms. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, **2017**, 14, 193-203	3	22
62	Variant-aware saturating mutagenesis using multiple Cas9 nucleases identifies regulatory elements at trait-associated loci. *Nature Genetics*, **2017**, 49, 625-634	36.3	73
61	Current Knowledge and Computational Techniques for Grapevine Meta-Omics Analysis. *Frontiers in Plant Science*, **2017**, 8, 2241	6.2	10
60	Dissecting hematopoietic and renal cell heterogeneity in adult zebrafish at single-cell resolution using RNA sequencing. *Journal of Experimental Medicine*, **2017**, 214, 2875-2887	16.6	82
59	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	
58	A novel computational method for inferring competing endogenous interactions. *Briefings in Bioinformatics*, **2017**, 18, 1071-1081	13.4	31
57	Post-transcriptional knowledge in pathway analysis increases the accuracy of phenotypes classification. *Oncotarget*, **2016**, 7, 54572-54582	3.3	23
56	Circulating Noncoding RNAs as Clinical Biomarkers **2016**, 239-258		3
55	Recommendation Techniques for Drug-Target Interaction Prediction and Drug Repositioning. *Methods in Molecular Biology*, **2016**, 1415, 441-62	1.4	24
54	APPAGATO: an APproximate PArallel and stochastic GrAph querying TOol for biological networks. *Bioinformatics*, **2016**, 32, 2159-66	7.2	8
53	A knowledge base for Vitis vinifera functional analysis. *BMC Systems Biology*, **2015**, 9 Suppl 3, S5	3.5	13
52	OCDB: a database collecting genes, miRNAs and drugs for obsessive-compulsive disorder. *Database: the Journal of Biological Databases and Curation*, **2015**, 2015, bav069	5	15
51	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 Suppl 3, S4	3.5	30
50	Knowledge in the Investigation of A-to-I RNA Editing Signals. *Frontiers in Bioengineering and Biotechnology*, **2015**, 3, 18	5.8	12

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49	SPECTRA: An Integrated Knowledge Base for Comparing Tissue and Tumor-Specific PPI Networks in Human. *Frontiers in Bioengineering and Biotechnology*, **2015**, 3, 58	5.8	11
48	NetMatchStar: an enhanced Cytoscape network querying app. *F1000Research*, **2015**, 4, 479	3.6	13
47	NetMatchStar: an enhanced Cytoscape network querying app. *F1000Research*, **2015**, 4, 479	3.6	8
46	Computational design of artificial RNA molecules for gene regulation. *Methods in Molecular Biology*, **2015**, 1269, 393-412	1.4	16
45	A knowledge base for the discovery of function, diagnostic potential and drug effects on cellular and extracellular miRNAs. *BMC Genomics*, **2014**, 15 Suppl 3, S4	4.5	21
44	Comprehensive reconstruction and visualization of non-coding regulatory networks in human. *Frontiers in Bioengineering and Biotechnology*, **2014**, 2, 69	5.8	20
43	ncPred: ncRNA-Disease Association Prediction through Tripartite Network-Based Inference. *Frontiers in Bioengineering and Biotechnology*, **2014**, 2, 71	5.8	39
42	Proteins comparison through probabilistic optimal structure local alignment. *Frontiers in Genetics*, **2014**, 5, 302	4.5	3
41	miR-Synth: a computational resource for the design of multi-site multi-target synthetic miRNAs. *Nucleic Acids Research*, **2014**, 42, 5416-25	20.1	28
40	GASOLINE: a Cytoscape app for multiple local alignment of PPI networks. *F1000Research*, **2014**, 3, 140	3.6	7
39	GASOLINE: a Cytoscape app for multiple local alignment of PPI networks. *F1000Research*, **2014**, 3, 140	3.6	8
38	GASOLINE: a Greedy And Stochastic algorithm for optimal Local multiple alignment of Interaction NEtworks. *PLoS ONE*, **2014**, 9, e98750	3.7	21
37	Dynamic Modeling and Simulation of Leukocyte Integrin Activation through an Electronic Design Automation Framework. *Lecture Notes in Computer Science*, **2014**, 143-154	0.9	2
36	Bioinformatics in Italy: BITS 2012, the ninth annual meeting of the Italian Society of Bioinformatics. *BMC Bioinformatics*, **2013**, 14 Suppl 7, S1	3.6	1
35	VIRGO: visualization of A-to-I RNA editing sites in genomic sequences. *BMC Bioinformatics*, **2013**, 14 Suppl 7, S5	3.6	9
34	A subgraph isomorphism algorithm and its application to biochemical data. *BMC Bioinformatics*, **2013**, 14 Suppl 7, S13	3.6	77
33	Enhancing density-based clustering: Parameter reduction and outlier detection. *Information Systems*, **2013**, 38, 317-330	2.7	63
32	Computational Approaches to RNAi and Gene Silencing **2013**, 169-194		

31	Elucidating the role of microRNAs in cancer through data mining techniques. *Advances in Experimental Medicine and Biology*, **2013**, 774, 291-315	3.6	6
30	Drug-target interaction prediction through domain-tuned network-based inference. *Bioinformatics*, **2013**, 29, 2004-8	7.2	124
29	Microarray Data Analysis: From Preparation To Classification **2013**, 657-674		
28	GRAPES: a software for parallel searching on biological graphs targeting multi-core architectures. *PLoS ONE*, **2013**, 8, e76911	3.7	18
27	Extracellular circulating viral microRNAs: current knowledge and perspectives. *Frontiers in Genetics*, **2013**, 4, 120	4.5	32
26	MIDClass: microarray data classification by association rules and gene expression intervals. *PLoS ONE*, **2013**, 8, e69873	3.7	13
25	miR-EdiTar: a database of predicted A-to-I edited miRNA target sites. *Bioinformatics*, **2012**, 28, 3166-8	7.2	23
24	miRandola: extracellular circulating microRNAs database. *PLoS ONE*, **2012**, 7, e47786	3.7	129
23	Tools and collaborative environments for bioinformatics research. *Briefings in Bioinformatics*, **2011**, 12, 549-61	13.4	46
22	Business Process Model Retrieval Based on Graph Indexing Method. *Lecture Notes in Business Information Processing*, **2011**, 238-250	0.6	1
21	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	3.7	43
20	SIGMA: a set-cover-based inexact graph matching algorithm. *Journal of Bioinformatics and Computational Biology*, **2010**, 8, 199-218	1	49
19	SING: subgraph search in non-homogeneous graphs. *BMC Bioinformatics*, **2010**, 11, 96	3.6	34
18	The neurology of coeliac disease in childhood: what is the evidence? A systematic review and meta-analysis. *Developmental Medicine and Child Neurology*, **2010**, 52, 700-7	3.3	80
17	Prediction of human targets for viral-encoded microRNAs by thermodynamics and empirical constraints. *Journal of Rnai and Gene Silencing*, **2010**, 6, 379-85		18
16	An Efficient Duplicate Record Detection Using q-Grams Array Inverted Index. *Lecture Notes in Computer Science*, **2010**, 309-323	0.9	5
15	Enhancing Graph Database Indexing by Suffix Tree Structure. *Lecture Notes in Computer Science*, **2010**, 195-203	0.9	14
14	MySQL Data Mining: Extending MySQL to Support Data Mining Primitives (Demo). *Lecture Notes in Computer Science*, **2010**, 438-444	0.9	

13	BitCube: A Bottom-Up Cubing Engineering. *Lecture Notes in Computer Science*, **2009**, 189-203	0.9	6
12	GraphFind: enhancing graph searching by low support data mining techniques. *BMC Bioinformatics*, **2008**, 9 Suppl 4, S10	3.6	12
11	Involvement of GTA protein NC2beta in neuroblastoma pathogenesis suggests that it physiologically participates in the regulation of cell proliferation. *Molecular Cancer*, **2008**, 7, 52	42.1	4
10	Involvement of GTA protein NC2beta in Neuroblastoma pathogenesis suggests that it physiologically participates in the regulation of cell proliferation. *Molecular Cancer*, **2008**, 7, 59	42.1	1
9	Sequence similarity is more relevant than species specificity in probabilistic backtranslation. *BMC Bioinformatics*, **2007**, 8, 58	3.6	4
8	Genomics, evolution, and expression of TBPL2, a member of the TBP family. *DNA and Cell Biology*, **2007**, 26, 369-85	3.6	4
7	In vitro and in silico cloning of Xenopus laevis SOD2 cDNA and its phylogenetic analysis. *DNA and Cell Biology*, **2005**, 24, 111-6	3.6	6
6	Multiple-Winners Randomized Tournaments with Consensus for Optimization Problems in Generic Metric Spaces. *Lecture Notes in Computer Science*, **2005**, 265-276	0.9	2
5	Efficient Boundary Values Generation in General Metric Spaces for Software Component Testing. *Lecture Notes in Computer Science*, **2003**, 318-331	0.9	
4	Algorithmics and applications of tree and graph searching **2002**,		180
3	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	0.9	55
2	Efficient Techniques for Graph Searching and Biological Network Mining. *Advances in Data Mining and Database Management Book Series*,89-111	0.6	
1	GRAFIMO: variant and haplotype aware motif scanning on pangenome graphs		1