

Rosalba Giugno

List of Publications by Year in descending order

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Version: 2024-02-01

150
papers

6,355
citations

126858

33
h-index

88593

70
g-index

162
all docs

162
docs citations

162
times ranked

9317
citing authors

#	ARTICLE	IF	CITATIONS
1	CRISPR prime editing with ribonucleoprotein complexes in zebrafish and primary human cells. <i>Nature Biotechnology</i> , 2022, 40, 189-193.	9.4	118
2	Targeting leukemia-specific dependence on the de novo purine synthesis pathway. <i>Leukemia</i> , 2022, 36, 383-393.	3.3	11
3	Interrupting the nitrosative stress fuels tumor-specific cytotoxic T lymphocytes in pancreatic cancer. <i>Cell</i> , 2022, 10, e003549.		22
4	Single-Cell RNA-Seq Analysis of Olfactory Mucosal Cells of Alzheimer's Disease Patients. <i>Cells</i> , 2022, 11, 676.	1.8	20
5	PANPROVA: pangenomic prokaryotic evolution of full assemblies. <i>Bioinformatics</i> , 2022, 38, 2631-2632.	1.8	1
6	Biometal Dyshomeostasis in Olfactory Mucosa of Alzheimer's Disease Patients. <i>International Journal of Molecular Sciences</i> , 2022, 23, 4123.	1.8	3
7	TUBE Project: Transport-Derived Ultrafines and the Brain Effects. <i>International Journal of Environmental Research and Public Health</i> , 2022, 19, 311.	1.2	1
8	Epigenetic Alterations in Keratinocyte Carcinoma. <i>Journal of Investigative Dermatology</i> , 2021, 141, 1207-1218.	0.3	9
9	Challenges in gene-oriented approaches for pangenome content discovery. <i>Briefings in Bioinformatics</i> , 2021, 22, .	3.2	8
10	A Code of Ethics for Gene Drive Research. <i>CRISPR Journal</i> , 2021, 4, 19-24.	1.4	24
11	PrimeDesign software for rapid and simplified design of prime editing guide RNAs. <i>Nature Communications</i> , 2021, 12, 1034.	5.8	105
12	Motif-Raptor: a cell type-specific and transcription factor centric approach for post-GWAS prioritization of causal regulators. <i>Bioinformatics</i> , 2021, 37, 2103-2111.	1.8	5
13	Transcription factor competition at the γ -globin promoters controls hemoglobin switching. <i>Nature Genetics</i> , 2021, 53, 511-520.	9.4	43
14	Exon-Intron Differential Analysis Reveals the Role of Competing Endogenous RNAs in Post-Transcriptional Regulation of Translation. <i>Non-coding RNA</i> , 2021, 7, 26.	1.3	3
15	GRAPES-DD: exploiting decision diagrams for index-driven search in biological graph databases. <i>BMC Bioinformatics</i> , 2021, 22, 209.	1.2	3
16	ZNF410 represses fetal globin by singular control of CHD4. <i>Nature Genetics</i> , 2021, 53, 719-728.	9.4	35
17	Dissecting ELANE neutropenia pathogenicity by human HSC gene editing. <i>Cell Stem Cell</i> , 2021, 28, 833-845.e5.	5.2	23
18	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.	1.3	8

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19	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
20	Augmenting and directing long-range CRISPR-mediated activation in human cells. Nature Methods, 2021, 18, 1075-1081.	9.0	17
21	GRAFIMO: Variant and haplotype aware motif scanning on pangenome graphs. PLoS Computational Biology, 2021, 17, e1009444.	1.5	5
22	Hedgehog interacting protein-expressing lung fibroblasts suppress lymphocytic inflammation in mice. JCI Insight, 2021, 6, .	2.3	9
23	Three subtypes of lung cancer fibroblasts define distinct therapeutic paradigms. Cancer Cell, 2021, 39, 1531-1547.e10.	7.7	106
24	singlecellVR: Interactive Visualization of Single-Cell Data in Virtual Reality. Frontiers in Genetics, 2021, 12, 764170.	1.1	14
25	Peripheral inflammation preceding ischemia impairs neuronal survival through mechanisms involving miR-127 in aged animals. Aging Cell, 2021, 20, e13287.	3.0	7
26	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
27	TEDAR: Temporal dynamic signal detection of adverse reactions. Artificial Intelligence in Medicine, 2021, 122, 102212.	3.8	2
28	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
29	Parallel Single-Cell RNA-Seq and Genetic Recording Reveals Lineage Decisions in Developing Embryoid Bodies. Cell Reports, 2020, 33, 108222.	2.9	16
30	Telemedicine and Virtual Reality for Cognitive Rehabilitation: A Roadmap for the COVID-19 Pandemic. Frontiers in Neurology, 2020, 11, 926.	1.1	102
31	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
32	Therapeutic base editing of human hematopoietic stem cells. Nature Medicine, 2020, 26, 535-541.	15.2	196
33	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
34	Technologies and Computational Analysis Strategies for CRISPR Applications. Molecular Cell, 2020, 79, 11-29.	4.5	28
35	Eleven grand challenges in single-cell data science. Genome Biology, 2020, 21, 31.	3.8	742
36	netDx: Software for building interpretable patient classifiers by multi-'omic data integration using patient similarity networks. F1000Research, 2020, 9, 1239.	0.8	2

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37	Ageing-Associated Alterations in Mammary Epithelia and Stroma Revealed by Single-Cell RNA Sequencing. <i>Cell Reports</i> , 2020, 33, 108566.	2.9	75
38	Centrality Speeds the Subgraph Isomorphism Search Up in Target Aware Contexts. <i>Lecture Notes in Computer Science</i> , 2020, , 19-26.	1.0	0
39	Characterization of Mammary Cells Co-expressing Separate Lineage Markers. <i>FASEB Journal</i> , 2020, 34, 1-1.	0.2	0
40	Multiplexed CRISPR <i>In Vivo</i> Editing of CLL Loss-of-Function Lesions Models Transformation of Chronic Lymphocytic Leukemia into Richter's Syndrome. <i>Blood</i> , 2020, 136, 2-3.	0.6	1
41	ZNF410 Represses Fetal Globin By Devoted Control of CHD4/NuRD. <i>Blood</i> , 2020, 136, 1-1.	0.6	0
42	LErNet: characterization of lncRNAs via context-aware network expansion and enrichment analysis. , 2019, , .		0
43	Parallel Searching on Biological Networks. , 2019, , .		1
44	Immunosuppression by monocytic myeloid-derived suppressor cells in patients with pancreatic ductal carcinoma is orchestrated by STAT3. , 2019, 7, 255.		123
45	PSEN1 ^{E9} , APP ^{swe} , and APOE4 Confer Disparate Phenotypes in Human iPSC-Derived Microglia. <i>Stem Cell Reports</i> , 2019, 13, 669-683.	2.3	132
46	Long Non-Coding RNAs as Molecular Signatures for Canine B-Cell Lymphoma Characterization. <i>Non-coding RNA</i> , 2019, 5, 47.	1.3	12
47	¹⁸ F-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.	1.0	19
48	Construction and Analysis of miRNA Regulatory Networks. <i>Methods in Molecular Biology</i> , 2019, 1970, 121-167.	0.4	0
49	Fast Subgraph Matching Strategies Based on Pattern-Only Heuristics. <i>Interdisciplinary Sciences, Computational Life Sciences</i> , 2019, 11, 21-32.	2.2	3
50	Highly efficient therapeutic gene editing of human hematopoietic stem cells. <i>Nature Medicine</i> , 2019, 25, 776-783.	15.2	344
51	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.	2.2	73
52	Fast methods for finding significant motifs on labelled multi-relational networks. <i>Journal of Complex Networks</i> , 2019, 7, 817-837.	1.1	1
53	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.	9.4	439
54	Assessment of computational methods for the analysis of single-cell ATAC-seq data. <i>Genome Biology</i> , 2019, 20, 241.	3.8	225

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55	Efficient Simulation and Parametrization of Stochastic Petri Nets in SystemC: A Case study from Systems Biology. , 2019, , .		1
56	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
57	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
58	CRISPR-Cas9 Screen Identifies XPO7 As a Potential Therapeutic Target for TP53-Mutated AML. Blood, 2019, 134, 3784-3784.	0.6	2
59	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
60	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
61	Paics, a De Novo Purine Synthetic Enzyme, Is a Novel Target for AML Therapy. Blood, 2019, 134, 1390-1390.	0.6	1
62	Impact of Genetic Variation on CRISPR-Cas Targeting. CRISPR Journal, 2018, 1, 159-170.	1.4	24
63	Integrated design, execution, and analysis of arrayed and pooled CRISPR genome-editing experiments. Nature Protocols, 2018, 13, 946-986.	5.5	70
64	Haystack: systematic analysis of the variation of epigenetic states and cell-type specific regulatory elements. Bioinformatics, 2018, 34, 1930-1933.	1.8	16
65	Response to "Unexpected mutations after CRISPR-Cas9 editing in vivo" Nature Methods, 2018, 15, 238-239.	9.0	25
66	miRandola 2017: a curated knowledge base of non-invasive biomarkers. Nucleic Acids Research, 2018, 46, D354-D359.	6.5	61
67	Fast analytical methods for finding significant labeled graph motifs. Data Mining and Knowledge Discovery, 2018, 32, 504-531.	2.4	18
68	An Efficient Implementation of a Subgraph Isomorphism Algorithm for GPUs.. , 2018, , .		1
69	Arena-Idb: a platform to build human non-coding RNA interaction networks. BMC Bioinformatics, 2018, 19, 350.	1.2	17
70	cuRnet: an R package for graph traversing on GPU. BMC Bioinformatics, 2018, 19, 356.	1.2	4
71	CRISPR-SURF: discovering regulatory elements by deconvolution of CRISPR tiling screen data. Nature Methods, 2018, 15, 992-993.	9.0	33
72	PanDelos: a dictionary-based method for pan-genome content discovery. BMC Bioinformatics, 2018, 19, 437.	1.2	13

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73	In vivo CRISPR editing with no detectable genome-wide off-target mutations. <i>Nature</i> , 2018, 561, 416-419.	13.7	274
74	Editorial: New Trends on Genome and Transcriptome Characterizations. <i>Frontiers in Genetics</i> , 2018, 9, 322.	1.1	0
75	INBIA: a boosting methodology for proteomic network inference. <i>BMC Bioinformatics</i> , 2018, 19, 188.	1.2	2
76	Genetic Alteration of MicroRNA Affecting Cancer Pathways. , 2018, , 269-287.		0
77	AmpUMI: design and analysis of unique molecular identifiers for deep amplicon sequencing. <i>Bioinformatics</i> , 2018, 34, i202-i210.	1.8	28
78	An APOBEC3A-Cas9 base editor with minimized bystander and off-target activities. <i>Nature Biotechnology</i> , 2018, 36, 977-982.	9.4	328
79	Ex Machina: Analytical platforms, Law and the Challenges of Computational Legal Science. <i>Future Internet</i> , 2018, 10, 37.	2.4	10
80	Highly Efficient Therapeutic Gene Editing of BCL11A enhancer in Human Hematopoietic Stem Cells from $\alpha\gamma$ -Hemoglobinopathy Patients for Fetal Hemoglobin Induction. <i>Blood</i> , 2018, 132, 3482-3482.	0.6	2
81	Comprehensive Integrated Genomic Perturbations Reveal Molecular Mechanisms of Red Blood Cell Trait Associations. <i>Blood</i> , 2018, 132, 532-532.	0.6	0
82	Rational Targeting of a NuRD Sub-Complex for Fetal Hemoglobin Induction Following Comprehensive in Situ Mutagenesis. <i>Blood</i> , 2018, 132, 2342-2342.	0.6	0
83	On the Variable Ordering in Subgraph Isomorphism Algorithms. <i>IEEE/ACM Transactions on Computational Biology and Bioinformatics</i> , 2017, 14, 193-203.	1.9	32
84	Variant-aware saturating mutagenesis using multiple Cas9 nucleases identifies regulatory elements at trait-associated loci. <i>Nature Genetics</i> , 2017, 49, 625-634.	9.4	96
85	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.	4.2	168
86	Current Knowledge and Computational Techniques for Grapevine Meta-Omics Analysis. <i>Frontiers in Plant Science</i> , 2017, 8, 2241.	1.7	24
87	Genome-Wide CRISPR/Cas9 Screen Reveals That the Dcps Scavenger Decapping Enzyme Is Essential for AML Cell Survival. <i>Blood</i> , 2017, 130, 782-782.	0.6	1
88	Circulating Noncoding RNAs as Clinical Biomarkers. , 2016, , 239-258.		4
89	A SystemC-based platform for assertion-based verification and mutation analysis in systems biology. , 2016, , .		1
90	Recommendation Techniques for Drug-Target Interaction Prediction and Drug Repositioning. <i>Methods in Molecular Biology</i> , 2016, 1415, 441-462.	0.4	33

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91	APPAGATO: an APproximate PARallel and stochastic GrAph querying TOol for biological networks. <i>Bioinformatics</i> , 2016, 32, 2159-2166.	1.8	10
92	A novel computational method for inferring competing endogenous interactions. <i>Briefings in Bioinformatics</i> , 2016, 18, bbw084.	3.2	37
93	SyQUAL: a platform for qualitative modelling and simulation of biological systems. , 2016, , .		0
94	Post-transcriptional knowledge in pathway analysis increases the accuracy of phenotypes classification. <i>Oncotarget</i> , 2016, 7, 54572-54582.	0.8	43
95	A knowledge base for <i>Vitis vinifera</i> functional analysis. <i>BMC Systems Biology</i> , 2015, 9, S5.	3.0	24
96	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.	1.4	18
97	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, S4.	3.0	38
98	Knowledge in the Investigation of A-to-I RNA Editing Signals. <i>Frontiers in Bioengineering and Biotechnology</i> , 2015, 3, 18.	2.0	17
99	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.	2.0	13
100	A SystemC Platform for Signal Transduction Modelling and Simulation in Systems Biology. , 2015, , .		2
101	Computational Design of Artificial RNA Molecules for Gene Regulation. <i>Methods in Molecular Biology</i> , 2015, 1269, 393-412.	0.4	28
102	NetMatchStar: an enhanced Cytoscape network querying App. <i>F1000Research</i> , 2015, 4, 479.	0.8	17
103	NetMatchStar: an enhanced Cytoscape network querying App. <i>F1000Research</i> , 2015, 4, 479.	0.8	11
104	Circular RNAs and Exosomes: The New Frontier of Cancer Diagnosis. <i>Forum on Immunopathological Diseases and Therapeutics</i> , 2015, 6, 181-186.	0.1	0
105	Comprehensive Reconstruction and Visualization of Non-Coding Regulatory Networks in Human. <i>Frontiers in Bioengineering and Biotechnology</i> , 2014, 2, 69.	2.0	25
106	ncPred: ncRNA-Disease Association Prediction through Tripartite Network-Based Inference. <i>Frontiers in Bioengineering and Biotechnology</i> , 2014, 2, 71.	2.0	56
107	Proteins comparison through probabilistic optimal structure local alignment. <i>Frontiers in Genetics</i> , 2014, 5, 302.	1.1	4
108	miR-Synth: a computational resource for the design of multi-site multi-target synthetic miRNAs. <i>Nucleic Acids Research</i> , 2014, 42, 5416-5425.	6.5	36

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109	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
110	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
111	GASOLINE: a Cytoscape app for multiple local alignment of PPI networks. F1000Research, 2014, 3, 140.	0.8	7
112	GASOLINE: a Cytoscape app for multiple local alignment of PPI networks. F1000Research, 2014, 3, 140.	0.8	10
113	GASOLINE: a Greedy And Stochastic algorithm for Optimal Local multiple alignment of Interaction NEtworks. PLoS ONE, 2014, 9, e98750.	1.1	28
114	Bioinformatics in Italy: BITS2012, the ninth annual meeting of the Italian Society of Bioinformatics. BMC Bioinformatics, 2013, 14, S1.	1.2	1
115	VIRGO: visualization of A-to-I RNA editing sites in genomic sequences. BMC Bioinformatics, 2013, 14, S5.	1.2	10
116	A subgraph isomorphism algorithm and its application to biochemical data. BMC Bioinformatics, 2013, 14, S13.	1.2	125
117	Enhancing density-based clustering: Parameter reduction and outlier detection. Information Systems, 2013, 38, 317-330.	2.4	97
118	Computational Approaches to RNAi and Gene Silencing. , 2013, , 169-194.		0
119	Elucidating the Role of microRNAs in Cancer Through Data Mining Techniques. Advances in Experimental Medicine and Biology, 2013, 774, 291-315.	0.8	6
120	Drug- [€] target interaction prediction through domain-tuned network-based inference. Bioinformatics, 2013, 29, 2004-2008.	1.8	146
121	GRAPES: A Software for Parallel Searching on Biological Graphs Targeting Multi-Core Architectures. PLoS ONE, 2013, 8, e76911.	1.1	33
122	Extracellular circulating viral microRNAs: current knowledge and perspectives. Frontiers in Genetics, 2013, 4, 120.	1.1	33
123	MIDClass: Microarray Data Classification by Association Rules and Gene Expression Intervals. PLoS ONE, 2013, 8, e69873.	1.1	17
124	miR-EdiTar: a database of predicted A-to-I edited miRNA target sites. Bioinformatics, 2012, 28, 3166-3168.	1.8	28
125	miRandola: Extracellular Circulating MicroRNAs Database. PLoS ONE, 2012, 7, e47786.	1.1	142
126	Preface - BITS 2012: Ninth Annual Meeting of the Bioinformatics Italian Society. EMBnet Journal, 2012, 18, 4.	0.2	0

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127	DBStrata. , 2011, , .		2
128	Editorial. Briefings in Bioinformatics, 2011, 12, 547-548.	3.2	2
129	Tools and collaborative environments for bioinformatics research. Briefings in Bioinformatics, 2011, 12, 549-561.	3.2	58
130	Business Process Model Retrieval Based on Graph Indexing Method. Lecture Notes in Business Information Processing, 2011, , 238-250.	0.8	1
131	SING: Subgraph search In Non-homogeneous Graphs. BMC Bioinformatics, 2010, 11, 96.	1.2	47
132	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.	1.1	92
133	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
134	SIGMA: A SET-COVER-BASED INEXACT GRAPH MATCHING ALGORITHM. Journal of Bioinformatics and Computational Biology, 2010, 08, 199-218.	0.3	61
135	An Efficient Duplicate Record Detection Using q-Grams Array Inverted Index. Lecture Notes in Computer Science, 2010, , 309-323.	1.0	6
136	Enhancing Graph Database Indexing by Suffix Tree Structure. Lecture Notes in Computer Science, 2010, , 195-203.	1.0	27
137	MySQL Data Mining: Extending MySQL to Support Data Mining Primitives (Demo). Lecture Notes in Computer Science, 2010, , 438-444.	1.0	1
138	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
139	Distributed randomized algorithms for low-support data mining. , 2009, , .		0
140	BitCube: A Bottom-Up Cubing Engineering. Lecture Notes in Computer Science, 2009, , 189-203.	1.0	10
141	GraphFind: enhancing graph searching by low support data mining techniques. BMC Bioinformatics, 2008, 9, S10.	1.2	15
142	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
143	Genomics, Evolution, and Expression of TBPL2, a Member of the TBP Family. DNA and Cell Biology, 2007, 26, 369-385.	0.9	5
144	Sequence similarity is more relevant than species specificity in probabilistic backtranslation. BMC Bioinformatics, 2007, 8, 58.	1.2	6

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145	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
146	Efficient Boundary Values Generation in General Metric Spaces for Software Component Testing. Lecture Notes in Computer Science, 2003, , 318-331.	1.0	0
147	Algorithmics and applications of tree and graph searching. , 2002, , .		240
148	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.	1.0	75
149	<title>Approximate search in image database</title>. , 1999, , .		0
150	Efficient Techniques for Graph Searching and Biological Network Mining. Advances in Data Mining and Database Management Book Series, 0, , 89-111.	0.4	0