Chiara Romualdi

List of Publications by Citations

159 papers	**6,274** citations
44 h-index	**73** g-index
178 ext. papers	**7,282** ext. citations
7.2 avg, IF	**5.39** L-index

#	Paper	IF	Citations
159	IDEG6: a web tool for detection of differentially expressed genes in multiple tag sampling experiments. *Physiological Genomics*, **2003**, 12, 159-62	3.6	310
158	Detection of cortical inflammatory lesions by double inversion recovery magnetic resonance imaging in patients with multiple sclerosis. *Archives of Neurology*, **2007**, 64, 1416-22		249
157	Life at depth: Photobacterium profundum genome sequence and expression analysis. *Science*, **2005**, 307, 1459-61	33.3	230
156	Cortical lesion load associates with progression of disability in multiple sclerosis. *Brain*, **2012**, 135, 2952-61	11.2	191
155	microRNA-181a has a critical role in ovarian cancer progression through the regulation of the epithelial-mesenchymal transition. *Nature Communications*, **2014**, 5, 2977	17.4	183
154	Cortical atrophy is relevant in multiple sclerosis at clinical onset. *Journal of Neurology*, **2007**, 254, 1212-20	5.5	182
153	Association between miR-200c and the survival of patients with stage I epithelial ovarian cancer: a retrospective study of two independent tumour tissue collections. *Lancet Oncology, The*, **2011**, 12, 273-85	21.7	163
152	Patterns of human diversity, within and among continents, inferred from biallelic DNA polymorphisms. *Genome Research*, **2002**, 12, 602-12	9.7	153
151	Ripening and genotype control stilbene accumulation in healthy grapes. *Journal of Agricultural and Food Chemistry*, **2008**, 56, 11773-85	5.7	150
150	MAGIA, a web-based tool for miRNA and Genes Integrated Analysis. *Nucleic Acids Research*, **2010**, 38, W352-9	20.1	135
149	graphite - a Bioconductor package to convert pathway topology to gene network. *BMC Bioinformatics*, **2012**, 13, 20	3.6	131
148	Inflammatory intrathecal profiles and cortical damage in multiple sclerosis. *Annals of Neurology*, **2018**, 83, 739-755	9.4	129
147	Resistance to platinum-based chemotherapy is associated with epithelial to mesenchymal transition in epithelial ovarian cancer. *European Journal of Cancer*, **2013**, 49, 520-30	7.5	121
146	Widespread cortical thinning characterizes patients with MS with mild cognitive impairment. *Neurology*, **2010**, 74, 321-8	6.5	118
145	miR148b is a major coordinator of breast cancer progression in a relapse-associated microRNA signature by targeting ITGA5, ROCK1, PIK3CA, NRAS, and CSF1. *FASEB Journal*, **2013**, 27, 1223-35	0.9	109
144	Cortical lesions in primary progressive multiple sclerosis: a 2-year longitudinal MR study. *Neurology*, **2009**, 72, 1330-6	6.5	108
143	MAGIA from miRNA and genes expression data integrative analysis to microRNA-transcription factor mixed regulatory circuits (2012 update). *Nucleic Acids Research*, **2012**, 40, W13-21	20.1	101

124	The cortical damage, early relapses, and onset of the progressive phase in multiple sclerosis. *Neurology*, **2018**, 90, e2107-e2118	6.5	51
123	MiRNA landscape in stage I epithelial ovarian cancer defines the histotype specificities. *Clinical Cancer Research*, **2013**, 19, 4114-23	12.9	50
122	Gene set analysis exploiting the topology of a pathway. *BMC Systems Biology*, **2010**, 4, 121	3.5	50
121	Detecting differentially expressed genes in multiple tag sampling experiments: comparative evaluation of statistical tests. *Human Molecular Genetics*, **2001**, 10, 2133-41	5.6	49
120	lncRNAs as Novel Indicators of PatientsPPrognosis in Stage I Epithelial Ovarian Cancer: A Retrospective and Multicentric Study. *Clinical Cancer Research*, **2017**, 23, 2356-2366	12.9	47
119	Analysis of differential miRNA expression in primary tumor and stroma of colorectal cancer patients. *BioMed Research International*, **2014**, 2014, 840921	3	46
118	Meta-analysis of expression signatures of muscle atrophy: gene interaction networks in early and late stages. *BMC Genomics*, **2008**, 9, 630	4.5	46
117	Single cell analysis reveals the involvement of the long non-coding RNA Pvt1 in the modulation of muscle atrophy and mitochondrial network. *Nucleic Acids Research*, **2019**, 47, 1653-1670	20.1	45
116	Gene expression profiling identifies potential relevant genes in alveolar rhabdomyosarcoma pathogenesis and discriminates PAX3-FKHR positive and negative tumors. *International Journal of Cancer*, **2006**, 118, 2772-81	7.5	44
115	COLOMBOS v3.0: leveraging gene expression compendia for cross-species analyses. *Nucleic Acids Research*, **2016**, 44, D620-3	20.1	41
114	Altered glucose metabolism and proteolysis in pancreatic cancer cell conditioned myoblasts: searching for a gene expression pattern with a microarray analysis of 5000 skeletal muscle genes. *Gut*, **2004**, 53, 1159-66	19.2	41
113	A modified LOESS normalization applied to microRNA arrays: a comparative evaluation. *Bioinformatics*, **2009**, 25, 2685-91	7.2	40
112	MIDAW: a web tool for statistical analysis of microarray data. *Nucleic Acids Research*, **2005**, 33, W644-9	20.1	40
111	Identification of high-grade serous ovarian cancer miRNA species associated with survival and drug response in patients receiving neoadjuvant chemotherapy: a retrospective longitudinal analysis using matched tumor biopsies. *Annals of Oncology*, **2016**, 27, 625-34	10.3	39
110	Aberrant DNA methylation profiles of inherited and sporadic colorectal cancer. *Clinical Epigenetics*, **2015**, 7, 131	7.7	39
109	Expression analysis of androgen-responsive genes in the prostate of veal calves treated with anabolic hormones. *Domestic Animal Endocrinology*, **2006**, 30, 38-55	2.3	39
108	Regional Distribution and Evolution of Gray Matter Damage in Different Populations of Multiple Sclerosis Patients. *PLoS ONE*, **2015**, 10, e0135428	3.7	39
107	Prognostic relevance of aberrant DNA methylation in g1 and g2 pancreatic neuroendocrine tumors. *Neuroendocrinology*, **2014**, 100, 26-34	5.6	38

106	Graphite Web: Web tool for gene set analysis exploiting pathway topology. *Nucleic Acids Research*, **2013**, 41, W89-97	20.1	38
105	Pattern recognition in gene expression profiling using DNA array: a comparative study of different statistical methods applied to cancer classification. *Human Molecular Genetics*, **2003**, 12, 823-36	5.6	38
104	Direct generation of human naive induced pluripotent stem cells from somatic cells in microfluidics. *Nature Cell Biology*, **2019**, 21, 275-286	23.4	38
103	The human adult skeletal muscle transcriptional profile reconstructed by a novel computational approach. *Genome Research*, **2000**, 10, 344-9	9.7	37
102	Transcriptomic Analysis of Single Isolated Myofibers Identifies miR-27a-3p and miR-142-3p as Regulators of Metabolism in Skeletal Muscle. *Cell Reports*, **2019**, 26, 3784-3797.e8	10.6	35
101	Disentangling the microRNA regulatory milieu in multiple myeloma: integrative genomics analysis outlines mixed miRNA-TF circuits and pathway-derived networks modulated in t(4;14) patients. *Oncotarget*, **2016**, 7, 2367-78	3.3	35
100	Wiring miRNAs to pathways: a topological approach to integrate miRNA and mRNA expression profiles. *Nucleic Acids Research*, **2014**, 42, e96	20.1	34
99	Defining the gene expression signature of rhabdomyosarcoma by meta-analysis. *BMC Genomics*, **2006**, 7, 287	4.5	34
98	Longitudinal analysis of immune cell phenotypes in early stage multiple sclerosis: distinctive patterns characterize MRI-active patients. *Brain*, **2006**, 129, 1993-2007	11.2	34
97	Expression profiling of skeletal muscle in young bulls treated with steroidal growth promoters. *Physiological Genomics*, **2009**, 38, 138-48	3.6	33
96	Impact of host genes and strand selection on miRNA and miRNA* expression. *PLoS ONE*, **2011**, 6, e23854	3.7	33
95	RAP: a new computer program for de novo identification of repeated sequences in whole genomes. *Bioinformatics*, **2005**, 21, 582-8	7.2	32
94	Territorial male gobies respond aggressively to sneakers but do not adjust their sperm expenditure. *Behavioral Ecology*, **2005**, 16, 1001-1007	2.3	31
93	Low degree of cortical pathology is associated with benign course of multiple sclerosis. *Multiple Sclerosis Journal*, **2013**, 19, 904-11	5	30
92	Beneficial Bacteria Isolated from Grapevine Inner Tissues Shape Arabidopsis thaliana Roots. *PLoS ONE*, **2015**, 10, e0140252	3.7	30
91	A founder MYBPC3 mutation results in HCM with a high risk of sudden death after the fourth decade of life. *Journal of Medical Genetics*, **2015**, 52, 338-47	5.8	30
90	Integration analysis of microRNA and mRNA expression profiles in human peripheral blood lymphocytes cultured in modeled microgravity. *BioMed Research International*, **2014**, 2014, 296747	3	30
89	Simplifying amino acid alphabets by means of a branch and bound algorithm and substitution matrices. *Bioinformatics*, **2002**, 18, 1102-8	7.2	30

88	Gene flow and genetic diversity: a comparison of freshwater bryozoan populations in Europe and North America. *Heredity*, **2000**, 85 Pt 5, 498-508	3.6	29
87	Profiling cancer gene mutations in longitudinal epithelial ovarian cancer biopsies by targeted next-generation sequencing: a retrospective study. *Annals of Oncology*, **2015**, 26, 1363-71	10.3	28
86	Polymorphisms in von Willebrand factor gene promoter influence the glucocorticoid-induced increase in von Willebrand factor: the lesson learned from Cushing syndrome. *British Journal of Haematology*, **2008**, 140, 230-5	4.5	24
85	Smokers and passive smokers gene expression profiles: correlation with the DNA oxidation damage. *Free Radical Biology and Medicine*, **2007**, 43, 415-22	7.8	24
84	Targeting p53 and histone methyltransferases restores exhausted CD8+ T cells in HCV infection. *Nature Communications*, **2020**, 11, 604	17.4	24
83	Pyrosequencing and de novo assembly of Antarctic krill (Euphausia superba) transcriptome to study the adaptability of krill to climate-induced environmental changes. *Molecular Ecology Resources*, **2015**, 15, 1460-71	8.4	23
82	A-MADMAN: annotation-based microarray data meta-analysis tool. *BMC Bioinformatics*, **2009**, 10, 201	3.6	23
81	The CSF Profile Linked to Cortical Damage Predicts Multiple Sclerosis Activity. *Annals of Neurology*, **2020**, 88, 562-573	9.4	22
80	Probability of conception on different days of the menstrual cycle: an ongoing exercise. *Advances in Contraception: the Official Journal of the Society for the Advancement of Contraception*, **1997**, 13, 105-15		22
79	Revertant fibers in the mdx murine model of Duchenne muscular dystrophy: an age- and muscle-related reappraisal. *PLoS ONE*, **2013**, 8, e72147	3.7	22
78	A leukemia-enriched cDNA microarray platform identifies new transcripts with relevance to the biology of pediatric acute lymphoblastic leukemia. *Haematologica*, **2005**, 90, 890-8	6.6	22
77	The self-morningness/eveningness (Self-ME): An extremely concise and totally subjective assessment of diurnal preference. *Chronobiology International*, **2015**, 32, 1192-200	3.6	21
76	Improved detection of differentially expressed genes in microarray experiments through multiple scanning and image integration. *Nucleic Acids Research*, **2003**, 31, e149	20.1	21
75	Circulating Cell-Free DNA in Dogs with Mammary Tumors: Short and Long Fragments and Integrity Index. *PLoS ONE*, **2017**, 12, e0169454	3.7	21
74	Assessment of statistical methods from single cell, bulk RNA-seq, and metagenomics applied to microbiome data. *Genome Biology*, **2020**, 21, 191	18.3	21
73	Genotype-specific mutations in the polymerase gene of hepatitis B virus potentially associated with resistance to oral antiviral therapy. *Antiviral Research*, **2012**, 96, 422-9	10.8	20
72	The Biological Connection Markup Language: a SBGN-compliant format for visualization, filtering and analysis of biological pathways. *Bioinformatics*, **2011**, 27, 2127-33	7.2	20
71	Microbiota changes induced by microencapsulated sodium butyrate in patients with inflammatory bowel disease. *Neurogastroenterology and Motility*, **2020**, 32, e13914	4	19

70	Gray matter pathology in MS: a 3-year longitudinal study in a pediatric population. *American Journal of Neuroradiology*, **2012**, 33, 1507-11	4.4	19
69	metaGraphite-a new layer of pathway annotation to get metabolite networks. *Bioinformatics*, **2019**, 35, 1258-1260	7.2	19
68	LINE-1 hypomethylation is associated to specific clinico-pathological features in Stage I non-small cell lung cancer. *Lung Cancer*, **2017**, 108, 83-89	5.9	18
67	Tissue-specific expression and regulatory networks of pig microRNAome. *PLoS ONE*, **2014**, 9, e89755	3.7	18
66	Selection of multipotent cells and enhanced muscle reconstruction by myogenic macrophage-secreted factors. *Experimental Cell Research*, **2009**, 315, 915-27	4.2	18
65	Disease genes and intracellular protein networks. *Physiological Genomics*, **2003**, 15, 223-7	3.6	18
64	A systems biology approach to characterize the regulatory networks leading to trabectedin resistance in an in vitro model of myxoid liposarcoma. *PLoS ONE*, **2012**, 7, e35423	3.7	17
63	Synthesis of mitochondrial DNA precursors during myogenesis, an analysis in purified C2C12 myotubes. *Journal of Biological Chemistry*, **2013**, 288, 5624-35	5.4	17
62	High IGFBP2 expression correlates with tumor severity in pediatric rhabdomyosarcoma. *American Journal of Pathology*, **2011**, 179, 2611-24	5.8	17
61	Genome-wide study of salivary miRNAs identifies miR-423-5p as promising diagnostic and prognostic biomarker in oral squamous cell carcinoma. *Theranostics*, **2021**, 11, 2987-2999	12.1	17
60	KrillDB: A de novo transcriptome database for the Antarctic krill (Euphausia superba). *PLoS ONE*, **2017**, 12, e0171908	3.7	16
59	FXYD5 (Dysadherin) upregulation predicts shorter survival and reveals platinum resistance in high-grade serous ovarian cancer patients. *British Journal of Cancer*, **2019**, 121, 584-592	8.7	15
58	Transcriptome Profiles of Human Visceral Adipocytes in Obesity and Colorectal Cancer Unravel the Effects of Body Mass Index and Polyunsaturated Fatty Acids on Genes and Biological Processes Related to Tumorigenesis. *Frontiers in Immunology*, **2019**, 10, 265	8.4	15
57	A prognostic regulatory pathway in stage I epithelial ovarian cancer: new hints for the poor prognosis assessment. *Annals of Oncology*, **2016**, 27, 1511-9	10.3	15
56	A comparison on effects of normalisations in the detection of differentially expressed genes. *BMC Bioinformatics*, **2009**, 10, 61	3.6	14
55	Novel genes, possibly relevant for molecular diagnosis or therapy of human rhabdomyosarcoma, detected by genomic expression profiling. *Gene*, **2005**, 348, 65-71	3.8	14
54	Usefulness of the Total Thrombus-Formation Analysis System (T-TAS) in the diagnosis and characterization of von Willebrand disease. *Haemophilia*, **2016**, 22, 949-956	3.3	13
53	A data-driven network model of primary myelofibrosis: transcriptional and post-transcriptional alterations in CD34+ cells. *Blood Cancer Journal*, **2016**, 6, e439	7	12

52	Individual Radiosensitivity in Oncological Patients: Linking Adverse Normal Tissue Reactions and Genetic Features. *Frontiers in Oncology*, **2019**, 9, 987	5.3	11
51	An aberrant microRNA signature in childhood T-cell lymphoblastic lymphoma affecting CDKN1B expression, NOTCH1 and growth factor signaling pathways. *Leukemia*, **2014**, 28, 1909-12	10.7	11
50	Global analysis of gene expression in mineralizing fish vertebra-derived cell lines: new insights into anti-mineralogenic effect of vanadate. *BMC Genomics*, **2011**, 12, 310	4.5	11
49	Regional and temporal heterogeneity of epithelial ovarian cancer tumor biopsies: implications for therapeutic strategies. *Oncotarget*, **2021**, 12, 2404-2417	3.3	11
48	Paradoxical GH Increase During OGTT Is Associated With First-Generation Somatostatin Analog Responsiveness in Acromegaly. *Journal of Clinical Endocrinology and Metabolism*, **2019**, 104, 856-862	5.6	10
47	Global DNA methylation profiling uncovers distinct methylation patterns of protocadherin alpha4 in metastatic and non-metastatic rhabdomyosarcoma. *BMC Cancer*, **2016**, 16, 886	4.8	10
46	Increased NK Cell Count in Multiple Sclerosis Patients Treated With Dimethyl Fumarate: A 2-Year Longitudinal Study. *Frontiers in Immunology*, **2019**, 10, 1666	8.4	10
45	timeClip: pathway analysis for time course data without replicates. *BMC Bioinformatics*, **2014**, 15 Suppl 5, S3	3.6	10
44	NELL1, whose high expression correlates with negative outcomes, has different methylation patterns in alveolar and embryonal rhabdomyosarcoma. *Oncotarget*, **2017**, 8, 33086-33099	3.3	10
43	Microsatellite (GT)(n) is part of the von Willebrand factor (VWF) promoter region that influences the glucocorticoid-induced increase in VWF in Cushing? syndrome. *Thrombosis Research*, **2010**, 125, e275-80	8.2	9
42	A global gene evolution analysis on Vibrionaceae family using phylogenetic profile. *BMC Bioinformatics*, **2007**, 8 Suppl 1, S23	3.6	9
41	Analysis of potential factors affecting allografts contamination at retrieval. *Cell and Tissue Banking*, **2017**, 18, 539-545	2.2	8
40	Filling gaps in PPAR-alpha signaling through comparative nutrigenomics analysis. *BMC Genomics*, **2009**, 10, 596	4.5	8
39	Multisite analysis of high-grade serous epithelial ovarian cancers identifies genomic regions of focal and recurrent copy number alteration in 3q26.2 and 8q24.3. *International Journal of Cancer*, **2019**, 145, 2670-2681	7.5	7
38	Systems biology approach to the dissection of the complexity of regulatory networks in the S. scrofa cardiocirculatory system. *International Journal of Molecular Sciences*, **2013**, 14, 23160-87	6.3	7
37	Impact of probe annotation on the integration of miRNA-mRNA expression profiles for miRNA target detection. *Nucleic Acids Research*, **2010**, 38, e97	20.1	7
36	Correlation between gene expression and clinical data through linear and nonlinear principal components analyses: muscular dystrophies as case studies. *OMICS A Journal of Integrative Biology*, **2009**, 13, 173-84	3.8	7
35	Genome-wide Copy-number Alterations in Circulating Tumor DNA as a Novel Biomarker for Patients with High-grade Serous Ovarian Cancer. *Clinical Cancer Research*, **2021**, 27, 2549-2559	12.9	7

34	Changes in Accident & Emergency Visits and Return Visits in Relation to the Enforcement of Daylight Saving Time and Photoperiod. *Journal of Biological Rhythms*, **2018**, 33, 555-564	3.2	7
33	The effect of fingolimod on focal and diffuse grey matter damage in active MS patients. *Journal of Neurology*, **2018**, 265, 2154-2161	5.5	7
32	A systems biology approach to investigate the mechanism of action of trabectedin in a model of myelomonocytic leukemia. *Pharmacogenomics Journal*, **2018**, 18, 56-63	3.5	6
31	Consequences of heat shock protein 72 (Hsp72) expression and activity on stress-induced apoptosis in CD30+ NPM-ALK+ anaplastic large-cell lymphomas. *Leukemia*, **2012**, 26, 1375-82	10.7	6
30	Microbiota of the Therapeutic Euganean Thermal Muds with a Focus on the Main Cyanobacteria Species. *Microorganisms*, **2020**, 8,	4.9	6
29	MOSClip: multi-omic and survival pathway analysis for the identification of survival associated gene and modules. *Nucleic Acids Research*, **2019**, 47, e80	20.1	5
28	Anticoagulant therapy for venous thromboembolism during pregnancy: a systematic review and a meta-analysis of the literature: a reply to a rebuttal. *Journal of Thrombosis and Haemostasis*, **2013**, 11, 788-9	15.4	5
27	Expression profiles of PRKG1, SDF2L1 and PPP1R12A are predictive and prognostic factors for therapy response and survival in high-grade serous ovarian cancer. *International Journal of Cancer*, **2020**, 147, 565-574	7.5	4
26	Statistical Test of Expression Pattern (STEPath): a new strategy to integrate gene expression data with genomic information in individual and meta-analysis studies. *BMC Bioinformatics*, **2011**, 12, 92	3.6	4
25	Expression profiling characterization of laminin alpha-2 positive MDC. *Biochemical and Biophysical Research Communications*, **2006**, 350, 345-51	3.4	4
24	TRAIT (TRAnscript Integrated Table): a knowledgebase of human skeletal muscle transcripts. *Bioinformatics*, **2003**, 19, 661-2	7.2	4
23	PsiNorm: a scalable normalization for single-cell RNA-seq data. *Bioinformatics*, **2021**,	7.2	4
22	rs4143815-, a New Potential Immunogenetic Biomarker of Biochemical Recurrence in Locally Advanced Prostate Cancer after Radiotherapy. *International Journal of Molecular Sciences*, **2019**, 20,	6.3	3
21	simPATHy: a new method for simulating data from perturbed biological PATHways. *Bioinformatics*, **2017**, 33, 456-457	7.2	3
20	SourceSet: A graphical model approach to identify primary genes in perturbed biological pathways. *PLoS Computational Biology*, **2019**, 15, e1007357	5	3
19	Graphical modeling for gene set analysis: A critical appraisal. *Biometrical Journal*, **2015**, 57, 852-66	1.5	3
18	A novel prognostic score to assess the risk of progression in relapsing-remitting multiple sclerosis patients. *European Journal of Neurology*, **2021**, 28, 2503-2512	6	3
17	MicroRNA expression profiling with a droplet digital PCR assay enables molecular diagnosis and prognosis of cancers of unknown primary. *Molecular Oncology*, **2021**, 15, 2732-2751	7.9	3

16	Transcriptional Characterization of Stage I Epithelial Ovarian Cancer: A Multicentric Study. *Cells*, **2019**, 8,	7.9	3
15	A TGF-□associated genetic score to define prognosis and platinum sensitivity in advanced epithelial ovarian cancer. *Gynecologic Oncology*, **2020**, 156, 233-242	4.9	2
14	Similarity Measures Based on the Overlap of Ranked Genes Are Effective for Comparison and Classification of Microarray Data. *Journal of Computational Biology*, **2016**, 23, 603-14	1.7	2
13	Antimicrobial use and microbiological testing in district general hospital ICUs of the Veneto region of north-east Italy. *European Journal of Clinical Microbiology and Infectious Diseases*, **2016**, 35, 1627-38	5.3	1
12	Sex identification from distinctive gene expression patterns in Antarctic krill (Euphausia superba). *Polar Biology*, **2019**, 42, 2205-2217	2	1
11	Headrace tunnel of the El Alto hydropower project in Panama / Druckstollen des Wasserkraftprojekts El Alto in Panama. *Geomechanik Und Tunnelbau*, **2013**, 6, 301-311	0.6	1
10	Assessment of statistical methods from single cell, bulk RNA-seq and metagenomics applied to microbiome data		1
9	Statistical Tools for Gene Expression Analysis and Systems Biology and Related Web Resources **2009**, 181-205		1
8	Comprehensive Profiling of Hypoxia-Related miRNAs Identifies miR-23a-3p Overexpression as a Marker of Platinum Resistance and Poor Prognosis in High-Grade Serous Ovarian Cancer. *Cancers*, **2021**, 13,	6.6	1
7	MyoData: An expression knowledgebase at single cell/nucleus level for the discovery of coding-noncoding RNA functional interactions in skeletal muscle. *Computational and Structural Biotechnology Journal*, **2021**, 19, 4142-4155	6.8	1
6	BrewerIX enables allelic expression analysis of imprinted and X-linked genes from bulk and single-cell transcriptomes.. *Communications Biology*, **2022**, 5, 146	6.7	1
5	NewWave: a scalable R/Bioconductor package for the dimensionality reduction and batch effect removal of single-cell RNA-seq data.. *Bioinformatics*, **2022**,	7.2	1
4	Searching for the Source of Difference: A Graphical Model Approach. *Lecture Notes in Computer Science*, **2020**, 131-138	0.9	
3	Pharmacogenetic score predicts overall survival, progression-free survival and platinum sensitivity in ovarian cancer. *Pharmacogenomics*, **2020**, 21, 995-1010	2.6	
2	Simulating gene silencing through intervention analysis. *Journal of the Royal Statistical Society Series C: Applied Statistics*, **2020**, 69, 887-907	1.5	
1	miRNA bioinformatics and pathway analysis **2022**, 141-150		