

Chun-Quan Li

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.

85
papers

2,081
citations

23
h-index

43
g-index

90
ext. papers

2,812
ext. citations

8
avg, IF

4.33
L-index

#	Paper	IF	Citations
85	TRmir: A Comprehensive Resource for Human Transcriptional Regulatory Information of MiRNAs.. <i>Frontiers in Genetics</i> , 2022 , 13, 808950	4.5	
84	TF-Marker: a comprehensive manually curated database for transcription factors and related markers in specific cell and tissue types in human.. <i>Nucleic Acids Research</i> , 2022 , 50, D402-D412	20.1	2
83	Characterization and Validation of ceRNA-Mediated Pathway-Pathway Crosstalk Networks Across Eight Major Cardiovascular Diseases.. <i>Frontiers in Cell and Developmental Biology</i> , 2022 , 10, 762129	5.7	0
82	TcoFBase: a comprehensive database for decoding the regulatory transcription co-factors in human and mouse. <i>Nucleic Acids Research</i> , 2021 ,	20.1	3
81	Cancer CRC: A Comprehensive Cancer Core Transcriptional Regulatory Circuit Resource and Analysis Platform. <i>Frontiers in Oncology</i> , 2021 , 11, 761700	5.3	1
80	OpenAnnotate: a web server to annotate the chromatin accessibility of genomic regions. <i>Nucleic Acids Research</i> , 2021 , 49, W483-W490	20.1	3
79	TRLnc: a comprehensive database for human transcriptional regulatory information of lncRNAs. <i>Briefings in Bioinformatics</i> , 2021 , 22, 1929-1939	13.4	12
78	LncSEA: a platform for long non-coding RNA related sets and enrichment analysis. <i>Nucleic Acids Research</i> , 2021 , 49, D969-D980	20.1	15
77	VARAdb: a comprehensive variation annotation database for human. <i>Nucleic Acids Research</i> , 2021 , 49, D1431-D1444	20.1	4
76	ATACdb: a comprehensive human chromatin accessibility database. <i>Nucleic Acids Research</i> , 2021 , 49, D55-D64	20.1	4
75	ComPAT: A Comprehensive Pathway Analysis Tools. <i>Lecture Notes in Computer Science</i> , 2021 , 109-120	0.9	1
74	Alterations of RNA splicing patterns in esophagus squamous cell carcinoma. <i>Cell and Bioscience</i> , 2021 , 11, 36	9.8	1
73	Large-scale and high-resolution mass spectrometry-based proteomics profiling defines molecular subtypes of esophageal cancer for therapeutic targeting. <i>Nature Communications</i> , 2021 , 12, 4961	17.4	9
72	Differential RNA expression profiles and competing endogenous RNA-associated regulatory networks during the progression of atherosclerosis. <i>Epigenomics</i> , 2021 , 13, 99-112	4.4	2
71	MiRNA-Mediated Subpathway Identification and Network Module Analysis to Reveal Prognostic Markers in Human Pancreatic Cancer. <i>Frontiers in Genetics</i> , 2020 , 11, 606940	4.5	1
70	Characterization of super-enhancer-associated functional lncRNAs acting as ceRNAs in ESCC. <i>Molecular Oncology</i> , 2020 , 14, 2203-2230	7.9	15
69	Identification of lncRNA-associated differential subnetworks in oesophageal squamous cell carcinoma by differential co-expression analysis. <i>Journal of Cellular and Molecular Medicine</i> , 2020 , 24, 4804-4818	5.6	4

68	TP63, SOX2, and KLF5 Establish a Core Regulatory Circuitry That Controls Epigenetic and Transcription Patterns in Esophageal Squamous Cell Carcinoma Cell Lines. <i>Gastroenterology</i> , 2020 , 159, 1311-1327.e19	13.3	29
67	ENdb: a manually curated database of experimentally supported enhancers for human and mouse. <i>Nucleic Acids Research</i> , 2020 , 48, D51-D57	20.1	15
66	KnockTF: a comprehensive human gene expression profile database with knockdown/knockout of transcription factors. <i>Nucleic Acids Research</i> , 2020 , 48, D93-D100	20.1	19
65	HiFreSP: A novel high-frequency sub-pathway mining approach to identify robust prognostic gene signatures. <i>Briefings in Bioinformatics</i> , 2020 , 21, 1411-1424	13.4	6
64	Macrophage-Enriched lncRNA RAPIA: A Novel Therapeutic Target for Atherosclerosis. <i>Arteriosclerosis, Thrombosis, and Vascular Biology</i> , 2020 , 40, 1464-1478	9.4	16
63	Integrative Epigenomic Analysis of Transcriptional Regulation of Human CircRNAs. <i>Frontiers in Genetics</i> , 2020 , 11, 590672	4.5	2
62	SEanalysis: a web tool for super-enhancer associated regulatory analysis. <i>Nucleic Acids Research</i> , 2019 , 47, W248-W255	20.1	24
61	ReCirc: prediction of circRNA expression and function through probe reannotation of non-circRNA microarrays. <i>Molecular Omics</i> , 2019 , 15, 150-163	4.4	3
60	Topologically inferring active miRNA-mediated subpathways toward precise cancer classification by directed random walk. <i>Molecular Oncology</i> , 2019 , 13, 2211-2226	7.9	5
59	TRCirc: a resource for transcriptional regulation information of circRNAs. <i>Briefings in Bioinformatics</i> , 2019 , 20, 2327-2333	13.4	35
58	Super-Enhancer-Associated Long Noncoding RNA HCCL5 Is Activated by ZEB1 and Promotes the Malignancy of Hepatocellular Carcinoma. <i>Cancer Research</i> , 2019 , 79, 572-584	10.1	66
57	ce-Subpathway: Identification of ceRNA-mediated subpathways via joint power of ceRNAs and pathway topologies. <i>Journal of Cellular and Molecular Medicine</i> , 2019 , 23, 967-984	5.6	9
56	SEdb: a comprehensive human super-enhancer database. <i>Nucleic Acids Research</i> , 2019 , 47, D235-D243	20.1	87
55	Super-Enhancer-Driven Long Non-Coding RNA LINC01503, Regulated by TP63, Is Over-Expressed and Oncogenic in Squamous Cell Carcinoma. <i>Gastroenterology</i> , 2018 , 154, 2137-2151.e1	13.3	108
54	Identification of distinct mutational patterns and new driver genes in oesophageal squamous cell carcinomas and adenocarcinomas. <i>Gut</i> , 2018 , 67, 1769-1779	19.2	62
53	Identification and analysis of a key long non-coding RNAs (lncRNAs)-associated module reveal functional lncRNAs in cardiac hypertrophy. <i>Journal of Cellular and Molecular Medicine</i> , 2018 , 22, 892-903	5.6	8
52	Co-activation of super-enhancer-driven CCAT1 by TP63 and SOX2 promotes squamous cancer progression. <i>Nature Communications</i> , 2018 , 9, 3619	17.4	104
51	MASAN: a novel staging system for prognosis of patients with oesophageal squamous cell carcinoma. <i>British Journal of Cancer</i> , 2018 , 118, 1476-1484	8.7	8

50	Inference of patient-specific subpathway activities reveals a functional signature associated with the prognosis of patients with breast cancer. <i>Journal of Cellular and Molecular Medicine</i> , 2018 , 22, 4304-4316	5.6	8
49	LncRNAs2Pathways: Identifying the pathways influenced by a set of lncRNAs of interest based on a global network propagation method. <i>Scientific Reports</i> , 2017 , 7, 46566	4.9	13
48	The global view of mRNA-related ceRNA cross-talks across cardiovascular diseases. <i>Scientific Reports</i> , 2017 , 7, 10185	4.9	22
47	The LncRNA Connectivity Map: Using LncRNA Signatures to Connect Small Molecules, LncRNAs, and Diseases. <i>Scientific Reports</i> , 2017 , 7, 6655	4.9	19
46	Integrative Pathway Analysis of Genes and Metabolites Reveals Metabolism Abnormal Subpathway Regions and Modules in Esophageal Squamous Cell Carcinoma. <i>Molecules</i> , 2017 , 22,	4.8	7
45	Subpathway-CorSP: Identification of metabolic subpathways via integrating expression correlations and topological features between metabolites and genes of interest within pathways. <i>Scientific Reports</i> , 2016 , 6, 33262	4.9	11
44	MiRSEA: Discovering the pathways regulated by dysfunctional MicroRNAs. <i>Oncotarget</i> , 2016 , 7, 55012-55025	5.0	9
43	RWCFusion: identifying phenotype-specific cancer driver gene fusions based on fusion pair random walk scoring method. <i>Oncotarget</i> , 2016 , 7, 61054-61068	3.3	4
42	Construction and analysis of cardiac hypertrophy-associated lncRNA-mRNA network based on competitive endogenous RNA reveal functional lncRNAs in cardiac hypertrophy. <i>Oncotarget</i> , 2016 , 7, 10827-40	3.3	87
41	Subpathway-LNCE: Identify dysfunctional subpathways competitively regulated by lncRNAs through integrating lncRNA-mRNA expression profile and pathway topologies. <i>Oncotarget</i> , 2016 , 7, 69837-69870	3.3	16
40	A truncated splice variant of human lysyl oxidase-like 2 promotes migration and invasion in esophageal squamous cell carcinoma. <i>International Journal of Biochemistry and Cell Biology</i> , 2016 , 75, 85-98	5.6	20
39	Protein-coding genes combined with long non-coding RNAs predict prognosis in esophageal squamous cell carcinoma patients as a novel clinical multi-dimensional signature. <i>Molecular BioSystems</i> , 2016 , 12, 3467-3477		29
38	Identification of a lncRNA involved functional module for esophageal cancer subtypes. <i>Molecular BioSystems</i> , 2016 , 12, 3312-3323		9
37	A novel dysregulated pathway-identification analysis based on global influence of within-pathway effects and crosstalk between pathways. <i>Journal of the Royal Society Interface</i> , 2015 , 12, 20140937	4.1	11
36	Integrative analysis of lung development-cancer expression associations reveals the roles of signatures with inverse expression patterns. <i>Molecular BioSystems</i> , 2015 , 11, 1271-84		7
35	Characterizing and optimizing human anticancer drug targets based on topological properties in the context of biological pathways. <i>Journal of Biomedical Informatics</i> , 2015 , 54, 132-40	10.2	1
34	Prioritization of rheumatoid arthritis risk subpathways based on global immune subpathway interaction network and random walk strategy. <i>Molecular BioSystems</i> , 2015 , 11, 2986-97		5
33	A global view of network of lncRNAs and their binding proteins. <i>Molecular BioSystems</i> , 2015 , 11, 656-63		19

32	Topologically inferring pathway activity toward precise cancer classification via integrating genomic and metabolomic data: prostate cancer as a case. <i>Scientific Reports</i> , 2015 , 5, 13192	4.9	22
31	ESEA: Discovering the Dysregulated Pathways based on Edge Set Enrichment Analysis. <i>Scientific Reports</i> , 2015 , 5, 13044	4.9	23
30	Global Prioritization of Disease Candidate Metabolites Based on a Multi-omics Composite Network. <i>Scientific Reports</i> , 2015 , 5, 17201	4.9	29
29	Identification of subtype specific miRNA-mRNA functional regulatory modules in matched miRNA-mRNA expression data: multiple myeloma as a case. <i>BioMed Research International</i> , 2015 , 2015, 501262	3	5
28	Systematic analysis of the associations between adverse drug reactions and pathways. <i>BioMed Research International</i> , 2015 , 2015, 670949	3	6
27	Integration of pathway structure information into a reweighted partial Cox regression approach for survival analysis on high-dimensional gene expression data. <i>Molecular BioSystems</i> , 2015 , 11, 1876-86		5
26	Subpathway-GMir: identifying miRNA-mediated metabolic subpathways by integrating condition-specific genes, microRNAs, and pathway topologies. <i>Oncotarget</i> , 2015 , 6, 39151-64	3.3	18
25	Functional combination strategy for prioritization of human miRNA target. <i>Gene</i> , 2014 , 533, 132-41	3.8	9
24	The detection of risk pathways, regulated by miRNAs, via the integration of sample-matched miRNA-mRNA profiles and pathway structure. <i>Journal of Biomedical Informatics</i> , 2014 , 49, 187-97	10.2	8
23	Identification of differentially expressed genes and their subpathways in recurrent versus primary bone giant cell tumors. <i>International Journal of Oncology</i> , 2014 , 45, 1133-42	4.4	7
22	Functional analysis of the mRNA profile of neutrophil gelatinase-associated lipocalin overexpression in esophageal squamous cell carcinoma using multiple bioinformatic tools. <i>Molecular Medicine Reports</i> , 2014 , 10, 1800-12	2.9	3
21	Network based analyses of gene expression profile of LCN2 overexpression in esophageal squamous cell carcinoma. <i>Scientific Reports</i> , 2014 , 4, 5403	4.9	21
20	MPINet: metabolite pathway identification via coupling of global metabolite network structure and metabolomic profile. <i>BioMed Research International</i> , 2014 , 2014, 325697	3	10
19	Identification of miRNA-mediated core gene module for glioma patient prediction by integrating high-throughput miRNA, mRNA expression and pathway structure. <i>PLoS ONE</i> , 2014 , 9, e96908	3.7	23
18	Prioritizing candidate disease metabolites based on global functional relationships between metabolites in the context of metabolic pathways. <i>PLoS ONE</i> , 2014 , 9, e104934	3.7	17
17	Walking the interactome to identify human miRNA-disease associations through the functional link between miRNA targets and disease genes. <i>BMC Systems Biology</i> , 2013 , 7, 101	3.5	184
16	Topologically inferring risk-active pathways toward precise cancer classification by directed random walk. <i>Bioinformatics</i> , 2013 , 29, 2169-77	7.2	46
15	Subpathway-GM: identification of metabolic subpathways via joint power of interesting genes and metabolites and their topologies within pathways. <i>Nucleic Acids Research</i> , 2013 , 41, e101	20.1	85

14	Allele-specific behavior of molecular networks: understanding small-molecule drug response in yeast. <i>PLoS ONE</i> , 2013 , 8, e53581	3.7	3
13	Dissection of miRNA-miRNA interaction in esophageal squamous cell carcinoma. <i>PLoS ONE</i> , 2013 , 8, e73191	3.7	24
12	Comprehensive bioinformatics analysis of the mRNA profile of fascin knockdown in esophageal squamous cell carcinoma. <i>Asian Pacific Journal of Cancer Prevention</i> , 2013 , 14, 7221-7	1.7	7
11	Identifying disease related sub-pathways for analysis of genome-wide association studies. <i>Gene</i> , 2012 , 503, 101-9	3.8	14
10	CNVd: text mining-based copy number variation in disease database. <i>Human Mutation</i> , 2012 , 33, E2375-81	4.7	23
9	Characterizing the network of drugs and their affected metabolic subpathways. <i>PLoS ONE</i> , 2012 , 7, e47326	3.7	26
8	Similarity measures for content-based image retrieval based on intuitionistic fuzzy set theory. <i>Journal of Computers</i> , 2012 , 7,	1.4	6
7	MiRNA-miRNA synergistic network: construction via co-regulating functional modules and disease miRNA topological features. <i>Nucleic Acids Research</i> , 2011 , 39, 825-36	20.1	218
6	The implications of relationships between human diseases and metabolic subpathways. <i>PLoS ONE</i> , 2011 , 6, e21131	3.7	39
5	DOSim: an R package for similarity between diseases based on Disease Ontology. <i>BMC Bioinformatics</i> , 2011 , 12, 266	3.6	65
4	Identification of pathways involved in paclitaxel activity in cervical cancer. <i>Asian Pacific Journal of Cancer Prevention</i> , 2011 , 12, 99-102	1.7	3
3	SubpathwayMiner: a software package for flexible identification of pathways. <i>Nucleic Acids Research</i> , 2009 , 37, e131	20.1	143
2	TP63, SOX2 and KLF5 Establish Core Regulatory Circuitry and Construct Cancer Specific Epigenome in Esophageal Squamous Cell Carcinoma		1
1	OpenAnnotate: a web server to annotate the chromatin accessibility of genomic regions		7