

# Chun-Quan Li

## List of Publications by Year in descending order

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Version: 2024-02-01

85  
papers

3,262  
citations

186209

28  
h-index

168321

53  
g-index

90  
all docs

90  
docs citations

90  
times ranked

3753  
citing authors

#	ARTICLE	IF	CITATIONS
1	MiRNAâ€™miRNA synergistic network: construction via co-regulating functional modules and disease miRNA topological features. <i>Nucleic Acids Research</i> , 2011, 39, 825-836.	6.5	245
2	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.	3.0	227
3	SubpathwayMiner: a software package for flexible identification of pathways. <i>Nucleic Acids Research</i> , 2009, 37, e131-e131.	6.5	195
4	Co-activation of super-enhancer-driven CCAT1 by TP63 and SOX2 promotes squamous cancer progression. <i>Nature Communications</i> , 2018, 9, 3619.	5.8	179
5	SEdb: a comprehensive human super-enhancer database. <i>Nucleic Acids Research</i> , 2019, 47, D235-D243.	6.5	166
6	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.	0.6	165
7	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-e101.	6.5	125
8	Identification of distinct mutational patterns and new driver genes in oesophageal squamous cell carcinomas and adenocarcinomas. <i>Gut</i> , 2018, 67, 1769-1779.	6.1	101
9	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, 10827-10840.	0.8	101
10	Super-Enhancerâ€™Associated Long Noncoding RNA HCCL5 Is Activated by ZEB1 and Promotes the Malignancy of Hepatocellular Carcinoma. <i>Cancer Research</i> , 2019, 79, 572-584.	0.4	97
11	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.	0.6	92
12	DOSim: An R package for similarity between diseases based on Disease Ontology. <i>BMC Bioinformatics</i> , 2011, 12, 266.	1.2	88
13	LncSEA: a platform for long non-coding RNA related sets and enrichment analysis. <i>Nucleic Acids Research</i> , 2021, 49, D969-D980.	6.5	76
14	KnockTF: a comprehensive human gene expression profile database with knockdown/knockout of transcription factors. <i>Nucleic Acids Research</i> , 2020, 48, D93-D100.	6.5	72
15	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.	5.8	63
16	Topologically inferring risk-active pathways toward precise cancer classification by directed random walk. <i>Bioinformatics</i> , 2013, 29, 2169-2177.	1.8	60
17	TRCirc: a resource for transcriptional regulation information of circRNAs. <i>Briefings in Bioinformatics</i> , 2019, 20, 2327-2333.	3.2	57
18	The Implications of Relationships between Human Diseases and Metabolic Subpathways. <i>PLoS ONE</i> , 2011, 6, e21131.	1.1	48

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19	SEanalysis: a web tool for super-enhancer associated regulatory analysis. <i>Nucleic Acids Research</i> , 2019, 47, W248-W255.	6.5	47
20	Global Prioritization of Disease Candidate Metabolites Based on a Multi-omics Composite Network. <i>Scientific Reports</i> , 2015, 5, 17201.	1.6	43
21	ENdb: a manually curated database of experimentally supported enhancers for human and mouse. <i>Nucleic Acids Research</i> , 2019, 48, D51-D57.	6.5	41
22	Macrophage-Enriched lncRNA RAPIA. <i>Arteriosclerosis, Thrombosis, and Vascular Biology</i> , 2020, 40, 1464-1478.	1.1	35
23	Subpathway-GMir: identifying miRNA-mediated metabolic subpathways by integrating condition-specific genes, microRNAs, and pathway topologies. <i>Oncotarget</i> , 2015, 6, 39151-39164.	0.8	33
24	Characterizing the Network of Drugs and Their Affected Metabolic Subpathways. <i>PLoS ONE</i> , 2012, 7, e47326.	1.1	32
25	ESEA: Discovering the Dysregulated Pathways based on Edge Set Enrichment Analysis. <i>Scientific Reports</i> , 2015, 5, 13044.	1.6	31
26	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.	2.9	31
27	The global view of mRNA-related ceRNA cross-talks across cardiovascular diseases. <i>Scientific Reports</i> , 2017, 7, 10185.	1.6	30
28	CNVD: Text mining-based copy number variation in disease database. <i>Human Mutation</i> , 2012, 33, E2375-E2381.	1.1	29
29	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.	1.6	29
30	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.	1.6	28
31	Characterization of super-enhancer-associated functional lncRNAs acting as ceRNAs in ESCC. <i>Molecular Oncology</i> , 2020, 14, 2203-2230.	2.1	28
32	Dissection of miRNA-miRNA Interaction in Esophageal Squamous Cell Carcinoma. <i>PLoS ONE</i> , 2013, 8, e73191.	1.1	27
33	ATACdb: a comprehensive human chromatin accessibility database. <i>Nucleic Acids Research</i> , 2021, 49, D55-D64.	6.5	27
34	Network based analyses of gene expression profile of LCN2 overexpression in esophageal squamous cell carcinoma. <i>Scientific Reports</i> , 2014, 4, 5403.	1.6	26
35	VARAdb: a comprehensive variation annotation database for human. <i>Nucleic Acids Research</i> , 2021, 49, D1431-D1444.	6.5	26
36	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.	1.1	26

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37	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.	1.6	25
38	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.	1.6	24
39	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.	1.2	23
40	ceâ€Subpathway: Identification of ce<scp>RNA</scp>â€mediated subpathways via joint power of ce<scp>RNA</scp>s and pathway topologies. <i>Journal of Cellular and Molecular Medicine</i> , 2019, 23, 967-984.	1.6	23
41	Prioritizing Candidate Disease Metabolites Based on Global Functional Relationships between Metabolites in the Context of Metabolic Pathways. <i>PLoS ONE</i> , 2014, 9, e104934.	1.1	23
42	The lncRNA Connectivity Map: Using lncRNA Signatures to Connect Small Molecules, lncRNAs, and Diseases. <i>Scientific Reports</i> , 2017, 7, 6655.	1.6	21
43	HiFreSP: A novel high-frequency sub-pathway mining approach to identify robust prognostic gene signatures. <i>Briefings in Bioinformatics</i> , 2020, 21, 1411-1424.	3.2	21
44	A global view of network of lncRNAs and their binding proteins. <i>Molecular BioSystems</i> , 2015, 11, 656-663.	2.9	20
45	Topologically inferring active miRNAâ€mediated subpathways toward precise cancer classification by directed random walk. <i>Molecular Oncology</i> , 2019, 13, 2211-2226.	2.1	20
46	TRlnc: a comprehensive database for human transcriptional regulatory information of lncRNAs. <i>Briefings in Bioinformatics</i> , 2021, 22, 1929-1939.	3.2	19
47	Subpathway-LNCE: Identify dysfunctional subpathways competitively regulated by lncRNAs through integrating lncRNA-mRNA expression profile and pathway topologies. <i>Oncotarget</i> , 2016, 7, 69857-69870.	0.8	18
48	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.	1.5	17
49	OpenAnnotate: a web server to annotate the chromatin accessibility of genomic regions. <i>Nucleic Acids Research</i> , 2021, 49, W483-W490.	6.5	17
50	TcoFBase: a comprehensive database for decoding the regulatory transcription co-factors in human and mouse. <i>Nucleic Acids Research</i> , 2022, 50, D391-D401.	6.5	16
51	Identifying disease related sub-pathways for analysis of genome-wide association studies. <i>Gene</i> , 2012, 503, 101-109.	1.0	15
52	Identification and analysis of a key long nonâ€coding RNAs (lncRNAs)â€associated module reveal functional lncRNAs in cardiac hypertrophy. <i>Journal of Cellular and Molecular Medicine</i> , 2018, 22, 892-903.	1.6	14
53	MASAN: a novel staging system for prognosis of patients with oesophageal squamous cell carcinoma. <i>British Journal of Cancer</i> , 2018, 118, 1476-1484.	2.9	13
54	MPINet: Metabolite Pathway Identification via Coupling of Global Metabolite Network Structure and Metabolomic Profile. <i>BioMed Research International</i> , 2014, 2014, 1-14.	0.9	12

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55	Alterations of RNA splicing patterns in esophagus squamous cell carcinoma. <i>Cell and Bioscience</i> , 2021, 11, 36.	2.1	12
56	OUP accepted manuscript. <i>Nucleic Acids Research</i> , 2022, 50, D402-D412.	6.5	12
57	Similarity measures for content-based image retrieval based on intuitionistic fuzzy set theory. <i>Journal of Computers</i> , 2012, 7, .	0.4	11
58	Functional combination strategy for prioritization of human miRNA target. <i>Gene</i> , 2014, 533, 132-141.	1.0	10
59	Identification of a lncRNA involved functional module for esophageal cancer subtypes. <i>Molecular BioSystems</i> , 2016, 12, 3312-3323.	2.9	10
60	MIRSEA: Discovering the pathways regulated by dysfunctional MicroRNAs. <i>Oncotarget</i> , 2016, 7, 55012-55025.	0.8	10
61	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, 187-197.	2.5	9
62	Integrative analysis of lung developmentâ€“cancer expression associations reveals the roles of signatures with inverse expression patterns. <i>Molecular BioSystems</i> , 2015, 11, 1271-1284.	2.9	9
63	Integrative Pathway Analysis of Genes and Metabolites Reveals Metabolism Abnormal Subpathway Regions and Modules in Esophageal Squamous Cell Carcinoma. <i>Molecules</i> , 2017, 22, 1599.	1.7	9
64	Comprehensive Bioinformation Analysis of the MRNA Profile of Fascin Knockdown in Esophageal Squamous Cell Carcinoma. <i>Asian Pacific Journal of Cancer Prevention</i> , 2013, 14, 7221-7227.	0.5	9
65	Identification of differentially expressed genes and their subpathways in recurrent versus primary bone giant cell tumors. <i>International Journal of Oncology</i> , 2014, 45, 1133-1142.	1.4	8
66	Prioritization of rheumatoid arthritis risk subpathways based on global immune subpathway interaction network and random walk strategy. <i>Molecular BioSystems</i> , 2015, 11, 2986-2997.	2.9	8
67	Identification of lncRNAâ€“associated differential subnetworks in oesophageal squamous cell carcinoma by differential coâ€“expression analysis. <i>Journal of Cellular and Molecular Medicine</i> , 2020, 24, 4804-4818.	1.6	8
68	Systematic Analysis of the Associations between Adverse Drug Reactions and Pathways. <i>BioMed Research International</i> , 2015, 2015, 1-12.	0.9	7
69	Allele-Specific Behavior of Molecular Networks: Understanding Small-Molecule Drug Response in Yeast. <i>PLoS ONE</i> , 2013, 8, e53581.	1.1	5
70	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, 1-15.	0.9	5
71	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, 1876-1886.	2.9	5
72	Differential RNA expression profiles and competing endogenous RNA-associated regulatory networks during the progression of atherosclerosis. <i>Epigenomics</i> , 2021, 13, 99-112.	1.0	5

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73	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, 132-140.	2.5	4
74	Integrative Epigenomic Analysis of Transcriptional Regulation of Human CircRNAs. <i>Frontiers in Genetics</i> , 2020, 11, 590672.	1.1	4
75	RWCFusion: identifying phenotype-specific cancer driver gene fusions based on fusion pair random walk scoring method. <i>Oncotarget</i> , 2016, 7, 61054-61068.	0.8	4
76	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, 1800-1812.	1.1	3
77	ReCirc: prediction of circRNA expression and function through probe reannotation of non-circRNA microarrays. <i>Molecular Omics</i> , 2019, 15, 150-163.	1.4	3
78	SENIES: DNA Shape Enhanced Two-layer Deep Learning Predictor for the Identification of Enhancers and Their Strength. <i>IEEE/ACM Transactions on Computational Biology and Bioinformatics</i> , 2022, PP, 1-1.	1.9	3
79	Identification of pathways involved in paclitaxel activity in cervical cancer. <i>Asian Pacific Journal of Cancer Prevention</i> , 2011, 12, 99-102.	0.5	3
80	MiRNA-Mediated Subpathway Identification and Network Module Analysis to Reveal Prognostic Markers in Human Pancreatic Cancer. <i>Frontiers in Genetics</i> , 2020, 11, 606940.	1.1	2
81	Cancer CRC: A Comprehensive Cancer Core Transcriptional Regulatory Circuit Resource and Analysis Platform. <i>Frontiers in Oncology</i> , 2021, 11, 761700.	1.3	2
82	A Heuristic Approach for Target SNP Mining Based on Genome-Wide IBD Profile. , 2007, , .		1
83	ComPAT: A Comprehensive Pathway Analysis Tools. <i>Lecture Notes in Computer Science</i> , 2021, , 109-120.	1.0	1
84	TRmir: A Comprehensive Resource for Human Transcriptional Regulatory Information of MiRNAs. <i>Frontiers in Genetics</i> , 2022, 13, 808950.	1.1	1
85	Characterization and Validation of ceRNA-Mediated Pathway Crosstalk Networks Across Eight Major Cardiovascular Diseases. <i>Frontiers in Cell and Developmental Biology</i> , 2022, 10, 762129.	1.8	1