Yuan-Yuan Li

List of Publications by Year
in descending order

33 papers	810 citations	623734 14 h-index	501196 28 g-index
33 all docs	33 docs citations	33 times ranked	1210 citing authors

#	Article	IF	Citations
1	The dynamic alteration of transcriptional regulation by crucial TFs during tumorigenesis of gastric cancer. Molecular Medicine, 2022, 28, 41.	4.4	4
2	DysRegSig: an R package for identifying gene dysregulations and building mechanistic signatures in cancer. Bioinformatics, 2021, 37, 429-430.	4.1	2
3	Gene dysregulation analysis builds a mechanistic signature for prognosis and therapeutic benefit in colorectal cancer. Journal of Molecular Cell Biology, 2021, 12, 881-893.	3.3	3
4	Identification of ARGLU1 as a potential therapeutic target for gastric cancer based on genome-wide functional screening data. EBioMedicine, 2021, 69, 103436.	6.1	12
5	TGPred: a tumor gene prediction webserver for analyzing structural and functional impacts of variants. Journal of Molecular Cell Biology, 2020, 12, 556-558.	3.3	0
6	Pan-Cancer Analysis of Head-to-Head Gene Pairs in Terms of Transcriptional Activity, Co-expression and Regulation. Frontiers in Genetics, 2020, 11, 560997.	2.3	6
7	DRAP: a toolbox for drug response analysis and visualization tailored for preclinical drug testing on patient-derived xenograft models. Journal of Translational Medicine, 2019, 17, 39.	4.4	13
8	Differential networking meta-analysis of gastric cancer across Asian and American racial groups. BMC Systems Biology, 2018, 12, 51.	3.0	7
9	A comparison of next-generation sequencing analysis methods for cancer xenograft samples. Journal of Genetics and Genomics, 2018, 45, 345-350.	3.9	5
10	Differential regulation analysis reveals dysfunctional regulatory mechanism involving transcription factors and microRNAs in gastric carcinogenesis. Artificial Intelligence in Medicine, 2017, 77, 12-22.	6.5	8
11	Ufm1 inhibits LPS-induced endothelial cell inflammatory responses through the NF-κB signaling pathway. International Journal of Molecular Medicine, 2017, 39, 1119-1126.	4.0	22
12	Differential Regulatory Analysis Based on Coexpression Network in Cancer Research. BioMed Research International, 2016, 2016, 1-8.	1.9	16
13	DNetDB: The human disease network database based on dysfunctional regulation mechanism. BMC Systems Biology, 2016, 10, 36.	3.0	23
14	A novel index of protein-protein interface propensity improves interface residue recognition. BMC Systems Biology, 2016, 10, 112.	3.0	18
15	A novel integrated gene coexpression analysis approach reveals a prognostic three-transcription-factor signature for glioma molecular subtypes. BMC Systems Biology, 2016, 10, 71.	3.0	9
16	The human disease network in terms of dysfunctional regulatory mechanisms. Biology Direct, 2015, 10, 60.	4.6	23
17	DSviaDRM: an R package for estimating disease similarity via dysfunctional regulation mechanism. Bioinformatics, 2015, 31, 3870-3872.	4.1	5
18	Differential network analysis reveals dysfunctional regulatory networks in gastric carcinogenesis. American Journal of Cancer Research, 2015, 5, 2605-25.	1.4	8

#	Article	IF	Citations
19	cGRNB: a web server for building combinatorial gene regulatory networks through integrated engineering of seed-matching sequence information and gene expression datasets. BMC Systems Biology, 2013, 7, S7.	3.0	13
20	Co-expression network with protein–protein interaction and transcription regulation in malaria parasite Plasmodium falciparum. Gene, 2013, 518, 7-16.	2.2	8
21	DCGL v2.0: An R Package for Unveiling Differential Regulation from Differential Co-expression. PLoS ONE, 2013, 8, e79729.	2.5	83
22	Teachers of Psychiatry meeting in Shanghai: A leadership training course. Asia-Pacific Psychiatry, 2012, 4, 87-89.	2.2	3
23	Combinatorial network of transcriptional regulation and microRNA regulation in human cancer. BMC Systems Biology, 2012, 6, 61.	3.0	22
24	Link-based quantitative methods to identify differentially coexpressed genes and gene Pairs. BMC Bioinformatics, 2011, 12, 315.	2.6	82
25	Analyses of Copy Number Variation of GK Rat Reveal New Putative Type 2 Diabetes Susceptibility Loci. PLoS ONE, 2010, 5, e14077.	2.5	10
26	DCGL: an R package for identifying differentially coexpressed genes and links from gene expression microarray data. Bioinformatics, 2010, 26, 2637-2638.	4.1	98
27	Exploring mitochondrial evolution and metabolism organization principles by comparative analysis of metabolic networks. Genomics, 2010, 95, 339-344.	2.9	15
28	Identifying Modules of Coexpressed Transcript Units and Their Organization of Saccharopolyspora erythraea from Time Series Gene Expression Profiles. PLoS ONE, 2010, 5, e12126.	2.5	16
29	Combinatorial network of primary and secondary microRNA-driven regulatory mechanisms. Nucleic Acids Research, 2009, 37, 5969-5980.	14.5	68
30	Recovering context-specific gene network modules from expression data: A brief review. Frontiers of Biology in China: Selected Publications From Chinese Universities, 2009, 4, 414-418.	0.2	1
31	Time-Resolved Transcriptome Analysis of Bacillus subtilis Responding to Valine, Glutamate, and Glutamine. PLoS ONE, 2009, 4, e7073.	2.5	24
32	In silico discovery of human natural antisense transcripts. BMC Bioinformatics, 2006, 7, 18.	2.6	38
33	Systematic Analysis of Head-to-Head Gene Organization: Evolutionary Conservation and Potential Biological Relevance. PLoS Computational Biology, 2006, 2, e74.	3.2	145