

Yuan-Yuan Li

List of Publications by Year in descending order

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Version: 2024-02-01

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	Systematic Analysis of Head-to-Head Gene Organization: Evolutionary Conservation and Potential Biological Relevance. <i>PLoS Computational Biology</i> , 2006, 2, e74.	3.2	145
2	DCGL: an R package for identifying differentially coexpressed genes and links from gene expression microarray data. <i>Bioinformatics</i> , 2010, 26, 2637-2638.	4.1	98
3	DCGL v2.0: An R Package for Unveiling Differential Regulation from Differential Co-expression. <i>PLoS ONE</i> , 2013, 8, e79729.	2.5	83
4	Link-based quantitative methods to identify differentially coexpressed genes and gene Pairs. <i>BMC Bioinformatics</i> , 2011, 12, 315.	2.6	82
5	Combinatorial network of primary and secondary microRNA-driven regulatory mechanisms. <i>Nucleic Acids Research</i> , 2009, 37, 5969-5980.	14.5	68
6	In silico discovery of human natural antisense transcripts. <i>BMC Bioinformatics</i> , 2006, 7, 18.	2.6	38
7	Time-Resolved Transcriptome Analysis of <i>Bacillus subtilis</i> Responding to Valine, Glutamate, and Glutamine. <i>PLoS ONE</i> , 2009, 4, e7073.	2.5	24
8	The human disease network in terms of dysfunctional regulatory mechanisms. <i>Biology Direct</i> , 2015, 10, 60.	4.6	23
9	DNetDB: The human disease network database based on dysfunctional regulation mechanism. <i>BMC Systems Biology</i> , 2016, 10, 36.	3.0	23
10	Combinatorial network of transcriptional regulation and microRNA regulation in human cancer. <i>BMC Systems Biology</i> , 2012, 6, 61.	3.0	22
11	Ufm1 inhibits LPS-induced endothelial cell inflammatory responses through the NF- κ B signaling pathway. <i>International Journal of Molecular Medicine</i> , 2017, 39, 1119-1126.	4.0	22
12	A novel index of protein-protein interface propensity improves interface residue recognition. <i>BMC Systems Biology</i> , 2016, 10, 112.	3.0	18
13	Differential Regulatory Analysis Based on Coexpression Network in Cancer Research. <i>BioMed Research International</i> , 2016, 2016, 1-8.	1.9	16
14	Identifying Modules of Coexpressed Transcript Units and Their Organization of <i>Saccharopolyspora erythraea</i> from Time Series Gene Expression Profiles. <i>PLoS ONE</i> , 2010, 5, e12126.	2.5	16
15	Exploring mitochondrial evolution and metabolism organization principles by comparative analysis of metabolic networks. <i>Genomics</i> , 2010, 95, 339-344.	2.9	15
16	cGRNB: a web server for building combinatorial gene regulatory networks through integrated engineering of seed-matching sequence information and gene expression datasets. <i>BMC Systems Biology</i> , 2013, 7, S7.	3.0	13
17	DRAP: a toolbox for drug response analysis and visualization tailored for preclinical drug testing on patient-derived xenograft models. <i>Journal of Translational Medicine</i> , 2019, 17, 39.	4.4	13
18	Identification of ARGLU1 as a potential therapeutic target for gastric cancer based on genome-wide functional screening data. <i>EBioMedicine</i> , 2021, 69, 103436.	6.1	12

#	ARTICLE	IF	CITATIONS
19	Analyses of Copy Number Variation of GK Rat Reveal New Putative Type 2 Diabetes Susceptibility Loci. <i>PLoS ONE</i> , 2010, 5, e14077.	2.5	10
20	A novel integrated gene coexpression analysis approach reveals a prognostic three-transcription-factor signature for glioma molecular subtypes. <i>BMC Systems Biology</i> , 2016, 10, 71.	3.0	9
21	Co-expression network with protein-protein interaction and transcription regulation in malaria parasite <i>Plasmodium falciparum</i> . <i>Gene</i> , 2013, 518, 7-16.	2.2	8
22	Differential regulation analysis reveals dysfunctional regulatory mechanism involving transcription factors and microRNAs in gastric carcinogenesis. <i>Artificial Intelligence in Medicine</i> , 2017, 77, 12-22.	6.5	8
23	Differential network analysis reveals dysfunctional regulatory networks in gastric carcinogenesis. <i>American Journal of Cancer Research</i> , 2015, 5, 2605-25.	1.4	8
24	Differential networking meta-analysis of gastric cancer across Asian and American racial groups. <i>BMC Systems Biology</i> , 2018, 12, 51.	3.0	7
25	Pan-Cancer Analysis of Head-to-Head Gene Pairs in Terms of Transcriptional Activity, Co-expression and Regulation. <i>Frontiers in Genetics</i> , 2020, 11, 560997.	2.3	6
26	DSviaDRM: an R package for estimating disease similarity via dysfunctional regulation mechanism. <i>Bioinformatics</i> , 2015, 31, 3870-3872.	4.1	5
27	A comparison of next-generation sequencing analysis methods for cancer xenograft samples. <i>Journal of Genetics and Genomics</i> , 2018, 45, 345-350.	3.9	5
28	The dynamic alteration of transcriptional regulation by crucial TFs during tumorigenesis of gastric cancer. <i>Molecular Medicine</i> , 2022, 28, 41.	4.4	4
29	Teachers of Psychiatry meeting in Shanghai: A leadership training course. <i>Asia-Pacific Psychiatry</i> , 2012, 4, 87-89.	2.2	3
30	Gene dysregulation analysis builds a mechanistic signature for prognosis and therapeutic benefit in colorectal cancer. <i>Journal of Molecular Cell Biology</i> , 2021, 12, 881-893.	3.3	3
31	DysRegSig: an R package for identifying gene dysregulations and building mechanistic signatures in cancer. <i>Bioinformatics</i> , 2021, 37, 429-430.	4.1	2
32	Recovering context-specific gene network modules from expression data: A brief review. <i>Frontiers of Biology in China: Selected Publications From Chinese Universities</i> , 2009, 4, 414-418.	0.2	1
33	TCPred: a tumor gene prediction webserver for analyzing structural and functional impacts of variants. <i>Journal of Molecular Cell Biology</i> , 2020, 12, 556-558.	3.3	0