

Jiaofang Shao

List of Publications by Year in descending order

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Version: 2024-02-01

30
papers

1,220
citations

394421

19
h-index

434195

31
g-index

31
all docs

31
docs citations

31
times ranked

1877
citing authors

#	ARTICLE	IF	CITATIONS
1	The SOX2 response program in glioblastoma multiforme: an integrated ChIP-seq, expression microarray, and microRNA analysis. <i>BMC Genomics</i> , 2011, 12, 11.	2.8	141
2	Enhancer RNA m6A methylation facilitates transcriptional condensate formation and gene activation. <i>Molecular Cell</i> , 2021, 81, 3368-3385.e9.	9.7	135
3	Analysis of banana transcriptome and global gene expression profiles in banana roots in response to infection by race 1 and tropical race 4 of <i>Fusarium oxysporum</i> f. sp. <i>cubense</i> . <i>BMC Genomics</i> , 2013, 14, 851.	2.8	112
4	Analysis of different strategies adapted by two cassava cultivars in response to drought stress: ensuring survival or continuing growth. <i>Journal of Experimental Botany</i> , 2015, 66, 1477-1488.	4.8	105
5	Gene transcription profiling of <i>Fusarium graminearum</i> treated with an azole fungicide tebuconazole. <i>Applied Microbiology and Biotechnology</i> , 2010, 85, 1105-1114.	3.6	78
6	Enhancer release and retargeting activates disease-susceptibility genes. <i>Nature</i> , 2021, 595, 735-740.	27.8	76
7	ChIP-seq and Functional Analysis of the SOX2 Gene in Colorectal Cancers. <i>OMICS A Journal of Integrative Biology</i> , 2010, 14, 369-384.	2.0	61
8	Inhibition of lung cancer growth and metastasis by DHA and its metabolite, RvD1, through miR-138-5p/FOXC1 pathway. <i>Journal of Experimental and Clinical Cancer Research</i> , 2019, 38, 479.	8.6	52
9	A Genome-Wide Hybrid Incompatibility Landscape between <i>Caenorhabditis briggsae</i> and <i>C. nigoni</i> . <i>PLoS Genetics</i> , 2015, 11, e1004993.	3.5	40
10	The SINEB1 element in the long non-coding RNA Malat1 is necessary for TDP-43 proteostasis. <i>Nucleic Acids Research</i> , 2020, 48, 2621-2642.	14.5	40
11	Cyclooxygenase-2 induced β 1-integrin expression in NSCLC and promoted cell invasion via the EP1/MAPK/E2F-1/FoxC2 signal pathway. <i>Scientific Reports</i> , 2016, 6, 33823.	3.3	38
12	The cell surface marker CD36 selectively identifies matured, mitochondria-rich hPSC-cardiomyocytes. <i>Cell Research</i> , 2020, 30, 626-629.	12.0	36
13	PTHGRN: unraveling post-translational hierarchical gene regulatory networks using PPI, ChIP-seq and gene expression data. <i>Nucleic Acids Research</i> , 2014, 42, W130-W136.	14.5	34
14	Unraveling Regulatory Programs for NF-kappaB, p53 and MicroRNAs in Head and Neck Squamous Cell Carcinoma. <i>PLoS ONE</i> , 2013, 8, e73656.	2.5	31
15	SOX4 inhibits GBM cell growth and induces G0/G1 cell cycle arrest through Akt-p53 axis. <i>BMC Neurology</i> , 2014, 14, 207.	1.8	31
16	Collaborative Regulation of Development but Independent Control of Metabolism by Two Epidermis-specific Transcription Factors in <i>Caenorhabditis elegans</i> . <i>Journal of Biological Chemistry</i> , 2013, 288, 33411-33426.	3.4	29
17	CMGRN: a web server for constructing multilevel gene regulatory networks using ChIP-seq and gene expression data. <i>Bioinformatics</i> , 2014, 30, 1190-1192.	4.1	29
18	Integrated transcriptional profiling and genomic analyses reveal RPN2 and HMGB1 as promising biomarkers in colorectal cancer. <i>Cell and Bioscience</i> , 2015, 5, 53.	4.8	29

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19	Systems-level quantification of division timing reveals a common genetic architecture controlling asynchrony and fate asymmetry. <i>Molecular Systems Biology</i> , 2015, 11, 814.	7.2	27
20	Implications of liver injury in risk-stratification and management of patients with COVID-19. <i>Hepatology International</i> , 2021, 15, 202-212.	4.2	15
21	Alternative Polyadenylation in Glioblastoma Multiforme and Changes in Predicted RNA Binding Protein Profiles. <i>OMICS A Journal of Integrative Biology</i> , 2013, 17, 136-149.	2.0	14
22	Dynamic regulation of genetic pathways and targets during aging in <i>Caenorhabditis elegans</i> . <i>Aging</i> , 2014, 6, 215-230.	3.1	13
23	miRNA Mediated Noise Making of 3' UTR Mutations in Cancer. <i>Genes</i> , 2018, 9, 545.	2.4	12
24	Next-Generation Sequencing of Colorectal Cancers in Chinese: Identification of a Recurrent Frame-Shift and Gain-of-Function Indel Mutation in the <i>TFDP1</i> Gene. <i>OMICS A Journal of Integrative Biology</i> , 2014, 18, 625-635.	2.0	9
25	Targeted Re-Sequencing Identified rs3106189 at the 5' UTR of <i>TAPBP</i> and rs1052918 at the 3' UTR of <i>TCF3</i> to Be Associated with the Overall Survival of Colorectal Cancer Patients. <i>PLoS ONE</i> , 2013, 8, e70307.	2.5	8
26	Association of blood glucose level and prognosis of inpatients with coexistent diabetes and COVID-19. <i>Endocrine</i> , 2022, 75, 1-9.	2.3	8
27	Identification of Novel SNPs by Next-Generation Sequencing of the Genomic Region Containing the <i>APC</i> Gene in Colorectal Cancer Patients in China. <i>OMICS A Journal of Integrative Biology</i> , 2010, 14, 315-325.	2.0	7
28	An Integrating Approach for Genome-Wide Screening of MicroRNA Polymorphisms Mediated Drug Response Alterations. <i>International Journal of Genomics</i> , 2017, 2017, 1-7.	1.6	5
29	The comprehensive transcriptional analysis in <i>Caenorhabditis elegans</i> by integrating ChIP-seq and gene expression data. <i>Genetical Research</i> , 2014, 96, e005.	0.9	2
30	Comparative proteome analysis between <i>C. briggsae</i> embryos and larvae reveals a role of chromatin modification proteins in embryonic cell division. <i>Scientific Reports</i> , 2017, 7, 4296.	3.3	2