

Dong Chen

List of Publications by Year in descending order

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Version: 2024-02-01

29
papers

910
citations

623574

14
h-index

552653

26
g-index

32
all docs

32
docs citations

32
times ranked

1088
citing authors

#	ARTICLE	IF	CITATIONS
1	CONSTITUTIVE EXPRESSER OF PATHOGENESIS-RELATED GENES 5 is an RNA-binding protein controlling plant immunity via an RNA processing complex. <i>Plant Cell</i> , 2022, 34, 1724-1744.	3.1	21
2	Iron metabolism protein transferrin receptor 1 involves in cervical cancer progression by affecting gene expression and alternative splicing in HeLa cells. <i>Genes and Genomics</i> , 2022, 44, 637-650.	0.5	9
3	PCBP1 is associated with rheumatoid arthritis by affecting RNA products of genes involved in immune response in Th1 cells. <i>Scientific Reports</i> , 2022, 12, 8398.	1.6	3
4	Study on microbial communities and higher alcohol formations in the fermentation of Chinese Xiaoku Baijiu produced by traditional and new mechanical technologies. <i>Food Research International</i> , 2021, 140, 109876.	2.9	38
5	ATP5A1 Participates in Transcriptional and Posttranscriptional Regulation of Cancer-Associated Genes by Modulating Their Expression and Alternative Splicing Profiles in HeLa Cells. <i>Technology in Cancer Research and Treatment</i> , 2021, 20, 153303382110391.	0.8	6
6	Dysregulated LncRNAs Act as Competitive Endogenous RNAs and Are Associated With Cervical Cancer Development in UYGHUR Women. <i>Technology in Cancer Research and Treatment</i> , 2021, 20, 153303382198971.	0.8	4
7	MACF1 promotes osteoblast differentiation by sequestering repressors in cytoplasm. <i>Cell Death and Differentiation</i> , 2021, 28, 2160-2178.	5.0	9
8	Comparison of lncRNA and mRNA expression in mouse brains infected by a wild-type and a lab-attenuated Rabies lyssavirus. <i>Journal of General Virology</i> , 2021, 102, .	1.3	8
9	Integrated Transcriptome Profiling Revealed That Elevated Long Non-Coding RNA-AC007278.2 Expression Repressed CCR7 Transcription in Systemic Lupus Erythematosus. <i>Frontiers in Immunology</i> , 2021, 12, 615859.	2.2	14
10	Dysregulated lncRNAs are Involved in the Progress of Sepsis by Constructing Regulatory Networks in Whole Blood Cells. <i>Frontiers in Pharmacology</i> , 2021, 12, 678256.	1.6	5
11	Sex-Specific Development in Haplodiploid Honeybee Is Controlled by the Female-Embryo-Specific Activation of Thousands of Intronic LncRNAs. <i>Frontiers in Cell and Developmental Biology</i> , 2021, 9, 690167.	1.8	0
12	Comparative study on seasonal hair follicle cycling by analysis of the transcriptomes from cashmere and milk goats. <i>Genomics</i> , 2020, 112, 332-345.	1.3	44
13	A novel antiviral lncRNA, EDAL, shields a T309 O-GlcNAcylation site to promote EZH2 lysosomal degradation. <i>Genome Biology</i> , 2020, 21, 228.	3.8	38
14	Chromatin modifier MTA1 regulates mitotic transition and tumorigenesis by orchestrating mitotic mRNA processing. <i>Nature Communications</i> , 2020, 11, 4455.	5.8	20
15	Transcriptome-wide study of the response of human trabecular meshwork cells to the substrate stiffness increase. <i>Journal of Cellular Biochemistry</i> , 2020, 121, 3112-3123.	1.2	14
16	Transcriptome profiling reveals the high incidence of hnRNPA1 exon 8 inclusion in chronic myeloid leukemia. <i>Journal of Advanced Research</i> , 2020, 24, 301-310.	4.4	18
17	Hfq Globally Binds and Destabilizes sRNAs and mRNAs in <i>Yersinia pestis</i> . <i>MSystems</i> , 2019, 4, .	1.7	7
18	Genome-wide identification of AGO18b-bound miRNAs and phasiRNAs in maize by cRIP-seq. <i>BMC Genomics</i> , 2019, 20, 656.	1.2	18

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19	Induced Expression of <i>VEGFC</i> , <i>ANGPT</i> , and <i>EFNB2</i> and Their Receptors Characterizes Neovascularization in Proliferative Diabetic Retinopathy. , 2019, 60, 4084.		28
20	Transcriptome analysis reveals downregulation of virulence-associated genes expression in a low virulence <i>Verticillium dahliae</i> strain. Archives of Microbiology, 2019, 201, 927-941.	1.0	23
21	The susceptibility of sea-island cotton recombinant inbred lines to <i>Fusarium oxysporum</i> f. sp. <i>vasinfectum</i> infection is characterized by altered expression of long noncoding RNAs. Scientific Reports, 2019, 9, 2894.	1.6	19
22	Transcriptome profiling reveals transcriptional and alternative splicing regulation in the early embryonic development of hair follicles in the cashmere goat. Scientific Reports, 2019, 9, 17735.	1.6	29
23	Annotation and functional clustering of circRNA expression in rhesus macaque brain during aging. Cell Discovery, 2018, 4, 48.	3.1	49
24	Diversity and Contributions to Nitrogen Cycling and Carbon Fixation of Soil Salinity Shaped Microbial Communities in Tarim Basin. Frontiers in Microbiology, 2018, 9, 431.	1.5	89
25	CELF1 preferentially binds to exon-intron boundary and regulates alternative splicing in HeLa cells. Biochimica Et Biophysica Acta - Gene Regulatory Mechanisms, 2017, 1860, 911-921.	0.9	111
26	Annotation and cluster analysis of spatiotemporal- and sex-related lncRNA expression in rhesus macaque brain. Genome Research, 2017, 27, 1608-1620.	2.4	113
27	A comparison of the low temperature transcriptomes of two tomato genotypes that differ in freezing tolerance: <i>Solanum lycopersicum</i> and <i>Solanum habrochaites</i> . BMC Plant Biology, 2015, 15, 132.	1.6	77
28	Integrative genome-wide analysis reveals HLP1, a novel RNA-binding protein, regulates plant flowering by targeting alternative polyadenylation. Cell Research, 2015, 25, 864-876.	5.7	94
29	Sex-Specific Development in Haplodiploid Honeybee is Controlled by the Female-Embryo-Specific Activation of Thousands of Intronic lncRNAs. SSRN Electronic Journal, 0, , .	0.4	0