

Ximiao He

List of Publications by Year in descending order

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43
papers

2,452
citations

471371

17
h-index

289141

40
g-index

45
all docs

45
docs citations

45
times ranked

4124
citing authors

#	ARTICLE	IF	CITATIONS
1	A novel multiplex assay system based on 10 methylation markers for forensic identification of body fluids. <i>Journal of Forensic Sciences</i> , 2022, 67, 136-148.	0.9	5
2	High-speed rail model reveals the gene tandem amplification mediated by short repeated sequence in eukaryote. <i>Scientific Reports</i> , 2022, 12, 2289.	1.6	0
3	Changes in transcriptomic landscape in human end-stage heart failure with distinct etiology. <i>IScience</i> , 2022, 25, 103935.	1.9	4
4	Exposure of mouse oocytes to N,N-dimethylformamide impairs mitochondrial functions and reduces oocyte quality. <i>Environmental Toxicology</i> , 2022, 37, 1563-1574.	2.1	5
5	Aberrant Expression of Mitochondrial SAM Transporter SLC25A26 Impairs Oocyte Maturation and Early Development in Mice. <i>Oxidative Medicine and Cellular Longevity</i> , 2022, 2022, 1-20.	1.9	4
6	Ppan is essential for preimplantation development in mice. <i>Biology of Reproduction</i> , 2022, , .	1.2	1
7	Genome-Wide Screen and Validation of Microglia Pro-Inflammatory Mediators in Stroke. , 2021, 12, 786.		17
8	Exogenous Coronavirus Interacts With Endogenous Retrotransposon in Human Cells. <i>Frontiers in Cellular and Infection Microbiology</i> , 2021, 11, 609160.	1.8	32
9	Two reactive behaviors of chondrocytes in an IL-1 β -induced inflammatory environment revealed by the single-cell RNA sequencing. <i>Aging</i> , 2021, 13, 11646-11664.	1.4	6
10	Cleavage-embryo genes and transposable elements are regulated by histone variant H2A.X. <i>Journal of Reproduction and Development</i> , 2021, 67, 307-312.	0.5	4
11	A Genome-Wide Investigation of Effects of Aberrant DNA Methylation on the Usage of Alternative Promoters in Hepatocellular Carcinoma. <i>Frontiers in Oncology</i> , 2021, 11, 780266.	1.3	5
12	High expression of TXNDC11 indicated unfavorable prognosis of glioma. <i>Translational Cancer Research</i> , 2021, 10, 5040-5051.	0.4	4
13	Midkine Prevents Calcification of Aortic Valve Interstitial Cells via Intercellular Crosstalk. <i>Frontiers in Cell and Developmental Biology</i> , 2021, 9, 794058.	1.8	6
14	Stable intronic sequence RNAs (sisRNAs) are selected regions in introns with distinct properties. <i>BMC Genomics</i> , 2020, 21, 287.	1.2	3
15	The impact factors of 3D genome organization. <i>Scientia Sinica Vitae</i> , 2020, 50, 465-483.	0.1	1
16	Transcriptome Sequencing Unravels Potential Biomarkers at Different Stages of Cerebral Ischemic Stroke. <i>Frontiers in Genetics</i> , 2019, 10, 814.	1.1	23
17	High levels of serum β 2-microglobulin predict severity of coronary artery disease. <i>BMC Cardiovascular Disorders</i> , 2017, 17, 71.	0.7	21
18	The Epstein-Barr Virus B-ZIP Protein Zta Recognizes Specific DNA Sequences Containing 5-Methylcytosine and 5-Hydroxymethylcytosine. <i>Biochemistry</i> , 2017, 56, 6200-6210.	1.2	17

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19	Genome-Wide Transcriptional Regulation and Chromosome Structural Arrangement by GalR in <i>E. coli</i> . <i>Frontiers in Molecular Biosciences</i> , 2016, 3, 74.	1.6	12
20	5-Hydroxymethylcytosine in E-box motifs ACAT GTG and ACAC GTG increases DNA-binding of the B-HLH transcription factor TCF4. <i>Integrative Biology (United Kingdom)</i> , 2016, 8, 936-945.	0.6	21
21	5-Methylcytosine (5mC) and 5-Hydroxymethylcytosine (5hmC) Enhance the DNA Binding of CREB1 to the C/EBP Half-Site Tetranucleotide GCAA. <i>Biochemistry</i> , 2016, 55, 6940-6948.	1.2	21
22	Integrating Epigenomics into the Understanding of Biomedical Insight. <i>Bioinformatics and Biology Insights</i> , 2016, 10, BBI.S38427.	1.0	22
23	GABP± Binding to Overlapping ETS and CRE DNA Motifs Is Enhanced by CREB1: Custom DNA Microarrays. <i>G3: Genes, Genomes, Genetics</i> , 2015, 5, 1909-1918.	0.8	4
24	A New Noncoding RNA Arranges Bacterial Chromosome Organization. <i>MBio</i> , 2015, 6, .	1.8	22
25	Methylated Cytosines Mutate to Transcription Factor Binding Sites that Drive Tetrapod Evolution. <i>Genome Biology and Evolution</i> , 2015, 7, 3155-3169.	1.1	20
26	Nucleosomes are enriched at the boundaries of hypomethylated regions (HMRS) in mouse dermal fibroblasts and keratinocytes. <i>Epigenetics and Chromatin</i> , 2014, 7, 34.	1.8	4
27	High-resolution genome-wide DNA methylation maps of mouse primary female dermal fibroblasts and keratinocytes. <i>Epigenetics and Chromatin</i> , 2014, 7, 35.	1.8	12
28	Contribution of nucleosome binding preferences and co-occurring DNA sequences to transcription factor binding. <i>BMC Genomics</i> , 2013, 14, 428.	1.2	20
29	CG methylated microarrays identify a novel methylated sequence bound by the CEBPB ATF4 heterodimer that is active in vivo. <i>Genome Research</i> , 2013, 23, 988-997.	2.4	111
30	Bookmarking by specific and nonspecific binding of FoxA1 pioneer factor to mitotic chromosomes. <i>Genes and Development</i> , 2013, 27, 251-260.	2.7	191
31	A Single-Nucleotide Polymorphism of Human Neuropeptide S Gene Originated from Europe Shows Decreased Bioactivity. <i>PLoS ONE</i> , 2013, 8, e83009.	1.1	8
32	Overlapping ETS and CRE Motifs (G/CCGGAAGTGACGTCA) Preferentially Bound by GABP± and CREB Proteins. <i>G3: Genes, Genomes, Genetics</i> , 2012, 2, 1243-1256.	0.8	11
33	Systematic evaluation of genome-wide methylated DNA enrichment using a CpG island array. <i>BMC Genomics</i> , 2011, 12, 10.	1.2	13
34	Evolution of an antifreeze protein by neofunctionalization under escape from adaptive conflict. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2010, 107, 21593-21598.	3.3	126
35	The Most Redundant Sequences in Human CpG Island Library Are Derived from Mitochondrial Genome. <i>Genomics, Proteomics and Bioinformatics</i> , 2010, 8, 81-91.	3.0	2
36	MethyCancer: the database of human DNA methylation and cancer. <i>Nucleic Acids Research</i> , 2007, 36, D836-D841.	6.5	127

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37	BGI-RIS V2. , 2007, 406, 275-299.		4
38	The Genomes of <i>Oryza sativa</i> : A History of Duplications. PLoS Biology, 2005, 3, e38.	2.6	808
39	BGI-RIS: an integrated information resource and comparative analysis workbench for rice genomics. Nucleic Acids Research, 2004, 32, 377D-382.	6.5	108
40	ChickVD: a sequence variation database for the chicken genome. Nucleic Acids Research, 2004, 33, D438-D441.	6.5	33
41	SilkDB: a knowledgebase for silkworm biology and genomics. Nucleic Acids Research, 2004, 33, D399-D402.	6.5	158
42	A genetic variation map for chicken with 2.8 million single-nucleotide polymorphisms. Nature, 2004, 432, 717-722.	13.7	391
43	The E Protein Is a Multifunctional Membrane Protein of SARS-CoV. Genomics, Proteomics and Bioinformatics, 2003, 1, 131-144.	3.0	41