Kan He

List of Publications by Year
in descending order

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38 papers	468 citations	687363 13 h-index	794594 19 g-index
40 all docs	40 docs citations	40 times ranked	901 citing authors

#	Article	IF	Citations
1	Wnt/Î²-catenin and LIF/Stat3 signaling pathways converge on Sp5 to promote mouse embryonic stem cell self-renewal. Journal of Cell Science, 2016, 129, 269-76.	2.0	43
2	Collaborative Regulation of Development but Independent Control of Metabolism by Two Epidermis-specific Transcription Factors in Caenorhabditis elegans. Journal of Biological Chemistry, 2013, 288, 33411-33426.	3.4	29
3	Association study between gene polymorphisms in PPAR signaling pathway and porcine meat quality traits. Mammalian Genome, 2013, 24, 322-331.	2.2	27
4	Systemsâ€level quantification of division timing reveals a common genetic architecture controlling asynchrony and fate asymmetry. Molecular Systems Biology, 2015, 11, 814.	7.2	27
5	1,3-Dicaffeoylquinic acid targeting 14-3-3 tau suppresses human breast cancer cell proliferation and metastasis through IL6/JAK2/PI3K pathway. Biochemical Pharmacology, 2020, 172, 113752.	4.4	26
6	Comprehensive tissue-specific gene set enrichment analysis and transcription factor analysis of breast cancer by integrating 14 gene expression datasets. Oncotarget, 2017, 8, 6775-6786.	1.8	26
7	Regulatory network reconstruction of five essential microRNAs for survival analysis in breast cancer by integrating miRNA and mRNA expression datasets. Functional and Integrative Genomics, 2019, 19, 645-658.	3.5	25
8	A cross-study gene set enrichment analysis identifies critical pathways in endometriosis. Reproductive Biology and Endocrinology, 2009, 7, 94.	3.3	20
9	A comparative genome analysis of gene expression reveals different regulatory mechanisms between mouse and human embryo pre-implantation development. Reproductive Biology and Endocrinology, 2010, 8, 41.	3.3	19
10	Depletion of Tcf3 and Lef1 maintains mouse embryonic stem cell self-renewal. Biology Open, 2017, 6, 511-517.	1.2	17
11	Identification of high-copper-responsive target pathways in Atp7b knockout mouse liver by GSEA on microarray data sets. Mammalian Genome, 2011, 22, 703-713.	2.2	16
12	A comprehensive meta-analysis of genetic associations between five key SNPs and colorectal cancer risk. Oncotarget, 2016, 7, 73945-73959.	1.8	16
13	Transcriptome Analysis of the Gene Expression Profiles Associated with Fungal Keratitis in Mice Based on RNA-Seq. , 2020, 61, 32.		15
14	Associations between gene polymorphisms in two crucial metabolic pathways and growth traits in pigs. Science Bulletin, 2012, 57, 2733-2740.	1.7	14
15	Gene set enrichment analysis of pathways and transcription factors associated with diabetic retinopathy using a microarray dataset. International Journal of Molecular Medicine, 2015, 36, 103-112.	4.0	14
16	Dynamic regulation of genetic pathways and targets during aging in Caenorhabditis elegans. Aging, 2014, 6, 215-230.	3.1	13
17	A Comparative Study of Mouse Hepatic and Intestinal Gene Expression Profiles under PPARÎ±Knockout by Gene Set Enrichment Analysis. PPAR Research, 2011, 2011, 1-10.	2.4	11
18	A systematic analysis of the association studies between CASP8 D302H polymorphisms and breast cancer risk. Journal of Genetics, 2017, 96, 283-289.	0.7	10

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19	Functional genomics study of protein inhibitor of activated STAT1 in mouse hippocampal neuronal cells revealed by RNA sequencing. Aging, 2021, 13, 9011-9027.	3.1	10
20	Comprehensive analysis of gene expression profiles associated with proliferative diabetic retinopathy. Experimental and Therapeutic Medicine, 2018, 16, 3539-3545.	1.8	9
21	Mechanism study of the beneficial effect of sodium selenite on metabolic disorders in imidacloprid-treated garlic plants. Ecotoxicology and Environmental Safety, 2020, 200, 110736.	6.0	9
22	Regulatory function of praja ring finger ubiquitin ligase 2 mediated by the P2rx3/P2rx7 axis in mouse hippocampal neuronal cells. American Journal of Physiology - Cell Physiology, 2020, 318, C1123-C1135.	4.6	9
23	Identification of hub ubiquitin ligase genes affecting Alzheimerâ€™s disease by analyzing transcriptome data from multiple brain regions. Science Progress, 2021, 104, 003685042110011.	1.9	9
24	Comprehensive identification of essential pathways and transcription factors related to epilepsy by gene set enrichment analysis on microarray datasets. International Journal of Molecular Medicine, 2014, 34, 715-724.	4.0	8
25	The stromal genome heterogeneity between breast and prostate tumors revealed by a comparative transcriptomic analysis. Oncotarget, 2015, 6, 8687-8697.	1.8	8
26	A transcriptomic study of myogenic differentiation under the overexpression of PPARÎ³ by RNA-Seq. Scientific Reports, 2017, 7, 15308.	3.3	8
27	A transcriptomic analysis of Nsmce1 overexpression in mouse hippocampal neuronal cell by RNA sequencing. Functional and Integrative Genomics, 2020, 20, 459-470.	3.5	5
28	Effect of selenium-enriched kiwifruit on body fat reduction and liver protection in hyperlipidaemic mice. Food and Function, 2021, 12, 2044-2057.	4.6	5
29	Transcriptome study of oleanolic acid in the inhibition of breast tumor growth based on high-throughput sequencing. Aging, 2021, 13, 22883-22897.	3.1	5
30	The prediction of the porcine pre-microRNAs in genome-wide based on support vector machine (SVM) and homology searching. BMC Genomics, 2012, 13, 729.	2.8	3
31	A transcriptomic study of selenium against liver injury induced by beta-cypermethrin in mice by RNA-seq. Functional and Integrative Genomics, 2020, 20, 343-353.	3.5	3
32	The comprehensive transcriptional analysis in Caenorhabditis elegans by integrating ChIP-seq and gene expression data. Genetical Research, 2014, 96, e005.	0.9	2
33	Comprehensive integrated analysis of gene expression datasets identifies key antiâ€cancer targets in different stages of breast cancer. Experimental and Therapeutic Medicine, 2018, 16, 802-810.	1.8	2
34	A meta-analysis study of gene expression datasets in mouse liver under PPARÎ± knockout. Genetical Research, 2013, 95, 78-88.	0.9	1
35	Wnt/Î²-catenin and LIFâ€“Stat3 signaling pathways converge on Sp5 to promote mouse embryonic stem cell self-renewal. Development (Cambridge), 2016, 143, e1.1-e1.1.	2.5	1
36	A comprehensive transcriptomic analysis of differentiating embryonic stem cells in response to the overexpression of Mesogenin 1. Aging, 2016, 8, 2324-2336.	3.1	1

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37	Comparative study of the promotion of porcine fetal fibroblast proliferation by overexpression of two transcriptional variants of SIRT6. Science Bulletin, 2013, 58, 1169-1174.	1.7	0
38	Study of the Mechanism of the Reyanning Mixture Involved in Treating Novel Coronavirus Pneumonia Based on Network Pharmacology. Natural Product Communications, 2020, 15, 1934578X2095459.	0.5	0