

# Kan He

## List of Publications by Year in descending order

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Version: 2024-02-01

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	Identification of hub ubiquitin ligase genes affecting Alzheimer's disease by analyzing transcriptome data from multiple brain regions. <i>Science Progress</i> , 2021, 104, 003685042110011.	1.9	9
2	Effect of selenium-enriched kiwifruit on body fat reduction and liver protection in hyperlipidaemic mice. <i>Food and Function</i> , 2021, 12, 2044-2057.	4.6	5
3	Functional genomics study of protein inhibitor of activated STAT1 in mouse hippocampal neuronal cells revealed by RNA sequencing. <i>Aging</i> , 2021, 13, 9011-9027.	3.1	10
4	Transcriptome study of oleanolic acid in the inhibition of breast tumor growth based on high-throughput sequencing. <i>Aging</i> , 2021, 13, 22883-22897.	3.1	5
5	A transcriptomic study of selenium against liver injury induced by beta-cypermethrin in mice by RNA-seq. <i>Functional and Integrative Genomics</i> , 2020, 20, 343-353.	3.5	3
6	1,3-Dicaffeoylquinic acid targeting 14-3-3 tau suppresses human breast cancer cell proliferation and metastasis through IL6/JAK2/PI3K pathway. <i>Biochemical Pharmacology</i> , 2020, 172, 113752.	4.4	26
7	A transcriptomic analysis of Nsmce1 overexpression in mouse hippocampal neuronal cell by RNA sequencing. <i>Functional and Integrative Genomics</i> , 2020, 20, 459-470.	3.5	5
8	Study of the Mechanism of the Reyaning Mixture Involved in Treating Novel Coronavirus Pneumonia Based on Network Pharmacology. <i>Natural Product Communications</i> , 2020, 15, 1934578X2095459.	0.5	0
9	Transcriptome Analysis of the Gene Expression Profiles Associated with Fungal Keratitis in Mice Based on RNA-Seq. , 2020, 61, 32.		15
10	Mechanism study of the beneficial effect of sodium selenite on metabolic disorders in imidacloprid-treated garlic plants. <i>Ecotoxicology and Environmental Safety</i> , 2020, 200, 110736.	6.0	9
11	Regulatory function of praja ring finger ubiquitin ligase 2 mediated by the <i>P2rx3/P2rx7</i> axis in mouse hippocampal neuronal cells. <i>American Journal of Physiology - Cell Physiology</i> , 2020, 318, C1123-C1135.	4.6	9
12	Regulatory network reconstruction of five essential microRNAs for survival analysis in breast cancer by integrating miRNA and mRNA expression datasets. <i>Functional and Integrative Genomics</i> , 2019, 19, 645-658.	3.5	25
13	Comprehensive analysis of gene expression profiles associated with proliferative diabetic retinopathy. <i>Experimental and Therapeutic Medicine</i> , 2018, 16, 3539-3545.	1.8	9
14	Comprehensive integrated analysis of gene expression datasets identifies key anti-cancer targets in different stages of breast cancer. <i>Experimental and Therapeutic Medicine</i> , 2018, 16, 802-810.	1.8	2
15	Depletion of <i>Tcf3</i> and <i>Lef1</i> maintains mouse embryonic stem cell self-renewal. <i>Biology Open</i> , 2017, 6, 511-517.	1.2	17
16	A transcriptomic study of myogenic differentiation under the overexpression of PPAR $\gamma$ by RNA-Seq. <i>Scientific Reports</i> , 2017, 7, 15308.	3.3	8
17	A systematic analysis of the association studies between CASP8 D302H polymorphisms and breast cancer risk. <i>Journal of Genetics</i> , 2017, 96, 283-289.	0.7	10
18	Comprehensive tissue-specific gene set enrichment analysis and transcription factor analysis of breast cancer by integrating 14 gene expression datasets. <i>Oncotarget</i> , 2017, 8, 6775-6786.	1.8	26

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19	Wnt/ $\beta$ -catenin and LIF/Stat3 signaling pathways converge on Sp5 to promote mouse embryonic stem cell self-renewal. <i>Journal of Cell Science</i> , 2016, 129, 269-76.	2.0	43
20	A comprehensive meta-analysis of genetic associations between five key SNPs and colorectal cancer risk. <i>Oncotarget</i> , 2016, 7, 73945-73959.	1.8	16
21	Wnt/ $\beta$ -catenin and LIF/Stat3 signaling pathways converge on Sp5 to promote mouse embryonic stem cell self-renewal. <i>Development (Cambridge)</i> , 2016, 143, e1.1-e1.1.	2.5	1
22	A comprehensive transcriptomic analysis of differentiating embryonic stem cells in response to the overexpression of Mesogenin 1. <i>Aging</i> , 2016, 8, 2324-2336.	3.1	1
23	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
24	The stromal genome heterogeneity between breast and prostate tumors revealed by a comparative transcriptomic analysis. <i>Oncotarget</i> , 2015, 6, 8687-8697.	1.8	8
25	Gene set enrichment analysis of pathways and transcription factors associated with diabetic retinopathy using a microarray dataset. <i>International Journal of Molecular Medicine</i> , 2015, 36, 103-112.	4.0	14
26	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
27	Comprehensive identification of essential pathways and transcription factors related to epilepsy by gene set enrichment analysis on microarray datasets. <i>International Journal of Molecular Medicine</i> , 2014, 34, 715-724.	4.0	8
28	Dynamic regulation of genetic pathways and targets during aging in <i>Caenorhabditis elegans</i> . <i>Aging</i> , 2014, 6, 215-230.	3.1	13
29	Association study between gene polymorphisms in PPAR signaling pathway and porcine meat quality traits. <i>Mammalian Genome</i> , 2013, 24, 322-331.	2.2	27
30	Comparative study of the promotion of porcine fetal fibroblast proliferation by overexpression of two transcriptional variants of SIRT6. <i>Science Bulletin</i> , 2013, 58, 1169-1174.	1.7	0
31	A meta-analysis study of gene expression datasets in mouse liver under PPAR $\alpha$ knockout. <i>Genetical Research</i> , 2013, 95, 78-88.	0.9	1
32	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
33	The prediction of the porcine pre-microRNAs in genome-wide based on support vector machine (SVM) and homology searching. <i>BMC Genomics</i> , 2012, 13, 729.	2.8	3
34	Associations between gene polymorphisms in two crucial metabolic pathways and growth traits in pigs. <i>Science Bulletin</i> , 2012, 57, 2733-2740.	1.7	14
35	Identification of high-copper-responsive target pathways in Atp7b knockout mouse liver by GSEA on microarray data sets. <i>Mammalian Genome</i> , 2011, 22, 703-713.	2.2	16
36	A Comparative Study of Mouse Hepatic and Intestinal Gene Expression Profiles under PPAR $\alpha$ Knockout by Gene Set Enrichment Analysis. <i>PPAR Research</i> , 2011, 2011, 1-10.	2.4	11

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37	A comparative genome analysis of gene expression reveals different regulatory mechanisms between mouse and human embryo pre-implantation development. <i>Reproductive Biology and Endocrinology</i> , 2010, 8, 41.	3.3	19
38	A cross-study gene set enrichment analysis identifies critical pathways in endometriosis. <i>Reproductive Biology and Endocrinology</i> , 2009, 7, 94.	3.3	20