

Fuhong He

List of Publications by Year in descending order

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Version: 2024-02-01

27
papers

1,103
citations

567281

15
h-index

713466

21
g-index

27
all docs

27
docs citations

27
times ranked

2472
citing authors

#	ARTICLE	IF	CITATIONS
1	Analyses of Long Noncoding RNA and mRNA Profiles in Subjects with the Phlegm-Dampness Constitution. <i>BioMed Research International</i> , 2021, 2021, 1-14.	1.9	4
2	Identification of Chemo-Resistant Residual Cell Population in Pediatric AML of Complete Remission By Single Cell RNA Sequencing. <i>Blood</i> , 2020, 136, 25-26.	1.4	0
3	Benzene metabolite hydroquinone promotes DNA homologous recombination repair via the NF- κ B pathway. <i>Carcinogenesis</i> , 2019, 40, 1021-1030.	2.8	12
4	Ecological principle meets cancer treatment: treating children with acute myeloid leukemia with low-dose chemotherapy. <i>National Science Review</i> , 2019, 6, 469-479.	9.5	9
5	PDGFRB mutation and tyrosine kinase inhibitor resistance in Ph-like acute lymphoblastic leukemia. <i>Blood</i> , 2018, 131, 2256-2261.	1.4	49
6	SETD2-mediated crosstalk between H3K36me3 and H3K79me2 in MLL-rearranged leukemia. <i>Leukemia</i> , 2018, 32, 890-899.	7.2	29
7	Chromatin regulator Asx1 loss and Nf1 haploinsufficiency cooperate to accelerate myeloid malignancy. <i>Journal of Clinical Investigation</i> , 2018, 128, 5383-5398.	8.2	25
8	Cooperative Epigenetic Regulation By ASXL1 and NF1 Loss on Leukemogenesis. <i>Blood</i> , 2018, 132, 652-652.	1.4	0
9	Loss of Asx2 leads to myeloid malignancies in mice. <i>Nature Communications</i> , 2017, 8, 15456.	12.8	23
10	Loss of Asx1 Alters Self-Renewal and Cell Fate of Bone Marrow Stromal Cells, Leading to Bohring-Opitz-like Syndrome in Mice. <i>Stem Cell Reports</i> , 2016, 6, 914-925.	4.8	18
11	Downregulation of SETD2-H3K36me3 Tumor Suppression Axis Promotes MLL Leukemia through Activation of DOT1L-H3K79me2 Axis. <i>Blood</i> , 2016, 128, 435-435.	1.4	0
12	Clinical Outcome and Non-Synonymous Mutation Clearance in Chinese Children with Acute Myeloid Leukemia Treated with a Low-Intensity Induction Chemotherapy Regimen. <i>Blood</i> , 2016, 128, 2848-2848.	1.4	0
13	Regulation of MEIS1 by distal enhancer elements in acute leukemia. <i>Leukemia</i> , 2014, 28, 138-146.	7.2	17
14	Reprogramming of MLL-AF9 leukemia cells into pluripotent stem cells. <i>Leukemia</i> , 2014, 28, 1071-1080.	7.2	40
15	Identification of functional cooperative mutations of SETD2 in human acute leukemia. <i>Nature Genetics</i> , 2014, 46, 287-293.	21.4	213
16	Rictor/mammalian target of rapamycin 2 regulates the development of notch1 induced murine T-cell acute lymphoblastic leukemia via forkhead box O3. <i>Experimental Hematology</i> , 2014, 42, 1031-1040.e4.	0.4	14
17	Downregulation of RUNX1/CBF β by MLL fusion proteins enhances hematopoietic stem cell self-renewal. <i>Blood</i> , 2014, 123, 1729-1738.	1.4	29
18	PLI.1 is essential for MLL leukemia partially via crosstalk with the MEIS/HOX pathway. <i>Leukemia</i> , 2014, 28, 1436-1448.	7.2	45

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19	PU.1 Is Essential For MLL Leukemia Via Activation Of The Meis/HOX Pathway and A Monocytic Cytokine Mediated Anti-Apoptotic Inflammatory Program. <i>Blood</i> , 2013, 122, 1276-1276.	1.4	0
20	Gene and Genome Parameters of Mammalian Liver Circadian Genes (LCGs). <i>PLoS ONE</i> , 2012, 7, e46961.	2.5	10
21	Whole-Genome Sequencing of a Monozygotic Twin Pair Reveals Functional Cooperative Mutations of SETD2 in Acute Leukemia. <i>Blood</i> , 2012, 120, 781-781.	1.4	0
22	MLL fusion proteins preferentially regulate a subset of wild-type MLL target genes in the leukemic genome. <i>Blood</i> , 2011, 117, 6895-6905.	1.4	103
23	A Novel Role for Minimal Introns: Routing mRNAs to the Cytosol. <i>PLoS ONE</i> , 2010, 5, e10144.	2.5	27
24	How Do Variable Substitution Rates Influence Ka and Ks Calculations?. <i>Genomics, Proteomics and Bioinformatics</i> , 2009, 7, 116-127.	6.9	42
25	How many human genes can be defined as housekeeping with current expression data?. <i>BMC Genomics</i> , 2008, 9, 172.	2.8	125
26	On the nature of human housekeeping genes. <i>Trends in Genetics</i> , 2008, 24, 481-484.	6.7	249
27	Modeling Transcriptome Based on Transcript-Sampling Data. <i>PLoS ONE</i> , 2008, 3, e1659.	2.5	20