Yuanhang Liu

List of Publications by Year in descending order

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933447 996975 20 252 10 15 citations h-index g-index papers 20 20 20 560 docs citations times ranked citing authors all docs

#	Article	IF	Citations
1	Global mapping of H3K4me3 and H3K27me3 reveals chromatin state-based regulation of human monocyte-derived dendritic cells in different environments. Genes and Immunity, 2012, 13, 311-320.	4.1	43
2	Gene expression differences between matched pairs of ovarian cancer patient tumors and patient-derived xenografts. Scientific Reports, 2019, 9, 6314.	3.3	33
3	Outcomes of <scp><i>TP53</i></scp> â€mutated <scp>AML</scp> with evolving frontline therapies: Impact of allogeneic stem cell transplantation on survival. American Journal of Hematology, 2022, 97, .	4.1	24
4	Ex Vivo Hepatocyte Reprograming Promotes Homologyâ€Directed DNA Repair to Correct Metabolic Disease in Mice After Transplantation. Hepatology Communications, 2019, 3, 558-573.	4.3	19
5	A combined gene expression and functional study reveals the crosstalk between N-Myc and differentiation-inducing microRNAs in neuroblastoma cells. Oncotarget, 2016, 7, 79372-79387.	1.8	16
6	Molecular and Immunohistochemical Analysis of Mucinous Cystic Neoplasm of the Liver. American Journal of Clinical Pathology, 2020, 154, 837-847.	0.7	14
7	Adenosine A $<$ sub $>$ 2A $<$ /sub $>$ receptor blockade prevents cisplatin-induced impairments in neurogenesis and cognitive function. Proceedings of the National Academy of Sciences of the United States of America, 2022, 119, .	7.1	14
8	Concomitant Erdheim hester disease and chronic myelomonocytic leukaemia: genomic insights into a common clonal origin. British Journal of Haematology, 2019, 187, e51-e54.	2.5	13
9	Dendritic Cell-Associated miRNAs Are Modulated via Chromatin Remodeling in Response to Different Environments. PLoS ONE, 2014, 9, e90231.	2.5	13
10	Differential expression analysis of RNA sequencing data by incorporating non-exonic mapped reads. BMC Genomics, 2015, 16, S14.	2.8	12
11	Bone marrow findings in Erdheim-Chester disease: increased prevalence of chronic myeloid neoplasms. Haematologica, 2020, 105, e84-e86.	3.5	12
12	XBSeq2: a fast and accurate quantification of differential expression and differential polyadenylation. BMC Bioinformatics, 2017, 18, 384.	2.6	11
13	Renal Artery Stenosis Alters Gene Expression in Swine Scattered Tubular-Like Cells. International Journal of Molecular Sciences, 2019, 20, 5069.	4.1	9
14	Impact of obesity on the molecular response to a single bout ofÂexercise in a preliminary human cohort. Obesity, 2022, 30, 1091-1104.	3.0	5
15	Differentially Expressed Functional LncRNAs in Human Subjects With Metabolic Syndrome Reflect a Competing Endogenous RNA Network in Circulating Extracellular Vesicles. Frontiers in Molecular Biosciences, 2021, 8, 667056.	3.5	4
16	MBDDiff: an R package designed specifically for processing MBDcap-seq datasets. BMC Genomics, 2016, 17, 432.	2.8	3
17	A microRNA Transcriptome-wide Association Study of Prostate Cancer Risk. Frontiers in Genetics, 2022, 13, 836841.	2.3	3
18	Somatic mutations in benign breast disease tissues and association with breast cancer risk. BMC Medical Genomics, 2021, 14, 185.	1.5	2

#	Article	IF	CITATIONS
19	2dFDR: a new approach to confounder adjustment substantially increases detection power in omics association studies. Genome Biology, 2021, 22, 208.	8.8	2
20	Model-based and context-specific background correction and differential methylation testing for MBDCap-seq., 2015,,.		0