Xiao-Ou Zhang

List of Publications by Citations

29	4,602	18	39
papers	citations	h-index	g-index

39	6,315	18	5.4
ext. papers	ext. citations	avg, IF	L-index

#	Paper	IF	Citations
29	Circular intronic long noncoding RNAs. *Molecular Cell*, **2013**, 51, 792-806	17.6	1352
28	Complementary sequence-mediated exon circularization. *Cell*, **2014**, 159, 134-147	56.2	1144
27	Diverse alternative back-splicing and alternative splicing landscape of circular RNAs. *Genome Research*, **2016**, 26, 1277-87	9.7	482
26	Human colorectal cancer-specific CCAT1-L lncRNA regulates long-range chromatin interactions at the MYC locus. *Cell Research*, **2014**, 24, 513-31	24.7	471
25	Expanded encyclopaedias of DNA elements in the human and mouse genomes. *Nature*, **2020**, 583, 699-710	30.4	360
24	Identification of multipotent mammary stem cells by protein C receptor expression. *Nature*, **2015**, 517, 81-4	50.4	236
23	CRISPR/Cas9-mediated genome editing induces exon skipping by alternative splicing or exon deletion. *Genome Biology*, **2017**, 18, 108	18.3	103
22	CircRNA-derived pseudogenes. *Cell Research*, **2016**, 26, 747-50	24.7	72
21	ADAR1 is required for differentiation and neural induction by regulating microRNA processing in a catalytically independent manner. *Cell Research*, **2015**, 25, 459-76	24.7	60
20	Species-specific alternative splicing leads to unique expression of sno-lncRNAs. *BMC Genomics*, **2014**, 15, 287	4.5	35
19	Mitochondrial DNA Stress Signalling Protects the Nuclear Genome. *Nature Metabolism*, **2019**, 1, 1209-1218	13.6	34
18	Chemical modifications of adenine base editor mRNA and guide RNA expand its application scope. *Nature Communications*, **2020**, 11, 1979	17.4	31
17	Genome-wide analysis of polymerase III-transcribed elements suggests cell-type-specific enhancer function. *Genome Research*, **2019**, 29, 1402-1414	9.7	31
16	Optimized RNA-targeting CRISPR/Cas13d technology outperforms shRNA in identifying functional circRNAs. *Genome Biology*, **2021**, 22, 41	18.3	27
15	Depletion of TRRAP Induces p53-Independent Senescence in Liver Cancer by Down-Regulating Mitotic Genes. *Hepatology*, **2020**, 71, 275-290	11.2	24
14	Comprehensive identification of alternative back-splicing in human tissue transcriptomes. *Nucleic Acids Research*, **2020**, 48, 1779-1789	20.1	22
13	Inhibition of protein arginine methyltransferase 5 enhances hepatic mitochondrial biogenesis. *Journal of Biological Chemistry*, **2018**, 293, 10884-10894	5.4	22

LIST OF PUBLICATIONS

12	Co-dependent Assembly of Drosophila piRNA Precursor Complexes and piRNA Cluster Heterochromatin. *Cell Reports*, **2018**, 24, 3413-3422.e4	10.6	18
11	Deletion and replacement of long genomic sequences using prime editing. *Nature Biotechnology*, **2021**,	44.5	13
10	Panning for Long Noncoding RNAs. *Biomolecules*, **2013**, 3, 226-41	5.9	12
9	Gene expression profiling of non-polyadenylated RNA-seq across species. *Genomics Data*, **2014**, 2, 237-41		11
8	The temporal landscape of recursive splicing during Pol II transcription elongation in human cells. *PLoS Genetics*, **2018**, 14, e1007579	6	9
7	YAP1 Withdrawal in Hepatoblastoma Drives Therapeutic Differentiation of Tumor Cells to Functional Hepatocyte-Like Cells. *Hepatology*, **2021**, 73, 1011-1027	11.2	6
6	Optimized RNA-targeting CRISPR/Cas13d technology outperforms shRNA in identifying essential circRNAs		5
5	5ᴰModifications improve potency and efficacy of DNA donors for precision genome editing. *ELife*, **2021**, 10,	8.9	4
4	Investigating the Potential Roles of SINEs in the Human Genome. *Annual Review of Genomics and Human Genetics*, **2021**, 22, 199-218	9.7	3
3	Programming large target genomic deletion and concurrent insertion via a prime editing-based method: PEDAR		1
2	Genetic and epigenetic features of promoters with ubiquitous chromatin accessibility support ubiquitous transcription of cell-essential genes. *Nucleic Acids Research*, **2021**, 49, 5705-5725	20.1	0
1	Modeling and identifying therapeutic targets in Hepatoblastoma.. *Journal of Clinical Oncology*, **2019**, 37, e21518-e21518	2.2	