## Xiao-Ou Zhang

List of Publications by Year in descending order

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#	Article	IF	CITATIONS
1	Circular Intronic Long Noncoding RNAs. Molecular Cell, 2013, 51, 792-806.	4.5	1,858
2	Complementary Sequence-Mediated Exon Circularization. Cell, 2014, 159, 134-147.	13.5	1,638
3	Expanded encyclopaedias of DNA elements in the human and mouse genomes. Nature, 2020, 583, 699-710.	13.7	1,252
4	Diverse alternative back-splicing and alternative splicing landscape of circular RNAs. Genome Research, 2016, 26, 1277-1287.	2.4	799
5	Human colorectal cancer-specific CCAT1-L IncRNA regulates long-range chromatin interactions at the MYC locus. Cell Research, 2014, 24, 513-531.	5.7	588
6	Identification of multipotent mammary stem cells by protein C receptor expression. Nature, 2015, 517, 81-84.	13.7	290
7	CRISPR/Cas9-mediated genome editing induces exon skipping by alternative splicing or exon deletion. Genome Biology, 2017, 18, 108.	3.8	141
8	CircRNA-derived pseudogenes. Cell Research, 2016, 26, 747-750.	5.7	96
9	Deletion and replacement of long genomic sequences using prime editing. Nature Biotechnology, 2022, 40, 227-234.	9.4	90
10	Mitochondrial DNA stress signalling protects the nuclear genome. Nature Metabolism, 2019, 1, 1209-1218.	5.1	87
11	Optimized RNA-targeting CRISPR/Cas13d technology outperforms shRNA in identifying functional circRNAs. Genome Biology, 2021, 22, 41.	3.8	75
12	ADAR1 is required for differentiation and neural induction by regulating microRNA processing in a catalytically independent manner. Cell Research, 2015, 25, 459-476.	5.7	73
13	Genome-wide analysis of polymerase III–transcribed <i>Alu</i> elements suggests cell-type–specific enhancer function. Genome Research, 2019, 29, 1402-1414.	2.4	69
14	Chemical modifications of adenine base editor mRNA and guide RNA expand its application scope. Nature Communications, 2020, 11, 1979.	5.8	66
15	Depletion of TRRAP Induces p53â€Independent Senescence in Liver Cancer by Downâ€Regulating Mitotic Genes. Hepatology, 2020, 71, 275-290.	3.6	43
16	Species-specific alternative splicing leads to unique expression of sno-lncRNAs. BMC Genomics, 2014, 15, 287.	1.2	42
17	Inhibition of protein arginine methyltransferase 5 enhances hepatic mitochondrial biogenesis. Journal of Biological Chemistry, 2018, 293, 10884-10894.	1.6	38
18	Comprehensive identification of alternative back-splicing in human tissue transcriptomes. Nucleic Acids Research. 2020. 48. 1779-1789.	6.5	33

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19	5′-Modifications improve potency and efficacy of DNA donors for precision genome editing. ELife, 2021, 10, .	2.8	30
20	Co-dependent Assembly of Drosophila piRNA Precursor Complexes and piRNA Cluster Heterochromatin. Cell Reports, 2018, 24, 3413-3422.e4.	2.9	29
21	PRMT5 activates AKT via methylation to promote tumor metastasis. Nature Communications, 2022, 13, .	5.8	25
22	The temporal landscape of recursive splicing during Pol II transcription elongation in human cells. PLoS Genetics, 2018, 14, e1007579.	1.5	17
23	Gene expression profiling of non-polyadenylated RNA-seq across species. Genomics Data, 2014, 2, 237-241.	1.3	16
24	Investigating the Potential Roles of SINEs in the Human Genome. Annual Review of Genomics and Human Genetics, 2021, 22, 199-218.	2.5	16
25	Panning for Long Noncoding RNAs. Biomolecules, 2013, 3, 226-241.	1.8	13
26	YAP1 Withdrawal in Hepatoblastoma Drives Therapeutic Differentiation of Tumor Cells to Functional Hepatocyteâ€Like Cells. Hepatology, 2021, 73, 1011-1027.	3.6	10
27	Genetic and epigenetic features of promoters with ubiquitous chromatin accessibility support ubiquitous transcription of cell-essential genes. Nucleic Acids Research, 2021, 49, 5705-5725.	6.5	10
28	Integration of high-resolution promoter profiling assays reveals novel, cell type–specific transcription start sites across 115 human cell and tissue types. Genome Research, 2022, 32, 389-402.	2.4	8
29	Abstract 3374: CRISPR/Cas9 mediated genome editing induces exon skipping by alternative splicing or exon deletion. , 2018, , .		2
30	Modeling and identifying therapeutic targets in Hepatoblastoma Journal of Clinical Oncology, 2019, 37, e21518-e21518.	0.8	0