

Xiao-Ou Zhang

List of Publications by Year in Descending Order

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The third column is the impact factor (IF) of the journal, and the fourth column is the number of citations of the article.

29
papers

4,602
citations

18
h-index

39
g-index

39
ext. papers

6,315
ext. citations

18
avg, IF

5.4
L-index

#	Paper	IF	Citations
29	Deletion and replacement of long genomic sequences using prime editing. <i>Nature Biotechnology</i> , 2021 ,	44.5	13
28	5dModifications improve potency and efficacy of DNA donors for precision genome editing. <i>ELife</i> , 2021 , 10,	8.9	4
27	Genetic and epigenetic features of promoters with ubiquitous chromatin accessibility support ubiquitous transcription of cell-essential genes. <i>Nucleic Acids Research</i> , 2021 , 49, 5705-5725	20.1	0
26	YAP1 Withdrawal in Hepatoblastoma Drives Therapeutic Differentiation of Tumor Cells to Functional Hepatocyte-Like Cells. <i>Hepatology</i> , 2021 , 73, 1011-1027	11.2	6
25	Investigating the Potential Roles of SINEs in the Human Genome. <i>Annual Review of Genomics and Human Genetics</i> , 2021 , 22, 199-218	9.7	3
24	Optimized RNA-targeting CRISPR/Cas13d technology outperforms shRNA in identifying functional circRNAs. <i>Genome Biology</i> , 2021 , 22, 41	18.3	27
23	Comprehensive identification of alternative back-splicing in human tissue transcriptomes. <i>Nucleic Acids Research</i> , 2020 , 48, 1779-1789	20.1	22
22	Chemical modifications of adenine base editor mRNA and guide RNA expand its application scope. <i>Nature Communications</i> , 2020 , 11, 1979	17.4	31
21	Expanded encyclopaedias of DNA elements in the human and mouse genomes. <i>Nature</i> , 2020 , 583, 699-710	40.4	360
20	Depletion of TRRAP Induces p53-Independent Senescence in Liver Cancer by Down-Regulating Mitotic Genes. <i>Hepatology</i> , 2020 , 71, 275-290	11.2	24
19	Genome-wide analysis of polymerase III-transcribed elements suggests cell-type-specific enhancer function. <i>Genome Research</i> , 2019 , 29, 1402-1414	9.7	31
18	Modeling and identifying therapeutic targets in Hepatoblastoma.. <i>Journal of Clinical Oncology</i> , 2019 , 37, e21518-e21518	2.2	
17	Mitochondrial DNA Stress Signalling Protects the Nuclear Genome. <i>Nature Metabolism</i> , 2019 , 1, 1209-1218	18.6	34
16	Co-dependent Assembly of Drosophila piRNA Precursor Complexes and piRNA Cluster Heterochromatin. <i>Cell Reports</i> , 2018 , 24, 3413-3422.e4	10.6	18
15	The temporal landscape of recursive splicing during Pol II transcription elongation in human cells. <i>PLoS Genetics</i> , 2018 , 14, e1007579	6	9
14	Inhibition of protein arginine methyltransferase 5 enhances hepatic mitochondrial biogenesis. <i>Journal of Biological Chemistry</i> , 2018 , 293, 10884-10894	5.4	22
13	CRISPR/Cas9-mediated genome editing induces exon skipping by alternative splicing or exon deletion. <i>Genome Biology</i> , 2017 , 18, 108	18.3	103

12	Diverse alternative back-splicing and alternative splicing landscape of circular RNAs. <i>Genome Research</i> , 2016 , 26, 1277-87	9.7	482
11	CircRNA-derived pseudogenes. <i>Cell Research</i> , 2016 , 26, 747-50	24.7	72
10	ADAR1 is required for differentiation and neural induction by regulating microRNA processing in a catalytically independent manner. <i>Cell Research</i> , 2015 , 25, 459-76	24.7	60
9	Identification of multipotent mammary stem cells by protein C receptor expression. <i>Nature</i> , 2015 , 517, 81-4	50.4	236
8	Gene expression profiling of non-polyadenylated RNA-seq across species. <i>Genomics Data</i> , 2014 , 2, 237-41		11
7	Complementary sequence-mediated exon circularization. <i>Cell</i> , 2014 , 159, 134-147	56.2	1144
6	Species-specific alternative splicing leads to unique expression of sno-lncRNAs. <i>BMC Genomics</i> , 2014 , 15, 287	4.5	35
5	Human colorectal cancer-specific CCAT1-L lncRNA regulates long-range chromatin interactions at the MYC locus. <i>Cell Research</i> , 2014 , 24, 513-31	24.7	471
4	Circular intronic long noncoding RNAs. <i>Molecular Cell</i> , 2013 , 51, 792-806	17.6	1352
3	Panning for Long Noncoding RNAs. <i>Biomolecules</i> , 2013 , 3, 226-41	5.9	12
2	Optimized RNA-targeting CRISPR/Cas13d technology outperforms shRNA in identifying essential circRNAs		5
1	Programming large target genomic deletion and concurrent insertion via a prime editing-based method: PEDAR		1