

# Xiao-Long Cui

## 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.

25  
papers

1,173  
citations

14  
h-index

30  
g-index

30  
ext. papers

1,900  
ext. citations

14.8  
avg, IF

4.2  
L-index

#	Paper	IF	Citations
25	The METTL5-TRMT112 N-methyladenosine methyltransferase complex regulates mRNA translation via 18S rRNA methylation.. <i>Journal of Biological Chemistry</i> , <b>2022</b> , 101590	5.4	2
24	FTO mediates LINE1 mA demethylation and chromatin regulation in mESCs and mouse development.. <i>Science</i> , <b>2022</b> , eabe9582	33.3	4
23	Autophagy of the mA mRNA demethylase FTO is impaired by low-level arsenic exposure to promote tumorigenesis. <i>Nature Communications</i> , <b>2021</b> , 12, 2183	17.4	19
22	Post-translational modification of RNA m6A demethylase ALKBH5 regulates ROS-induced DNA damage response. <i>Nucleic Acids Research</i> , <b>2021</b> , 49, 5779-5797	20.1	13
21	Multi-cancer detection and tissue of origin determination based on 5-hydroxymethylcytosine biomarkers in circulating cell-free DNA.. <i>Journal of Clinical Oncology</i> , <b>2021</b> , 39, 3123-3123	2.2	0
20	Alterations of 5-hydroxymethylation in circulating cell-free DNA reflect molecular distinctions of subtypes of non-Hodgkin lymphoma. <i>Npj Genomic Medicine</i> , <b>2021</b> , 6, 11	6.2	3
19	A Critical Role of Nuclear m6A Reader YTHDC1 in Leukemogenesis by Regulating MCM Complex-Mediated DNA Replication. <i>Blood</i> , <b>2021</b> ,	2.2	9
18	METTL14 facilitates global genome repair and suppresses skin tumorigenesis. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , <b>2021</b> , 118,	11.5	15
17	An integrative analysis of genome-wide 5-hydroxymethylcytosines in circulating cell-free DNA detects noninvasive diagnostic markers for gliomas. <i>Neuro-Oncology Advances</i> , <b>2021</b> , 3, vdab049	0.9	4
16	N-Deoxyadenosine Methylation in Mammalian Mitochondrial DNA. <i>Molecular Cell</i> , <b>2020</b> , 78, 382-395.e8	17.6	66
15	DNA 5-Methylcytosine-Specific Amplification and Sequencing. <i>Journal of the American Chemical Society</i> , <b>2020</b> , 142, 4539-4543	16.4	8
14	A metabolic labeling method detects mA transcriptome-wide at single base resolution. <i>Nature Chemical Biology</i> , <b>2020</b> , 16, 887-895	11.7	70
13	An integrated multi-omics approach identifies epigenetic alterations associated with Alzheimer's disease. <i>Nature Genetics</i> , <b>2020</b> , 52, 1024-1035	36.3	53
12	A human tissue map of 5-hydroxymethylcytosines exhibits tissue specificity through gene and enhancer modulation. <i>Nature Communications</i> , <b>2020</b> , 11, 6161	17.4	21
11	Control of Early B Cell Development by the RNA N-Methyladenosine Methylation. <i>Cell Reports</i> , <b>2020</b> , 31, 107819	10.6	25
10	Evolution of a reverse transcriptase to map N-methyladenosine in human messenger RNA. <i>Nature Methods</i> , <b>2019</b> , 16, 1281-1288	21.6	55
9	Jump-seq: Genome-Wide Capture and Amplification of 5-Hydroxymethylcytosine Sites. <i>Journal of the American Chemical Society</i> , <b>2019</b> , 141, 8694-8697	16.4	14

8	VIRMA mediates preferential mA mRNA methylation in 3'UTR and near stop codon and associates with alternative polyadenylation. <i>Cell Discovery</i> , <b>2018</b> , 4, 10	22.3	332
7	OGT binds a conserved C-terminal domain of TET1 to regulate TET1 activity and function in development. <i>ELife</i> , <b>2018</b> , 7,	8.9	27
6	Differential mA, mA, and mA Demethylation Mediated by FTO in the Cell Nucleus and Cytoplasm. <i>Molecular Cell</i> , <b>2018</b> , 71, 973-985.e5	17.6	289
5	Targeted inhibition of STAT/TET1 axis as a therapeutic strategy for acute myeloid leukemia. <i>Nature Communications</i> , <b>2017</b> , 8, 2099	17.4	36
4	Targeted Inhibition of STAT/TET1 Axis As a Potent Therapeutic Strategy for Acute Myeloid Leukemia. <i>Blood</i> , <b>2017</b> , 130, 857-857	2.2	1
3	Generation and Application of Mouse-Rat Allodiploid Embryonic Stem Cells. <i>Cell</i> , <b>2016</b> , 164, 279-292	56.2	32
2	Co-participation of paternal and maternal genomes before the blastocyst stage is not required for full-term development of mouse embryos. <i>Journal of Molecular Cell Biology</i> , <b>2015</b> , 7, 486-8	6.3	3
1	Genetic modification and screening in rat using haploid embryonic stem cells. <i>Cell Stem Cell</i> , <b>2014</b> , 14, 404-14	18	71