Miao Yu

List of Publications by Year
in descending order

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48 papers	10,840 citations	136950 32 h-index	206112 48 g-index
60 all docs	60 docs citations	60 times ranked	16169 citing authors

#	Article	IF	Citations
1	A METTL3â€“METTL14 complex mediates mammalian nuclear RNA N6-adenosine methylation. Nature Chemical Biology, 2014, 10, 93-95.	8.0	2,342
2	Global Epigenomic Reconfiguration During Mammalian Brain Development. Science, 2013, 341, 1237905.	12.6	1,609
3	Base-Resolution Analysis of 5-Hydroxymethylcytosine in the Mammalian Genome. Cell, 2012, 149, 1368-1380.	28.9	912
4	An efficient organocatalytic method for constructing biaryls through aromatic Câ€“H activation. Nature Chemistry, 2010, 2, 1044-1049.	13.6	601
5	Brain cell typeâ€“specific enhancerâ€“promoter interactome maps and disease - risk association. Science, 2019, 366, 1134-1139.	12.6	486
6	N6-Methyldeoxyadenosine Marks Active Transcription Start Sites in Chlamydomonas. Cell, 2015, 161, 879-892.	28.9	477
7	Sperm, but Not Oocyte, DNA Methylome Is Inherited by Zebrafish Early Embryos. Cell, 2013, 153, 773-784.	28.9	428
8	Circular ecDNA promotes accessible chromatin and high oncogene expression. Nature, 2019, 575, 699-703.	27.8	343
9	The Three-Dimensional Organization of Mammalian Genomes. Annual Review of Cell and Developmental Biology, 2017, 33, 265-289.	9.4	320
10	Mapping of long-range chromatin interactions by proximity ligation-assisted ChIP-seq. Cell Research, 2016, 26, 1345-1348.	12.0	264
11	An ultra high-throughput method for single-cell joint analysis of open chromatin and transcriptome. Nature Structural and Molecular Biology, 2019, 26, 1063-1070.	8.2	239
12	Tet-assisted bisulfite sequencing of 5-hydroxymethylcytosine. Nature Protocols, 2012, 7, 2159-2170.	12.0	236
13	Whole-genome analysis of 5-hydroxymethylcytosine and 5-methylcytosine at base resolution in the human brain. Genome Biology, 2014, 15, R49.	9.6	232
14	Bacterial infection remodels the DNA methylation landscape of human dendritic cells. Genome Research, 2015, 25, 1801-1811.	5.5	195
15	Impairment of DNA Methylation Maintenance Is the Main Cause of Global Demethylation in Naive Embryonic Stem Cells. Molecular Cell, 2016, 62, 848-861.	9.7	189
16	Promoter-proximal CTCF binding promotes distal enhancer-dependent gene activation. Nature Structural and Molecular Biology, 2021, 28, 152-161.	8.2	172
17	Analysis of Genetically Diverse Macrophages Reveals Local and Domain-wide Mechanisms that Control Transcription Factor Binding and Function. Cell, 2018, 173, 1796-1809.e17.	28.9	165
18	Carbonâˆ’Carbon Formation via Ni-Catalyzed Suzukiâˆ’Miyaura Coupling through Câˆ’CN Bond Cleavage of Aryl Nitrile. Organic Letters, 2009, 11, 3374-3377.	4.6	119

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19	MeCP2 recognizes cytosine methylated tri-nucleotide and di-nucleotide sequences to tune transcription in the mammalian brain. PLoS Genetics, 2017, 13, e1006793.	3.5	117
20	miR-22 has a potent anti-tumour role with therapeutic potential in acute myeloid leukaemia. Nature Communications, 2016, 7, 11452.	12.8	113
21	MAPS: Model-based analysis of long-range chromatin interactions from PLAC-seq and HiChIP experiments. PLoS Computational Biology, 2019, 15, e1006982.	3.2	94
22	Hydroxymethylation at Gene Regulatory Regions Directs Stem/Early Progenitor Cell Commitment during Erythropoiesis. Cell Reports, 2014, 6, 231-244.	6.4	93
23	Characterization of eukaryotic DNA N6-methyladenine by a highly sensitive restriction enzyme-assisted sequencing. Nature Communications, 2016, 7, 11301.	12.8	93
24	The Catalytic Ability of Various Transition Metals in the Direct Functionalization of Aromatic Cï£¿H Bonds. Chemistry - A European Journal, 2011, 17, 3593-3597.	3.3	90
25	CTCF mediates dosage- and sequence-context-dependent transcriptional insulation by forming local chromatin domains. Nature Genetics, 2021, 53, 1064-1074.	21.4	90
26	Tet2 loss leads to hypermutagenicity in haematopoietic stem/progenitor cells. Nature Communications, 2017, 8, 15102.	12.8	88
27	Subtelomeric hotspots of aberrant 5-hydroxymethylcytosine-mediated epigenetic modifications during reprogramming to pluripotency. Nature Cell Biology, 2013, 15, 700-711.	10.3	87
28	The dynamics of DNA methylation fidelity during mouse embryonic stem cell self-renewal and differentiation. Genome Research, 2014, 24, 1296-1307.	5.5	72
29	Base-resolution detection of<i>N</i>⁴-methylcytosine in genomic DNA using 4mC-Tet-assisted-bisulfite- sequencing. Nucleic Acids Research, 2015, 43, gkv738.	14.5	58
30	A TET Homologue Protein from <i>Coprinopsis cinerea</i> (CcTET) That Biochemically Converts 5-Methylcytosine to 5-Hydroxymethylcytosine, 5-Formylcytosine, and 5-Carboxylcytosine. Journal of the American Chemical Society, 2014, 136, 4801-4804.	13.7	56
31	Tet-mediated covalent labelling of 5-methylcytosine for its genome-wide detection and sequencing. Nature Communications, 2013, 4, 1517.	12.8	48
32	SnapHiC: a computational pipeline to identify chromatin loops from single-cell Hi-C data. Nature Methods, 2021, 18, 1056-1059.	19.0	46
33	ZNF143 mediates CTCF-bound promoterâ€“enhancer loops required for murine hematopoietic stem and progenitor cell function. Nature Communications, 2021, 12, 43.	12.8	45
34	Quantitative modelling predicts the impact of DNA methylation on RNA polymerase II traffic. Proceedings of the National Academy of Sciences of the United States of America, 2019, 116, 14995-15000.	7.1	42
35	Direct DNA crosslinking with CAP-C uncovers transcription-dependent chromatin organization at high resolution. Nature Biotechnology, 2021, 39, 225-235.	17.5	37
36	Detection of 5-hydroxymethylcytosine in a combined glycosylation restriction analysis (CGRA) using restriction enzyme TaqÎ±I. Bioorganic and Medicinal Chemistry Letters, 2011, 21, 5075-5077.	2.2	33

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37	Application of a low cost array-based technique â€” TAB-Array â€” for quantifying and mapping both 5mC and 5hmC at single base resolution in human pluripotent stem cells. Genomics, 2014, 104, 358-367.	2.9	33
38	Tet-Assisted Bisulfite Sequencing (TAB-seq). Methods in Molecular Biology, 2018, 1708, 645-663.	0.9	23
39	Detection of 5â€Hydroxymethylcytosine in DNA by Transferring a Ketoâ€Glucose by Using T4 Phage Î²â€Glucosyltransferase. ChemBioChem, 2011, 12, 1682-1685.	2.6	21
40	Parallel characterization of cis-regulatory elements for multiple genes using CRISPRpath. Science Advances, 2021, 7, eabi4360.	10.3	16
41	Znhit1 controls meiotic initiation in male germ cells by coordinating with Stra8 to activate meiotic gene expression. Developmental Cell, 2022, 57, 901-913.e4.	7.0	16
42	Detection of mismatched 5-hydroxymethyluracil in DNA by selective chemical labeling. Methods, 2015, 72, 16-20.	3.8	14
43	Subsets of Visceral Adipose Tissue Nuclei with Distinct Levels of 5-Hydroxymethylcytosine. PLoS ONE, 2016, 11, e0154949.	2.5	9
44	Mapping chromatin loops in single cells. Trends in Genetics, 2022, 38, 637-640.	6.7	9
45	SnapHiC2: A computationally efficient loop caller for single cell Hi-C data. Computational and Structural Biotechnology Journal, 2022, 20, 2778-2783.	4.1	7
46	Proximity Ligation-Assisted ChIP-Seq (PLAC-Seq). Methods in Molecular Biology, 2021, 2351, 181-199.	0.9	6
47	Mouse Tet1 Protein can Oxidize 5mC to 5hmC and 5caC on Single-stranded DNA. Acta Chimica Sinica, 2012, 70, 2123.	1.4	6
48	DNA cytosine hydroxymethylation levels are distinct among non-overlapping classes of peripheral blood leukocytes. Journal of Immunological Methods, 2016, 436, 1-15.	1.4	5