

Miao Yu

List of Publications by Year in descending order

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Version: 2024-02-01

48
papers

10,840
citations

136740

32
h-index

205818

48
g-index

60
all docs

60
docs citations

60
times ranked

16169
citing authors

#	ARTICLE	IF	CITATIONS
1	A METTL3-METTL14 complex mediates mammalian nuclear RNA N6-adenosine methylation. <i>Nature Chemical Biology</i> , 2014, 10, 93-95.	3.9	2,342
2	Global Epigenomic Reconfiguration During Mammalian Brain Development. <i>Science</i> , 2013, 341, 1237905.	6.0	1,609
3	Base-Resolution Analysis of 5-Hydroxymethylcytosine in the Mammalian Genome. <i>Cell</i> , 2012, 149, 1368-1380.	13.5	912
4	An efficient organocatalytic method for constructing biaryls through aromatic C-H activation. <i>Nature Chemistry</i> , 2010, 2, 1044-1049.	6.6	601
5	Brain cell type-specific enhancer-promoter interactome maps and disease risk association. <i>Science</i> , 2019, 366, 1134-1139.	6.0	486
6	N6-Methyldeoxyadenosine Marks Active Transcription Start Sites in <i>Chlamydomonas</i> . <i>Cell</i> , 2015, 161, 879-892.	13.5	477
7	Sperm, but Not Oocyte, DNA Methylome Is Inherited by Zebrafish Early Embryos. <i>Cell</i> , 2013, 153, 773-784.	13.5	428
8	Circular ecDNA promotes accessible chromatin and high oncogene expression. <i>Nature</i> , 2019, 575, 699-703.	13.7	343
9	The Three-Dimensional Organization of Mammalian Genomes. <i>Annual Review of Cell and Developmental Biology</i> , 2017, 33, 265-289.	4.0	320
10	Mapping of long-range chromatin interactions by proximity ligation-assisted ChIP-seq. <i>Cell Research</i> , 2016, 26, 1345-1348.	5.7	264
11	An ultra high-throughput method for single-cell joint analysis of open chromatin and transcriptome. <i>Nature Structural and Molecular Biology</i> , 2019, 26, 1063-1070.	3.6	239
12	Tet-assisted bisulfite sequencing of 5-hydroxymethylcytosine. <i>Nature Protocols</i> , 2012, 7, 2159-2170.	5.5	236
13	Whole-genome analysis of 5-hydroxymethylcytosine and 5-methylcytosine at base resolution in the human brain. <i>Genome Biology</i> , 2014, 15, R49.	13.9	232
14	Bacterial infection remodels the DNA methylation landscape of human dendritic cells. <i>Genome Research</i> , 2015, 25, 1801-1811.	2.4	195
15	Impairment of DNA Methylation Maintenance Is the Main Cause of Global Demethylation in Naive Embryonic Stem Cells. <i>Molecular Cell</i> , 2016, 62, 848-861.	4.5	189
16	Promoter-proximal CTCF binding promotes distal enhancer-dependent gene activation. <i>Nature Structural and Molecular Biology</i> , 2021, 28, 152-161.	3.6	172
17	Analysis of Genetically Diverse Macrophages Reveals Local and Domain-wide Mechanisms that Control Transcription Factor Binding and Function. <i>Cell</i> , 2018, 173, 1796-1809.e17.	13.5	165
18	Carbon-Carbon Formation via Ni-Catalyzed Suzuki-Miyaura Coupling through C-CN Bond Cleavage of Aryl Nitrile. <i>Organic Letters</i> , 2009, 11, 3374-3377.	2.4	119

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19	MeCP2 recognizes cytosine methylated tri-nucleotide and di-nucleotide sequences to tune transcription in the mammalian brain. <i>PLoS Genetics</i> , 2017, 13, e1006793.	1.5	117
20	miR-22 has a potent anti-tumour role with therapeutic potential in acute myeloid leukaemia. <i>Nature Communications</i> , 2016, 7, 11452.	5.8	113
21	MAPS: Model-based analysis of long-range chromatin interactions from PLAC-seq and HiChIP experiments. <i>PLoS Computational Biology</i> , 2019, 15, e1006982.	1.5	94
22	Hydroxymethylation at Gene Regulatory Regions Directs Stem/Early Progenitor Cell Commitment during Erythropoiesis. <i>Cell Reports</i> , 2014, 6, 231-244.	2.9	93
23	Characterization of eukaryotic DNA N6-methyladenine by a highly sensitive restriction enzyme-assisted sequencing. <i>Nature Communications</i> , 2016, 7, 11301.	5.8	93
24	The Catalytic Ability of Various Transition Metals in the Direct Functionalization of Aromatic C-H Bonds. <i>Chemistry - A European Journal</i> , 2011, 17, 3593-3597.	1.7	90
25	CTCF mediates dosage- and sequence-context-dependent transcriptional insulation by forming local chromatin domains. <i>Nature Genetics</i> , 2021, 53, 1064-1074.	9.4	90
26	Tet2 loss leads to hypermutagenicity in haematopoietic stem/progenitor cells. <i>Nature Communications</i> , 2017, 8, 15102.	5.8	88
27	Subtelomeric hotspots of aberrant 5-hydroxymethylcytosine-mediated epigenetic modifications during reprogramming to pluripotency. <i>Nature Cell Biology</i> , 2013, 15, 700-711.	4.6	87
28	The dynamics of DNA methylation fidelity during mouse embryonic stem cell self-renewal and differentiation. <i>Genome Research</i> , 2014, 24, 1296-1307.	2.4	72
29	Base-resolution detection of 5-methylcytosine in genomic DNA using 4mC-Tet-assisted-bisulfite- sequencing. <i>Nucleic Acids Research</i> , 2015, 43, gkv738.	6.5	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. <i>Journal of the American Chemical Society</i> , 2014, 136, 4801-4804.	6.6	56
31	Tet-mediated covalent labelling of 5-methylcytosine for its genome-wide detection and sequencing. <i>Nature Communications</i> , 2013, 4, 1517.	5.8	48
32	SnapHiC: a computational pipeline to identify chromatin loops from single-cell Hi-C data. <i>Nature Methods</i> , 2021, 18, 1056-1059.	9.0	46
33	ZNF143 mediates CTCF-bound promoter-enhancer loops required for murine hematopoietic stem and progenitor cell function. <i>Nature Communications</i> , 2021, 12, 43.	5.8	45
34	Quantitative modelling predicts the impact of DNA methylation on RNA polymerase II traffic. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2019, 116, 14995-15000.	3.3	42
35	Direct DNA crosslinking with CAP-C uncovers transcription-dependent chromatin organization at high resolution. <i>Nature Biotechnology</i> , 2021, 39, 225-235.	9.4	37
36	Detection of 5-hydroxymethylcytosine in a combined glycosylation restriction analysis (CGRA) using restriction enzyme TaqI. <i>Bioorganic and Medicinal Chemistry Letters</i> , 2011, 21, 5075-5077.	1.0	33

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37	Application of a low cost array-based technique " TAB-Array " for quantifying and mapping both 5mC and 5hmC at single base resolution in human pluripotent stem cells. <i>Genomics</i> , 2014, 104, 358-367.	1.3	33
38	Tet-Assisted Bisulfite Sequencing (TAB-seq). <i>Methods in Molecular Biology</i> , 2018, 1708, 645-663.	0.4	23
39	Detection of 5-Hydroxymethylcytosine in DNA by Transferring a Keto-Glucose by Using T4 Phage β -Glucosyltransferase. <i>ChemBioChem</i> , 2011, 12, 1682-1685.	1.3	21
40	Parallel characterization of cis-regulatory elements for multiple genes using CRISPRpath. <i>Science Advances</i> , 2021, 7, eabi4360.	4.7	16
41	Znhit1 controls meiotic initiation in male germ cells by coordinating with Stra8 to activate meiotic gene expression. <i>Developmental Cell</i> , 2022, 57, 901-913.e4.	3.1	16
42	Detection of mismatched 5-hydroxymethyluracil in DNA by selective chemical labeling. <i>Methods</i> , 2015, 72, 16-20.	1.9	14
43	Subsets of Visceral Adipose Tissue Nuclei with Distinct Levels of 5-Hydroxymethylcytosine. <i>PLoS ONE</i> , 2016, 11, e0154949.	1.1	9
44	Mapping chromatin loops in single cells. <i>Trends in Genetics</i> , 2022, 38, 637-640.	2.9	9
45	SnapHiC2: A computationally efficient loop caller for single cell Hi-C data. <i>Computational and Structural Biotechnology Journal</i> , 2022, 20, 2778-2783.	1.9	7
46	Proximity Ligation-Assisted CHIP-Seq (PLAC-Seq). <i>Methods in Molecular Biology</i> , 2021, 2351, 181-199.	0.4	6
47	Mouse Tet1 Protein can Oxidize 5mC to 5hmC and 5caC on Single-stranded DNA. <i>Acta Chimica Sinica</i> , 2012, 70, 2123.	0.5	6
48	DNA cytosine hydroxymethylation levels are distinct among non-overlapping classes of peripheral blood leukocytes. <i>Journal of Immunological Methods</i> , 2016, 436, 1-15.	0.6	5