

Miao Yu

List of Publications by Year in descending order

Source: <https://exaly.com/author-pdf/11942797/publications.pdf>

Version: 2024-02-01

48
papers

10,840
citations

156536

32
h-index

232693

48
g-index

60
all docs

60
docs citations

60
times ranked

17962
citing authors

#	ARTICLE	IF	CITATIONS
1	Mapping chromatin loops in single cells. Trends in Genetics, 2022, 38, 637-640.	2.9	9
2	Znhit1 controls meiotic initiation in male germ cells by coordinating with Stra8 to activate meiotic gene expression. Developmental Cell, 2022, 57, 901-913.e4.	3.1	16
3	SnapHiC2: A computationally efficient loop caller for single cell Hi-C data. Computational and Structural Biotechnology Journal, 2022, 20, 2778-2783.	1.9	7
4	Direct DNA crosslinking with CAP-C uncovers transcription-dependent chromatin organization at high resolution. Nature Biotechnology, 2021, 39, 225-235.	9.4	37
5	ZNF143 mediates CTCF-bound promoter-enhancer loops required for murine hematopoietic stem and progenitor cell function. Nature Communications, 2021, 12, 43.	5.8	45
6	CTCF mediates dosage- and sequence-context-dependent transcriptional insulation by forming local chromatin domains. Nature Genetics, 2021, 53, 1064-1074.	9.4	90
7	SnapHiC: a computational pipeline to identify chromatin loops from single-cell Hi-C data. Nature Methods, 2021, 18, 1056-1059.	9.0	46
8	Parallel characterization of cis-regulatory elements for multiple genes using CRISPRpath. Science Advances, 2021, 7, eabi4360.	4.7	16
9	Proximity Ligation-Assisted ChIP-Seq (PLAC-Seq). Methods in Molecular Biology, 2021, 2351, 181-199.	0.4	6
10	Promoter-proximal CTCF binding promotes distal enhancer-dependent gene activation. Nature Structural and Molecular Biology, 2021, 28, 152-161.	3.6	172
11	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.	3.3	42
12	Brain cell type-specific enhancer-promoter interactome maps and disease risk association. Science, 2019, 366, 1134-1139.	6.0	486
13	MAPS: Model-based analysis of long-range chromatin interactions from PLAC-seq and HiChIP experiments. PLoS Computational Biology, 2019, 15, e1006982.	1.5	94
14	Circular ecDNA promotes accessible chromatin and high oncogene expression. Nature, 2019, 575, 699-703.	13.7	343
15	An ultra high-throughput method for single-cell joint analysis of open chromatin and transcriptome. Nature Structural and Molecular Biology, 2019, 26, 1063-1070.	3.6	239
16	Tet-Assisted Bisulfite Sequencing (TAB-seq). Methods in Molecular Biology, 2018, 1708, 645-663.	0.4	23
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.	13.5	165
18	Tet2 loss leads to hypermutagenicity in haematopoietic stem/progenitor cells. Nature Communications, 2017, 8, 15102.	5.8	88

#	ARTICLE	IF	CITATIONS
19	The Three-Dimensional Organization of Mammalian Genomes. <i>Annual Review of Cell and Developmental Biology</i> , 2017, 33, 265-289.	4.0	320
20	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
21	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
22	Mapping of long-range chromatin interactions by proximity ligation-assisted ChIP-seq. <i>Cell Research</i> , 2016, 26, 1345-1348.	5.7	264
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	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
25	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
26	Subsets of Visceral Adipose Tissue Nuclei with Distinct Levels of 5-Hydroxymethylcytosine. <i>PLoS ONE</i> , 2016, 11, e0154949.	1.1	9
27	Base-resolution detection of 4-methylcytosine in genomic DNA using 4mC-Tet-assisted-bisulfite-sequencing. <i>Nucleic Acids Research</i> , 2015, 43, gkv738.	6.5	58
28	N6-Methyldeoxyadenosine Marks Active Transcription Start Sites in <i>Chlamydomonas</i> . <i>Cell</i> , 2015, 161, 879-892.	13.5	477
29	Bacterial infection remodels the DNA methylation landscape of human dendritic cells. <i>Genome Research</i> , 2015, 25, 1801-1811.	2.4	195
30	Detection of mismatched 5-hydroxymethyluracil in DNA by selective chemical labeling. <i>Methods</i> , 2015, 72, 16-20.	1.9	14
31	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
32	Hydroxymethylation at Gene Regulatory Regions Directs Stem/Early Progenitor Cell Commitment during Erythropoiesis. <i>Cell Reports</i> , 2014, 6, 231-244.	2.9	93
33	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
34	A METTL3-METTL14 complex mediates mammalian nuclear RNA N6-adenosine methylation. <i>Nature Chemical Biology</i> , 2014, 10, 93-95.	3.9	2,342
35	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
36	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

#	ARTICLE	IF	CITATIONS
37	Global Epigenomic Reconfiguration During Mammalian Brain Development. <i>Science</i> , 2013, 341, 1237905.	6.0	1,609
38	Tet-mediated covalent labelling of 5-methylcytosine for its genome-wide detection and sequencing. <i>Nature Communications</i> , 2013, 4, 1517.	5.8	48
39	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
40	Sperm, but Not Oocyte, DNA Methylome Is Inherited by Zebrafish Early Embryos. <i>Cell</i> , 2013, 153, 773-784.	13.5	428
41	Tet-assisted bisulfite sequencing of 5-hydroxymethylcytosine. <i>Nature Protocols</i> , 2012, 7, 2159-2170.	5.5	236
42	Base-Resolution Analysis of 5-Hydroxymethylcytosine in the Mammalian Genome. <i>Cell</i> , 2012, 149, 1368-1380.	13.5	912
43	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
44	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
45	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
46	Detection of 5-Hydroxymethylcytosine in DNA by Transferring a Keto-Glucose by Using T4 Phage Î²-Glucosyltransferase. <i>ChemBioChem</i> , 2011, 12, 1682-1685.	1.3	21
47	An efficient organocatalytic method for constructing biaryls through aromatic C-H activation. <i>Nature Chemistry</i> , 2010, 2, 1044-1049.	6.6	601
48	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