

Wei Xie

List of Publications by Year in descending order

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Version: 2024-02-01

79
papers

18,870
citations

71102

41
h-index

66911

78
g-index

92
all docs

92
docs citations

92
times ranked

30549
citing authors

#	ARTICLE	IF	CITATIONS
1	Integrative analysis of 111 reference human epigenomes. <i>Nature</i> , 2015, 518, 317-330.	27.8	5,653
2	Directly Reprogrammed Fibroblasts Show Global Epigenetic Remodeling and Widespread Tissue Contribution. <i>Cell Stem Cell</i> , 2007, 1, 55-70.	11.1	1,596
3	Chromatin architecture reorganization during stem cell differentiation. <i>Nature</i> , 2015, 518, 331-336.	27.8	1,442
4	Induced Pluripotent Stem Cells and Embryonic Stem Cells Are Distinguished by Gene Expression Signatures. <i>Cell Stem Cell</i> , 2009, 5, 111-123.	11.1	915
5	Epigenomic Analysis of Multilineage Differentiation of Human Embryonic Stem Cells. <i>Cell</i> , 2013, 153, 1134-1148.	28.9	689
6	The landscape of accessible chromatin in mammalian preimplantation embryos. <i>Nature</i> , 2016, 534, 652-657.	27.8	550
7	Dnmt3a-Dependent Nonpromoter DNA Methylation Facilitates Transcription of Neurogenic Genes. <i>Science</i> , 2010, 329, 444-448.	12.6	544
8	Allelic reprogramming of the histone modification H3K4me3 in early mammalian development. <i>Nature</i> , 2016, 537, 553-557.	27.8	516
9	Base-Resolution Analyses of Sequence and Parent-of-Origin Dependent DNA Methylation in the Mouse Genome. <i>Cell</i> , 2012, 148, 816-831.	28.9	478
10	The role of 3D genome organization in development and cell differentiation. <i>Nature Reviews Molecular Cell Biology</i> , 2019, 20, 535-550.	37.0	451
11	3D Chromatin Structures of Mature Gametes and Structural Reprogramming during Mammalian Embryogenesis. <i>Cell</i> , 2017, 170, 367-381.e20.	28.9	415
12	Allelic reprogramming of 3D chromatin architecture during early mammalian development. <i>Nature</i> , 2017, 547, 232-235.	27.8	406
13	Resetting Epigenetic Memory by Reprogramming of Histone Modifications in Mammals. <i>Molecular Cell</i> , 2016, 63, 1066-1079.	9.7	327
14	Multi-omics profiling of mouse gastrulation at single-cell resolution. <i>Nature</i> , 2019, 576, 487-491.	27.8	307
15	Chromatin analysis in human early development reveals epigenetic transition during ZGA. <i>Nature</i> , 2018, 557, 256-260.	27.8	241
16	BMP restricts stemness of intestinal Lgr5+ stem cells by directly suppressing their signature genes. <i>Nature Communications</i> , 2017, 8, 13824.	12.8	214
17	Epigenetic Reprogramming by Adenovirus e1a. <i>Science</i> , 2008, 321, 1086-1088.	12.6	207
18	SETD2 regulates the maternal epigenome, genomic imprinting and embryonic development. <i>Nature Genetics</i> , 2019, 51, 844-856.	21.4	207

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19	RFECS: A Random-Forest Based Algorithm for Enhancer Identification from Chromatin State. PLoS Computational Biology, 2013, 9, e1002968.	3.2	205
20	Integrative analysis of haplotype-resolved epigenomes across human tissues. Nature, 2015, 518, 350-354.	27.8	201
21	Histone H3 Lysine 56 Acetylation Is Linked to the Core Transcriptional Network in Human Embryonic Stem Cells. Molecular Cell, 2009, 33, 417-427.	9.7	176
22	Resetting histone modifications during human parental-to-zygotic transition. Science, 2019, 365, 353-360.	12.6	170
23	Dynamic epigenomic landscapes during early lineage specification in mouse embryos. Nature Genetics, 2018, 50, 96-105.	21.4	164
24	Epigenome in Early Mammalian Development: Inheritance, Reprogramming and Establishment. Trends in Cell Biology, 2018, 28, 237-253.	7.9	158
25	Sir2 Deacetylates Histone H3 Lysine 56 to Regulate Telomeric Heterochromatin Structure in Yeast. Molecular Cell, 2007, 27, 890-900.	9.7	145
26	Selective recognition of histone crotonylation by double PHD fingers of MOZ and DPF2. Nature Chemical Biology, 2016, 12, 1111-1118.	8.0	144
27	Bisulfite-free, base-resolution analysis of 5-formylcytosine at the genome scale. Nature Methods, 2015, 12, 1047-1050.	19.0	141
28	Reprogramming of Meiotic Chromatin Architecture during Spermatogenesis. Molecular Cell, 2019, 73, 547-561.e6.	9.7	122
29	Slc6a8-Mediated Creatine Uptake and Accumulation Reprogram Macrophage Polarization via Regulating Cytokine Responses. Immunity, 2019, 51, 272-284.e7.	14.3	121
30	Polycomb Group Proteins Regulate Chromatin Architecture in Mouse Oocytes and Early Embryos. Molecular Cell, 2020, 77, 825-839.e7.	9.7	105
31	Homotypic clustering of L1 and B1/Alu repeats compartmentalizes the 3D genome. Cell Research, 2021, 31, 613-630.	12.0	105
32	Genome-wide analyses reveal a role of Polycomb in promoting hypomethylation of DNA methylation valleys. Genome Biology, 2018, 19, 18.	8.8	103
33	Isoform Switch of TET1 Regulates DNA Demethylation and Mouse Development. Molecular Cell, 2016, 64, 1062-1073.	9.7	91
34	Activity-induced histone modifications govern Neurexin-1 mRNA splicing and memory preservation. Nature Neuroscience, 2017, 20, 690-699.	14.8	91
35	Regulation of DNA methylation turnover at LTR retrotransposons and imprinted loci by the histone methyltransferase Setdb1. Proceedings of the National Academy of Sciences of the United States of America, 2014, 111, 6690-6695.	7.1	89
36	The landscape of RNA Pol II binding reveals a stepwise transition during ZGA. Nature, 2020, 587, 139-144.	27.8	71

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37	Epigenomic analysis of gastrulation identifies a unique chromatin state for primed pluripotency. <i>Nature Genetics</i> , 2020, 52, 95-105.	21.4	69
38	Imprecise DNMT1 activity coupled with neighbor-guided correction enables robust yet flexible epigenetic inheritance. <i>Nature Genetics</i> , 2020, 52, 828-839.	21.4	69
39	Widespread Enhancer Dememorization and Promoter Priming during Parental-to-Zygotic Transition. <i>Molecular Cell</i> , 2018, 72, 673-686.e6.	9.7	57
40	Ultrasensitive Ribo-seq reveals translational landscapes during mammalian oocyte-to-embryo transition and pre-implantation development. <i>Nature Cell Biology</i> , 2022, 24, 968-980.	10.3	57
41	Mutant Kras co-opts a proto-oncogenic enhancer network in inflammation-induced metaplastic progenitor cells to initiate pancreatic cancer. <i>Nature Cancer</i> , 2021, 2, 49-65.	13.2	54
42	Formative pluripotent stem cells show features of epiblast cells poised for gastrulation. <i>Cell Research</i> , 2021, 31, 526-541.	12.0	53
43	Rebooting the Epigenomes during Mammalian Early Embryogenesis. <i>Stem Cell Reports</i> , 2020, 15, 1158-1175.	4.8	52
44	Genome-wide R-loop Landscapes during Cell Differentiation and Reprogramming. <i>Cell Reports</i> , 2020, 32, 107870.	6.4	51
45	Hoxc-Dependent Mesenchymal Niche Heterogeneity Drives Regional Hair Follicle Regeneration. <i>Cell Stem Cell</i> , 2018, 23, 487-500.e6.	11.1	49
46	Generation and characterization of stable pig pregastrulation epiblast stem cell lines. <i>Cell Research</i> , 2022, 32, 383-400.	12.0	48
47	Metabolic remodelling during early mouse embryo development. <i>Nature Metabolism</i> , 2021, 3, 1372-1384.	11.9	45
48	Comparative Transcriptomic and Epigenomic Analyses Reveal New Regulators of Murine Brown Adipogenesis. <i>PLoS Genetics</i> , 2016, 12, e1006474.	3.5	44
49	TELP, a sensitive and versatile library construction method for next-generation sequencing. <i>Nucleic Acids Research</i> , 2015, 43, e35-e35.	14.5	43
50	Evolutionary epigenomic analyses in mammalian early embryos reveal species-specific innovations and conserved principles of imprinting. <i>Science Advances</i> , 2021, 7, eabi6178.	10.3	42
51	Analysis of Genome Architecture during SCNT Reveals a Role of Cohesin in Impeding Minor ZGA. <i>Molecular Cell</i> , 2020, 79, 234-250.e9.	9.7	39
52	Conversion of random X-inactivation to imprinted X-inactivation by maternal PRC2. <i>ELife</i> , 2019, 8, .	6.0	38
53	Simultaneous epigenetic perturbation and genome imaging reveal distinct roles of H3K9me3 in chromatin architecture and transcription. <i>Genome Biology</i> , 2020, 21, 296.	8.8	37
54	Narciclasine attenuates diet-induced obesity by promoting oxidative metabolism in skeletal muscle. <i>PLoS Biology</i> , 2017, 15, e1002597.	5.6	37

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55	Enhancing Pluripotency and Lineage Specification. <i>Science</i> , 2013, 341, 245-247.	12.6	36
56	The loss of heterochromatin is associated with multiscale three-dimensional genome reorganization and aberrant transcription during cellular senescence. <i>Genome Research</i> , 2021, 31, 1121-1135.	5.5	36
57	A permissive chromatin state regulated by ZFP281-AFF3 in controlling the imprinted Meg3 polycistron. <i>Nucleic Acids Research</i> , 2017, 45, 1177-1185.	14.5	35
58	Epigenetic Reprogramming in Early Animal Development. <i>Cold Spring Harbor Perspectives in Biology</i> , 2022, 14, a039677.	5.5	28
59	DEAD-Box Helicase 18 Counteracts PRC2 to Safeguard Ribosomal DNA in Pluripotency Regulation. <i>Cell Reports</i> , 2020, 30, 81-97.e7.	6.4	25
60	β H2A is a component of yeast heterochromatin required for telomere elongation. <i>Cell Cycle</i> , 2011, 10, 293-300.	2.6	24
61	Creating a monomeric endonuclease TALE-I-SceI with high specificity and low genotoxicity in human cells. <i>Nucleic Acids Research</i> , 2015, 43, 1112-1122.	14.5	24
62	Stiffness-Controlled Thermoresponsive Hydrogels for Cell Harvesting with Sustained Mechanical Memory. <i>Advanced Healthcare Materials</i> , 2017, 6, 1601152.	7.6	22
63	Epigenetic dysregulation of Oxtr in Tet1-deficient mice has implications for neuropsychiatric disorders. <i>JCI Insight</i> , 2018, 3, .	5.0	22
64	Differential regulation of H3S10 phosphorylation, mitosis progression and cell fate by Aurora Kinase B and C in mouse preimplantation embryos. <i>Protein and Cell</i> , 2017, 8, 662-674.	11.0	21
65	Heterochromatin remodeling by CDK12 contributes to learning in <i>Drosophila</i> . <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2015, 112, 13988-13993.	7.1	17
66	H3K18ac Primes Mesendodermal Differentiation upon Nodal Signaling. <i>Stem Cell Reports</i> , 2019, 13, 642-656.	4.8	16
67	Proteasome activator PA200 maintains stability of histone marks during transcription and aging. <i>Theranostics</i> , 2021, 11, 1458-1472.	10.0	13
68	ZFP57 dictates allelic expression switch of target imprinted genes. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2021, 118, .	7.1	12
69	Methylome inheritance and enhancer dememorization reset an epigenetic gate safeguarding embryonic programs. <i>Science Advances</i> , 2021, 7, eabl3858.	10.3	12
70	Activin/Smad2 and Wnt/ β -catenin up-regulate HAS2 and ALDH3A2 to facilitate mesendoderm differentiation of human embryonic stem cells. <i>Journal of Biological Chemistry</i> , 2018, 293, 18444-18453.	3.4	10
71	High-mobility group nucleosomal binding domain 2 protects against microcephaly by maintaining global chromatin accessibility during corticogenesis. <i>Journal of Biological Chemistry</i> , 2020, 295, 468-480.	3.4	10
72	The chromatin remodeler <i>SRCAP</i> promotes self-renewal of intestinal stem cells. <i>EMBO Journal</i> , 2020, 39, e103786.	7.8	10

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73	CpG island reconfiguration for the establishment and synchronization of polycomb functions upon exit from naive pluripotency. <i>Molecular Cell</i> , 2022, 82, 1169-1185.e7.	9.7	10
74	Building the genome architecture during the maternal to zygotic transition. <i>Current Opinion in Genetics and Development</i> , 2022, 72, 91-100.	3.3	8
75	Parental methylome reprogramming in human uniparental blastocysts reveals germline memory transition. <i>Genome Research</i> , 2021, 31, 1519-1530.	5.5	4
76	Progressive Domain Segregation in Early Embryonic Development and Underlying Correlation to Genetic and Epigenetic Changes. <i>Cells</i> , 2021, 10, 2521.	4.1	4
77	Zfp57 Exerts Maternal and Sexually Dimorphic Effects on Genomic Imprinting. <i>Frontiers in Cell and Developmental Biology</i> , 2022, 10, 784128.	3.7	2
78	DE MERVLs are Enriched Around Two-Cell-Specific Genes During Zygotic Genome Activation in Mouse. , 2018, , .		0
79	Tracking in and Low-Input Samples Using Ultrasensitive STAR. <i>Methods in Molecular Biology</i> , 2021, 2214, 241-252.	0.9	0