

# Wei Xie

## List of Publications by Year in descending order

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79  
papers

18,870  
citations

70961

41  
h-index

66788

78  
g-index

92  
all docs

92  
docs citations

92  
times ranked

30549  
citing authors

#	ARTICLE	IF	CITATIONS
1	Epigenetic Reprogramming in Early Animal Development. Cold Spring Harbor Perspectives in Biology, 2022, 14, a039677.	2.3	28
2	Generation and characterization of stable pig pregastrulation epiblast stem cell lines. Cell Research, 2022, 32, 383-400.	5.7	48
3	Building the genome architecture during the maternal to zygotic transition. Current Opinion in Genetics and Development, 2022, 72, 91-100.	1.5	8
4	Zfp57 Exerts Maternal and Sexually Dimorphic Effects on Genomic Imprinting. Frontiers in Cell and Developmental Biology, 2022, 10, 784128.	1.8	2
5	CpG island reconfiguration for the establishment and synchronization of polycomb functions upon exit from naive pluripotency. Molecular Cell, 2022, 82, 1169-1185.e7.	4.5	10
6	Ultrasensitive Ribo-seq reveals translational landscapes during mammalian oocyte-to-embryo transition and pre-implantation development. Nature Cell Biology, 2022, 24, 968-980.	4.6	57
7	Mutant Kras co-opts a proto-oncogenic enhancer network in inflammation-induced metaplastic progenitor cells to initiate pancreatic cancer. Nature Cancer, 2021, 2, 49-65.	5.7	54
8	Formative pluripotent stem cells show features of epiblast cells poised for gastrulation. Cell Research, 2021, 31, 526-541.	5.7	53
9	The loss of heterochromatin is associated with multiscale three-dimensional genome reorganization and aberrant transcription during cellular senescence. Genome Research, 2021, 31, 1121-1135.	2.4	36
10	Parental methylome reprogramming in human uniparental blastocysts reveals germline memory transition. Genome Research, 2021, 31, 1519-1530.	2.4	4
11	Progressive Domain Segregation in Early Embryonic Development and Underlying Correlation to Genetic and Epigenetic Changes. Cells, 2021, 10, 2521.	1.8	4
12	ZFP57 dictates allelic expression switch of target imprinted genes. Proceedings of the National Academy of Sciences of the United States of America, 2021, 118, .	3.3	12
13	Proteasome activator PA200 maintains stability of histone marks during transcription and aging. Theranostics, 2021, 11, 1458-1472.	4.6	13
14	Homotypic clustering of L1 and B1/Alu repeats compartmentalizes the 3D genome. Cell Research, 2021, 31, 613-630.	5.7	105
15	Metabolic remodelling during early mouse embryo development. Nature Metabolism, 2021, 3, 1372-1384.	5.1	45
16	Tracking in and Low-Input Samples Using Ultrasensitive STAR. Methods in Molecular Biology, 2021, 2214, 241-252.	0.4	0
17	Evolutionary epigenomic analyses in mammalian early embryos reveal species-specific innovations and conserved principles of imprinting. Science Advances, 2021, 7, eabi6178.	4.7	42
18	Methylome inheritance and enhancer dememorization reset an epigenetic gate safeguarding embryonic programs. Science Advances, 2021, 7, eabl3858.	4.7	12

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19	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.	1.6	10
20	DEAD-Box Helicase 18 Counteracts PRC2 to Safeguard Ribosomal DNA in Pluripotency Regulation. <i>Cell Reports</i> , 2020, 30, 81-97.e7.	2.9	25
21	Epigenomic analysis of gastrulation identifies a unique chromatin state for primed pluripotency. <i>Nature Genetics</i> , 2020, 52, 95-105.	9.4	69
22	Polycomb Group Proteins Regulate Chromatin Architecture in Mouse Oocytes and Early Embryos. <i>Molecular Cell</i> , 2020, 77, 825-839.e7.	4.5	105
23	Rebooting the Epigenomes during Mammalian Early Embryogenesis. <i>Stem Cell Reports</i> , 2020, 15, 1158-1175.	2.3	52
24	Imprecise DNMT1 activity coupled with neighbor-guided correction enables robust yet flexible epigenetic inheritance. <i>Nature Genetics</i> , 2020, 52, 828-839.	9.4	69
25	The landscape of RNA Pol II binding reveals a stepwise transition during ZGA. <i>Nature</i> , 2020, 587, 139-144.	13.7	71
26	The chromatin remodeler <sc>SRCAP</sc> promotes self-renewal of intestinal stem cells. <i>EMBO Journal</i> , 2020, 39, e103786.	3.5	10
27	Simultaneous epigenetic perturbation and genome imaging reveal distinct roles of H3K9me3 in chromatin architecture and transcription. <i>Genome Biology</i> , 2020, 21, 296.	3.8	37
28	Analysis of Genome Architecture during SCNT Reveals a Role of Cohesin in Impeding Minor ZGA. <i>Molecular Cell</i> , 2020, 79, 234-250.e9.	4.5	39
29	Genome-wide R-loop Landscapes during Cell Differentiation and Reprogramming. <i>Cell Reports</i> , 2020, 32, 107870.	2.9	51
30	Slc6a8-Mediated Creatine Uptake and Accumulation Reprogram Macrophage Polarization via Regulating Cytokine Responses. <i>Immunity</i> , 2019, 51, 272-284.e7.	6.6	121
31	Resetting histone modifications during human parental-to-zygotic transition. <i>Science</i> , 2019, 365, 353-360.	6.0	170
32	H3K18ac Primes Mesendodermal Differentiation upon Nodal Signaling. <i>Stem Cell Reports</i> , 2019, 13, 642-656.	2.3	16
33	Conversion of random X-inactivation to imprinted X-inactivation by maternal PRC2. <i>ELife</i> , 2019, 8, .	2.8	38
34	The role of 3D genome organization in development and cell differentiation. <i>Nature Reviews Molecular Cell Biology</i> , 2019, 20, 535-550.	16.1	451
35	SETD2 regulates the maternal epigenome, genomic imprinting and embryonic development. <i>Nature Genetics</i> , 2019, 51, 844-856.	9.4	207
36	Reprogramming of Meiotic Chromatin Architecture during Spermatogenesis. <i>Molecular Cell</i> , 2019, 73, 547-561.e6.	4.5	122

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37	Multi-omics profiling of mouse gastrulation at single-cell resolution. <i>Nature</i> , 2019, 576, 487-491.	13.7	307
38	Genome-wide analyses reveal a role of Polycomb in promoting hypomethylation of DNA methylation valleys. <i>Genome Biology</i> , 2018, 19, 18.	3.8	103
39	Chromatin analysis in human early development reveals epigenetic transition during ZGA. <i>Nature</i> , 2018, 557, 256-260.	13.7	241
40	Epigenome in Early Mammalian Development: Inheritance, Reprogramming and Establishment. <i>Trends in Cell Biology</i> , 2018, 28, 237-253.	3.6	158
41	Dynamic epigenomic landscapes during early lineage specification in mouse embryos. <i>Nature Genetics</i> , 2018, 50, 96-105.	9.4	164
42	DE MERVLs are Enriched Around Two-Cell-Specific Genes During Zygotic Genome Activation in Mouse. , 2018, , .		0
43	Epigenetic dysregulation of Oxt in Tet1-deficient mice has implications for neuropsychiatric disorders. <i>JCI Insight</i> , 2018, 3, .	2.3	22
44	Widespread Enhancer Dememorization and Promoter Priming during Parental-to-Zygotic Transition. <i>Molecular Cell</i> , 2018, 72, 673-686.e6.	4.5	57
45	Activin/Smad2 and Wnt/ $\beta$ -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.	1.6	10
46	Hoxc-Dependent Mesenchymal Niche Heterogeneity Drives Regional Hair Follicle Regeneration. <i>Cell Stem Cell</i> , 2018, 23, 487-500.e6.	5.2	49
47	Stiffness- Controlled Thermo-responsive Hydrogels for Cell Harvesting with Sustained Mechanical Memory. <i>Advanced Healthcare Materials</i> , 2017, 6, 1601152.	3.9	22
48	BMP restricts stemness of intestinal Lgr5+ stem cells by directly suppressing their signature genes. <i>Nature Communications</i> , 2017, 8, 13824.	5.8	214
49	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.	4.8	21
50	Activity-induced histone modifications govern Neurexin-1 mRNA splicing and memory preservation. <i>Nature Neuroscience</i> , 2017, 20, 690-699.	7.1	91
51	3D Chromatin Structures of Mature Gametes and Structural Reprogramming during Mammalian Embryogenesis. <i>Cell</i> , 2017, 170, 367-381.e20.	13.5	415
52	Allelic reprogramming of 3D chromatin architecture during early mammalian development. <i>Nature</i> , 2017, 547, 232-235.	13.7	406
53	A permissive chromatin state regulated by ZFP281-AFF3 in controlling the imprinted Meg3 polycistron. <i>Nucleic Acids Research</i> , 2017, 45, 1177-1185.	6.5	35
54	Narciclasine attenuates diet-induced obesity by promoting oxidative metabolism in skeletal muscle. <i>PLoS Biology</i> , 2017, 15, e1002597.	2.6	37

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55	Comparative Transcriptomic and Epigenomic Analyses Reveal New Regulators of Murine Brown Adipogenesis. <i>PLoS Genetics</i> , 2016, 12, e1006474.	1.5	44
56	Isoform Switch of TET1 Regulates DNA Demethylation and Mouse Development. <i>Molecular Cell</i> , 2016, 64, 1062-1073.	4.5	91
57	Allelic reprogramming of the histone modification H3K4me3 in early mammalian development. <i>Nature</i> , 2016, 537, 553-557.	13.7	516
58	Resetting Epigenetic Memory by Reprogramming of Histone Modifications in Mammals. <i>Molecular Cell</i> , 2016, 63, 1066-1079.	4.5	327
59	Selective recognition of histone crotonylation by double PHD fingers of MOZ and DPF2. <i>Nature Chemical Biology</i> , 2016, 12, 1111-1118.	3.9	144
60	The landscape of accessible chromatin in mammalian preimplantation embryos. <i>Nature</i> , 2016, 534, 652-657.	13.7	550
61	Integrative analysis of haplotype-resolved epigenomes across human tissues. <i>Nature</i> , 2015, 518, 350-354.	13.7	201
62	Integrative analysis of 111 reference human epigenomes. <i>Nature</i> , 2015, 518, 317-330.	13.7	5,653
63	Chromatin architecture reorganization during stem cell differentiation. <i>Nature</i> , 2015, 518, 331-336.	13.7	1,442
64	TELP, a sensitive and versatile library construction method for next-generation sequencing. <i>Nucleic Acids Research</i> , 2015, 43, e35-e35.	6.5	43
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.	3.3	17
66	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.	6.5	24
67	Bisulfite-free, base-resolution analysis of 5-formylcytosine at the genome scale. <i>Nature Methods</i> , 2015, 12, 1047-1050.	9.0	141
68	Regulation of DNA methylation turnover at LTR retrotransposons and imprinted loci by the histone methyltransferase Setdb1. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2014, 111, 6690-6695.	3.3	89
69	Enhancing Pluripotency and Lineage Specification. <i>Science</i> , 2013, 341, 245-247.	6.0	36
70	Epigenomic Analysis of Multilineage Differentiation of Human Embryonic Stem Cells. <i>Cell</i> , 2013, 153, 1134-1148.	13.5	689
71	RFECs: A Random-Forest Based Algorithm for Enhancer Identification from Chromatin State. <i>PLoS Computational Biology</i> , 2013, 9, e1002968.	1.5	205
72	Base-Resolution Analyses of Sequence and Parent-of-Origin Dependent DNA Methylation in the Mouse Genome. <i>Cell</i> , 2012, 148, 816-831.	13.5	478

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73	H2A is a component of yeast heterochromatin required for telomere elongation. <i>Cell Cycle</i> , 2011, 10, 293-300.	1.3	24
74	Dnmt3a-Dependent Nonpromoter DNA Methylation Facilitates Transcription of Neurogenic Genes. <i>Science</i> , 2010, 329, 444-448.	6.0	544
75	Induced Pluripotent Stem Cells and Embryonic Stem Cells Are Distinguished by Gene Expression Signatures. <i>Cell Stem Cell</i> , 2009, 5, 111-123.	5.2	915
76	Histone H3 Lysine 56 Acetylation Is Linked to the Core Transcriptional Network in Human Embryonic Stem Cells. <i>Molecular Cell</i> , 2009, 33, 417-427.	4.5	176
77	Epigenetic Reprogramming by Adenovirus e1a. <i>Science</i> , 2008, 321, 1086-1088.	6.0	207
78	Directly Reprogrammed Fibroblasts Show Global Epigenetic Remodeling and Widespread Tissue Contribution. <i>Cell Stem Cell</i> , 2007, 1, 55-70.	5.2	1,596
79	Sir2 Deacetylates Histone H3 Lysine 56 to Regulate Telomeric Heterochromatin Structure in Yeast. <i>Molecular Cell</i> , 2007, 27, 890-900.	4.5	145