

Keji Zhao

List of Publications by Year in descending order

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203
papers

37,180
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4370

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213
all docs

213
docs citations

213
times ranked

43539
citing authors

#	ARTICLE	IF	CITATIONS
1	High-Resolution Profiling of Histone Methylations in the Human Genome. <i>Cell</i> , 2007, 129, 823-837.	13.5	6,036
2	Combinatorial patterns of histone acetylations and methylations in the human genome. <i>Nature Genetics</i> , 2008, 40, 897-903.	9.4	2,034
3	Dynamic Regulation of Nucleosome Positioning in the Human Genome. <i>Cell</i> , 2008, 132, 887-898.	13.5	1,211
4	Genome-wide Mapping of HATs and HDACs Reveals Distinct Functions in Active and Inactive Genes. <i>Cell</i> , 2009, 138, 1019-1031.	13.5	1,174
5	Global Mapping of H3K4me3 and H3K27me3 Reveals Specificity and Plasticity in Lineage Fate Determination of Differentiating CD4+ T Cells. <i>Immunity</i> , 2009, 30, 155-167.	6.6	1,005
6	A clustering approach for identification of enriched domains from histone modification ChIP-Seq data. <i>Bioinformatics</i> , 2009, 25, 1952-1958.	1.8	936
7	c-Myc Is a Universal Amplifier of Expressed Genes in Lymphocytes and Embryonic Stem Cells. <i>Cell</i> , 2012, 151, 68-79.	13.5	907
8	Control of Cell Identity Genes Occurs in Insulated Neighborhoods in Mammalian Chromosomes. <i>Cell</i> , 2014, 159, 374-387.	13.5	793
9	Rapid and Phosphoinositol-Dependent Binding of the SWI/SNF-like BAF Complex to Chromatin after T Lymphocyte Receptor Signaling. <i>Cell</i> , 1998, 95, 625-636.	13.5	683
10	H3.3/H2A.Z double variant-containing nucleosomes mark 'nucleosome-free regions' of active promoters and other regulatory regions. <i>Nature Genetics</i> , 2009, 41, 941-945.	9.4	679
11	Global analysis of the insulator binding protein CTCF in chromatin barrier regions reveals demarcation of active and repressive domains. <i>Genome Research</i> , 2009, 19, 24-32.	2.4	587
12	Dual functions of Tet1 in transcriptional regulation in mouse embryonic stem cells. <i>Nature</i> , 2011, 473, 389-393.	13.7	581
13	Chromatin Signatures in Multipotent Human Hematopoietic Stem Cells Indicate the Fate of Bivalent Genes during Differentiation. <i>Cell Stem Cell</i> , 2009, 4, 80-93.	5.2	548
14	Genome-wide identification of <i>in vivo</i> protein-DNA binding sites from ChIP-Seq data. <i>Nucleic Acids Research</i> , 2008, 36, 5221-5231.	6.5	500
15	Intragenic DNA methylation modulates alternative splicing by recruiting MeCP2 to promote exon recognition. <i>Cell Research</i> , 2013, 23, 1256-1269.	5.7	489
16	Genome-wide analysis of 5-hydroxymethylcytosine distribution reveals its dual function in transcriptional regulation in mouse embryonic stem cells. <i>Genes and Development</i> , 2011, 25, 679-684.	2.7	488
17	GATA3 controls Foxp3+ regulatory T cell fate during inflammation in mice. <i>Journal of Clinical Investigation</i> , 2011, 121, 4503-4515.	3.9	462
18	The genomic landscape of histone modifications in human T cells. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2006, 103, 15782-15787.	3.3	432

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19	Nucleosome dynamics define transcriptional enhancers. <i>Nature Genetics</i> , 2010, 42, 343-347.	9.4	426
20	Expression and regulation of intergenic long noncoding RNAs during T cell development and differentiation. <i>Nature Immunology</i> , 2013, 14, 1190-1198.	7.0	414
21	Active chromatin domains are defined by acetylation islands revealed by genome-wide mapping. <i>Genes and Development</i> , 2005, 19, 542-552.	2.7	398
22	An embryonic stem cell chromatin remodeling complex, esBAF, is an essential component of the core pluripotency transcriptional network. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2009, 106, 5187-5191.	3.3	374
23	IL-1 family members and STAT activators induce cytokine production by Th2, Th17, and Th1 cells. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2009, 106, 13463-13468.	3.3	362
24	Novel Foxo1-dependent transcriptional programs control Treg cell function. <i>Nature</i> , 2012, 491, 554-559.	13.7	348
25	Genome-wide approaches to studying chromatin modifications. <i>Nature Reviews Genetics</i> , 2008, 9, 179-191.	7.7	343
26	The Transcription Factor GATA3 Is Critical for the Development of All IL-7R α -Expressing Innate Lymphoid Cells. <i>Immunity</i> , 2014, 40, 378-388.	6.6	320
27	Regulation of CSF1 Promoter by the SWI/SNF-like BAF Complex. <i>Cell</i> , 2001, 106, 309-318.	13.5	315
28	Visualization of chromosomal domains with boundary element-associated factor BEAF-32. <i>Cell</i> , 1995, 81, 879-889.	13.5	303
29	Genome-wide detection of DNase I hypersensitive sites in single cells and FFPE tissue samples. <i>Nature</i> , 2015, 528, 142-146.	13.7	303
30	Genome-wide Analyses of Transcription Factor GATA3-Mediated Gene Regulation in Distinct T Cell Types. <i>Immunity</i> , 2011, 35, 299-311.	6.6	293
31	H2A.Z Facilitates Access of Active and Repressive Complexes to Chromatin in Embryonic Stem Cell Self-Renewal and Differentiation. <i>Cell Stem Cell</i> , 2013, 12, 180-192.	5.2	272
32	The Transcription Factor T-bet Is Induced by Multiple Pathways and Prevents an Endogenous Th2 Cell Program during Th1 Cell Responses. <i>Immunity</i> , 2012, 37, 660-673.	6.6	269
33	Histone H4K20/H3K9 demethylase PHF8 regulates zebrafish brain and craniofacial development. <i>Nature</i> , 2010, 466, 503-507.	13.7	263
34	Genome-wide Analysis of Histone Methylation Reveals Chromatin State-Based Regulation of Gene Transcription and Function of Memory CD8 $^{+}$ T Cells. <i>Immunity</i> , 2009, 30, 912-925.	6.6	256
35	Establishing Chromatin Regulatory Landscape during Mouse Preimplantation Development. <i>Cell</i> , 2016, 165, 1375-1388.	13.5	254
36	Characterization of genome-wide enhancer-promoter interactions reveals co-expression of interacting genes and modes of higher order chromatin organization. <i>Cell Research</i> , 2012, 22, 490-503.	5.7	238

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37	Priming for T helper type 2 differentiation by interleukin 2-mediated induction of interleukin 4 receptor α -chain expression. <i>Nature Immunology</i> , 2008, 9, 1288-1296.	7.0	234
38	Reciprocal regulation of CD4/CD8 expression by SWI/SNF-like BAF complexes. <i>Nature</i> , 2002, 418, 195-199.	13.7	230
39	BAF complexes facilitate decatenation of DNA by topoisomerase II. <i>Nature</i> , 2013, 497, 624-627.	13.7	230
40	Searching for a function for nuclear actin. <i>Trends in Cell Biology</i> , 2000, 10, 92-97.	3.6	224
41	PAX3-mediated FOXO1 Establishes Myogenic Super Enhancers and Confers BET Bromodomain Vulnerability. <i>Cancer Discovery</i> , 2017, 7, 884-899.	7.7	221
42	PfSETvs methylation of histone H3K36 represses virulence genes in <i>Plasmodium falciparum</i> . <i>Nature</i> , 2013, 499, 223-227.	13.7	219
43	CTCF-Mediated Enhancer-Promoter Interaction Is a Critical Regulator of Cell-to-Cell Variation of Gene Expression. <i>Molecular Cell</i> , 2017, 67, 1049-1058.e6.	4.5	219
44	Phosphatidylinositol-dependent actin filament binding by the SWI/SNF-like BAF chromatin remodeling complex. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2002, 99, 2824-2829.	3.3	215
45	PBAF chromatin-remodeling complex requires a novel specificity subunit, BAF200, to regulate expression of selective interferon-responsive genes. <i>Genes and Development</i> , 2005, 19, 1662-1667.	2.7	214
46	RNA Polymerase II Regulates Topoisomerase 1 Activity to Favor Efficient Transcription. <i>Cell</i> , 2016, 165, 357-371.	13.5	211
47	SMARCB1 is required for widespread BAF complex-mediated activation of enhancers and bivalent promoters. <i>Nature Genetics</i> , 2017, 49, 1613-1623.	9.4	207
48	High-resolution genome-wide mapping of histone modifications. <i>Nature Biotechnology</i> , 2004, 22, 1013-1016.	9.4	199
49	ChIP-Seq: technical considerations for obtaining high-quality data. <i>Nature Immunology</i> , 2011, 12, 918-922.	7.0	199
50	Transformation of Accessible Chromatin and 3D Nucleome Underlies Lineage Commitment of Early T Cells. <i>Immunity</i> , 2018, 48, 227-242.e8.	6.6	188
51	The Transcription Factors T-bet and Runx Are Required for the Ontogeny of Pathogenic Interferon- γ -Producing T Helper 17 Cells. <i>Immunity</i> , 2014, 40, 355-366.	6.6	183
52	miR-155 Activates Cytokine Gene Expression in Th17 Cells by Regulating the DNA-Binding Protein Jarid2 to Relieve Polycomb-Mediated Repression. <i>Immunity</i> , 2014, 40, 865-879.	6.6	178
53	Intrinsic Dynamics of a Human Gene Reveal the Basis of Expression Heterogeneity. <i>Cell</i> , 2019, 176, 213-226.e18.	13.5	168
54	Smarca4 ATPase mutations disrupt direct eviction of PRC1 from chromatin. <i>Nature Genetics</i> , 2017, 49, 282-288.	9.4	165

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55	Epigenome Mapping in Normal and Disease States. <i>Circulation Research</i> , 2010, 107, 327-339.	2.0	164
56	The epigenetic basis of cellular heterogeneity. <i>Nature Reviews Genetics</i> , 2021, 22, 235-250.	7.7	163
57	Pol II and its associated epigenetic marks are present at Pol III-transcribed noncoding RNA genes. <i>Nature Structural and Molecular Biology</i> , 2010, 17, 629-634.	3.6	161
58	Regulation of nucleosome landscape and transcription factor targeting at tissue-specific enhancers by BRG1. <i>Genome Research</i> , 2011, 21, 1650-1658.	2.4	160
59	Genomic location analysis by ChIP-seq. <i>Journal of Cellular Biochemistry</i> , 2009, 107, 11-18.	1.2	153
60	Detection of single nucleotide variations in expressed exons of the human genome using RNA-Seq. <i>Nucleic Acids Research</i> , 2009, 37, e106-e106.	6.5	152
61	The Transcription Factor GATA3 Actively Represses RUNX3 Protein-Regulated Production of Interferon- β . <i>Immunity</i> , 2010, 32, 507-517.	6.6	151
62	Characterization of human epigenomes. <i>Current Opinion in Genetics and Development</i> , 2009, 19, 127-134.	1.5	144
63	Single-cell chromatin immunocleavage sequencing (scChIC-seq) to profile histone modification. <i>Nature Methods</i> , 2019, 16, 323-325.	9.0	144
64	The FUSE/FBP/FIR/TFIIH system is a molecular machine programming a pulse of c-myc expression. <i>EMBO Journal</i> , 2006, 25, 2119-2130.	3.5	140
65	Dominant-negative SMARCA4 mutants alter the accessibility landscape of tissue-unrestricted enhancers. <i>Nature Structural and Molecular Biology</i> , 2018, 25, 61-72.	3.6	140
66	PTIP Promotes Chromatin Changes Critical for Immunoglobulin Class Switch Recombination. <i>Science</i> , 2010, 329, 917-923.	6.0	137
67	Critical role of histone demethylase Jmjd3 in the regulation of CD4+ T-cell differentiation. <i>Nature Communications</i> , 2014, 5, 5780.	5.8	136
68	Chromatin poises miRNA- and protein-coding genes for expression. <i>Genome Research</i> , 2009, 19, 1742-1751.	2.4	135
69	Principles of nucleosome organization revealed by single-cell micrococcal nuclease sequencing. <i>Nature</i> , 2018, 562, 281-285.	13.7	135
70	Down-regulation of Gfi-1 expression by TGF- β 2 is important for differentiation of Th17 and CD103+ inducible regulatory T cells. <i>Journal of Experimental Medicine</i> , 2009, 206, 329-341.	4.2	124
71	Genome-wide incorporation dynamics reveal distinct categories of turnover for the histone variant H3.3. <i>Genome Biology</i> , 2013, 14, R121.	13.9	123
72	Group 3 innate lymphoid cells continuously require the transcription factor GATA-3 after commitment. <i>Nature Immunology</i> , 2016, 17, 169-178.	7.0	116

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73	The transcription factor Bhlhe40 is a switch of inflammatory versus antiinflammatory Th1 cell fate determination. <i>Journal of Experimental Medicine</i> , 2018, 215, 1813-1821.	4.2	115
74	Genome-wide prediction of conserved and nonconserved enhancers by histone acetylation patterns. <i>Genome Research</i> , 2006, 17, 74-81.	2.4	113
75	Histone hyperacetylation disrupts core gene regulatory architecture in rhabdomyosarcoma. <i>Nature Genetics</i> , 2019, 51, 1714-1722.	9.4	113
76	BRG1 Controls the Activity of the Retinoblastoma Protein via Regulation of p21 CIP1/WAF1/SDI. <i>Molecular and Cellular Biology</i> , 2004, 24, 1188-1199.	1.1	111
77	Mapping histone modifications in low cell number and single cells using antibody-guided chromatin tagmentation (ACT-seq). <i>Nature Communications</i> , 2019, 10, 3747.	5.8	111
78	Dynamic regulation of alternative splicing and chromatin structure in <i>Drosophila</i> gonads revealed by RNA-seq. <i>Cell Research</i> , 2010, 20, 763-783.	5.7	107
79	Maximal Induction of a Subset of Interferon Target Genes Requires the Chromatin-Remodeling Activity of the BAF Complex. <i>Molecular and Cellular Biology</i> , 2002, 22, 6471-6479.	1.1	104
80	MEK inhibition induces MYOG and remodels super-enhancers in RAS-driven rhabdomyosarcoma. <i>Science Translational Medicine</i> , 2018, 10, .	5.8	104
81	Chromatin Immunoprecipitation Indirect Peaks Highlight Long-Range Interactions of Insulator Proteins and Pol II Pausing. <i>Molecular Cell</i> , 2014, 53, 672-681.	4.5	102
82	Cooperative Activity of BRG1 and Z-DNA Formation in Chromatin Remodeling. <i>Molecular and Cellular Biology</i> , 2006, 26, 2550-2559.	1.1	99
83	Transcriptional Regulation of Rod Photoreceptor Homeostasis Revealed by In Vivo NRL Targetome Analysis. <i>PLoS Genetics</i> , 2012, 8, e1002649.	1.5	99
84	Lineage relationship of CD8 ⁺ T cell subsets is revealed by progressive changes in the epigenetic landscape. <i>Cellular and Molecular Immunology</i> , 2016, 13, 502-513.	4.8	99
85	Global intron retention mediated gene regulation during CD4 ⁺ T cell activation. <i>Nucleic Acids Research</i> , 2016, 44, 6817-6829.	6.5	96
86	Chromatin accessibility profiling methods. <i>Nature Reviews Methods Primers</i> , 2021, 1, .	11.8	95
87	Novel Mechanism of Positive versus Negative Regulation by Thyroid Hormone Receptor β 1 (TR β 1) Identified by Genome-wide Profiling of Binding Sites in Mouse Liver. <i>Journal of Biological Chemistry</i> , 2014, 289, 13113-13128.	1.6	92
88	Epigenomics of T cell activation, differentiation, and memory. <i>Current Opinion in Immunology</i> , 2010, 22, 341-347.	2.4	91
89	Nuclear adaptor Ldb1 regulates a transcriptional program essential for the maintenance of hematopoietic stem cells. <i>Nature Immunology</i> , 2011, 12, 129-136.	7.0	91
90	Report of the National Heart, Lung, and Blood Institute Working Group on Epigenetics and Hypertension. <i>Hypertension</i> , 2012, 59, 899-905.	1.3	91

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91	Methylation of Histone H3 on Lysine 79 Associates with a Group of Replication Origins and Helps Limit DNA Replication Once per Cell Cycle. <i>PLoS Genetics</i> , 2013, 9, e1003542.	1.5	88
92	The Chromatin-Remodeling BAF Complex Mediates Cellular Antiviral Activities by Promoter Priming. <i>Molecular and Cellular Biology</i> , 2004, 24, 4476-4486.	1.1	87
93	Genome-Wide Approaches to Determining Nucleosome Occupancy in Metazoans Using MNase-Seq. <i>Methods in Molecular Biology</i> , 2012, 833, 413-419.	0.4	87
94	The transcription factor TCF-1 enforces commitment to the innate lymphoid cell lineage. <i>Nature Immunology</i> , 2019, 20, 1150-1160.	7.0	81
95	Ldb1-nucleated transcription complexes function as primary mediators of global erythroid gene activation. <i>Blood</i> , 2013, 121, 4575-4585.	0.6	78
96	Integrated Expression Profiling and ChIP-seq Analyses of the Growth Inhibition Response Program of the Androgen Receptor. <i>PLoS ONE</i> , 2009, 4, e6589.	1.1	77
97	Lsh, chromatin remodeling family member, modulates genome-wide cytosine methylation patterns at nonrepeat sequences. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2011, 108, 5626-5631.	3.3	76
98	Cell Fate Determination Factor Dachshund Reprograms Breast Cancer Stem Cell Function. <i>Journal of Biological Chemistry</i> , 2011, 286, 2132-2142.	1.6	74
99	Trac-looping measures genome structure and chromatin accessibility. <i>Nature Methods</i> , 2018, 15, 741-747.	9.0	74
100	Regulation of Pluripotency and Self-Renewal of ESCs through Epigenetic-Threshold Modulation and mRNA Pruning. <i>Cell</i> , 2012, 151, 576-589.	13.5	71
101	DNA Break Mapping Reveals Topoisomerase II Activity Genome-Wide. <i>International Journal of Molecular Sciences</i> , 2014, 15, 13111-13122.	1.8	70
102	GABP controls a critical transcription regulatory module that is essential for maintenance and differentiation of hematopoietic stem/progenitor cells. <i>Blood</i> , 2011, 117, 2166-2178.	0.6	69
103	The conservation and signatures of lincRNAs in Marek's disease of chicken. <i>Scientific Reports</i> , 2015, 5, 15184.	1.6	69
104	MECP2 truncating mutations cause histone H4 hyperacetylation in Rett syndrome. <i>Human Molecular Genetics</i> , 2001, 10, 1085-1092.	1.4	68
105	Epigenetic control of the variable expression of a <i>Plasmodium falciparum</i> receptor protein for erythrocyte invasion. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2010, 107, 2224-2229.	3.3	68
106	Transient T-bet expression functionally specifies a distinct T follicular helper subset. <i>Journal of Experimental Medicine</i> , 2018, 215, 2705-2714.	4.2	68
107	TOP2 synergizes with BAF chromatin remodeling for both resolution and formation of facultative heterochromatin. <i>Nature Structural and Molecular Biology</i> , 2017, 24, 344-352.	3.6	66
108	Monovalent and unpoised status of most genes in undifferentiated cell-enriched <i>Drosophila</i> testis. <i>Genome Biology</i> , 2010, 11, R42.	13.9	65

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109	The DNA-binding inhibitor Id3 regulates IL-9 production in CD4+ T cells. <i>Nature Immunology</i> , 2015, 16, 1077-1084.	7.0	63
110	MLL4 prepares the enhancer landscape for Foxp3 induction via chromatin looping. <i>Nature Immunology</i> , 2017, 18, 1035-1045.	7.0	63
111	Genome-Wide Distribution of MacroH2A1 Histone Variants in Mouse Liver Chromatin. <i>Molecular and Cellular Biology</i> , 2010, 30, 5473-5483.	1.1	60
112	Application of CHIP-Seq and Related Techniques to the Study of Immune Function. <i>Immunity</i> , 2011, 34, 830-842.	6.6	60
113	Genome-Wide uH2A Localization Analysis Highlights Bmi1-Dependent Deposition of the Mark at Repressed Genes. <i>PLoS Genetics</i> , 2009, 5, e1000506.	1.5	58
114	Attenuation of Forkhead signaling by the retinal determination factor DACH1. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2010, 107, 6864-6869.	3.3	58
115	Extended Self-Renewal and Accelerated Reprogramming in the Absence of Kdm5b. <i>Molecular and Cellular Biology</i> , 2013, 33, 4793-4810.	1.1	58
116	USF1 and hSET1A Mediated Epigenetic Modifications Regulate Lineage Differentiation and HoxB4 Transcription. <i>PLoS Genetics</i> , 2013, 9, e1003524.	1.5	57
117	Mapping of INS promoter interactions reveals its role in long-range regulation of SYT8 transcription. <i>Nature Structural and Molecular Biology</i> , 2011, 18, 372-378.	3.6	55
118	Phosphorylation of H4 Ser 47 promotes HIRA-mediated nucleosome assembly. <i>Genes and Development</i> , 2011, 25, 1359-1364.	2.7	52
119	Differential Expression of the Transcription Factor GATA3 Specifies Lineage and Functions of Innate Lymphoid Cells. <i>Immunity</i> , 2020, 52, 83-95.e4.	6.6	52
120	DNMT gene expression and methylome in Marek's disease resistant and susceptible chickens prior to and following infection by MDV. <i>Epigenetics</i> , 2013, 8, 431-444.	1.3	50
121	Stage-Dependent and Locus-Specific Role of Histone Demethylase Jumonji D3 (JMJD3) in the Embryonic Stages of Lung Development. <i>PLoS Genetics</i> , 2014, 10, e1004524.	1.5	50
122	DNA double-strand breaks induced by high NaCl occur predominantly in gene deserts. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2011, 108, 20796-20801.	3.3	48
123	Interleukin-21 Receptor Gene Induction in Human T Cells Is Mediated by T-Cell Receptor-Induced Sp1 Activity. <i>Molecular and Cellular Biology</i> , 2005, 25, 9741-9752.	1.1	46
124	Hybrid DNA virus in Chinese patients with seronegative hepatitis discovered by deep sequencing. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2013, 110, 10264-10269.	3.3	45
125	SMYD5 regulates H4K20me3-marked heterochromatin to safeguard ES cell self-renewal and prevent spurious differentiation. <i>Epigenetics and Chromatin</i> , 2017, 10, 8.	1.8	45
126	Genomic Profiling of HMGN1 Reveals an Association with Chromatin at Regulatory Regions. <i>Molecular and Cellular Biology</i> , 2011, 31, 700-709.	1.1	44

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127	Division of labor between IRF1 and IRF2 in regulating different stages of transcriptional activation in cellular antiviral activities. <i>Cell and Bioscience</i> , 2015, 5, 17.	2.1	44
128	TGF- β 2 induces ST2 and programs ILC2 development. <i>Nature Communications</i> , 2020, 11, 35.	5.8	43
129	Dynamic regulation of epigenomic landscapes during hematopoiesis. <i>BMC Genomics</i> , 2013, 14, 193.	1.2	41
130	The Epigenomics of Embryonic Stem Cell Differentiation. <i>International Journal of Biological Sciences</i> , 2013, 9, 1134-1144.	2.6	41
131	Genome-wide mapping of DNase I hypersensitive sites in rare cell populations using single-cell DNase sequencing. <i>Nature Protocols</i> , 2017, 12, 2342-2354.	5.5	41
132	Bcl11b, a novel GATA3-interacting protein, suppresses Th1 while limiting Th2 cell differentiation. <i>Journal of Experimental Medicine</i> , 2018, 215, 1449-1462.	4.2	41
133	Comparison of REST Cistromes across Human Cell Types Reveals Common and Context-Specific Functions. <i>PLoS Computational Biology</i> , 2014, 10, e1003671.	1.5	40
134	Genome-Wide H3K4me3 Analysis in Angus Cattle with Divergent Tenderness. <i>PLoS ONE</i> , 2015, 10, e0115358.	1.1	40
135	Setd1a and NURF mediate chromatin dynamics and gene regulation during erythroid lineage commitment and differentiation. <i>Nucleic Acids Research</i> , 2016, 44, gkw327.	6.5	39
136	Rapid Recall Ability of Memory T cells is Encoded in their Epigenome. <i>Scientific Reports</i> , 2017, 7, 39785.	1.6	39
137	Genome-wide analysis of H3.3 dissociation reveals high nucleosome turnover at distal regulatory regions of embryonic stem cells. <i>Epigenetics and Chromatin</i> , 2014, 7, 38.	1.8	38
138	A Non-Cell Autonomous Role of E β 2 to Prevent Germ Cells from Turning on a Somatic Cell Marker. <i>Science</i> , 2014, 343, 1513-1516.	6.0	38
139	Multiple Layers of Chimerism in a Single-Stranded DNA Virus Discovered by Deep Sequencing. <i>Genome Biology and Evolution</i> , 2015, 7, 993-1001.	1.1	37
140	O-GlcNAcase Is an RNA Polymerase II Elongation Factor Coupled to Pausing Factors SPT5 and TIF1 β . <i>Journal of Biological Chemistry</i> , 2016, 291, 22703-22713.	1.6	35
141	Insulators recruit histone methyltransferase <i>Mes4</i> to regulate chromatin of flanking genes. <i>EMBO Journal</i> , 2014, 33, 1599-1613.	3.5	34
142	A novel genetic strategy reveals unexpected roles of the Swi β -like chromatin-remodeling BAF complex in thymocyte development. <i>Journal of Experimental Medicine</i> , 2008, 205, 2813-2825.	4.2	33
143	Response: Mapping Nucleosome Positions Using ChIP-Seq Data. <i>Cell</i> , 2007, 131, 832-833.	13.5	32
144	The ATP-dependent Chromatin Remodeling Enzyme Fun30 Represses Transcription by Sliding Promoter-proximal Nucleosomes. <i>Journal of Biological Chemistry</i> , 2013, 288, 23182-23193.	1.6	31

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145	Gcn5 and PCAF negatively regulate interferon β production through HAT β -independent inhibition of TBK1. EMBO Reports, 2014, 15, 1192-1201.	2.0	31
146	Differential Histone Distribution Patterns in Induced Asymmetrically Dividing Mouse Embryonic Stem Cells. Cell Reports, 2020, 32, 108003.	2.9	31
147	SWI/SNF-mediated chromatin remodeling induces Z-DNA formation on a nucleosome. Cell and Bioscience, 2012, 2, 3.	2.1	29
148	Single-cyst transcriptome analysis of <i>Drosophila</i> male germline stem cell lineage. Development (Cambridge), 2020, 147, .	1.2	29
149	Histone demethylases UTX and JMJD3 are required for NKT cell development in mice. Cell and Bioscience, 2017, 7, 25.	2.1	28
150	Induction of DNMT3B by PGE2 and IL6 at Distant Metastatic Sites Promotes Epigenetic Modification and Breast Cancer Colonization. Cancer Research, 2020, 80, 2612-2627.	0.4	28
151	Topoisomerase 3 β interacts with RNAi machinery to promote heterochromatin formation and transcriptional silencing in <i>Drosophila</i> . Nature Communications, 2018, 9, 4946.	5.8	27
152	Genome-Wide Mapping of Nucleosome Occupancy, Histone Modifications, and Gene Expression Using Next-Generation Sequencing Technology. Methods in Enzymology, 2012, 513, 297-313.	0.4	24
153	A Novel Human Polycomb Binding Site Acts As a Functional Polycomb Response Element in <i>Drosophila</i> . PLoS ONE, 2012, 7, e36365.	1.1	24
154	RUNX1 and CBF β -SMMHC transactivate target genes together in abnormal myeloid progenitors for leukemia development. Blood, 2020, 136, 2373-2385.	0.6	24
155	cLoops2: a full-stack comprehensive analytical tool for chromatin interactions. Nucleic Acids Research, 2022, 50, 57-71.	6.5	24
156	SMYD5 Controls Heterochromatin and Chromosome Integrity during Embryonic Stem Cell Differentiation. Cancer Research, 2017, 77, 6729-6745.	0.4	23
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