

Keji Zhao

List of Publications by Year in descending order

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Version: 2024-02-01

203
papers

37,180
citations

4370

86
h-index

3257

185
g-index

213
all docs

213
docs citations

213
times ranked

43539
citing authors

#	ARTICLE	IF	CITATIONS
1	Differential regulation of transcription factor T-bet induction during NK cell development and T helper-1 cell differentiation. <i>Immunity</i> , 2022, 55, 639-655.e7.	6.6	11
2	cLoops2: a full-stack comprehensive analytical tool for chromatin interactions. <i>Nucleic Acids Research</i> , 2022, 50, 57-71.	6.5	24
3	A dual-activity topoisomerase complex regulates mRNA translation and turnover. <i>Nucleic Acids Research</i> , 2022, 50, 7013-7033.	6.5	9
4	scPCOR-seq enables co-profiling of chromatin occupancy and RNAs in single cells. <i>Communications Biology</i> , 2022, 5, .	2.0	7
5	The epigenetic basis of cellular heterogeneity. <i>Nature Reviews Genetics</i> , 2021, 22, 235-250.	7.7	163
6	Genome-wide chromatin occupancy of BRDT and gene expression analysis suggest transcriptional partners and specific epigenetic landscapes that regulate gene expression during spermatogenesis. <i>Molecular Reproduction and Development</i> , 2021, 88, 141-157.	1.0	9
7	Multiplex indexing approach for the detection of DNase I hypersensitive sites in single cells. <i>Nucleic Acids Research</i> , 2021, 49, e56-e56.	6.5	11
8	Profiling single-cell histone modifications using indexing chromatin immunocleavage sequencing. <i>Genome Research</i> , 2021, 31, 1831-1842.	2.4	17
9	The Toolbox for Untangling Chromosome Architecture in Immune Cells. <i>Frontiers in Immunology</i> , 2021, 12, 670884.	2.2	3
10	B cell residency but not T cell-independent IgA switching in the gut requires innate lymphoid cells. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2021, 118, .	3.3	10
11	Chromatin accessibility profiling methods. <i>Nature Reviews Methods Primers</i> , 2021, 1, .	11.8	95
12	Concurrent mapping of multiple epigenetic marks and co-occupancy using ACT2-seq. <i>Cell and Bioscience</i> , 2021, 11, 198.	2.1	2
13	TGF- β 2 induces ST2 and programs ILC2 development. <i>Nature Communications</i> , 2020, 11, 35.	5.8	43
14	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
15	Genome-wide profiling of nucleosome position and chromatin accessibility in single cells using scMNase-seq. <i>Nature Protocols</i> , 2020, 15, 68-85.	5.5	17
16	Diploid genome architecture revealed by multi-omic data of hybrid mice. <i>Genome Research</i> , 2020, 30, 1097-1106.	2.4	18
17	Differential Histone Distribution Patterns in Induced Asymmetrically Dividing Mouse Embryonic Stem Cells. <i>Cell Reports</i> , 2020, 32, 108003.	2.9	31
18	Altered 3D chromatin structure permits inversional recombination at the <i>IgH</i> locus. <i>Science Advances</i> , 2020, 6, eaaz8850.	4.7	13

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19	RUNX1 and CBF β -SMMHC transactivate target genes together in abnormal myeloid progenitors for leukemia development. <i>Blood</i> , 2020, 136, 2373-2385.	0.6	24
20	Genome-Wide Transcriptional Regulation of the Long Non-coding RNA Steroid Receptor RNA Activator in Human Erythroblasts. <i>Frontiers in Genetics</i> , 2020, 11, 850.	1.1	6
21	Ldb1 is required for Lmo2 oncogene-induced thymocyte self-renewal and T-cell acute lymphoblastic leukemia. <i>Blood</i> , 2020, 135, 2252-2265.	0.6	7
22	Topoisomerase 3 β knockout mice show transcriptional and behavioural impairments associated with neurogenesis and synaptic plasticity. <i>Nature Communications</i> , 2020, 11, 3143.	5.8	22
23	Single-cyst transcriptome analysis of <i>Drosophila</i> male germline stem cell lineage. <i>Development (Cambridge)</i> , 2020, 147, .	1.2	29
24	Alteration of CTCF-associated chromatin neighborhood inhibits TAL1-driven oncogenic transcription program and leukemogenesis. <i>Nucleic Acids Research</i> , 2020, 48, 3119-3133.	6.5	19
25	Oncogene-dependent function of BRG1 in hepatocarcinogenesis. <i>Cell Death and Disease</i> , 2020, 11, 91.	2.7	23
26	Induction of DNMT3B by PGE2 and IL6 at Distant Metastatic Sites Promotes Epigenetic Modification and Breast Cancer Colonization. <i>Cancer Research</i> , 2020, 80, 2612-2627.	0.4	28
27	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
28	The transcription factor TCF-1 enforces commitment to the innate lymphoid cell lineage. <i>Nature Immunology</i> , 2019, 20, 1150-1160.	7.0	81
29	CTCF and cellular heterogeneity. <i>Cell and Bioscience</i> , 2019, 9, 83.	2.1	14
30	Single-cell chromatin immunocleavage sequencing (scChIC-seq) to profile histone modification. <i>Nature Methods</i> , 2019, 16, 323-325.	9.0	144
31	Histone hyperacetylation disrupts core gene regulatory architecture in rhabdomyosarcoma. <i>Nature Genetics</i> , 2019, 51, 1714-1722.	9.4	113
32	Intrinsic Dynamics of a Human Gene Reveal the Basis of Expression Heterogeneity. <i>Cell</i> , 2019, 176, 213-226.e18.	13.5	168
33	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
34	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
35	DNA Methylation and Regulatory Elements during Chicken Germline Stem Cell Differentiation. <i>Stem Cell Reports</i> , 2018, 10, 1793-1806.	2.3	19
36	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

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37	Topoisomerase 3 ¹² interacts with RNAi machinery to promote heterochromatin formation and transcriptional silencing in <i>Drosophila</i> . <i>Nature Communications</i> , 2018, 9, 4946.	5.8	27
38	The gene repressor complex NuRD interacts with the histone variant H3.3 at promoters of active genes. <i>Genome Research</i> , 2018, 28, 1646-1655.	2.4	17
39	Principles of nucleosome organization revealed by single-cell micrococcal nuclease sequencing. <i>Nature</i> , 2018, 562, 281-285.	13.7	135
40	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
41	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
42	MEK inhibition induces MYOG and remodels super-enhancers in RAS-driven rhabdomyosarcoma. <i>Science Translational Medicine</i> , 2018, 10, .	5.8	104
43	Trac-looping measures genome structure and chromatin accessibility. <i>Nature Methods</i> , 2018, 15, 741-747.	9.0	74
44	Rapid Recall Ability of Memory T cells is Encoded in their Epigenome. <i>Scientific Reports</i> , 2017, 7, 39785.	1.6	39
45	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
46	A General Non-radioactive ATPase Assay for Chromatin Remodeling Complexes. <i>Current Protocols in Chemical Biology</i> , 2017, 9, 1-10.	1.7	7
47	Polycomb Group Gene E(z) Is Required for Spermatogonial Dedifferentiation in <i>Drosophila</i> Adult Testis. <i>Journal of Molecular Biology</i> , 2017, 429, 2030-2041.	2.0	11
48	PAX3 ¹² FOXO1 Establishes Myogenic Super Enhancers and Confers BET Bromodomain Vulnerability. <i>Cancer Discovery</i> , 2017, 7, 884-899.	7.7	221
49	Smarca4 ATPase mutations disrupt direct eviction of PRC1 from chromatin. <i>Nature Genetics</i> , 2017, 49, 282-288.	9.4	165
50	SMARCB1 is required for widespread BAF complex ¹² mediated activation of enhancers and bivalent promoters. <i>Nature Genetics</i> , 2017, 49, 1613-1623.	9.4	207
51	SMYD5 Controls Heterochromatin and Chromosome Integrity during Embryonic Stem Cell Differentiation. <i>Cancer Research</i> , 2017, 77, 6729-6745.	0.4	23
52	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
53	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
54	Genome-wide identification of histone H2A and histone variant H2A.Z-interacting proteins by bPPI-seq. <i>Cell Research</i> , 2017, 27, 1258-1274.	5.7	14

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55	MLL4 prepares the enhancer landscape for Foxp3 induction via chromatin looping. <i>Nature Immunology</i> , 2017, 18, 1035-1045.	7.0	63
56	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
57	Histone demethylases UTX and JMJD3 are required for NKT cell development in mice. <i>Cell and Bioscience</i> , 2017, 7, 25.	2.1	28
58	Global intron retention mediated gene regulation during CD4 ⁺ T cell activation. <i>Nucleic Acids Research</i> , 2016, 44, 6817-6829.	6.5	96
59	RNA Polymerase II Regulates Topoisomerase 1 Activity to Favor Efficient Transcription. <i>Cell</i> , 2016, 165, 357-371.	13.5	211
60	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
61	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
62	O-GlcNAcase Is an RNA Polymerase II Elongation Factor Coupled to Pausing Factors SPT5 and TIF1 ² . <i>Journal of Biological Chemistry</i> , 2016, 291, 22703-22713.	1.6	35
63	Looping around Bcl6 in Germinal Center to Sharpen B Cell Immunity. <i>Immunity</i> , 2016, 45, 459-461.	6.6	2
64	Establishing Chromatin Regulatory Landscape during Mouse Preimplantation Development. <i>Cell</i> , 2016, 165, 1375-1388.	13.5	254
65	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
66	The conservation and signatures of lincRNAs in Marek's disease of chicken. <i>Scientific Reports</i> , 2015, 5, 15184.	1.6	69
67	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
68	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
69	Histone modifications induced by MDV infection at early cytotytic and latency phases. <i>BMC Genomics</i> , 2015, 16, 311.	1.2	13
70	The DNA-binding inhibitor Id3 regulates IL-9 production in CD4 ⁺ T cells. <i>Nature Immunology</i> , 2015, 16, 1077-1084.	7.0	63
71	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
72	Methylome Analysis in Chickens Immunized with Infectious Laryngotracheitis Vaccine. <i>PLoS ONE</i> , 2015, 10, e0100476.	1.1	10

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73	Genome-Wide H3K4me3 Analysis in Angus Cattle with Divergent Tenderness. <i>PLoS ONE</i> , 2015, 10, e0115358.	1.1	40
74	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
75	DNA Break Mapping Reveals Topoisomerase II Activity Genome-Wide. <i>International Journal of Molecular Sciences</i> , 2014, 15, 13111-13122.	1.8	70
76	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
77	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
78	Critical role of histone demethylase Jmjd3 in the regulation of CD4+ T-cell differentiation. <i>Nature Communications</i> , 2014, 5, 5780.	5.8	136
79	Reply to Naccache et al: Viral sequences of NIH-CQV virus, a contamination of DNA extraction method. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2014, 111, E977-E977.	3.3	11
80	The Transcription Factors T-bet and Runx Are Required for the Ontogeny of Pathogenic Interferon- β -Producing T Helper 17 Cells. <i>Immunity</i> , 2014, 40, 355-366.	6.6	183
81	A Non-Cell Autonomous Role of E-cadherin to Prevent Germ Cells from Turning on a Somatic Cell Marker. <i>Science</i> , 2014, 343, 1513-1516.	6.0	38
82	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
83	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
84	Telbivudine treatment corrects HBV-induced epigenetic alterations in liver cells of patients with chronic hepatitis B. <i>Carcinogenesis</i> , 2014, 35, 53-61.	1.3	13
85	Gcn5 and PCAF negatively regulate interferon β production through HAT-independent inhibition of TBK1. <i>EMBO Reports</i> , 2014, 15, 1192-1201.	2.0	31
86	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, 1313-1328.	1.6	92
87	Control of Cell Identity Genes Occurs in Insulated Neighborhoods in Mammalian Chromosomes. <i>Cell</i> , 2014, 159, 374-387.	13.5	793
88	Insulators recruit histone methyltransferase MeKs4 to regulate chromatin of flanking genes. <i>EMBO Journal</i> , 2014, 33, 1599-1613.	3.5	34
89	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
90	Efficient Library Preparation for Next-Generation Sequencing Analysis of Genome-Wide Epigenetic and Transcriptional Landscapes in Embryonic Stem Cells. <i>Methods in Molecular Biology</i> , 2014, 1150, 3-20.	0.4	17

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91	Dynamic regulation of epigenomic landscapes during hematopoiesis. <i>BMC Genomics</i> , 2013, 14, 193.	1.2	41
92	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
93	Extended Self-Renewal and Accelerated Reprogramming in the Absence of Kdm5b. <i>Molecular and Cellular Biology</i> , 2013, 33, 4793-4810.	1.1	58
94	Ldb1-nucleated transcription complexes function as primary mediators of global erythroid gene activation. <i>Blood</i> , 2013, 121, 4575-4585.	0.6	78
95	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
96	BAF complexes facilitate decatenation of DNA by topoisomerase II α . <i>Nature</i> , 2013, 497, 624-627.	13.7	230
97	PfSETvs methylation of histone H3K36 represses virulence genes in <i>Plasmodium falciparum</i> . <i>Nature</i> , 2013, 499, 223-227.	13.7	219
98	USF1 and hSET1A Mediated Epigenetic Modifications Regulate Lineage Differentiation and HoxB4 Transcription. <i>PLoS Genetics</i> , 2013, 9, e1003524.	1.5	57
99	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
100	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
101	Intragenic DNA methylation modulates alternative splicing by recruiting MeCP2 to promote exon recognition. <i>Cell Research</i> , 2013, 23, 1256-1269.	5.7	489
102	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
103	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
104	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
105	The Epigenomics of Embryonic Stem Cell Differentiation. <i>International Journal of Biological Sciences</i> , 2013, 9, 1134-1144.	2.6	41
106	Transcriptional Regulation of Rod Photoreceptor Homeostasis Revealed by In Vivo NRL Targetome Analysis. <i>PLoS Genetics</i> , 2012, 8, e1002649.	1.5	99
107	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
108	T-cell Acute Leukemia 1 (TAL1) Regulation of Erythropoietin Receptor and Association with Excessive Erythrocytosis. <i>Journal of Biological Chemistry</i> , 2012, 287, 36720-36731.	1.6	13

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109	Novel Foxo1-dependent transcriptional programs control Treg cell function. <i>Nature</i> , 2012, 491, 554-559.	13.7	348
110	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
111	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
112	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
113	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
114	An anti-cancer Smurf. <i>Cell and Bioscience</i> , 2012, 2, 10.	2.1	1
115	Genome-Wide Mapping of Nucleosome Occupancy, Histone Modifications, and Gene Expression Using Next-Generation Sequencing Technology. <i>Methods in Enzymology</i> , 2012, 513, 297-313.	0.4	24
116	A Novel Human Polycomb Binding Site Acts As a Functional Polycomb Response Element in <i>Drosophila</i> . <i>PLoS ONE</i> , 2012, 7, e36365.	1.1	24
117	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
118	SWI/SNF-mediated chromatin remodeling induces Z-DNA formation on a nucleosome. <i>Cell and Bioscience</i> , 2012, 2, 3.	2.1	29
119	CTCF Mediated Enhancer and Promoter Interaction Regulates Differential Expression of TAL1 Oncogene in Normal and Malignant Hematopoiesis. <i>Blood</i> , 2012, 120, 281-281.	0.6	2
120	Histone Methylation Analysis and Pathway Predictions in Chickens after MDV Infection. <i>PLoS ONE</i> , 2012, 7, e41849.	1.1	21
121	The fragile X mental retardation protein FMRP plays a role in the DNA damage response. <i>FASEB Journal</i> , 2012, 26, 88.1.	0.2	1
122	Identification and Characterization of a Novel Parvovirus-Like Virus in Seronegative Hepatitis Patients by Next Generation Sequencing. <i>Blood</i> , 2012, 120, 273-273.	0.6	0
123	A T-Cell Specific Element Activates the TAL1 Oncogene Via an Interchromosomal Interaction During Leukemogenesis. <i>Blood</i> , 2012, 120, 3507-3507.	0.6	0
124	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
125	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
126	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

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127	ChIP-Seq: technical considerations for obtaining high-quality data. <i>Nature Immunology</i> , 2011, 12, 918-922.	7.0	199
128	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
129	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
130	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
131	Dual functions of Tet1 in transcriptional regulation in mouse embryonic stem cells. <i>Nature</i> , 2011, 473, 389-393.	13.7	581
132	Effect of PCR extension temperature on high-throughput sequencing. <i>Molecular and Biochemical Parasitology</i> , 2011, 176, 64-67.	0.5	19
133	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
134	3C-based methods to detect long-range chromatin interactions. <i>Frontiers in Biology</i> , 2011, 6, 76-81.	0.7	4
135	Application of ChIP-Seq and Related Techniques to the Study of Immune Function. <i>Immunity</i> , 2011, 34, 830-842.	6.6	60
136	Phosphorylation of H4 Ser 47 promotes HIRA-mediated nucleosome assembly. <i>Genes and Development</i> , 2011, 25, 1359-1364.	2.7	52
137	A Barrier-Only Boundary Element Delimits the Formation of Facultative Heterochromatin in <i>Drosophila melanogaster</i> and Vertebrates. <i>Molecular and Cellular Biology</i> , 2011, 31, 2729-2741.	1.1	19
138	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
139	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
140	Cell Fate Determination Factor Dachshund Reprograms Breast Cancer Stem Cell Function. <i>Journal of Biological Chemistry</i> , 2011, 286, 2132-2142.	1.6	74
141	GATA3 controls Foxp3+ regulatory T cell fate during inflammation in mice. <i>Journal of Clinical Investigation</i> , 2011, 121, 4503-4515.	3.9	462
142	Role of hSET1 Complex in Epigenetic Controls of HoxB4 Expression and Development of Hematopoietic Stem Cells. <i>Blood</i> , 2011, 118, 212-212.	0.6	2
143	The Transcription Factor GATA3 Actively Represses RUNX3 Protein-Regulated Production of Interferon- β . <i>Immunity</i> , 2010, 32, 507-517.	6.6	151
144	Epigenomics of T cell activation, differentiation, and memory. <i>Current Opinion in Immunology</i> , 2010, 22, 341-347.	2.4	91

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145	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
146	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
147	Histone H4K20/H3K9 demethylase PHF8 regulates zebrafish brain and craniofacial development. <i>Nature</i> , 2010, 466, 503-507.	13.7	263
148	Nucleosome dynamics define transcriptional enhancers. <i>Nature Genetics</i> , 2010, 42, 343-347.	9.4	426
149	Genome-Wide Distribution of MacroH2A1 Histone Variants in Mouse Liver Chromatin. <i>Molecular and Cellular Biology</i> , 2010, 30, 5473-5483.	1.1	60
150	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
151	PTIP Promotes Chromatin Changes Critical for Immunoglobulin Class Switch Recombination. <i>Science</i> , 2010, 329, 917-923.	6.0	137
152	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
153	Epigenome Mapping in Normal and Disease States. <i>Circulation Research</i> , 2010, 107, 327-339.	2.0	164
154	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
155	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
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