

Keji Zhao

List of Publications by Year in descending order

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Version: 2024-02-01

203
papers

37,180
citations

5126

86
h-index

3782

185
g-index

213
all docs

213
docs citations

213
times ranked

48315
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 cytolitic 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. PLoS ONE, 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. Epigenetics and Chromatin, 2014, 7, 38.	1.8	38
75	DNA Break Mapping Reveals Topoisomerase II Activity Genome-Wide. International Journal of Molecular Sciences, 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. PLoS Genetics, 2014, 10, e1004524.	1.5	50
77	Comparison of REST Cistromes across Human Cell Types Reveals Common and Context-Specific Functions. PLoS Computational Biology, 2014, 10, e1003671.	1.5	40
78	Critical role of histone demethylase Jmjd3 in the regulation of CD4+ T-cell differentiation. Nature Communications, 2014, 5, 5780.	5.8	136
79	Reply to Naccache et al: Viral sequences of NIH-CQV virus, a contamination of DNA extraction method. Proceedings of the National Academy of Sciences of the United States of America, 2014, 111, E977-E977.	3.3	11
80	The Transcription Factors T-bet and Runx Are Required for the Ontogeny of Pathogenic Interferon- γ -Producing T Helper 17 Cells. Immunity, 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. Science, 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. Immunity, 2014, 40, 378-388.	6.6	320
83	Chromatin Immunoprecipitation Indirect Peaks Highlight Long-Range Interactions of Insulator Proteins and Pol II Pausing. Molecular Cell, 2014, 53, 672-681.	4.5	102
84	Telbivudine treatment corrects HBV-induced epigenetic alterations in liver cells of patients with chronic hepatitis B. Carcinogenesis, 2014, 35, 53-61.	1.3	13
85	Gcn5 and PCAF negatively regulate interferon β production through HAT-independent inhibition of TBK1. EMBO Reports, 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. Journal of Biological Chemistry, 2014, 289, 1313-1328.	1.6	92
87	Control of Cell Identity Genes Occurs in Insulated Neighborhoods in Mammalian Chromosomes. Cell, 2014, 159, 374-387.	13.5	793
88	Insulators recruit histone methyltransferase MeKs4 to regulate chromatin of flanking genes. EMBO Journal, 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. Immunity, 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. Methods in Molecular Biology, 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 β . <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
156	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
157	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
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