

Keji Zhao

List of PR Articles by Year in descending order

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178

PR articles

26,534

PR citations

4517

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PR h-index

3757

160

g-index

204

documents

36238

doc citations

3448

87

h-index

46515

citing authors

#	ARTICLE	IF	PR CITATIONS
1	Three-dimensional chromatin reorganization regulates B cell development during ageing. <i>Nature Cell Biology</i> , 2024, 26, 991-1002.	16.9	21
2	Acute depletion of BRG1 reveals its primary function as an activator of transcription. <i>Nature Communications</i> , 2024, 15, .	13.9	13
3	The <i>Drosophila</i> histone methyltransferase SET1 coordinates multiple signaling pathways in regulating male germline stem cell maintenance and differentiation. <i>Development (Cambridge)</i> , 2024, 151, .	3.1	1
4	Hi-TrAC detects active sub-TADs and reveals internal organizations of super-enhancers. <i>Nucleic Acids Research</i> , 2023, 51, 6172-6189.	15.7	13
5	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.	23.3	41
6	cLoops2: a full-stack comprehensive analytical tool for chromatin interactions. <i>Nucleic Acids Research</i> , 2022, 50, 57-71.	15.7	41
7	A dual-activity topoisomerase complex regulates mRNA translation and turnover. <i>Nucleic Acids Research</i> , 2022, 50, 7013-7033.	15.7	26
8	scPCOR-seq enables co-profiling of chromatin occupancy and RNAs in single cells. <i>Communications Biology</i> , 2022, 5, .	4.4	16
9	Opposing functions of circadian protein DBP and atypical E2F family E2F8 in anti-tumor Th9 cell differentiation. <i>Nature Communications</i> , 2022, 13, .	13.9	19
10	Hi-TrAC reveals division of labor of transcription factors in organizing chromatin loops. <i>Nature Communications</i> , 2022, 13, .	13.9	38
11	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.	2.9	17
12	Multiplex indexing approach for the detection of DNase I hypersensitive sites in single cells. <i>Nucleic Acids Research</i> , 2021, 49, e56-e56.	15.7	18
13	Profiling single-cell histone modifications using indexing chromatin immunocleavage sequencing. <i>Genome Research</i> , 2021, 31, 1831-1842.	4.6	25
14	The Toolbox for Untangling Chromosome Architecture in Immune Cells. <i>Frontiers in Immunology</i> , 2021, 12, .	5.1	4
15	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, .	7.6	16
16	Chromatin accessibility profiling methods. <i>Nature Reviews Methods Primers</i> , 2021, 1, .	51.0	162
17	Concurrent mapping of multiple epigenetic marks and co-occupancy using ACT2-seq. <i>Cell and Bioscience</i> , 2021, 11, .	5.6	2
18	TGF- β 2 induces ST2 and programs ILC2 development. <i>Nature Communications</i> , 2020, 11, .	13.9	57

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19	Differential Expression of the Transcription Factor GATA3 Specifies Lineage and Functions of Innate Lymphoid Cells. <i>Immunity</i> , 2020, 52, 83-95.e4.	23.3	84
20	Diploid genome architecture revealed by multi-omic data of hybrid mice. <i>Genome Research</i> , 2020, 30, 1097-1106.	4.6	27
21	Altered 3D chromatin structure permits inversional recombination at the <i>IgH</i> locus. <i>Science Advances</i> , 2020, 6, .	11.0	21
22	RUNX1 and CBF β -SMMHC transactivate target genes together in abnormal myeloid progenitors for leukemia development. <i>Blood</i> , 2020, 136, 2373-2385.	4.2	37
23	Genome-Wide Transcriptional Regulation of the Long Non-coding RNA Steroid Receptor RNA Activator in Human Erythroblasts. <i>Frontiers in Genetics</i> , 2020, 11, .	2.4	6
24	Ldb1 is required for Lmo2 oncogene-induced thymocyte self-renewal and T-cell acute lymphoblastic leukemia. <i>Blood</i> , 2020, 135, 2252-2265.	4.2	11
25	Topoisomerase 3 β knockout mice show transcriptional and behavioural impairments associated with neurogenesis and synaptic plasticity. <i>Nature Communications</i> , 2020, 11, .	13.9	35
26	Single-cyst transcriptome analysis of <i>Drosophila</i> male germline stem cell lineage. <i>Development (Cambridge)</i> , 2020, 147, .	3.1	35
27	Alteration of CTCF-associated chromatin neighborhood inhibits TAL1-driven oncogenic transcription program and leukemogenesis. <i>Nucleic Acids Research</i> , 2020, 48, 3119-3133.	15.7	28
28	Oncogene-dependent function of BRG1 in hepatocarcinogenesis. <i>Cell Death and Disease</i> , 2020, 11, .	8.7	29
29	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.	0.6	40
30	The epigenetic basis of cellular heterogeneity. <i>Nature Reviews Genetics</i> , 2020, 22, 235-250.	47.6	279
31	Mapping histone modifications in low cell number and single cells using antibody-guided chromatin tagmentation (ACT-seq). <i>Nature Communications</i> , 2019, 10, .	13.9	146
32	The transcription factor TCF-1 enforces commitment to the innate lymphoid cell lineage. <i>Nature Immunology</i> , 2019, 20, 1150-1160.	24.2	120
33	CTCF and cellular heterogeneity. <i>Cell and Bioscience</i> , 2019, 9, .	5.6	17
34	Single-cell chromatin immunocleavage sequencing (scChIC-seq) to profile histone modification. <i>Nature Methods</i> , 2019, 16, 323-325.	25.9	178
35	Histone hyperacetylation disrupts core gene regulatory architecture in rhabdomyosarcoma. <i>Nature Genetics</i> , 2019, 51, 1714-1722.	26.1	153
36	Intrinsic Dynamics of a Human Gene Reveal the Basis of Expression Heterogeneity. <i>Cell</i> , 2019, 176, 213-226.e18.	34.1	258

#	ARTICLE	IF	PR CITATIONS
37	Trac-looping protocol. Protocol Exchange, 2019, , .	0.0	1
38	A single-cell chromatin immunocleavage sequencing (scChIC-seq). Protocol Exchange, 2019, , .	0.0	1
39	Transformation of Accessible Chromatin and 3D Nucleome Underlies Lineage Commitment of Early T Cells. <i>Immunity</i> , 2018, 48, 227-242.e8.	23.3	210
40	Bcl11b, a novel GATA3-interacting protein, suppresses Th1 while limiting Th2 cell differentiation. <i>Journal of Experimental Medicine</i> , 2018, 215, 1449-1462.	9.4	52
41	DNA Methylation and Regulatory Elements during Chicken Germline Stem Cell Differentiation. <i>Stem Cell Reports</i> , 2018, 10, 1793-1806.	4.5	27
42	Topoisomerase 3 ^β interacts with RNAi machinery to promote heterochromatin formation and transcriptional silencing in <i>Drosophila</i> . <i>Nature Communications</i> , 2018, 9, .	13.9	36
43	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.	4.6	22
44	MEK inhibition induces MYOG and remodels super-enhancers in RAS-driven rhabdomyosarcoma. <i>Science Translational Medicine</i> , 2018, 10, .	12.7	131
45	Trac-looping measures genome structure and chromatin accessibility. <i>Nature Methods</i> , 2018, 15, 741-747.	25.9	90
46	Rapid Recall Ability of Memory T cells is Encoded in their Epigenome. <i>Scientific Reports</i> , 2017, 7, .	3.5	50
47	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.	8.7	85
48	A General Non- ³² P-ATPase Assay for Chromatin Remodeling Complexes. <i>Current Protocols in Chemical Biology</i> , 2017, 9, 1-10.	1.4	12
49	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.	4.2	14
50	PAX3-FOXO1 Establishes Myogenic Super Enhancers and Confers BET Bromodomain Vulnerability. <i>Cancer Discovery</i> , 2017, 7, 884-899.	25.6	298
51	SMARCB1 is required for widespread BAF complex-mediated activation of enhancers and bivalent promoters. <i>Nature Genetics</i> , 2017, 49, 1613-1623.	26.1	270
52	SMYD5 Controls Heterochromatin and Chromosome Integrity during Embryonic Stem Cell Differentiation. <i>Cancer Research</i> , 2017, 77, 6729-6745.	0.6	34
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.	13.4	260
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.	12.5	20

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55	MLL4 prepares the enhancer landscape for Foxp3 induction via chromatin looping. <i>Nature Immunology</i> , 2017, 18, 1035-1045.	24.2	83
56	SMYD5 regulates H4K20me3-marked heterochromatin to safeguard ES cell self-renewal and prevent spurious differentiation. <i>Epigenetics and Chromatin</i> , 2017, 10, .	3.3	63
57	Histone demethylases UTX and JMJD3 are required for NKT cell development in mice. <i>Cell and Bioscience</i> , 2017, 7, .	5.6	32
58	Dominant-negative SMARCA4 mutants alter the accessibility landscape of tissue-unrestricted enhancers. <i>Nature Structural and Molecular Biology</i> , 2017, 25, 61-72.	8.7	164
59	Global intron retention mediated gene regulation during CD4 ⁺ T cell activation. <i>Nucleic Acids Research</i> , 2016, 44, 6817-6829.	15.7	108
60	RNA Polymerase II Regulates Topoisomerase 1 Activity to Favor Efficient Transcription. <i>Cell</i> , 2016, 165, 357-371.	34.1	266
61	Setd1a and NURF mediate chromatin dynamics and gene regulation during erythroid lineage commitment and differentiation. <i>Nucleic Acids Research</i> , 2016, , gkw327.	15.7	43
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.	2.2	43
63	Establishing Chromatin Regulatory Landscape during Mouse Preimplantation Development. <i>Cell</i> , 2016, 165, 1375-1388.	34.1	326
64	The conservation and signatures of lincRNAs in Marek's disease of chicken. <i>Scientific Reports</i> , 2015, 5, .	3.5	74
65	Multiple Layers of Chimerism in a Single-Stranded DNA Virus Discovered by Deep Sequencing. <i>Genome Biology and Evolution</i> , 2015, 7, 993-1001.	2.4	41
66	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, .	5.6	57
67	Histone modifications induced by MDV infection at early cytolitic and latency phases. <i>BMC Genomics</i> , 2015, 16, .	3.3	15
68	The DNA-binding inhibitor Id3 regulates IL-9 production in CD4 ⁺ T cells. <i>Nature Immunology</i> , 2015, 16, 1077-1084.	24.2	75
69	Lineage relationship of CD8 ⁺ T cell subsets is revealed by progressive changes in the epigenetic landscape. <i>Cellular and Molecular Immunology</i> , 2015, 13, 502-513.	15.6	115
70	Group 3 innate lymphoid cells continuously require the transcription factor GATA-3 after commitment. <i>Nature Immunology</i> , 2015, 17, 169-178.	24.2	140
71	Methylome Analysis in Chickens Immunized with Infectious Laryngotracheitis Vaccine. <i>PLoS ONE</i> , 2015, 10, e0100476.	2.4	10
72	Genome-Wide H3K4me3 Analysis in Angus Cattle with Divergent Tenderness. <i>PLoS ONE</i> , 2015, 10, e0115358.	2.4	43

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73	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, .	3.3	41
74	DNA Break Mapping Reveals Topoisomerase II Activity Genome-Wide. <i>International Journal of Molecular Sciences</i> , 2014, 15, 13111-13122.	4.5	84
75	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.	3.3	52
76	Comparison of REST Cistromes across Human Cell Types Reveals Common and Context-Specific Functions. <i>PLoS Computational Biology</i> , 2014, 10, e1003671.	3.1	45
77	Critical role of histone demethylase Jmjd3 in the regulation of CD4+ T-cell differentiation. <i>Nature Communications</i> , 2014, 5, .	13.9	152
78	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.	23.3	354
79	Chromatin Immunoprecipitation Indirect Peaks Highlight Long-Range Interactions of Insulator Proteins and Pol II Pausing. <i>Molecular Cell</i> , 2014, 53, 672-681.	13.4	113
80	Telbivudine treatment corrects HBV-induced epigenetic alterations in liver cells of patients with chronic hepatitis B. <i>Carcinogenesis</i> , 2014, 35, 53-61.	2.9	13
81	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.	2.2	100
82	Control of Cell Identity Genes Occurs in Insulated Neighborhoods in Mammalian Chromosomes. <i>Cell</i> , 2014, 159, 374-387.	34.1	883
83	Insulators recruit histone methyltransferase <i>Mes4</i> to regulate chromatin of flanking genes. <i>EMBO Journal</i> , 2014, 33, 1599-1613.	7.4	40
84	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.	23.3	187
85	Dynamic regulation of epigenomic landscapes during hematopoiesis. <i>BMC Genomics</i> , 2013, 14, .	3.3	43
86	Expression and regulation of intergenic long noncoding RNAs during T cell development and differentiation. <i>Nature Immunology</i> , 2013, 14, 1190-1198.	24.2	438
87	Extended Self-Renewal and Accelerated Reprogramming in the Absence of Kdm5b. <i>Molecular and Cellular Biology</i> , 2013, 33, 4793-4810.	2.5	64
88	Ldb1-nucleated transcription complexes function as primary mediators of global erythroid gene activation. <i>Blood</i> , 2013, 121, 4575-4585.	4.2	94
89	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.	16.8	304
90	USF1 and hSET1A Mediated Epigenetic Modifications Regulate Lineage Differentiation and HoxB4 Transcription. <i>PLoS Genetics</i> , 2013, 9, e1003524.	3.3	60

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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.	3.3	91
92	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.	3.1	51
93	Intragenic DNA methylation modulates alternative splicing by recruiting MeCP2 to promote exon recognition. <i>Cell Research</i> , 2013, 23, 1256-1269.	12.5	535
94	The ATP-dependent Chromatin Remodeling Enzyme Fun30 Represses Transcription by Sliding Promoter-proximal Nucleosomes. <i>Journal of Biological Chemistry</i> , 2013, 288, 23182-23193.	2.2	38
95	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.	7.6	51
96	Genome-wide incorporation dynamics reveal distinct categories of turnover for the histone variant H3.3. <i>Genome Biology</i> , 2013, 14, .	8.2	134
97	The Epigenomics of Embryonic Stem Cell Differentiation. <i>International Journal of Biological Sciences</i> , 2013, 9, 1134-1144.	8.8	44
98	Transcriptional Regulation of Rod Photoreceptor Homeostasis Revealed by In Vivo NRL Targetome Analysis. <i>PLoS Genetics</i> , 2012, 8, e1002649.	3.3	115
99	Report of the National Heart, Lung, and Blood Institute Working Group on Epigenetics and Hypertension. <i>Hypertension</i> , 2012, 59, 899-905.	6.9	92
100	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.	2.2	16
101	Novel Foxo1-dependent transcriptional programs control Treg cell function. <i>Nature</i> , 2012, 491, 554-559.	38.7	392
102	c-Myc Is a Universal Amplifier of Expressed Genes in Lymphocytes and Embryonic Stem Cells. <i>Cell</i> , 2012, 151, 68-79.	34.1	999
103	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.	23.3	309
104	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.	12.5	260
105	Regulation of Pluripotency and Self-Renewal of ESCs through Epigenetic-Threshold Modulation and mRNA Pruning. <i>Cell</i> , 2012, 151, 576-589.	34.1	78
106	A Novel Human Polycomb Binding Site Acts As a Functional Polycomb Response Element in Drosophila. <i>PLoS ONE</i> , 2012, 7, e36365.	2.4	26
107	SWI/SNF-mediated chromatin remodeling induces Z-DNA formation on a nucleosome. <i>Cell and Bioscience</i> , 2012, 2, .	5.6	41
108	CTCF Mediated Enhancer and Promoter Interaction Regulates Differential Expression of TAL1 Oncogene in Normal and Malignant Hematopoiesis. <i>Blood</i> , 2012, 120, 281-281.	4.2	3

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109	Histone Methylation Analysis and Pathway Predictions in Chickens after MDV Infection. PLoS ONE, 2012, 7, e41849.	2.4	23
110	Identification and Characterization of a Novel Parvovirus-Like Virus in Seronegative Hepatitis Patients by Next Generation Sequencing. Blood, 2012, 120, 273-273.	4.2	0
111	A T-Cell Specific Element Activates the TAL1 Oncogene Via an Interchromosomal Interaction During Leukemogenesis. Blood, 2012, 120, 3507-3507.	4.2	0
112	GABP controls a critical transcription regulatory module that is essential for maintenance and differentiation of hematopoietic stem/progenitor cells. Blood, 2011, 117, 2166-2178.	4.2	76
113	Genome-wide analysis of 5-hydroxymethylcytosine distribution reveals its dual function in transcriptional regulation in mouse embryonic stem cells. Genes and Development, 2011, 25, 679-684.	4.7	517
114	Regulation of nucleosome landscape and transcription factor targeting at tissue-specific enhancers by BRG1. Genome Research, 2011, 21, 1650-1658.	4.6	175
115	Genome-wide Analyses of Transcription Factor GATA3-Mediated Gene Regulation in Distinct T Cell Types. Immunity, 2011, 35, 299-311.	23.3	331
116	Mapping of INS promoter interactions reveals its role in long-range regulation of SYT8 transcription. Nature Structural and Molecular Biology, 2011, 18, 372-378.	8.7	59
117	Effect of PCR extension temperature on high-throughput sequencing. Molecular and Biochemical Parasitology, 2011, 176, 64-67.	1.3	20
118	DNA double-strand breaks induced by high NaCl occur predominantly in gene deserts. Proceedings of the National Academy of Sciences of the United States of America, 2011, 108, 20796-20801.	7.6	54
119	3C-based methods to detect long-range chromatin interactions. Frontiers in Biology, 2011, 6, 76-81.	0.8	4
120	Application of CHIP-Seq and Related Techniques to the Study of Immune Function. Immunity, 2011, 34, 830-842.	23.3	62
121	Phosphorylation of H4 Ser 47 promotes HIRA-mediated nucleosome assembly. Genes and Development, 2011, 25, 1359-1364.	4.7	53
122	A Barrier-Only Boundary Element Delimits the Formation of Facultative Heterochromatin in Drosophila melanogaster and Vertebrates. Molecular and Cellular Biology, 2011, 31, 2729-2741.	2.5	19
123	Lsh, chromatin remodeling family member, modulates genome-wide cytosine methylation patterns at nonrepeat sequences. Proceedings of the National Academy of Sciences of the United States of America, 2011, 108, 5626-5631.	7.6	84
124	Genomic Profiling of HMGN1 Reveals an Association with Chromatin at Regulatory Regions. Molecular and Cellular Biology, 2011, 31, 700-709.	2.5	48
125	Cell Fate Determination Factor Dachshund Reprograms Breast Cancer Stem Cell Function. Journal of Biological Chemistry, 2011, 286, 2132-2142.	2.2	77
126	GATA3 controls Foxp3+ regulatory T cell fate during inflammation in mice. Journal of Clinical Investigation, 2011, 121, 4503-4515.	10.7	523

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127	Role of hSET1 Complex in Epigenetic Controls of HoxB4 Expression and Development of Hematopoietic Stem Cells. <i>Blood</i> , 2011, 118, 212-212.	4.2	2
128	The Transcription Factor GATA3 Actively Represses RUNX3 Protein-Regulated Production of Interferon- β . <i>Immunity</i> , 2010, 32, 507-517.	23.3	165
129	Epigenomics of T cell activation, differentiation, and memory. <i>Current Opinion in Immunology</i> , 2010, 22, 341-347.	5.3	99
130	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.	8.7	180
131	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.	12.5	112
132	Genome-Wide Distribution of MacroH2A1 Histone Variants in Mouse Liver Chromatin. <i>Molecular and Cellular Biology</i> , 2010, 30, 5473-5483.	2.5	63
133	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.	7.6	59
134	PTIP Promotes Chromatin Changes Critical for Immunoglobulin Class Switch Recombination. <i>Science</i> , 2010, 329, 917-923.	36.4	152
135	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.	7.6	71
136	Epigenome Mapping in Normal and Disease States. <i>Circulation Research</i> , 2010, 107, 327-339.	12.5	180
137	Monovalent and unpoised status of most genes in undifferentiated cell-enriched <i>Drosophila</i> testis. <i>Genome Biology</i> , 2010, 11, .	8.2	70
138	Nuclear adaptor Ldb1 regulates a transcriptional program essential for the maintenance of hematopoietic stem cells. <i>Nature Immunology</i> , 2010, 12, 129-136.	24.2	103
139	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.	4.6	612
140	Detection of single nucleotide variations in expressed exons of the human genome using RNA-Seq. <i>Nucleic Acids Research</i> , 2009, 37, e106-e106.	15.7	161
141	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.	7.6	398
142	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.	7.6	396
143	Genome-Wide uH2A Localization Analysis Highlights Bmi1-Dependent Deposition of the Mark at Repressed Genes. <i>PLoS Genetics</i> , 2009, 5, e1000506.	3.3	62
144	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.	9.4	131

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145	Chromatin poises miRNA- and protein-coding genes for expression. <i>Genome Research</i> , 2009, 19, 1742-1751.	4.6	137
146	Genomic location analysis by ChIP-seq. <i>Journal of Cellular Biochemistry</i> , 2009, 107, 11-18.	3.1	158
147	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.	23.3	1,071
148	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.	23.3	279
149	A clustering approach for identification of enriched domains from histone modification ChIP-Seq data. <i>Bioinformatics</i> , 2009, 25, 1952-1958.	4.8	1,030
150	Genome-wide Mapping of HATs and HDACs Reveals Distinct Functions in Active and Inactive Genes. <i>Cell</i> , 2009, 138, 1019-1031.	34.1	1,278
151	Characterization of human epigenomes. <i>Current Opinion in Genetics and Development</i> , 2009, 19, 127-134.	3.2	147
152	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.	16.8	575
153	Integrated Expression Profiling and ChIP-seq Analyses of the Growth Inhibition Response Program of the Androgen Receptor. <i>PLoS ONE</i> , 2009, 4, e6589.	2.4	78
154	Serine Phosphorylation On TAL1 Regulates Its Interaction with Histone Demethylase LSD1.. <i>Blood</i> , 2009, 114, 1460-1460.	4.2	2
155	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.	24.2	261
156	Genome-wide approaches to studying chromatin modifications. <i>Nature Reviews Genetics</i> , 2008, 9, 179-191.	47.6	351
157	Transcriptional enhancer factor 1 (TEF/TEAD1) mediates activation of <i>IFITM3</i> gene by BRG1. <i>FEBS Letters</i> , 2008, 582, 391-397.	2.7	8
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