

# Kairong Cui

## List of Publications by Year in descending order

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84  
papers

24,173  
citations

31976

53  
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53230

85  
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86  
docs citations

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times ranked

31164  
citing authors

#	ARTICLE	IF	CITATIONS
1	High-Resolution Profiling of Histone Methylations in the Human Genome. <i>Cell</i> , 2007, 129, 823-837.	28.9	6,036
2	Combinatorial patterns of histone acetylations and methylations in the human genome. <i>Nature Genetics</i> , 2008, 40, 897-903.	21.4	2,034
3	Dynamic Regulation of Nucleosome Positioning in the Human Genome. <i>Cell</i> , 2008, 132, 887-898.	28.9	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.	28.9	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.	14.3	1,005
6	A clustering approach for identification of enriched domains from histone modification ChIP-Seq data. <i>Bioinformatics</i> , 2009, 25, 1952-1958.	4.1	936
7	c-Myc Is a Universal Amplifier of Expressed Genes in Lymphocytes and Embryonic Stem Cells. <i>Cell</i> , 2012, 151, 68-79.	28.9	907
8	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.	21.4	679
9	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.	5.5	587
10	Dual functions of Tet1 in transcriptional regulation in mouse embryonic stem cells. <i>Nature</i> , 2011, 473, 389-393.	27.8	581
11	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.	11.1	548
12	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.	14.5	500
13	Intragenic DNA methylation modulates alternative splicing by recruiting MeCP2 to promote exon recognition. <i>Cell Research</i> , 2013, 23, 1256-1269.	12.0	489
14	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.	5.9	488
15	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.	7.1	432
16	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.	7.1	374
17	Directional gene expression and antisense transcripts in sexual and asexual stages of <i>Plasmodium falciparum</i> . <i>BMC Genomics</i> , 2011, 12, 587.	2.8	309
18	Genome-wide detection of DNase I hypersensitive sites in single cells and FFPE tissue samples. <i>Nature</i> , 2015, 528, 142-146.	27.8	303

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19	Genome-wide Analyses of Transcription Factor GATA3-Mediated Gene Regulation in Distinct T Cell Types. <i>Immunity</i> , 2011, 35, 299-311.	14.3	293
20	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.	11.1	272
21	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.	14.3	256
22	Priming for T helper type 2 differentiation by interleukin 2-mediated induction of interleukin 4 receptor $\alpha$ -chain expression. <i>Nature Immunology</i> , 2008, 9, 1288-1296.	14.5	234
23	BAF complexes facilitate decatenation of DNA by topoisomerase II $\beta$ . <i>Nature</i> , 2013, 497, 624-627.	27.8	230
24	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.	9.7	219
25	RNA Polymerase II Regulates Topoisomerase 1 Activity to Favor Efficient Transcription. <i>Cell</i> , 2016, 165, 357-371.	28.9	211
26	SMARCB1 is required for widespread BAF complex-mediated activation of enhancers and bivalent promoters. <i>Nature Genetics</i> , 2017, 49, 1613-1623.	21.4	207
27	High-resolution genome-wide mapping of histone modifications. <i>Nature Biotechnology</i> , 2004, 22, 1013-1016.	17.5	199
28	Transformation of Accessible Chromatin and 3D Nucleome Underlies Lineage Commitment of Early T Cells. <i>Immunity</i> , 2018, 48, 227-242.e8.	14.3	188
29	The Transcription Factors T-bet and Runx Are Required for the Ontogeny of Pathogenic Interferon- $\gamma$ -Producing T Helper 17 Cells. <i>Immunity</i> , 2014, 40, 355-366.	14.3	183
30	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.	8.2	161
31	Regulation of nucleosome landscape and transcription factor targeting at tissue-specific enhancers by BRG1. <i>Genome Research</i> , 2011, 21, 1650-1658.	5.5	160
32	Single-cell chromatin immunocleavage sequencing (scChIC-seq) to profile histone modification. <i>Nature Methods</i> , 2019, 16, 323-325.	19.0	144
33	Chromatin poises miRNA- and protein-coding genes for expression. <i>Genome Research</i> , 2009, 19, 1742-1751.	5.5	135
34	Principles of nucleosome organization revealed by single-cell micrococcal nuclease sequencing. <i>Nature</i> , 2018, 562, 281-285.	27.8	135
35	Down-regulation of Gfi-1 expression by TGF- $\beta$ 2 is important for differentiation of Th17 and CD103+ inducible regulatory T cells. <i>Journal of Experimental Medicine</i> , 2009, 206, 329-341.	8.5	124
36	Group 3 innate lymphoid cells continuously require the transcription factor GATA-3 after commitment. <i>Nature Immunology</i> , 2016, 17, 169-178.	14.5	116

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37	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.	12.0	107
38	Transcriptional Regulation of Rod Photoreceptor Homeostasis Revealed by In Vivo NRL Targetome Analysis. <i>PLoS Genetics</i> , 2012, 8, e1002649.	3.5	99
39	Global intron retention mediated gene regulation during CD4 <sup>+</sup> T cell activation. <i>Nucleic Acids Research</i> , 2016, 44, 6817-6829.	14.5	96
40	Nuclear adaptor Ldb1 regulates a transcriptional program essential for the maintenance of hematopoietic stem cells. <i>Nature Immunology</i> , 2011, 12, 129-136.	14.5	91
41	The Chromatin-Remodeling BAF Complex Mediates Cellular Antiviral Activities by Promoter Priming. <i>Molecular and Cellular Biology</i> , 2004, 24, 4476-4486.	2.3	87
42	Genome-Wide Approaches to Determining Nucleosome Occupancy in Metazoans Using MNase-Seq. <i>Methods in Molecular Biology</i> , 2012, 833, 413-419.	0.9	87
43	Negative reciprocal regulation between Sirt1 and Per2 modulates the circadian clock and aging. <i>Scientific Reports</i> , 2016, 6, 28633.	3.3	80
44	Ldb1-nucleated transcription complexes function as primary mediators of global erythroid gene activation. <i>Blood</i> , 2013, 121, 4575-4585.	1.4	78
45	Trac-looping measures genome structure and chromatin accessibility. <i>Nature Methods</i> , 2018, 15, 741-747.	19.0	74
46	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.	1.4	69
47	Transient T-bet expression functionally specifies a distinct T follicular helper subset. <i>Journal of Experimental Medicine</i> , 2018, 215, 2705-2714.	8.5	68
48	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.	8.2	66
49	Monovalent and unpoised status of most genes in undifferentiated cell-enriched <i>Drosophila</i> testis. <i>Genome Biology</i> , 2010, 11, R42.	9.6	65
50	The DNA-binding inhibitor Id3 regulates IL-9 production in CD4 <sup>+</sup> T cells. <i>Nature Immunology</i> , 2015, 16, 1077-1084.	14.5	63
51	MLL4 prepares the enhancer landscape for Foxp3 induction via chromatin looping. <i>Nature Immunology</i> , 2017, 18, 1035-1045.	14.5	63
52	Genome-Wide Distribution of MacroH2A1 Histone Variants in Mouse Liver Chromatin. <i>Molecular and Cellular Biology</i> , 2010, 30, 5473-5483.	2.3	60
53	Genome-Wide uH2A Localization Analysis Highlights Bmi1-Dependent Deposition of the Mark at Repressed Genes. <i>PLoS Genetics</i> , 2009, 5, e1000506.	3.5	58
54	USF1 and hSET1A Mediated Epigenetic Modifications Regulate Lineage Differentiation and HoxB4 Transcription. <i>PLoS Genetics</i> , 2013, 9, e1003524.	3.5	57

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55	Differential Expression of the Transcription Factor GATA3 Specifies Lineage and Functions of Innate Lymphoid Cells. <i>Immunity</i> , 2020, 52, 83-95.e4.	14.3	52
56	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.	7.1	48
57	SMYD5 regulates H4K20me3-marked heterochromatin to safeguard ES cell self-renewal and prevent spurious differentiation. <i>Epigenetics and Chromatin</i> , 2017, 10, 8.	3.9	45
58	Genomic Profiling of HMG1 Reveals an Association with Chromatin at Regulatory Regions. <i>Molecular and Cellular Biology</i> , 2011, 31, 700-709.	2.3	44
59	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.	4.8	44
60	TGF- $\beta$ 2 induces ST2 and programs ILC2 development. <i>Nature Communications</i> , 2020, 11, 35.	12.8	43
61	Dynamic regulation of epigenomic landscapes during hematopoiesis. <i>BMC Genomics</i> , 2013, 14, 193.	2.8	41
62	Bcl11b, a novel GATA3-interacting protein, suppresses Th1 while limiting Th2 cell differentiation. <i>Journal of Experimental Medicine</i> , 2018, 215, 1449-1462.	8.5	41
63	Response: Mapping Nucleosome Positions Using ChIP-Seq Data. <i>Cell</i> , 2007, 131, 832-833.	28.9	32
64	Single-cyst transcriptome analysis of <i>Drosophila</i> male germline stem cell lineage. <i>Development (Cambridge)</i> , 2020, 147, .	2.5	29
65	Histone demethylases UTX and JMJD3 are required for NKT cell development in mice. <i>Cell and Bioscience</i> , 2017, 7, 25.	4.8	28
66	Native Chromatin Preparation and Illumina/Solexa Library Construction. <i>Cold Spring Harbor Protocols</i> , 2009, 2009, pdb.prot5237.	0.3	26
67	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.	1.0	24
68	A Novel Human Polycomb Binding Site Acts As a Functional Polycomb Response Element in <i>Drosophila</i> . <i>PLoS ONE</i> , 2012, 7, e36365.	2.5	24
69	Oncogene-dependent function of BRG1 in hepatocarcinogenesis. <i>Cell Death and Disease</i> , 2020, 11, 91.	6.3	23
70	Histone Methylation Analysis and Pathway Predictions in Chickens after MDV Infection. <i>PLoS ONE</i> , 2012, 7, e41849.	2.5	21
71	Effect of PCR extension temperature on high-throughput sequencing. <i>Molecular and Biochemical Parasitology</i> , 2011, 176, 64-67.	1.1	19
72	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.	2.3	19

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73	Diploid genome architecture revealed by multi-omic data of hybrid mice. <i>Genome Research</i> , 2020, 30, 1097-1106.	5.5	18
74	Marek's disease virus infection induces widespread differential chromatin marks in inbred chicken lines. <i>BMC Genomics</i> , 2012, 13, 557.	2.8	17
75	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.	5.5	17
76	Genome-wide identification of histone H2A and histone variant H2A.Z-interacting proteins by bPPI-seq. <i>Cell Research</i> , 2017, 27, 1258-1274.	12.0	14
77	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.	3.4	13
78	Histone modifications induced by MDV infection at early cytotytic and latency phases. <i>BMC Genomics</i> , 2015, 16, 311.	2.8	13
79	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	11
80	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.	14.3	11
81	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.	2.0	9
82	Ldb1 is required for Lmo2 oncogene-induced thymocyte self-renewal and T-cell acute lymphoblastic leukemia. <i>Blood</i> , 2020, 135, 2252-2265.	1.4	7
83	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.	2.3	6
84	Genome-Wide Approaches to Studying Yeast Chromatin Modifications. <i>Methods in Molecular Biology</i> , 2011, 759, 61-71.	0.9	4