

# Kairong Cui

## List of Publications by Year in descending order

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84  
papers

24,173  
citations

31902

53  
h-index

53109

85  
g-index

86  
all docs

86  
docs citations

86  
times ranked

31164  
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	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
3	TGF- $\beta^2$ induces ST2 and programs ILC2 development. <i>Nature Communications</i> , 2020, 11, 35.	5.8	43
4	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
5	Diploid genome architecture revealed by multi-omic data of hybrid mice. <i>Genome Research</i> , 2020, 30, 1097-1106.	2.4	18
6	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
7	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
8	Single-cyst transcriptome analysis of <i>Drosophila</i> male germline stem cell lineage. <i>Development (Cambridge)</i> , 2020, 147, .	1.2	29
9	Oncogene-dependent function of BRG1 in hepatocarcinogenesis. <i>Cell Death and Disease</i> , 2020, 11, 91.	2.7	23
10	Single-cell chromatin immunocleavage sequencing (scChIC-seq) to profile histone modification. <i>Nature Methods</i> , 2019, 16, 323-325.	9.0	144
11	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
12	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
13	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
14	Principles of nucleosome organization revealed by single-cell micrococcal nuclease sequencing. <i>Nature</i> , 2018, 562, 281-285.	13.7	135
15	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
16	Trac-looping measures genome structure and chromatin accessibility. <i>Nature Methods</i> , 2018, 15, 741-747.	9.0	74
17	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
18	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

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19	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
20	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
21	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
22	MLL4 prepares the enhancer landscape for Foxp3 induction via chromatin looping. <i>Nature Immunology</i> , 2017, 18, 1035-1045.	7.0	63
23	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
24	Histone demethylases UTX and JMJD3 are required for NKT cell development in mice. <i>Cell and Bioscience</i> , 2017, 7, 25.	2.1	28
25	Global intron retention mediated gene regulation during CD4 <sup>+</sup> T cell activation. <i>Nucleic Acids Research</i> , 2016, 44, 6817-6829.	6.5	96
26	Negative reciprocal regulation between Sirt1 and Per2 modulates the circadian clock and aging. <i>Scientific Reports</i> , 2016, 6, 28633.	1.6	80
27	RNA Polymerase II Regulates Topoisomerase 1 Activity to Favor Efficient Transcription. <i>Cell</i> , 2016, 165, 357-371.	13.5	211
28	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
29	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
30	Histone modifications induced by MDV infection at early cytolitic and latency phases. <i>BMC Genomics</i> , 2015, 16, 311.	1.2	13
31	The DNA-binding inhibitor Id3 regulates IL-9 production in CD4 <sup>+</sup> T cells. <i>Nature Immunology</i> , 2015, 16, 1077-1084.	7.0	63
32	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
33	The Transcription Factors T-bet and Runx Are Required for the Ontogeny of Pathogenic Interferon- $\beta$ -Producing T Helper 17 Cells. <i>Immunity</i> , 2014, 40, 355-366.	6.6	183
34	Dynamic regulation of epigenomic landscapes during hematopoiesis. <i>BMC Genomics</i> , 2013, 14, 193.	1.2	41
35	Ldb1-nucleated transcription complexes function as primary mediators of global erythroid gene activation. <i>Blood</i> , 2013, 121, 4575-4585.	0.6	78
36	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

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37	BAF complexes facilitate decatenation of DNA by topoisomerase II $\beta$ . <i>Nature</i> , 2013, 497, 624-627.	13.7	230
38	USF1 and hSET1A Mediated Epigenetic Modifications Regulate Lineage Differentiation and HoxB4 Transcription. <i>PLoS Genetics</i> , 2013, 9, e1003524.	1.5	57
39	Intragenic DNA methylation modulates alternative splicing by recruiting MeCP2 to promote exon recognition. <i>Cell Research</i> , 2013, 23, 1256-1269.	5.7	489
40	Transcriptional Regulation of Rod Photoreceptor Homeostasis Revealed by In Vivo NRL Targetome Analysis. <i>PLoS Genetics</i> , 2012, 8, e1002649.	1.5	99
41	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
42	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
43	Marek's disease virus infection induces widespread differential chromatin marks in inbred chicken lines. <i>BMC Genomics</i> , 2012, 13, 557.	1.2	17
44	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
45	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
46	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
47	Histone Methylation Analysis and Pathway Predictions in Chickens after MDV Infection. <i>PLoS ONE</i> , 2012, 7, e41849.	1.1	21
48	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
49	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
50	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
51	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
52	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
53	Dual functions of Tet1 in transcriptional regulation in mouse embryonic stem cells. <i>Nature</i> , 2011, 473, 389-393.	13.7	581
54	Effect of PCR extension temperature on high-throughput sequencing. <i>Molecular and Biochemical Parasitology</i> , 2011, 176, 64-67.	0.5	19

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55	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.	3.3	48
56	Directional gene expression and antisense transcripts in sexual and asexual stages of Plasmodium falciparum. BMC Genomics, 2011, 12, 587.	1.2	309
57	A Barrier-Only Boundary Element Delimits the Formation of Facultative Heterochromatin in Drosophila melanogaster and Vertebrates. Molecular and Cellular Biology, 2011, 31, 2729-2741.	1.1	19
58	Genomic Profiling of HMGN1 Reveals an Association with Chromatin at Regulatory Regions. Molecular and Cellular Biology, 2011, 31, 700-709.	1.1	44
59	Genome-Wide Approaches to Studying Yeast Chromatin Modifications. Methods in Molecular Biology, 2011, 759, 61-71.	0.4	4
60	Pol II and its associated epigenetic marks are present at Pol III-transcribed noncoding RNA genes. Nature Structural and Molecular Biology, 2010, 17, 629-634.	3.6	161
61	Dynamic regulation of alternative splicing and chromatin structure in Drosophila gonads revealed by RNA-seq. Cell Research, 2010, 20, 763-783.	5.7	107
62	Genome-Wide Distribution of MacroH2A1 Histone Variants in Mouse Liver Chromatin. Molecular and Cellular Biology, 2010, 30, 5473-5483.	1.1	60
63	Monovalent and unpoised status of most genes in undifferentiated cell-enriched Drosophila testis. Genome Biology, 2010, 11, R42.	13.9	65
64	Global analysis of the insulator binding protein CTCF in chromatin barrier regions reveals demarcation of active and repressive domains. Genome Research, 2009, 19, 24-32.	2.4	587
65	Native Chromatin Preparation and Illumina/Solexa Library Construction. Cold Spring Harbor Protocols, 2009, 2009, pdb.prot5237.	0.2	26
66	An embryonic stem cell chromatin remodeling complex, esBAF, is an essential component of the core pluripotency transcriptional network. Proceedings of the National Academy of Sciences of the United States of America, 2009, 106, 5187-5191.	3.3	374
67	Genome-Wide uH2A Localization Analysis Highlights Bmi1-Dependent Deposition of the Mark at Repressed Genes. PLoS Genetics, 2009, 5, e1000506.	1.5	58
68	Down-regulation of Gfi-1 expression by TGF- $\beta$ 2 is important for differentiation of Th17 and CD103+ inducible regulatory T cells. Journal of Experimental Medicine, 2009, 206, 329-341.	4.2	124
69	Chromatin poises miRNA- and protein-coding genes for expression. Genome Research, 2009, 19, 1742-1751.	2.4	135
70	H3.3/H2A.Z double variant-containing nucleosomes mark 'nucleosome-free regions' of active promoters and other regulatory regions. Nature Genetics, 2009, 41, 941-945.	9.4	679
71	Global Mapping of H3K4me3 and H3K27me3 Reveals Specificity and Plasticity in Lineage Fate Determination of Differentiating CD4+ T Cells. Immunity, 2009, 30, 155-167.	6.6	1,005
72	Genome-wide Analysis of Histone Methylation Reveals Chromatin State-Based Regulation of Gene Transcription and Function of Memory CD8+ T Cells. Immunity, 2009, 30, 912-925.	6.6	256

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73	A clustering approach for identification of enriched domains from histone modification ChIP-Seq data. <i>Bioinformatics</i> , 2009, 25, 1952-1958.	1.8	936
74	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
75	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
76	Combinatorial patterns of histone acetylations and methylations in the human genome. <i>Nature Genetics</i> , 2008, 40, 897-903.	9.4	2,034
77	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.	7.0	234
78	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
79	Dynamic Regulation of Nucleosome Positioning in the Human Genome. <i>Cell</i> , 2008, 132, 887-898.	13.5	1,211
80	High-Resolution Profiling of Histone Methylations in the Human Genome. <i>Cell</i> , 2007, 129, 823-837.	13.5	6,036
81	Response: Mapping Nucleosome Positions Using ChIP-Seq Data. <i>Cell</i> , 2007, 131, 832-833.	13.5	32
82	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
83	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
84	High-resolution genome-wide mapping of histone modifications. <i>Nature Biotechnology</i> , 2004, 22, 1013-1016.	9.4	199