

## List of Publications by Year in descending order

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138  
papers

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10424

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docs citations

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times ranked

61438  
citing authors

#	ARTICLE	IF	CITATIONS
1	Characterizing cis-regulatory elements using single-cell epigenomics. <i>Nature Reviews Genetics</i> , 2023, 24, 21-43.	7.7	72
2	Improved epicardial cardiac fibroblast generation from iPSCs. <i>Journal of Molecular and Cellular Cardiology</i> , 2022, 164, 58-68.	0.9	3
3	Single nucleus multi-omics identifies human cortical cell regulatory genome diversity. <i>Cell Genomics</i> , 2022, 2, 100107.	3.0	58
4	Chromothripsis drives the evolution of gene amplification in cancer. <i>Nature</i> , 2021, 591, 137-141.	13.7	228
5	Direct DNA crosslinking with CAP-C uncovers transcription-dependent chromatin organization at high resolution. <i>Nature Biotechnology</i> , 2021, 39, 225-235.	9.4	37
6	ZNF143 mediates CTCF-bound promoter-enhancer loops required for murine hematopoietic stem and progenitor cell function. <i>Nature Communications</i> , 2021, 12, 43.	5.8	45
7	FIREcaller: Detecting frequently interacting regions from Hi-C data. <i>Computational and Structural Biotechnology Journal</i> , 2021, 19, 355-362.	1.9	22
8	Pancreatic progenitor epigenome maps prioritize type 2 diabetes risk genes with roles in development. <i>ELife</i> , 2021, 10, .	2.8	15
9	A $\beta$ -catenin-driven switch in TCF/LEF transcription factor binding to DNA target sites promotes commitment of mammalian nephron progenitor cells. <i>ELife</i> , 2021, 10, .	2.8	32
10	Joint profiling of histone modifications and transcriptome in single cells from mouse brain. <i>Nature Methods</i> , 2021, 18, 283-292.	9.0	171
11	Comprehensive analysis of single cell ATAC-seq data with SnapATAC. <i>Nature Communications</i> , 2021, 12, 1337.	5.8	253
12	Iterative single-cell multi-omic integration using online learning. <i>Nature Biotechnology</i> , 2021, 39, 1000-1007.	9.4	53
13	CTCF mediates dosage- and sequence-context-dependent transcriptional insulation by forming local chromatin domains. <i>Nature Genetics</i> , 2021, 53, 1064-1074.	9.4	90
14	Cardiac cell type-specific gene regulatory programs and disease risk association. <i>Science Advances</i> , 2021, 7, .	4.7	63
15	SnapHiC: a computational pipeline to identify chromatin loops from single-cell Hi-C data. <i>Nature Methods</i> , 2021, 18, 1056-1059.	9.0	46
16	Parallel characterization of cis-regulatory elements for multiple genes using CRISPRpath. <i>Science Advances</i> , 2021, 7, eabi4360.	4.7	16
17	Proximity Ligation-Assisted ChIP-Seq (PLAC-Seq). <i>Methods in Molecular Biology</i> , 2021, 2351, 181-199.	0.4	6
18	Systematic analysis of binding of transcription factors to noncoding variants. <i>Nature</i> , 2021, 591, 147-151.	13.7	89

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19	Promoter-proximal CTCF binding promotes distal enhancer-dependent gene activation. <i>Nature Structural and Molecular Biology</i> , 2021, 28, 152-161.	3.6	172
20	An atlas of gene regulatory elements in adult mouse cerebrum. <i>Nature</i> , 2021, 598, 129-136.	13.7	95
21	A transcriptomic and epigenomic cell atlas of the mouse primary motor cortex. <i>Nature</i> , 2021, 598, 103-110.	13.7	166
22	Comparative cellular analysis of motor cortex in human, marmoset and mouse. <i>Nature</i> , 2021, 598, 111-119.	13.7	361
23	A multimodal cell census and atlas of the mammalian primary motor cortex. <i>Nature</i> , 2021, 598, 86-102.	13.7	316
24	DNA methylation atlas of the mouse brain at single-cell resolution. <i>Nature</i> , 2021, 598, 120-128.	13.7	135
25	Sequence logic at enhancers governs a dual mechanism of endodermal organ fate induction by FOXA pioneer factors. <i>Nature Communications</i> , 2021, 12, 6636.	5.8	31
26	A single-cell atlas of chromatin accessibility in the human genome. <i>Cell</i> , 2021, 184, 5985-6001.e19.	13.5	194
27	Single-cell multimodal omics: the power of many. <i>Nature Methods</i> , 2020, 17, 11-14.	9.0	277
28	An atlas of dynamic chromatin landscapes in mouse fetal development. <i>Nature</i> , 2020, 583, 744-751.	13.7	257
29	Spatiotemporal DNA methylome dynamics of the developing mouse fetus. <i>Nature</i> , 2020, 583, 752-759.	13.7	84
30	Perspectives on ENCODE. <i>Nature</i> , 2020, 583, 693-698.	13.7	123
31	Expanded encyclopaedias of DNA elements in the human and mouse genomes. <i>Nature</i> , 2020, 583, 699-710.	13.7	1,252
32	The changing mouse embryo transcriptome at whole tissue and single-cell resolution. <i>Nature</i> , 2020, 583, 760-767.	13.7	131
33	Genome-wide association and multi-omic analyses reveal ACTN2 as a gene linked to heart failure. <i>Nature Communications</i> , 2020, 11, 1122.	5.8	57
34	CTCF mediates chromatin looping via N-terminal domain-dependent cohesin retention. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2020, 117, 2020-2031.	3.3	156
35	Transcriptionally active HERV-H retrotransposons demarcate topologically associating domains in human pluripotent stem cells. <i>Nature Genetics</i> , 2019, 51, 1380-1388.	9.4	236
36	Joint profiling of DNA methylation and chromatin architecture in single cells. <i>Nature Methods</i> , 2019, 16, 991-993.	9.0	155

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37	Brain cell type-specific enhancer-promoter interactome maps and disease risk association. <i>Science</i> , 2019, 366, 1134-1139.	6.0	486
38	A compendium of promoter-centered long-range chromatin interactions in the human genome. <i>Nature Genetics</i> , 2019, 51, 1442-1449.	9.4	267
39	Transcription Factor-Directed Re-wiring of Chromatin Architecture for Somatic Cell Nuclear Reprogramming toward trans-Differentiation. <i>Molecular Cell</i> , 2019, 76, 453-472.e8.	4.5	67
40	Single-Cell Chromatin Analysis of Mammary Gland Development Reveals Cell-State Transcriptional Regulators and Lineage Relationships. <i>Cell Reports</i> , 2019, 29, 495-510.e6.	2.9	66
41	Comparing 3D Genome Organization in Multiple Species Using Phylo-HMRF. <i>Cell Systems</i> , 2019, 8, 494-505.e14.	2.9	27
42	DNA replication acts as an error correction mechanism to maintain centromere identity by restricting CENP-A to centromeres. <i>Nature Cell Biology</i> , 2019, 21, 743-754.	4.6	65
43	Pancreatic islet chromatin accessibility and conformation reveals distal enhancer networks of type 2 diabetes risk. <i>Nature Communications</i> , 2019, 10, 2078.	5.8	82
44	MAPS: Model-based analysis of long-range chromatin interactions from PLAC-seq and HiChIP experiments. <i>PLoS Computational Biology</i> , 2019, 15, e1006982.	1.5	94
45	Multi-platform discovery of haplotype-resolved structural variation in human genomes. <i>Nature Communications</i> , 2019, 10, 1784.	5.8	636
46	Dynamic reorganization of the genome shapes the recombination landscape in meiotic prophase. <i>Nature Structural and Molecular Biology</i> , 2019, 26, 164-174.	3.6	123
47	Ranking of non-coding pathogenic variants and putative essential regions of the human genome. <i>Nature Communications</i> , 2019, 10, 5241.	5.8	65
48	Common DNA sequence variation influences 3-dimensional conformation of the human genome. <i>Genome Biology</i> , 2019, 20, 255.	3.8	65
49	Circular ecDNA promotes accessible chromatin and high oncogene expression. <i>Nature</i> , 2019, 575, 699-703.	13.7	343
50	An ultra high-throughput method for single-cell joint analysis of open chromatin and transcriptome. <i>Nature Structural and Molecular Biology</i> , 2019, 26, 1063-1070.	3.6	239
51	The human noncoding genome defined by genetic diversity. <i>Nature Genetics</i> , 2018, 50, 333-337.	9.4	137
52	Single-nucleus analysis of accessible chromatin in developing mouse forebrain reveals cell-type-specific transcriptional regulation. <i>Nature Neuroscience</i> , 2018, 21, 432-439.	7.1	290
53	Identification of H3K4me1-associated proteins at mammalian enhancers. <i>Nature Genetics</i> , 2018, 50, 73-82.	9.4	177
54	Histone H3 lysine 4 monomethylation modulates long-range chromatin interactions at enhancers. <i>Cell Research</i> , 2018, 28, 204-220.	5.7	131

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55	Transcriptional regulatory control of mammalian nephron progenitors revealed by multi-factor cistromic analysis and genetic studies. <i>PLoS Genetics</i> , 2018, 14, e1007181.	1.5	40
56	A Scalable Epitope Tagging Approach for High Throughput ChIP-Seq Analysis. <i>ACS Synthetic Biology</i> , 2017, 6, 1034-1042.	1.9	19
57	Human centromeric CENP-A chromatin is a homotypic, octameric nucleosome at all cell cycle points. <i>Journal of Cell Biology</i> , 2017, 216, 607-621.	2.3	53
58	Extrachromosomal oncogene amplification drives tumour evolution and genetic heterogeneity. <i>Nature</i> , 2017, 543, 122-125.	13.7	530
59	Improved regulatory element prediction based on tissue-specific local epigenomic signatures. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2017, 114, E1633-E1640.	3.3	78
60	A tiling-deletion-based genetic screen for cis-regulatory element identification in mammalian cells. <i>Nature Methods</i> , 2017, 14, 629-635.	9.0	217
61	HUGIn: Hi-C Unifying Genomic Interrogator. <i>Bioinformatics</i> , 2017, 33, 3793-3795.	1.8	69
62	The 4D nucleome project. <i>Nature</i> , 2017, 549, 219-226.	13.7	579
63	The Three-Dimensional Organization of Mammalian Genomes. <i>Annual Review of Cell and Developmental Biology</i> , 2017, 33, 265-289.	4.0	320
64	High-Resolution Mapping of Chromatin Conformation in Cardiac Myocytes Reveals Structural Remodeling of the Epigenome in Heart Failure. <i>Circulation</i> , 2017, 136, 1613-1625.	1.6	135
65	Genome-wide mapping and analysis of chromosome architecture. <i>Nature Reviews Molecular Cell Biology</i> , 2016, 17, 743-755.	16.1	324
66	Mapping of long-range chromatin interactions by proximity ligation-assisted ChIP-seq. <i>Cell Research</i> , 2016, 26, 1345-1348.	5.7	264
67	Broad histone H3K4me3 domains in mouse oocytes modulate maternal-to-zygotic transition. <i>Nature</i> , 2016, 537, 548-552.	13.7	484
68	The International Human Epigenome Consortium: A Blueprint for Scientific Collaboration and Discovery. <i>Cell</i> , 2016, 167, 1145-1149.	13.5	404
69	A Compendium of Chromatin Contact Maps Reveals Spatially Active Regions in the Human Genome. <i>Cell Reports</i> , 2016, 17, 2042-2059.	2.9	745
70	Genome-wide compendium and functional assessment of in vivo heart enhancers. <i>Nature Communications</i> , 2016, 7, 12923.	5.8	83
71	Chromatin Domains: The Unit of Chromosome Organization. <i>Molecular Cell</i> , 2016, 62, 668-680.	4.5	653
72	A new class of temporarily phenotypic enhancers identified by CRISPR/Cas9-mediated genetic screening. <i>Genome Research</i> , 2016, 26, 397-405.	2.4	111

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73	Complete haplotype phasing of the MHC and KIR loci with targeted HaploSeq. BMC Genomics, 2015, 16, 900.	1.2	10
74	A CRISPR Connection between Chromatin Topology and Genetic Disorders. Cell, 2015, 161, 955-957.	13.5	13
75	Human body epigenome maps reveal noncanonical DNA methylation variation. Nature, 2015, 523, 212-216.	13.7	605
76	Identification of global regulators of T-helper cell lineage specification. Genome Medicine, 2015, 7, 122.	3.6	38
77	Transcriptional Enhancers: Bridging the Genome and Phenome. Cold Spring Harbor Symposia on Quantitative Biology, 2015, 80, 17-26.	2.0	28
78	Integrative analysis of haplotype-resolved epigenomes across human tissues. Nature, 2015, 518, 350-354.	13.7	201
79	Integrative analysis of 111 reference human epigenomes. Nature, 2015, 518, 317-330.	13.7	5,653
80	Chromatin architecture reorganization during stem cell differentiation. Nature, 2015, 518, 331-336.	13.7	1,442
81	MPE-seq, a new method for the genome-wide analysis of chromatin structure. Proceedings of the National Academy of Sciences of the United States of America, 2015, 112, E3457-65.	3.3	66
82	Epigenetic Priming of Enhancers Predicts Developmental Competence of hESC-Derived Endodermal Lineage Intermediates. Cell Stem Cell, 2015, 16, 386-399.	5.2	222
83	CRISPR Inversion of CTCF Sites Alters Genome Topology and Enhancer/Promoter Function. Cell, 2015, 162, 900-910.	13.5	846
84	EGFR Mutation Promotes Glioblastoma through Epigenome and Transcription Factor Network Remodeling. Molecular Cell, 2015, 60, 307-318.	4.5	161
85	Comparative analyses of CTCF and BORIS occupancies uncover two distinct classes of CTCF binding genomic regions. Genome Biology, 2015, 16, 161.	3.8	83
86	CRISPR Reveals a Distal Super-Enhancer Required for Sox2 Expression in Mouse Embryonic Stem Cells. PLoS ONE, 2014, 9, e114485.	1.1	168
87	Defining functional DNA elements in the human genome. Proceedings of the National Academy of Sciences of the United States of America, 2014, 111, 6131-6138.	3.3	635
88	Distinct and Predictive Histone Lysine Acetylation Patterns at Promoters, Enhancers, and Gene Bodies. G3: Genes, Genomes, Genetics, 2014, 4, 2051-2063.	0.8	39
89	Tissue-specific SMARCA4 binding at active and repressed regulatory elements during embryogenesis. Genome Research, 2014, 24, 920-929.	2.4	63
90	Regulation of DNA methylation turnover at LTR retrotransposons and imprinted loci by the histone methyltransferase Setdb1. Proceedings of the National Academy of Sciences of the United States of America, 2014, 111, 6690-6695.	3.3	89

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91	Cohesin and CTCF differentially affect chromatin architecture and gene expression in human cells. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2014, 111, 996-1001.	3.3	700
92	A comparative encyclopedia of DNA elements in the mouse genome. <i>Nature</i> , 2014, 515, 355-364.	13.7	1,444
93	Topologically associating domains are stable units of replication-timing regulation. <i>Nature</i> , 2014, 515, 402-405.	13.7	779
94	5mC Oxidation by Tet2 Modulates Enhancer Activity and Timing of Transcriptome Reprogramming during Differentiation. <i>Molecular Cell</i> , 2014, 56, 286-297.	4.5	285
95	The 3D Genome in Transcriptional Regulation and Pluripotency. <i>Cell Stem Cell</i> , 2014, 14, 762-775.	5.2	353
96	A high-resolution map of the three-dimensional chromatin interactome in human cells. <i>Nature</i> , 2013, 503, 290-294.	13.7	1,074
97	Whole-genome haplotype reconstruction using proximity-ligation and shotgun sequencing. <i>Nature Biotechnology</i> , 2013, 31, 1111-1118.	9.4	257
98	Epigenetic memory at embryonic enhancers identified in DNA methylation maps from adult mouse tissues. <i>Nature Genetics</i> , 2013, 45, 1198-1206.	9.4	431
99	Mapping Human Epigenomes. <i>Cell</i> , 2013, 155, 39-55.	13.5	481
100	Genome organization and long-range regulation of gene expression by enhancers. <i>Current Opinion in Cell Biology</i> , 2013, 25, 387-394.	2.6	139
101	Global Chromatin State Analysis Reveals Lineage-Specific Enhancers during the Initiation of Human T helper 1 and T helper 2 Cell Polarization. <i>Immunity</i> , 2013, 38, 1271-1284.	6.6	83
102	Epigenomic Analysis of Multilineage Differentiation of Human Embryonic Stem Cells. <i>Cell</i> , 2013, 153, 1134-1148.	13.5	689
103	Fine Tuning of Craniofacial Morphology by Distant-Acting Enhancers. <i>Science</i> , 2013, 342, 1241006.	6.0	209
104	RFECs: A Random-Forest Based Algorithm for Enhancer Identification from Chromatin State. <i>PLoS Computational Biology</i> , 2013, 9, e1002968.	1.5	205
105	HiCNorm: removing biases in Hi-C data via Poisson regression. <i>Bioinformatics</i> , 2012, 28, 3131-3133.	1.8	228
106	Base-Resolution Analyses of Sequence and Parent-of-Origin Dependent DNA Methylation in the Mouse Genome. <i>Cell</i> , 2012, 148, 816-831.	13.5	478
107	Base-Resolution Analysis of 5-Hydroxymethylcytosine in the Mammalian Genome. <i>Cell</i> , 2012, 149, 1368-1380.	13.5	912
108	Topological domains in mammalian genomes identified by analysis of chromatin interactions. <i>Nature</i> , 2012, 485, 376-380.	13.7	5,786

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109	A map of the cis-regulatory sequences in the mouse genome. <i>Nature</i> , 2012, 488, 116-120.	13.7	1,306
110	Identification of 67 Histone Marks and Histone Lysine Crotonylation as a New Type of Histone Modification. <i>Cell</i> , 2011, 146, 1016-1028.	13.5	1,462
111	Dynamic chromatin states in human ES cells reveal potential regulatory sequences and genes involved in pluripotency. <i>Cell Research</i> , 2011, 21, 1393-1409.	5.7	91
112	A cis-regulatory map of the <i>Drosophila</i> genome. <i>Nature</i> , 2011, 471, 527-531.	13.7	477
113	PU.1 and C/EBP $\beta$ synergistically program distinct response to NF- $\kappa$ B activation through establishing monocyte specific enhancers. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2011, 108, 5290-5295.	3.3	79
114	Integrating 5-Hydroxymethylcytosine into the Epigenomic Landscape of Human Embryonic Stem Cells. <i>PLoS Genetics</i> , 2011, 7, e1002154.	1.5	250
115	The NIH Roadmap Epigenomics Mapping Consortium. <i>Nature Biotechnology</i> , 2010, 28, 1045-1048.	9.4	1,705
116	ChIP-Seq identification of weakly conserved heart enhancers. <i>Nature Genetics</i> , 2010, 42, 806-810.	9.4	395
117	Next-generation genomics: an integrative approach. <i>Nature Reviews Genetics</i> , 2010, 11, 476-486.	7.7	554
118	Identification of Functional Elements and Regulatory Circuits by <i>Drosophila</i> modENCODE. <i>Science</i> , 2010, 330, 1787-1797.	6.0	1,124
119	Distinct Epigenomic Landscapes of Pluripotent and Lineage-Committed Human Cells. <i>Cell Stem Cell</i> , 2010, 6, 479-491.	5.2	747
120	Uncovering a conserved role for JMJD2 histone triâ€demethylases from worm to human. <i>FASEB Journal</i> , 2010, 24, 456.13.	0.2	0
121	Discovery and Annotation of Functional Chromatin Signatures in the Human Genome. <i>PLoS Computational Biology</i> , 2009, 5, e1000566.	1.5	143
122	ChIP-seq accurately predicts tissue-specific activity of enhancers. <i>Nature</i> , 2009, 457, 854-858.	13.7	1,526
123	Histone modifications at human enhancers reflect global cell-type-specific gene expression. <i>Nature</i> , 2009, 459, 108-112.	13.7	2,225
124	Human DNA methylomes at base resolution show widespread epigenomic differences. <i>Nature</i> , 2009, 462, 315-322.	13.7	4,063
125	Prediction of regulatory elements in mammalian genomes using chromatin signatures. <i>BMC Bioinformatics</i> , 2008, 9, 547.	1.2	92
126	ChromaSig: A Probabilistic Approach to Finding Common Chromatin Signatures in the Human Genome. <i>PLoS Computational Biology</i> , 2008, 4, e1000201.	1.5	135



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127	Identification and Characterization of Cell Type-Specific and Ubiquitous Chromatin Regulatory Structures in the Human Genome. <i>PLoS Genetics</i> , 2007, 3, e136.	1.5	196
128	Analysis of the Vertebrate Insulator Protein CTCF-Binding Sites in the Human Genome. <i>Cell</i> , 2007, 128, 1231-1245.	13.5	910
129	Distinct and predictive chromatin signatures of transcriptional promoters and enhancers in the human genome. <i>Nature Genetics</i> , 2007, 39, 311-318.	9.4	2,898
130	The transcriptional regulatory code of eukaryotic cells – insights from genome-wide analysis of chromatin organization and transcription factor binding. <i>Current Opinion in Cell Biology</i> , 2006, 18, 291-298.	2.6	108
131	Genome-wide location analysis: insights on transcriptional regulation. <i>Human Molecular Genetics</i> , 2006, 15, R1-R7.	1.4	30
132	Î2-Catenin activates the growth factor endothelin-1 in colon cancer cells. <i>Oncogene</i> , 2005, 24, 597-604.	2.6	90
133	A high-resolution map of active promoters in the human genome. <i>Nature</i> , 2005, 436, 876-880.	13.7	841
134	Direct isolation and identification of promoters in the human genome. <i>Genome Research</i> , 2005, 15, 830-839.	2.4	76
135	Use of Chromatin Immunoprecipitation Assays in Genome-Wide Location Analysis of Mammalian Transcription Factors. <i>Methods in Enzymology</i> , 2003, 376, 304-315.	0.4	79
136	A global transcriptional regulatory role for c-Myc in Burkitt's lymphoma cells. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2003, 100, 8164-8169.	3.3	447
137	E2F integrates cell cycle progression with DNA repair, replication, and G2/M checkpoints. <i>Genes and Development</i> , 2002, 16, 245-256.	2.7	1,002
138	Transcriptional Regulatory Networks in <i>Saccharomyces cerevisiae</i> . <i>Science</i> , 2002, 298, 799-804.	6.0	2,706