List of Publications by Year in descending order

138 papers	65,070 citations	4388 86 h-index	10445 139 g-index
183 all docs	183 docs citations	183 times ranked	61438 citing authors

#	Article	IF	Citations
1	Topological domains in mammalian genomes identified by analysis of chromatin interactions. Nature, 2012, 485, 376-380.	27.8	5,786
2	Integrative analysis of 111 reference human epigenomes. Nature, 2015, 518, 317-330.	27.8	5,653
3	Human DNA methylomes at base resolution show widespread epigenomic differences. Nature, 2009, 462, 315-322.	27.8	4,063
4	Distinct and predictive chromatin signatures of transcriptional promoters and enhancers in the human genome. Nature Genetics, 2007, 39, 311-318.	21.4	2,898
5	Transcriptional Regulatory Networks in Saccharomyces cerevisiae. Science, 2002, 298, 799-804.	12.6	2,706
6	Histone modifications at human enhancers reflect global cell-type-specific gene expression. Nature, 2009, 459, 108-112.	27.8	2,225
7	The NIH Roadmap Epigenomics Mapping Consortium. Nature Biotechnology, 2010, 28, 1045-1048.	17.5	1,705
8	ChIP-seq accurately predicts tissue-specific activity of enhancers. Nature, 2009, 457, 854-858.	27.8	1,526
9	Identification of 67 Histone Marks and Histone Lysine Crotonylation as a New Type of Histone Modification. Cell, 2011, 146, 1016-1028.	28.9	1,462
10	A comparative encyclopedia of DNA elements in the mouse genome. Nature, 2014, 515, 355-364.	27.8	1,444
11	Chromatin architecture reorganization during stem cell differentiation. Nature, 2015, 518, 331-336.	27.8	1,442
12	A map of the cis-regulatory sequences in the mouse genome. Nature, 2012, 488, 116-120.	27.8	1,306
13	Expanded encyclopaedias of DNA elements in the human and mouse genomes. Nature, 2020, 583, 699-710.	27.8	1,252
14	Identification of Functional Elements and Regulatory Circuits by Drosophila modENCODE. Science, 2010, 330, 1787-1797.	12.6	1,124
15	A high-resolution map of the three-dimensional chromatin interactome in human cells. Nature, 2013, 503, 290-294.	27.8	1,074
16	E2F integrates cell cycle progression with DNA repair, replication, and G₂/M checkpoints. Genes and Development, 2002, 16, 245-256.	5.9	1,002
17	Base-Resolution Analysis of 5-Hydroxymethylcytosine in the Mammalian Genome. Cell, 2012, 149, 1368-1380.	28.9	912
18	Analysis of the Vertebrate Insulator Protein CTCF-Binding Sites in the Human Genome. Cell, 2007, 128, 1231-1245.	28.9	910

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19	CRISPR Inversion of CTCF Sites Alters Genome Topology and Enhancer/Promoter Function. Cell, 2015, 162, 900-910.	28.9	846
20	A high-resolution map of active promoters in the human genome. Nature, 2005, 436, 876-880.	27.8	841
21	Topologically associating domains are stable units of replication-timing regulation. Nature, 2014, 515, 402-405.	27.8	779
22	Distinct Epigenomic Landscapes of Pluripotent and Lineage-Committed Human Cells. Cell Stem Cell, 2010, 6, 479-491.	11.1	747
23	A Compendium of Chromatin Contact Maps Reveals Spatially Active Regions in the Human Genome. Cell Reports, 2016, 17, 2042-2059.	6.4	745
24	Cohesin and CTCF differentially affect chromatin architecture and gene expression in human cells. Proceedings of the National Academy of Sciences of the United States of America, 2014, 111, 996-1001.	7.1	700
25	Epigenomic Analysis of Multilineage Differentiation of Human Embryonic Stem Cells. Cell, 2013, 153, 1134-1148.	28.9	689
26	Chromatin Domains: The Unit of Chromosome Organization. Molecular Cell, 2016, 62, 668-680.	9.7	653
27	Multi-platform discovery of haplotype-resolved structural variation in human genomes. Nature Communications, 2019, 10, 1784.	12.8	636
28	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.	7.1	635
29	Human body epigenome maps reveal noncanonical DNA methylation variation. Nature, 2015, 523, 212-216.	27.8	605
30	The 4D nucleome project. Nature, 2017, 549, 219-226.	27.8	579
31	Next-generation genomics: an integrative approach. Nature Reviews Genetics, 2010, 11, 476-486.	16.3	554
32	Extrachromosomal oncogene amplification drives tumour evolution and genetic heterogeneity. Nature, 2017, 543, 122-125.	27.8	530
33	Brain cell typeâ€“specific enhancerâ€“promoter interactome maps and disease - risk association. Science, 2019, 366, 1134-1139.	12.6	486
34	Broad histone H3K4me3 domains in mouse oocytes modulate maternal-to-zygotic transition. Nature, 2016, 537, 548-552.	27.8	484
35	Mapping Human Epigenomes. Cell, 2013, 155, 39-55.	28.9	481
36	Base-Resolution Analyses of Sequence and Parent-of-Origin Dependent DNA Methylation in the Mouse Genome. Cell, 2012, 148, 816-831.	28.9	478

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37	A cis-regulatory map of the Drosophila genome. Nature, 2011, 471, 527-531.	27.8	477
38	A global transcriptional regulatory role for c-Myc in Burkitt's lymphoma cells. Proceedings of the National Academy of Sciences of the United States of America, 2003, 100, 8164-8169.	7.1	447
39	Epigenetic memory at embryonic enhancers identified in DNA methylation maps from adult mouse tissues. Nature Genetics, 2013, 45, 1198-1206.	21.4	431
40	The International Human Epigenome Consortium: A Blueprint for Scientific Collaboration and Discovery. Cell, 2016, 167, 1145-1149.	28.9	404
41	ChIP-Seq identification of weakly conserved heart enhancers. Nature Genetics, 2010, 42, 806-810.	21.4	395
42	Comparative cellular analysis of motor cortex in human, marmoset and mouse. Nature, 2021, 598, 111-119.	27.8	361
43	The 3D Genome in Transcriptional Regulation and Pluripotency. Cell Stem Cell, 2014, 14, 762-775.	11.1	353
44	Circular ecDNA promotes accessible chromatin and high oncogene expression. Nature, 2019, 575, 699-703.	27.8	343
45	Genome-wide mapping and analysis of chromosome architecture. Nature Reviews Molecular Cell Biology, 2016, 17, 743-755.	37.0	324
46	The Three-Dimensional Organization of Mammalian Genomes. Annual Review of Cell and Developmental Biology, 2017, 33, 265-289.	9.4	320
47	A multimodal cell census and atlas of the mammalian primary motor cortex. Nature, 2021, 598, 86-102.	27.8	316
48	Single-nucleus analysis of accessible chromatin in developing mouse forebrain reveals cell-type-specific transcriptional regulation. Nature Neuroscience, 2018, 21, 432-439.	14.8	290
49	5mC Oxidation by Tet2 Modulates Enhancer Activity and Timing of Transcriptome Reprogramming during Differentiation. Molecular Cell, 2014, 56, 286-297.	9.7	285
50	Single-cell multimodal omics: the power of many. Nature Methods, 2020, 17, 11-14.	19.0	277
51	A compendium of promoter-centered long-range chromatin interactions in the human genome. Nature Genetics, 2019, 51, 1442-1449.	21.4	267
52	Mapping of long-range chromatin interactions by proximity ligation-assisted ChIP-seq. Cell Research, 2016, 26, 1345-1348.	12.0	264
53	Whole-genome haplotype reconstruction using proximity-ligation and shotgun sequencing. Nature Biotechnology, 2013, 31, 1111-1118.	17.5	257
54	An atlas of dynamic chromatin landscapes in mouse fetal development. Nature, 2020, 583, 744-751.	27.8	257

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55	Comprehensive analysis of single cell ATAC-seq data with SnapATAC. Nature Communications, 2021, 12, 1337.	12.8	253
56	Integrating 5-Hydroxymethylcytosine into the Epigenomic Landscape of Human Embryonic Stem Cells. PLoS Genetics, 2011, 7, e1002154.	3.5	250
57	An ultra high-throughput method for single-cell joint analysis of open chromatin and transcriptome. Nature Structural and Molecular Biology, 2019, 26, 1063-1070.	8.2	239
58	Transcriptionally active HERV-H retrotransposons demarcate topologically associating domains in human pluripotent stem cells. Nature Genetics, 2019, 51, 1380-1388.	21.4	236
59	HiCNorm: removing biases in Hi-C data via Poisson regression. Bioinformatics, 2012, 28, 3131-3133.	4.1	228
60	Chromothripsis drives the evolution of gene amplification in cancer. Nature, 2021, 591, 137-141.	27.8	228
61	Epigenetic Priming of Enhancers Predicts Developmental Competence of hESC-Derived Endodermal Lineage Intermediates. Cell Stem Cell, 2015, 16, 386-399.	11.1	222
62	A tiling-deletion-based genetic screen for cis-regulatory element identification in mammalian cells. Nature Methods, 2017, 14, 629-635.	19.0	217
63	Fine Tuning of Craniofacial Morphology by Distant-Acting Enhancers. Science, 2013, 342, 1241006.	12.6	209
64	RFECS: A Random-Forest Based Algorithm for Enhancer Identification from Chromatin State. PLoS Computational Biology, 2013, 9, e1002968.	3.2	205
65	Integrative analysis of haplotype-resolved epigenomes across human tissues. Nature, 2015, 518, 350-354.	27.8	201
66	Identification and Characterization of Cell Typeâ€“Specific and Ubiquitous Chromatin Regulatory Structures in the Human Genome. PLoS Genetics, 2007, 3, e136.	3.5	196
67	A single-cell atlas of chromatin accessibility in the human genome. Cell, 2021, 184, 5985-6001.e19.	28.9	194
68	Identification of H3K4me1-associated proteins at mammalian enhancers. Nature Genetics, 2018, 50, 73-82.	21.4	177
69	Promoter-proximal CTCF binding promotes distal enhancer-dependent gene activation. Nature Structural and Molecular Biology, 2021, 28, 152-161.	8.2	172
70	Joint profiling of histone modifications and transcriptome in single cells from mouse brain. Nature Methods, 2021, 18, 283-292.	19.0	171
71	CRISPR Reveals a Distal Super-Enhancer Required for Sox2 Expression in Mouse Embryonic Stem Cells. PLoS ONE, 2014, 9, e114485.	2.5	168
72	A transcriptomic and epigenomic cell atlas of the mouse primary motor cortex. Nature, 2021, 598, 103-110.	27.8	166

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73	EGFR Mutation Promotes Glioblastoma through Epigenome and Transcription Factor Network Remodeling. Molecular Cell, 2015, 60, 307-318.	9.7	161
74	CTCF mediates chromatin looping via N-terminal domain-dependent cohesin retention. Proceedings of the National Academy of Sciences of the United States of America, 2020, 117, 2020-2031.	7.1	156
75	Joint profiling of DNA methylation and chromatin architecture in single cells. Nature Methods, 2019, 16, 991-993.	19.0	155
76	Discovery and Annotation of Functional Chromatin Signatures in the Human Genome. PLoS Computational Biology, 2009, 5, e1000566.	3.2	143
77	Genome organization and long-range regulation of gene expression by enhancers. Current Opinion in Cell Biology, 2013, 25, 387-394.	5.4	139
78	The human noncoding genome defined by genetic diversity. Nature Genetics, 2018, 50, 333-337.	21.4	137
79	ChromaSig: A Probabilistic Approach to Finding Common Chromatin Signatures in the Human Genome. PLoS Computational Biology, 2008, 4, e1000201.	3.2	135
80	High-Resolution Mapping of Chromatin Conformation in Cardiac Myocytes Reveals Structural Remodeling of the Epigenome in Heart Failure. Circulation, 2017, 136, 1613-1625.	1.6	135
81	DNA methylation atlas of the mouse brain at single-cell resolution. Nature, 2021, 598, 120-128.	27.8	135
82	Histone H3 lysine 4 monomethylation modulates long-range chromatin interactions at enhancers. Cell Research, 2018, 28, 204-220.	12.0	131
83	The changing mouse embryo transcriptome at whole tissue and single-cell resolution. Nature, 2020, 583, 760-767.	27.8	131
84	Dynamic reorganization of the genome shapes the recombination landscape in meiotic prophase. Nature Structural and Molecular Biology, 2019, 26, 164-174.	8.2	123
85	Perspectives on ENCODE. Nature, 2020, 583, 693-698.	27.8	123
86	A new class of temporarily phenotypic enhancers identified by CRISPR/Cas9-mediated genetic screening. Genome Research, 2016, 26, 397-405.	5.5	111
87	The transcriptional regulatory code of eukaryotic cells â€“ insights from genome-wide analysis of chromatin organization and transcription factor binding. Current Opinion in Cell Biology, 2006, 18, 291-298.	5.4	108
88	An atlas of gene regulatory elements in adult mouse cerebrum. Nature, 2021, 598, 129-136.	27.8	95
89	MAPS: Model-based analysis of long-range chromatin interactions from PLAC-seq and HiChIP experiments. PLoS Computational Biology, 2019, 15, e1006982.	3.2	94
90	Prediction of regulatory elements in mammalian genomes using chromatin signatures. BMC Bioinformatics, 2008, 9, 547.	2.6	92

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91	Dynamic chromatin states in human ES cells reveal potential regulatory sequences and genes involved in pluripotency. Cell Research, 2011, 21, 1393-1409.	12.0	91
92	Î²-Catenin activates the growth factor endothelin-1 in colon cancer cells. Oncogene, 2005, 24, 597-604.	5.9	90
93	CTCF mediates dosage- and sequence-context-dependent transcriptional insulation by forming local chromatin domains. Nature Genetics, 2021, 53, 1064-1074.	21.4	90
94	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.	7.1	89
95	Systematic analysis of binding of transcription factors to noncoding variants. Nature, 2021, 591, 147-151.	27.8	89
96	Spatiotemporal DNA methylome dynamics of the developing mouse fetus. Nature, 2020, 583, 752-759.	27.8	84
97	Global Chromatin State Analysis Reveals Lineage-Specific Enhancers during the Initiation of Human T helper 1 and T helper 2 Cell Polarization. Immunity, 2013, 38, 1271-1284.	14.3	83
98	Comparative analyses of CTCF and BORIS occupancies uncover two distinct classes of CTCF binding genomic regions. Genome Biology, 2015, 16, 161.	8.8	83
99	Genome-wide compendium and functional assessment of in vivo heart enhancers. Nature Communications, 2016, 7, 12923.	12.8	83
100	Pancreatic islet chromatin accessibility and conformation reveals distal enhancer networks of type 2 diabetes risk. Nature Communications, 2019, 10, 2078.	12.8	82
101	Use of Chromatin Immunoprecipitation Assays in Genome-Wide Location Analysis of Mammalian Transcription Factors. Methods in Enzymology, 2003, 376, 304-315.	1.0	79
102	PU.1 and C/EBPÎ± synergistically program distinct response to NF-ÎºB activation through establishing monocyte specific enhancers. Proceedings of the National Academy of Sciences of the United States of America, 2011, 108, 5290-5295.	7.1	79
103	Improved regulatory element prediction based on tissue-specific local epigenomic signatures. Proceedings of the National Academy of Sciences of the United States of America, 2017, 114, E1633-E1640.	7.1	78
104	Direct isolation and identification of promoters in the human genome. Genome Research, 2005, 15, 830-839.	5.5	76
105	Characterizing cis-regulatory elements using single-cell epigenomics. Nature Reviews Genetics, 2023, 24, 21-43.	16.3	72
106	HUGIn: Hi-C Unifying Genomic Interrogator. Bioinformatics, 2017, 33, 3793-3795.	4.1	69
107	Transcription Factor-Directed Re-wiring of Chromatin Architecture for Somatic Cell Nuclear Reprogramming toward trans-Differentiation. Molecular Cell, 2019, 76, 453-472.e8.	9.7	67
108	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.	7.1	66

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109	Single-Cell Chromatin Analysis of Mammary Gland Development Reveals Cell-State Transcriptional Regulators and Lineage Relationships. Cell Reports, 2019, 29, 495-510.e6.	6.4	66
110	DNA replication acts as an error correction mechanism to maintain centromere identity by restricting CENP-A to centromeres. Nature Cell Biology, 2019, 21, 743-754.	10.3	65
111	Ranking of non-coding pathogenic variants and putative essential regions of the human genome. Nature Communications, 2019, 10, 5241.	12.8	65
112	Common DNA sequence variation influences 3-dimensional conformation of the human genome. Genome Biology, 2019, 20, 255.	8.8	65
113	Tissue-specific SMARCA4 binding at active and repressed regulatory elements during embryogenesis. Genome Research, 2014, 24, 920-929.	5.5	63
114	Cardiac cell typeâ€“specific gene regulatory programs and disease risk association. Science Advances, 2021, 7, .	10.3	63
115	Single nucleus multi-omics identifies human cortical cell regulatory genome diversity. Cell Genomics, 2022, 2, 100107.	6.5	58
116	Genome-wide association and multi-omic analyses reveal ACTN2 as a gene linked to heart failure. Nature Communications, 2020, 11, 1122.	12.8	57
117	Human centromeric CENP-A chromatin is a homotypic, octameric nucleosome at all cell cycle points. Journal of Cell Biology, 2017, 216, 607-621.	5.2	53
118	Iterative single-cell multi-omic integration using online learning. Nature Biotechnology, 2021, 39, 1000-1007.	17.5	53
119	SnapHiC: a computational pipeline to identify chromatin loops from single-cell Hi-C data. Nature Methods, 2021, 18, 1056-1059.	19.0	46
120	ZNF143 mediates CTCF-bound promoterâ€“enhancer loops required for murine hematopoietic stem and progenitor cell function. Nature Communications, 2021, 12, 43.	12.8	45
121	Transcriptional regulatory control of mammalian nephron progenitors revealed by multi-factor cistromic analysis and genetic studies. PLoS Genetics, 2018, 14, e1007181.	3.5	40
122	Distinct and Predictive Histone Lysine Acetylation Patterns at Promoters, Enhancers, and Gene Bodies. G3: Genes, Genomes, Genetics, 2014, 4, 2051-2063.	1.8	39
123	Identification of global regulators of T-helper cell lineage specification. Genome Medicine, 2015, 7, 122.	8.2	38
124	Direct DNA crosslinking with CAP-C uncovers transcription-dependent chromatin organization at high resolution. Nature Biotechnology, 2021, 39, 225-235.	17.5	37
125	A Î²-catenin-driven switch in TCF/LEF transcription factor binding to DNA target sites promotes commitment of mammalian nephron progenitor cells. ELife, 2021, 10, .	6.0	32
126	Sequence logic at enhancers governs a dual mechanism of endodermal organ fate induction by FOXA pioneer factors. Nature Communications, 2021, 12, 6636.	12.8	31

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127	Genome-wide location analysis: insights on transcriptional regulation. Human Molecular Genetics, 2006, 15, R1-R7.	2.9	30
128	Transcriptional Enhancers: Bridging the Genome and Phenome. Cold Spring Harbor Symposia on Quantitative Biology, 2015, 80, 17-26.	1.1	28
129	Comparing 3D Genome Organization in Multiple Species Using Phylo-HMRF. Cell Systems, 2019, 8, 494-505.e14.	6.2	27
130	FIREcaller: Detecting frequently interacting regions from Hi-C data. Computational and Structural Biotechnology Journal, 2021, 19, 355-362.	4.1	22
131	A Scalable Epitope Tagging Approach for High Throughput ChIP-Seq Analysis. ACS Synthetic Biology, 2017, 6, 1034-1042.	3.8	19
132	Parallel characterization of cis-regulatory elements for multiple genes using CRISPRpath. Science Advances, 2021, 7, eabi4360.	10.3	16
133	Pancreatic progenitor epigenome maps prioritize type 2 diabetes risk genes with roles in development. ELife, 2021, 10, .	6.0	15
134	A CRISPR Connection between Chromatin Topology and Genetic Disorders. Cell, 2015, 161, 955-957.	28.9	13
135	Complete haplotype phasing of the MHC and KIR loci with targeted HaploSeq. BMC Genomics, 2015, 16, 900.	2.8	10
136	Proximity Ligation-Assisted ChIP-Seq (PLAC-Seq). Methods in Molecular Biology, 2021, 2351, 181-199.	0.9	6
137	Improved epicardial cardiac fibroblast generation from iPSCs. Journal of Molecular and Cellular Cardiology, 2022, 164, 58-68.	1.9	3
138	Uncovering a conserved role for JMJD2 histone triâ€demethylases from worm to human. FASEB Journal, 2010, 24, 456.13.	0.5	0