Transposition of native chromatin for fast and sensitive
chromatin, DNA-binding proteins and nucleosome posi

Nature Methods

10, 1213-1218

DOI: 10.1038/nmeth.2688

Citation Report

#	Article	IF	Citations
2	237. Transgenic Expression of Dp116 in Muscle Does Not Ameliorate Dystrophy in mdx Mice. Molecular Therapy, 2004, 9, S91.	3.7	1
3	Gene-Environment Interaction for Hypertension Among African American Women Across Generations. Biological Research for Nursing, 2010, 12, 149-155.	1.0	30
4	High-resolution mapping of transcription factor binding sites on native chromatin. Epigenetics and Chromatin, 2013, 6, .	1.8	0
5	Chromatin accessibility: a window into the genome. Epigenetics and Chromatin, 2014, 7, 33.	1.8	326
6	Map of open and closed chromatin domains in Drosophila genome. BMC Genomics, 2014, 15, 988.	1.2	19
7	Open Chromatin in Plant Genomes. Cytogenetic and Genome Research, 2014, 143, 18-27.	0.6	19
8	An Integrated Cell Purification and Genomics Strategy Reveals Multiple Regulators of Pancreas Development. PLoS Genetics, 2014, 10, e1004645.	1.5	49
9	MORC1 represses transposable elements in the mouse male germline. Nature Communications, 2014, 5, 5795.	5.8	108
10	Genotet: An Interactive Web-based Visual Exploration Framework to Support Validation of Gene Regulatory Networks. IEEE Transactions on Visualization and Computer Graphics, 2014, 20, 1903-1912.	2.9	11
11	Perspective for special Gurdon issue for differentiation: Can cell fusion inform nuclear reprogramming?. Differentiation, 2014, 88, 27-28.	1.0	2
12	In vitro, long-range sequence information for de novo genome assembly via transposase contiguity. Genome Research, 2014, 24, 2041-2049.	2.4	150
13	The epigenomic tool kit. Drug Discovery Today: Disease Models, 2014, 12, 27-33.	1.2	0
14	Tissue-Resident Macrophage Enhancer Landscapes Are Shaped by the Local Microenvironment. Cell, 2014, 159, 1312-1326.	13.5	1,705
15	Protection of CpG islands against de novo DNA methylation during oogenesis is associated with the recognition site of E2f1 and E2f2. Epigenetics and Chromatin, 2014, 7, 26.	1.8	30
16	Transcriptional enhancers: from properties to genome-wide predictions. Nature Reviews Genetics, 2014, 15, 272-286.	7.7	1,136
17	Dissecting the Causal Genetic Mechanisms of Coronary Heart Disease. Current Atherosclerosis Reports, 2014, 16, 406.	2.0	11
18	Functional interpretation of nonâ€coding sequence variation: Concepts and challenges. BioEssays, 2014, 36, 191-199.	1.2	47
19	Quantitative analysis of RNA-protein interactions on a massively parallel array reveals biophysical and evolutionary landscapes. Nature Biotechnology, 2014, 32, 562-568.	9.4	202

#	Article	IF	Citations
20	Plasticity in the transcriptional and epigenetic circuits regulating dendritic cell lineage specification and function. Current Opinion in Immunology, 2014, 30, 1-8.	2.4	24
21	High-resolution mapping of transcription factor binding sites on native chromatin. Nature Methods, 2014, 11, 203-209.	9.0	170
22	The genome shows its sensitive side. Nature Methods, 2014, 11, 39-40.	9.0	4
23	A Negative Feedback Loop of Transcription Factors Specifies Alternative Dendritic Cell Chromatin States. Molecular Cell, 2014, 56, 749-762.	4.5	58
24	When genetics meets epigenetics: deciphering the mechanisms controlling inter-individual variation in immune responses to infection. Current Opinion in Immunology, 2014, 29, 119-126.	2.4	13
25	Enhancer alterations in cancer: a source for a cell identity crisis. Genome Medicine, 2014, 6, 77.	3.6	47
26	pENCODE: A Plant Encyclopedia of DNA Elements. Annual Review of Genetics, 2014, 48, 49-70.	3.2	38
27	Sequencing the AML Genome, Transcriptome, and Epigenome. Seminars in Hematology, 2014, 51, 250-258.	1.8	13
28	Enhancing the understanding of asthma. Nature Immunology, 2014, 15, 701-703.	7.0	10
29	H3K4me3 Breadth Is Linked to Cell Identity and Transcriptional Consistency. Cell, 2014, 158, 673-688.	13.5	404
30	Chromatin state dynamics during blood formation. Science, 2014, 345, 943-949.	6.0	699
31	The role of chromatin dynamics in immune cell development. Immunological Reviews, 2014, 261, 9-22.	2.8	57
32	Transcriptional and epigenetic networks of helper T and innate lymphoid cells. Immunological Reviews, 2014, 261, 23-49.	2.8	76
33	High-resolution digital profiling of the epigenome. Nature Reviews Genetics, 2014, 15, 814-827.	7.7	112
34	Absence of a simple code: how transcription factors read the genome. Trends in Biochemical Sciences, 2014, 39, 381-399.	3.7	447
35	From Cancer Genomics to Precision Oncologyâ€"Tissueâ€™s Still an Issue. Cell, 2014, 157, 1509-1514.	13.5	26
36	Identifying and mitigating bias in next-generation sequencing methods for chromatin biology. Nature Reviews Genetics, 2014, 15, 709-721.	7.7	295
37	In pursuit of design principles of regulatory sequences. Nature Reviews Genetics, 2014, 15, 453-468.	7.7	196

#	Article	IF	Citations
38	Epigenetics: A New Player in the Regulation of Mammalian Puberty. Neuroendocrinology, 2014, 99, 139-155.	1.2	34
39	Genomic-wide transcriptional profiling in primary myoblasts reveals Runx1-regulated genes in muscle regeneration. Genomics Data, 2015, 6, 120-122.	1.3	7
40	Transcriptional enhancers: functional insights and role in human disease. Current Opinion in Genetics and Development, 2015, 33, 71-76.	1.5	35
41	Prioritization Of Nonsynonymous Single Nucleotide Variants For Exome Sequencing Studies Via Integrative Learning On Multiple Genomic Data. Scientific Reports, 2015, 5, 14955.	1.6	10
42	Tunicates: exploring the sea shores and roaming the open ocean. A tribute to Thomas Huxley. Open Biology, 2015, 5, 150053.	1.5	16
43	Taking Stock of Regulatory Variation. Cell Systems, 2015, 1, 18-21.	2.9	4
44	A novel ATAC-seq approach reveals lineage-specific reinforcement of the open chromatin landscape via cooperation between BAF and p63. Genome Biology, 2015, 16, 284.	3.8	135
45	cChIP-seq: a robust small-scale method for investigation of histone modifications. BMC Genomics, 2015, 16, 1083.	1.2	14
46	Improved DNase-seq protocol facilitates high resolution mapping of DNase I hypersensitive sites in roots in Arabidopsis thaliana. Plant Methods, 2015, 11, 42.	1.9	20
47	Reconstructing A/B compartments as revealed by Hi-C using long-range correlations in epigenetic data. Genome Biology, 2015, 16, 180.	3.8	232
48	Making sense of GWAS: using epigenomics and genome engineering to understand the functional relevance of SNPs in non-coding regions of the human genome. Epigenetics and Chromatin, 2015, 8, 57.	1.8	277
49	Epigenetic States of Nephron Progenitors and Epithelial Differentiation. Journal of Cellular Biochemistry, 2015, 116, 893-902.	1.2	15
50	On Accounting for Sequence-Specific Bias in Genome-Wide Chromatin Accessibility Experiments: Recent Advances and Contradictions. Frontiers in Bioengineering and Biotechnology, 2015, 3, 144.	2.0	23
51	Transcriptional Enhancers in the Regulation of T Cell Differentiation. Frontiers in Immunology, 2015, 6, 462.	2.2	17
52	Runx1 Transcription Factor Is Required for Myoblasts Proliferation during Muscle Regeneration. PLoS Genetics, 2015, 11, e1005457.	1.5	67
53	The chromatin remodeler Brg1 activates enhancer repertoires to establish B cell identity and modulate cell growth. Nature Immunology, 2015, 16, 775-784.	7.0	107
54	cMonkey₂: Automated, systematic, integrated detection of co-regulated gene modules for any organism. Nucleic Acids Research, 2015, 43, e87-e87.	6.5	45
55	Long Noncoding RNA in Hematopoiesis and Immunity. Immunity, 2015, 42, 792-804.	6.6	161

#	Article	IF	Citations
56	High-Throughput Sequencing Technologies. Molecular Cell, 2015, 58, 586-597.	4.5	968
57	Recent developments in epigenetics of acute and chronic kidney diseases. Kidney International, 2015, 88, 250-261.	2.6	88
58	A virus that infects a hyperthermophile encapsidates A-form DNA. Science, 2015, 348, 914-917.	6.0	98
59	BinDNase: a discriminatory approach for transcription factor binding prediction using DNase I hypersensitivity data. Bioinformatics, 2015, 31, 2852-2859.	1.8	54
60	A Genome-Wide Perspective on Metabolism. Handbook of Experimental Pharmacology, 2015, 233, 1-28.	0.9	3
61	Characterization of functional methylomes by next-generation capture sequencing identifies novel disease-associated variants. Nature Communications, 2015, 6, 7211.	5.8	84
62	Proteinâ€“DNA binding in high-resolution. Critical Reviews in Biochemistry and Molecular Biology, 2015, 50, 269-283.	2.3	41
63	Integrating motif, DNA accessibility and gene expression data to build regulatory maps in an organism. Nucleic Acids Research, 2015, 43, 3998-4012.	6.5	36
64	The histone chaperone CAF-1 safeguards somatic cell identity. Nature, 2015, 528, 218-224.	13.7	244
65	The Genotype and Phenotype (GaP) registry: a living biobank for the analysis of quantitative traits. Immunologic Research, 2015, 63, 107-112.	1.3	14
66	Genome-Wide Epigenetic Studies in Human Disease: A Primer on -Omic Technologies. American Journal of Epidemiology, 2016, 183, kwv187.	1.6	23
67	Glioma Stem-like Cells Keep Their H3.3 Variant Levels at Bay. Cancer Cell, 2015, 28, 679-680.	7.7	0
68	Dual Function of DNA Sequences: Protein-Coding Sequences Function as Transcriptional Enhancers. Perspectives in Biology and Medicine, 2015, 58, 182-195.	0.3	12
69	Single-cell ATAC-seq: strength in numbers. Genome Biology, 2015, 16, 172.	3.8	62
70	Transcriptional Enhancers: Bridging the Genome and Phenome. Cold Spring Harbor Symposia on Quantitative Biology, 2015, 80, 17-26.	2.0	28
71	Intrauterine growth restriction perturbs nucleosome depletion at a growth hormone-responsive element in the mouse IGF-1 gene. Physiological Genomics, 2015, 47, 634-643.	1.0	6
72	Identifying transcriptional cisâ€regulatory modules in animal genomes. Wiley Interdisciplinary Reviews: Developmental Biology, 2015, 4, 59-84.	5.9	54
73	ATACâ€seq: A Method for Assaying Chromatin Accessibility Genomeâ€Wide. Current Protocols in Molecular Biology, 2015, 109, 21.29.1-21.29.9.	2.9	2,391

#	Article	IF	Citations
74	Enhancer Evolution across 20 Mammalian Species. Cell, 2015, 160, 554-566.	13.5	671
75	Epigenomic analysis of the HOX gene loci reveals mechanisms that may control canonical expression patterns in AML and normal hematopoietic cells. Leukemia, 2015, 29, 1279-1289.	3.3	96
76	Identification of altered cis-regulatory elements in human disease. Trends in Genetics, 2015, 31, 67-76.	2.9	99
77	Path from schizophrenia genomics to biology: gene regulation and perturbation in neurons derived from induced pluripotent stem cells and genome editing. Neuroscience Bulletin, 2015, 31, 113-127.	1.5	12
78	The â€˜dark matterâ€™ in the plant genomes: non-coding and unannotated DNA sequences associated with open chromatin. Current Opinion in Plant Biology, 2015, 24, 17-23.	3.5	49
79	Transcription-coupled recruitment of human CHD1 and CHD2 influences chromatin accessibility and histone H3 and H3.3 occupancy at active chromatin regions. Epigenetics and Chromatin, 2015, 8, 4.	1.8	42
80	Investigating the Transcriptional Control of Cardiovascular Development. Circulation Research, 2015, 116, 700-714.	2.0	77
81	Functional annotation of native enhancers with a Cas9â€“histone demethylase fusion. Nature Methods, 2015, 12, 401-403.	9.0	548
82	Transcription factors and target genes of pre-TCR signaling. Cellular and Molecular Life Sciences, 2015, 72, 2305-2321.	2.4	17
83	An Integrative Breakage Model of genome architecture, reshuffling and evolution. BioEssays, 2015, 37, 479-488.	1.2	54
84	Genome-wide CIITA-binding profile identifies sequence preferences that dictate function versus recruitment. Nucleic Acids Research, 2015, 43, 3128-3142.	6.5	28
85	Epigenomic Signatures of Neuronal Diversity in the Mammalian Brain. Neuron, 2015, 86, 1369-1384.	3.8	640
86	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
87	Recent advances in functional assays of transcriptional enhancers. Genomics, 2015, 106, 137-139.	1.3	16
88	RAG Represents a Widespread Threat to the Lymphocyte Genome. Cell, 2015, 162, 751-765.	13.5	98
89	Single-cell transcriptome analysis reveals coordinated ectopic gene-expression patterns in medullary thymic epithelial cells. Nature Immunology, 2015, 16, 933-941.	7.0	148
90	Uncovering correlated variability in epigenomic datasets using the Karhunen-Loeve transform. BioData Mining, 2015, 8, 20.	2.2	15
91	Inhibitory Synapses Get Madd for Neuroligin. Neuron, 2015, 86, 1321-1324.	3.8	2

#	Article	IF	Citations
92	Systems biology and gene networks in neurodevelopmental and neurodegenerative disorders. Nature Reviews Genetics, 2015, 16, 441-458.	7.7	378
93	SeqGL Identifies Context-Dependent Binding Signals in Genome-Wide Regulatory Element Maps. PLoS Computational Biology, 2015, 11, e1004271.	1.5	67
94	Transient acquisition of pluripotency during somatic cell transdifferentiation with iPSC reprogramming factors. Nature Biotechnology, 2015, 33, 769-774.	9.4	124
95	Decoding enhancers using massively parallel reporter assays. Genomics, 2015, 106, 159-164.	1.3	208
96	Third Report on Chicken Genes and Chromosomes 2015. Cytogenetic and Genome Research, 2015, 145, 78-179.	0.6	97
97	Single-cell chromatin accessibility reveals principles of regulatory variation. Nature, 2015, 523, 486-490.	13.7	1,798
98	Epigenomic Landscapes Reflect Neuronal Diversity. Neuron, 2015, 86, 1319-1321.	3.8	1
99	Using transgenic reporter assays to functionally characterize enhancers in animals. Genomics, 2015, 106, 185-192.	1.3	63
101	Discovery of Transcription Factors and Regulatory Regions Driving In Vivo Tumor Development by ATAC-seq and FAIRE-seq Open Chromatin Profiling. PLoS Genetics, 2015, 11, e1004994.	1.5	155
102	Lessons from modENCODE. Annual Review of Genomics and Human Genetics, 2015, 16, 31-53.	2.5	46
103	Genetic and Genomic Approaches to Understanding Macrophage Identity and Function. Arteriosclerosis, Thrombosis, and Vascular Biology, 2015, 35, 755-762.	1.1	21
104	Characterization of TCF21 Downstream Target Regions Identifies a Transcriptional Network Linking Multiple Independent Coronary Artery Disease Loci. PLoS Genetics, 2015, 11, e1005202.	1.5	41
105	Myogenesis in the Genomics Era. Journal of Molecular Biology, 2015, 427, 2023-2038.	2.0	10
106	Unraveling the 3D genome: genomics tools for multiscale exploration. Trends in Genetics, 2015, 31, 357-372.	2.9	62
107	Organogenesis in deep time: A problem in genomics, development, and paleontology. Proceedings of the National Academy of Sciences of the United States of America, 2015, 112, 4871-4876.	3.3	23
108	Coordinated international action to accelerate genome-to-phenome with FAANG, the Functional Annotation of Animal Genomes project. Genome Biology, 2015, 16, 57.	3.8	331
109	The Ensembl Regulatory Build. Genome Biology, 2015, 16, 56.	3.8	382
110	Gene regulatory mechanisms orchestrated by p63 in epithelial development and related disorders. Biochimica Et Biophysica Acta - Gene Regulatory Mechanisms, 2015, 1849, 590-600.	0.9	27

#	Article	IF	Citations
111	Multiplex single-cell profiling of chromatin accessibility by combinatorial cellular indexing. Science, 2015, 348, 910-914.	6.0	1,045
112	Identification of active transcriptional regulatory elements from GRO-seq data. Nature Methods, 2015, 12, 433-438.	9.0	198
113	DOT1L inhibits SIRT1-mediated epigenetic silencing to maintain leukemic gene expression in MLL-rearranged leukemia. Nature Medicine, 2015, 21, 335-343.	15.2	200
114	Epigenome Mapping Reveals Distinct Modes of Gene Regulation and Widespread Enhancer Reprogramming by the Oncogenic Fusion Protein EWS-FLI1. Cell Reports, 2015, 10, 1082-1095.	2.9	183
115	Epigenomics and the structure of the living genome. Genome Research, 2015, 25, 1482-1490.	2.4	48
116	Defining cell types and states with single-cell genomics. Genome Research, 2015, 25, 1491-1498.	2.4	636
117	Genomic approaches for understanding the genetics of complex disease. Genome Research, 2015, 25, 1432-1441.	2.4	75
118	Hematopoietic Differentiation Is Required for Initiation of Acute Myeloid Leukemia. Cell Stem Cell, 2015, 17, 611-623.	5.2	97
119	Genomic approaches to studying human-specific developmental traits. Development (Cambridge), 2015, 142, 3100-3112.	1.2	26
120	Early enhancer establishment and regulatory locus complexity shape transcriptional programs in hematopoietic differentiation. Nature Genetics, 2015, 47, 1249-1259.	9.4	83
121	Bacterial infection remodels the DNA methylation landscape of human dendritic cells. Genome Research, 2015, 25, 1801-1811.	2.4	195
122	Structured nucleosome fingerprints enable high-resolution mapping of chromatin architecture within regulatory regions. Genome Research, 2015, 25, 1757-1770.	2.4	334
123	Glioblastoma Stem Cells Respond to Differentiation Cues but Fail to Undergo Commitment and Terminal Cell-Cycle Arrest. Stem Cell Reports, 2015, 5, 829-842.	2.3	93
124	Leukemia-Associated Cohesin Mutants Dominantly Enforce Stem Cell Programs and Impair Human Hematopoietic Progenitor Differentiation. Cell Stem Cell, 2015, 17, 675-688.	5.2	177
125	BioWardrobe: an integrated platform for analysis of epigenomics and transcriptomics data. Genome Biology, 2015, 16, 158.	3.8	74
126	Making the case for chromatin profiling: a new tool to investigate the immune-regulatory landscape. Nature Reviews Immunology, 2015, 15, 585-594.	10.6	32
127	Technological advances transforming rheumatology. Nature Reviews Rheumatology, 2015, 11, 626-628.	3.5	7
128	Dose-dependent role of the cohesin complex in normal and malignant hematopoiesis. Journal of Experimental Medicine, 2015, 212, 1819-1832.	4.2	137

#	Article	IF	Citations
129	Removing reference mapping biases using limited or no genotype data identifies allelic differences in protein binding at disease-associated loci. BMC Medical Genomics, 2015, 8, 43.	0.7	13
130	Genomic Views of Transcriptional Enhancers: Essential Determinants of Cellular Identity and Activity-Dependent Responses in the CNS. Journal of Neuroscience, 2015, 35, 13819-13826.	1.7	33
131	Single-cell epigenomics: techniques and emerging applications. Nature Reviews Genetics, 2015, 16, 716-726.	7.7	219
132	Dynamics of chromatin accessibility and epigenetic state in response to UV damage. Journal of Cell Science, 2015, 128, 4380-94.	1.2	31
133	Histone reader BRWD1 targets and restricts recombination to the Igk locus. Nature Immunology, 2015, 16, 1094-1103.	7.0	37
134	Homology in the Age of Developmental Genomics. , 2015, , 25-43.		6
135	Exploiting genomics and natural genetic variation to decode macrophage enhancers. Trends in Immunology, 2015, 36, 507-518.	2.9	32
136	New approaches to understanding the immune response to vaccination and infection. Vaccine, 2015, 33, 5271-5281.	1.7	103
137	Super-enhancers: Asset management in immune cell genomes. Trends in Immunology, 2015, 36, 519-526.	2.9	36
138	ChIPmentation: fast, robust, low-input ChIP-seq for histones and transcription factors. Nature Methods, 2015, 12, 963-965.	9.0	417
139	Architectural and Functional Commonalities between Enhancers and Promoters. Cell, 2015, 162, 948-959.	13.5	277
140	Discovering enhancers by mapping chromatin features in primary tissue. Genomics, 2015, 106, 140-144.	1.3	13
141	Comparative Analysis of Gene Regulatory Networks: From Network Reconstruction to Evolution. Annual Review of Cell and Developmental Biology, 2015, 31, 399-428.	4.0	170
142	Enhancer Divergence and cis-Regulatory Evolution in the Human and Chimp Neural Crest. Cell, 2015, 163, 68-83.	13.5	299
144	Insect Regulatory Genomics. True Bugs (Heteroptera) of the Neotropics, 2015, , 119-155.	1.2	1
145	Individuality and Variation of Personal Regulomes in Primary Human T Cells. Cell Systems, 2015, 1, 51-61.	2.9	128
146	Control of plant cell differentiation by histone modification and DNA methylation. Current Opinion in Plant Biology, 2015, 28, 60-67.	3.5	81
147	MLL5 Orchestrates a Cancer Self-Renewal State by Repressing the Histone Variant H3.3 and Globally Reorganizing Chromatin. Cancer Cell, 2015, 28, 715-729.	7.7	90

#	Article	IF	Citations
148	Regulation and Evolution of the RAG Recombinase. Advances in Immunology, 2015, 128, 1-39.	1.1	70
149	Deep conservation of wrist and digit enhancers in fish. Proceedings of the National Academy of Sciences of the United States of America, 2015, 112, 803-808.	3.3	121
150	Promoter or enhancer, what's the difference? Deconstruction of established distinctions and presentation of a unifying model. BioEssays, 2015, 37, 314-323.	1.2	92
151	TP53 engagement with the genome occurs in distinct local chromatin environments via pioneer factor activity. Genome Research, 2015, 25, 179-188.	2.4	95
152	Assaying the epigenome in limited numbers of cells. Methods, 2015, 72, 51-56.	1.9	16
153	Closing the genotypeâ€“phenotype gap: Emerging technologies for evolutionary genetics in ecological model vertebrate systems. BioEssays, 2015, 37, 213-226.	1.2	59
154	Single molecule and single cell epigenomics. Methods, 2015, 72, 41-50.	1.9	35
155	GC Content Heterogeneity Transition of Conserved Noncoding Sequences Occurred at the Emergence of Vertebrates. Genome Biology and Evolution, 2016, 8, 3377-3392.	1.1	11
156	4C-ker: A Method to Reproducibly Identify Genome-Wide Interactions Captured by 4C-Seq Experiments. PLoS Computational Biology, 2016, 12, e1004780.	1.5	84
157	Which Genetics Variants in DNase-Seq Footprints Are More Likely to Alter Binding?. PLoS Genetics, 2016, 12, e1005875.	1.5	56
158	Cancer Epigenetics. , 2016, , 41-59.		2
159	Advancing haematopoietic stem and progenitor cell biology through singleâ€cell profiling. FEBS Letters, 2016, 590, 4052-4067.	1.3	6
160	Principles of metadata organization at the ENCODE data coordination center. Database: the Journal of Biological Databases and Curation, 2016, 2016, baw001.	1.4	40
161	Gene regulation at a distance: From remote enhancers to 3D regulatory ensembles. Seminars in Cell and Developmental Biology, 2016, 57, 57-67.	2.3	78
162	Genetic dissection of the Î±-globin super-enhancer in vivo. Nature Genetics, 2016, 48, 895-903.	9.4	308
163	Cellular and chromatin dynamics of antibodyâ€secreting plasma cells. Wiley Interdisciplinary Reviews: Developmental Biology, 2016, 5, 136-149.	5.9	12
164	Impact of the X Chromosome and sex on regulatory variation. Genome Research, 2016, 26, 768-777.	2.4	88
165	Ensembl regulation resources. Database: the Journal of Biological Databases and Curation, 2016, 2016, bav119.	1.4	45

#	Article	IF	Citations
166	Nfib Promotes Metastasis through a Widespread Increase in Chromatin Accessibility. Cell, 2016, 166, 328-342.	13.5	304
167	Meeting report: processing, translation, decay â€“ three ways to keep RNA sizzling. Plant, Cell and Environment, 2016, 39, 2624-2628.	2.8	0
168	Identification and in silico modeling of enhancers reveals new features of the cardiac differentiation network. Development (Cambridge), 2016, 143, 4533-4542.	1.2	5
169	Impact of the gut microbiota on enhancer accessibility in gut intraepithelial lymphocytes. Proceedings of the National Academy of Sciences of the United States of America, 2016, 113, 14805-14810.	3.3	37
170	Can T cells be too exhausted to fight back?. Science, 2016, 354, 1104-1105.	6.0	12
171	Transcriptional and postâ€transcriptional regulation of histone variant H2A.Z during sea urchin development. Development Growth and Differentiation, 2016, 58, 727-740.	0.6	5
172	MNase titration reveals differences between nucleosome occupancy and chromatin accessibility. Nature Communications, 2016, 7, 11485.	5.8	185
173	Tumor Interferon Signaling Regulates a Multigenic Resistance Program to Immune Checkpoint Blockade. Cell, 2016, 167, 1540-1554.e12.	13.5	830
174	Conserved Noncoding Elements in the Most Distant Genera of Cephalochordates: The Goldilocks Principle. Genome Biology and Evolution, 2016, 8, 2387-2405.	1.1	23
175	Enhancers reside in a unique epigenetic environment during early zebrafish development. Genome Biology, 2016, 17, 146.	3.8	41
176	Leukaemia cell of origin identified by chromatin landscape of bulk tumour cells. Nature Communications, 2016, 7, 12166.	5.8	47
177	Expression of Terminal Effector Genes in Mammalian Neurons Is Maintained by a Dynamic Relay of Transient Enhancers. Neuron, 2016, 92, 1252-1265.	3.8	70
178	Genome-wide epigenomic profiling for biomarker discovery. Clinical Epigenetics, 2016, 8, 122.	1.8	67
179	DeFCoM: analysis and modeling of transcription factor binding sites using a motif-centric genomic footprinter. Bioinformatics, 2017, 33, 956-963.	1.8	30
180	ALTRE: workflow for defining ALTered Regulatory Elements using chromatin accessibility data. Bioinformatics, 2017, 33, 740-742.	1.8	3
181	Transcription Factor Hand-offs â€œEnhanceâ€•Motor Neuron Differentiation. Neuron, 2016, 92, 1149-1151.	3.8	1
182	An atlas of transcriptional, chromatin accessibility, and surface marker changes in human mesoderm development. Scientific Data, 2016, 3, 160109.	2.4	47
183	- Protein-Protein Functional Linkage Predictions: Bringing Regulation to Context. , 2016, , 172-191.		0

#	Article	IF	Citations
184	Epigenetic Changes During Food-Specific Immunotherapy. Current Allergy and Asthma Reports, 2016, 16, 87.	2.4	10
185	Disease Model of GATA4 Mutation Reveals Transcription Factor Cooperativity in Human Cardiogenesis. Cell, 2016, 167, 1734-1749.e22.	13.5	195
186	Dynamic Changes in Chromatin Accessibility Occur in CD8 + T Cells Responding to Viral Infection. Immunity, 2016, 45, 1327-1340.	6.6	231
187	The genetic regulatory signature of type 2 diabetes in human skeletal muscle. Nature Communications, 2016, 7, 11764.	5.8	114
188	Clonal conversion of B lymphoid leukemia reveals cross-lineage transfer of malignant states. Genes and Development, 2016, 30, 2486-2499.	2.7	16
189	RAG1 targeting in the genome is dominated by chromatin interactions mediated by the non-core regions of RAG1 and RAG2. Nucleic Acids Research, 2016, 44, gkw633.	6.5	19
190	Computational Prediction of the Global Functional Genomic Landscape: Applications, Methods, and Challenges. Human Heredity, 2016, 81, 88-105.	0.4	3
191	ATAC-seq on biobanked specimens defines a unique chromatin accessibility structure in naÃ¯ve SLE B cells. Scientific Reports, 2016, 6, 27030.	1.6	88
192	The Functionality and Evolution of Eukaryotic Transcriptional Enhancers. Advances in Genetics, 2016, 96, 143-206.	0.8	27
193	Genome-Wide Approaches to Defining Macrophage Identity and Function. Microbiology Spectrum, 2016, 4, .	1.2	21
194	Transcriptomics in type 2 diabetes: Bridging the gap between genotype and phenotype. Genomics Data, 2016, 8, 25-36.	1.3	37
195	The Dynamic Regulatory Genome of Capsaspora and the Origin of Animal Multicellularity. Cell, 2016, 165, 1224-1237.	13.5	139
196	OVOL2 Maintains the Transcriptional Program of Human Corneal Epithelium by Suppressing Epithelial-to-Mesenchymal Transition. Cell Reports, 2016, 15, 1359-1368.	2.9	66
197	Decoding transcriptional enhancers: Evolving from annotation to functional interpretation. Seminars in Cell and Developmental Biology, 2016, 57, 40-50.	2.3	11
198	GATA3-dependent cellular reprogramming requires activation-domain dependent recruitment of a chromatin remodeler. Genome Biology, 2016, 17, 36.	3.8	121
199	Medial HOXA genes demarcate haematopoietic stem cell fate during human development. Nature Cell Biology, 2016, 18, 595-606.	4.6	81
200	Coming of age: ten years of next-generation sequencing technologies. Nature Reviews Genetics, 2016, 17, 333-351.	7.7	3,160
201	DNA Transposition at Work. Chemical Reviews, 2016, 116, 12758-12784.	23.0	89

#	Article	IF	Citations
202	Characterization of chromatin accessibility with a transposome hypersensitive sites sequencing (THS-seq) assay. Genome Biology, 2016, 17, 20.	3.8	55
203	ANISEED 2015: a digital framework for the comparative developmental biology of ascidians. Nucleic Acids Research, 2016, 44, D808-D818.	6.5	68
204	Self-renewal of tumor cells: epigenetic determinants of the cancer stem cell phenotype. Current Opinion in Genetics and Development, 2016, 36, 92-99.	1.5	18
205	Age-Dependent Pancreatic Gene Regulation Reveals Mechanisms Governing Human Î² Cell Function. Cell Metabolism, 2016, 23, 909-920.	7.2	205
206	Distinct Gene Regulatory Pathways for Human Innate versus Adaptive Lymphoid Cells. Cell, 2016, 165, 1134-1146.	13.5	134
207	Developmental Acquisition of Regulomes Underlies Innate Lymphoid Cell Functionality. Cell, 2016, 165, 1120-1133.	13.5	273
208	Network-based approaches for analysis of complex biological systems. Current Opinion in Biotechnology, 2016, 39, 157-166.	3.3	71
209	Evolution of Gene Regulation in Humans. Annual Review of Genomics and Human Genetics, 2016, 17, 45-67.	2.5	52
210	Techniques and Approaches to Genetic Analyses in Nephrological Disorders. Journal of Pediatric Genetics, 2016, 05, 002-014.	0.3	0
211	BACH2 regulates CD8+ T cell differentiation by controlling access of AP-1 factors to enhancers. Nature Immunology, 2016, 17, 851-860.	7.0	221
212	Genetics and Genomics of Coronary Artery Disease. Current Cardiology Reports, 2016, 18, 102.	1.3	31
213	Exploiting Chromatin Biology to Understand Immunology. Methods in Enzymology, 2016, 574, 365-383.	0.4	0
214	Epigenomic Consequences of Coding and Noncoding Driver Mutations. Trends in Cancer, 2016, 2, 585-605.	3.8	8
215	The dark side of the human genome. Nature, 2016, 538, 275-277.	13.7	44
216	Divergence and rewiring of regulatory networks for neural development between human and other species. Neurogenesis (Austin, Tex), 2016, 3, e1231495.	1.5	6
217	Identifying Coopted Networks and Causative Mutations in the Origin of Novel Complex Traits. Current Topics in Developmental Biology, 2016, 119, 205-226.	1.0	21
218	An inducible long noncoding RNA amplifies DNA damage signaling. Nature Genetics, 2016, 48, 1370-1376.	9.4	195
219	Chromatin Control of Developmental Dynamics and Plasticity. Developmental Cell, 2016, 38, 610-620.	3.1	127

#	Article	IF	Citations
220	High-resolution interrogation of functional elements in the noncoding genome. Science, 2016, 353, 1545-1549.	6.0	251
221	Epigenetics, Energy Balance, and Cancer. Energy Balance and Cancer, 2016, , .	0.2	2
222	Epigenetics, Enhancers, and Cancer. Energy Balance and Cancer, 2016, , 29-53.	0.2	1
223	Suppression by TFR cells leads to durable and selective inhibition of B cell effector function. Nature Immunology, 2016, 17, 1436-1446.	7.0	189
224	Chromatin immunoprecipitation and an open chromatin assay in zebrafish erythrocytes. Methods in Cell Biology, 2016, 135, 387-412.	0.5	5
225	Open chromatin profiling as a novel strategy for identifying cancer cell of origin. Molecular and Cellular Oncology, 2016, 3, e1236770.	0.3	0
226	Chromatin, Nuclear Organization, and Genome Stability in Mammals. , 2016, , 391-407.		0
227	Past Roadblocks and New Opportunities in Transcription Factor Network Mapping. Trends in Genetics, 2016, 32, 736-750.	2.9	23
228	Histone Deacetylase 5 Is Overexpressed in Scleroderma Endothelial Cells and Impairs Angiogenesis via Repression of Proangiogenic Factors. Arthritis and Rheumatology, 2016, 68, 2975-2985.	2.9	62
229	Memory of Inflammation in Regulatory T Cells. Cell, 2016, 166, 977-990.	13.5	148
230	The Transcriptional Repressor Polycomb Group Factor 6, PCGF6, Negatively Regulates Dendritic Cell Activation and Promotes Quiescence. Cell Reports, 2016, 16, 1829-1837.	2.9	32
231	Epigenetic memory: A macrophage perspective. Seminars in Immunology, 2016, 28, 359-367.	2.7	49
232	Network pharmacology of JAK inhibitors. Proceedings of the National Academy of Sciences of the United States of America, 2016, 113, 9852-9857.	3.3	59
233	A Highly Sensitive and Robust Method for Genome-wide 5hmC Profiling of Rare Cell Populations. Molecular Cell, 2016, 63, 711-719.	4.5	128
234	Epigenetic Variation between Human Induced Pluripotent Stem Cell Lines Is an Indicator of Differentiation Capacity. Cell Stem Cell, 2016, 19, 341-354.	5.2	179
235	Cell typeâ€specific epigenome profiling using affinityâ€purified nuclei. Genesis, 2016, 54, 160-169.	0.8	4
236	Advances, practice, and clinical perspectives in highâ€throughput sequencing. Oral Diseases, 2016, 22, 353-364.	1.5	11
237	The epigenome in Alzheimerâ€™s disease: current state and approaches for a new path to gene discovery and understanding disease mechanism. Acta Neuropathologica, 2016, 132, 503-514.	3.9	44

#	Article	IF	Citations
238	Fast and Furious 800. The Retinal Determination Gene Network in Drosophila. , 2016, , 95-124.		13
239	Lineage-specific and single-cell chromatin accessibility charts human hematopoiesis and leukemia evolution. Nature Genetics, 2016, 48, 1193-1203.	9.4	952
240	The Spectrum and Regulatory Landscape of Intestinal Innate Lymphoid Cells Are Shaped by the Microbiome. Cell, 2016, 166, 1231-1246.e13.	13.5	465
241	Applications of integrative OMICs approaches to gene regulation studies. Quantitative Biology, 2016, 4, 283-301.	0.3	6
242	NRL-Regulated Transcriptome Dynamics of Developing Rod Photoreceptors. Cell Reports, 2016, 17, 2460-2473.	2.9	104
243	Integrative functional genomics identifies regulatory mechanisms at coronary artery disease loci. Nature Communications, 2016, 7, 12092.	5.8	123
244	Macrophage Ontogeny Underlies Differences in Tumor-Specific Education in Brain Malignancies. Cell Reports, 2016, 17, 2445-2459.	2.9	450
245	Strategies for targeting primate neural circuits with viral vectors. Journal of Neurophysiology, 2016, 116, 122-134.	0.9	34
246	Manual of Cardiovascular Proteomics. , 2016, , .		4
247	Polarized regulatory landscape and Wnt responsiveness underlie Hox activation in embryos. Genes and Development, 2016, 30, 1937-1942.	2.7	77
248	Plant Enhancers: A Call for Discovery. Trends in Plant Science, 2016, 21, 974-987.	4.3	115
249	EGRINs (Environmental Gene Regulatory Influence Networks) in Rice That Function in the Response to Water Deficit, High Temperature, and Agricultural Environments. Plant Cell, 2016, 28, 2365-2384.	3.1	139
250	Sensing and Remembering Cellular States Through Chromatin. , 2016, , 343-363.		0
251	HiChIP: efficient and sensitive analysis of protein-directed genome architecture. Nature Methods, 2016, 13, 919-922.	9.0	853
252	G-quadruplex structures mark human regulatory chromatin. Nature Genetics, 2016, 48, 1267-1272.	9.4	683
253	<scp>GO</scp>â€<scp>FAANG</scp> meeting: a Gathering On Functional Annotation of <scp>An</scp>imal Genomes. Animal Genetics, 2016, 47, 528-533.	0.6	65
254	Hormoneâ€induced repression of genes requires <scp>BRG</scp> 1â€mediated H1.2 deposition at target promoters. EMBO Journal, 2016, 35, 1822-1843.	3.5	33
255	A synergistic DNA logic predicts genome-wide chromatin accessibility. Genome Research, 2016, 26, 1430-1440.	2.4	18

#	Article	IF	Citations
256	Modeling cis-regulation with a compendium of genome-wide histone H3K27ac profiles. Genome Research, 2016, 26, 1417-1429.	2.4	75
257	Piwi Modulates Chromatin Accessibility by Regulating Multiple Factors Including Histone H1 to Repress Transposons. Molecular Cell, 2016, 63, 408-419.	4.5	110
258	Neuroepigenomics and Human Disease. , 2016, , 73-91.		0
259	Mapping the Pairwise Choices Leading from Pluripotency to Human Bone, Heart, and Other Mesoderm Cell Types. Cell, 2016, 166, 451-467.	13.5	367
260	Mutant IDH1 Downregulates ATM and Alters DNA Repair and Sensitivity to DNA Damage Independent of TET2. Cancer Cell, 2016, 30, 337-348.	7.7	166
261	Structural organization of the inactive X chromosome in the mouse. Nature, 2016, 535, 575-579.	13.7	369
262	Identification of multi-loci hubs from 4C-seq demonstrates the functional importance of simultaneous interactions. Nucleic Acids Research, 2016, 44, 8714-8725.	6.5	47
263	Assay for transposase-accessible chromatin and circularized chromosome conformation capture, two methods to explore the regulatory landscapes of genes in zebrafish. Methods in Cell Biology, 2016, 135, 413-430.	0.5	28
264	A tissue checkpoint regulates type 2 immunity. Nature Immunology, 2016, 17, 1381-1387.	7.0	184
265	ATAC-see reveals the accessible genome by transposase-mediated imaging and sequencing. Nature Methods, 2016, 13, 1013-1020.	9.0	199
266	A Druggable TCF4- and BRD4-Dependent Transcriptional Network Sustains Malignancy in Blastic Plasmacytoid Dendritic Cell Neoplasm. Cancer Cell, 2016, 30, 764-778.	7.7	116
267	Cell freezing protocol suitable for ATAC-Seq on motor neurons derived from human induced pluripotent stem cells. Scientific Reports, 2016, 6, 25474.	1.6	49
268	SnapShot: Epigenomic Assays. Cell, 2016, 167, 1430-1430.e1.	13.5	2
269	Most brain disease-associated and eQTL haplotypes are not located within transcription factor DNase-seq footprints in brain. Human Molecular Genetics, 2016, 26, ddw369.	1.4	4
270	Chromatin accessibility maps of chronic lymphocytic leukaemia identify subtype-specific epigenome signatures and transcription regulatory networks. Nature Communications, 2016, 7, 11938.	5.8	131
271	Current and Emerging Technologies for the Analysis of the Genome-Wide and Locus-Specific DNA Methylation Patterns. Advances in Experimental Medicine and Biology, 2016, 945, 343-430.	0.8	22
272	Deregulation of DUX4 and ERG in acute lymphoblastic leukemia. Nature Genetics, 2016, 48, 1481-1489.	9.4	231
273	Local regulation of gene expression by lncRNA promoters, transcription and splicing. Nature, 2016, 539, 452-455.	13.7	1,056

#	Article	IF	Citations
274	The epigenetic landscape of T cell exhaustion. Science, 2016, 354, 1165-1169.	6.0	694
275	Epigenetic stability of exhausted T cells limits durability of reinvigoration by PD-1 blockade. Science, 2016, 354, 1160-1165.	6.0	939
276	Defining cell type with chromatin profiling. Nature Biotechnology, 2016, 34, 1126-1128.	9.4	4
277	Mechanism for DNA transposons to generate introns on genomic scales. Nature, 2016, 538, 533-536.	13.7	83
278	Genome-wide identification of Drosophila dorso-ventral enhancers by differential histone acetylation analysis. Genome Biology, 2016, 17, 196.	3.8	54
279	Genetic Ancestry and Natural Selection Drive Population Differences in Immune Responses to Pathogens. Cell, 2016, 167, 657-669.e21.	13.5	419
280	Authentication and characterisation of a new oesophageal adenocarcinoma cell line: MFD-1. Scientific Reports, 2016, 6, 32417.	1.6	20
281	Widespread Chromatin Accessibility at Repetitive Elements Links Stem Cells with Human Cancer. Cell Reports, 2016, 17, 1607-1620.	2.9	32
282	An Emerging Regulatory Landscape for Skeletal Development. Trends in Genetics, 2016, 32, 774-787.	2.9	16
283	Resolving TYK2 locus genotype-to-phenotype differences in autoimmunity. Science Translational Medicine, 2016, 8, 363ra149.	5.8	186
285	The appeasement of Doug: a synthetic approach to enhancer biology. Integrative Biology (United) Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50	0.6	42
286	Screening for Functional Non-coding Genetic Variants Using Electrophoretic Mobility Shift Assay (EMSA) and DNA-affinity Precipitation Assay (DAPA). Journal of Visualized Experiments, 2016, , .	0.2	11
287	Identifying peaks in *-seq data using shape information. BMC Bioinformatics, 2016, 17, 206.	1.2	17
288	Novel tools for primary immunodeficiency diagnosis: making a case for deep profiling. Current Opinion in Allergy and Clinical Immunology, 2016, 16, 549-556.	1.1	10
289	An enduring role for quiescent stem cells. Developmental Dynamics, 2016, 245, 718-726.	0.8	17
290	Diversity and Divergence of Dinoflagellate Histone Proteins. G3: Genes, Genomes, Genetics, 2016, 6, 397-422.	0.8	38
291	Modeling the causal regulatory network by integrating chromatin accessibility and transcriptome data. National Science Review, 2016, 3, 240-251.	4.6	14
292	Active and Inactive Enhancers Cooperate to Exert Localized and Long-Range Control of Gene Regulation. Cell Reports, 2016, 15, 2159-2169.	2.9	35

#	Article	IF	Citations
293	Microglia development follows a stepwise program to regulate brain homeostasis. Science, 2016, 353, aad8670.	6.0	911
294	Whole genome sequencing and its applications in medical genetics. Quantitative Biology, 2016, 4, 115-128.	0.3	7
295	Establishing Chromatin Regulatory Landscape during Mouse Preimplantation Development. Cell, 2016, 165, 1375-1388.	13.5	254
296	Simultaneous Pathway Activity Inference and Gene Expression Analysis Using RNA Sequencing. Cell Systems, 2016, 2, 323-334.	2.9	26
297	Smash and DASH with Cas9. Genome Biology, 2016, 17, 42.	3.8	5
298	Single-cell epigenomics: powerful new methods for understanding gene regulation and cell identity. Genome Biology, 2016, 17, 72.	3.8	253
299	A Long Noncoding RNA lincRNA-EPS Acts as a Transcriptional Brake to Restrain Inflammation. Cell, 2016, 165, 1672-1685.	13.5	399
300	Molecular functions of the transcription factors E2A and E2-2 in controlling germinal center B cell and plasma cell development. Journal of Experimental Medicine, 2016, 213, 1201-1221.	4.2	106
301	Next generation sequencing technology and genomewide data analysis: Perspectives for retinal research. Progress in Retinal and Eye Research, 2016, 55, 1-31.	7.3	58
302	The landscape of accessible chromatin in mammalian preimplantation embryos. Nature, 2016, 534, 652-657.	13.7	550
303	High-density genotyping of immune-related loci identifies new SLE risk variants in individuals with Asian ancestry. Nature Genetics, 2016, 48, 323-330.	9.4	219
304	Integration of ATAC-seq and RNA-seq identifies human alpha cell and beta cell signature genes. Molecular Metabolism, 2016, 5, 233-244.	3.0	233
305	Genome-wide nucleosome specificity and function of chromatin remodellers in ES cells. Nature, 2016, 530, 113-116.	13.7	211
306	A zebrafish melanoma model reveals emergence of neural crest identity during melanoma initiation. Science, 2016, 351, aad2197.	6.0	339
307	Multifunctional role of the transcription factor Blimp-1 in coordinating plasma cell differentiation. Nature Immunology, 2016, 17, 331-343.	7.0	284
308	Parsing the Interferon Transcriptional Network and Its Disease Associations. Cell, 2016, 164, 564-578.	13.5	250
309	Transcription factors LRF and BCL11A independently repress expression of fetal hemoglobin. Science, 2016, 351, 285-289.	6.0	260
310	Mapping nucleosome positions using DNase-seq. Genome Research, 2016, 26, 351-364.	2.4	46

#	Article	IF	Citations
311	Cis-regulatory programs in the development and evolution of vertebrate paired appendages. Seminars in Cell and Developmental Biology, 2016, 57, 31-39.	2.3	32
312	The mechanisms shaping the single-cell transcriptional landscape. Current Opinion in Genetics and Development, 2016, 37, 27-35.	1.5	7
313	Enhanced Identification of Transcriptional Enhancers Provides Mechanistic Insights into Diseases. Trends in Genetics, 2016, 32, 76-88.	2.9	87
314	Favorable genomic environments for cis-regulatory evolution: A novel theoretical framework. Seminars in Cell and Developmental Biology, 2016, 57, 2-10.	2.3	16
315	Massively parallel cis-regulatory analysis in the mammalian central nervous system. Genome Research, 2016, 26, 238-255.	2.4	106
316	Fine-mapping cellular QTLs with RASQUAL and ATAC-seq. Nature Genetics, 2016, 48, 206-213.	9.4	199
317	Recent advances in ChIP-seq analysis: from quality management to whole-genome annotation. Briefings in Bioinformatics, 2017, 18, bbw023.	3.2	107
318	Genome-Scale Analysis of Cell-Specific Regulatory Codes Using Nuclear Enzymes. Methods in Molecular Biology, 2016, 1418, 225-240.	0.4	11
319	Statistical Genomics. Methods in Molecular Biology, 2016, , .	0.4	21
320	CD44+ Cells in Head and Neck Squamous Cell Carcinoma Suppress T-Cellâ€“Mediated Immunity by Selective Constitutive and Inducible Expression of PD-L1. Clinical Cancer Research, 2016, 22, 3571-3581.	3.2	177
321	7SK-BAF axis controls pervasive transcription at enhancers. Nature Structural and Molecular Biology, 2016, 23, 231-238.	3.6	92
322	From Loci to Biology. Circulation Research, 2016, 118, 586-606.	2.0	54
323	The Histone Variant MacroH2A1.2 Is Necessary for the Activation of Muscle Enhancers and Recruitment of the Transcription Factor Pbx1. Cell Reports, 2016, 14, 1156-1168.	2.9	49
324	Foxc1 reinforces quiescence in self-renewing hair follicle stem cells. Science, 2016, 351, 613-617.	6.0	109
325	Understanding the genetic liability to schizophrenia through the neuroepigenome. Schizophrenia Research, 2016, 177, 115-124.	1.1	22
326	A single three-dimensional chromatin compartment in amphioxus indicates a stepwise evolution of vertebrate Hox bimodal regulation. Nature Genetics, 2016, 48, 336-341.	9.4	113
327	C/EBPÎ± creates elite cells for iPSC reprogramming by upregulating Klf4 and increasing the levels of Lsd1 andÂBrd4. Nature Cell Biology, 2016, 18, 371-381.	4.6	94
328	Genome-wide footprinting: ready for prime time?. Nature Methods, 2016, 13, 222-228.	9.0	66

#	Article	IF	Citations
329	Genomic footprinting. Nature Methods, 2016, 13, 213-221.	9.0	97
330	Active DNA demethylation at enhancers during the vertebrate phylotypic period. Nature Genetics, 2016, 48, 417-426.	9.4	210
331	Understanding Celiac Disease by Genomics. Trends in Genetics, 2016, 32, 295-308.	2.9	78
332	Epigenetics - A Different Way of Looking at Genetics. Epigenetics and Human Health, 2016, , .	0.2	0
333	Regulatory T cell memory. Nature Reviews Immunology, 2016, 16, 90-101.	10.6	287
334	Multiplexed analysis of chromosome conformation at vastly improved sensitivity. Nature Methods, 2016, 13, 74-80.	9.0	225
335	Toward understanding the evolution of vertebrate gene regulatory networks: comparative genomics and epigenomic approaches. Briefings in Functional Genomics, 2016, 15, 315-321.	1.3	7
336	Genetics of congenital heart disease: the contribution of the noncoding regulatory genome. Journal of Human Genetics, 2016, 61, 13-19.	1.1	52
337	Identification of plant transcription factor target sequences. Biochimica Et Biophysica Acta - Gene Regulatory Mechanisms, 2017, 1860, 21-30.	0.9	36
338	Epigenetic regulation of bone cells. Connective Tissue Research, 2017, 58, 76-89.	1.1	27
339	Landscape of monoallelic DNA accessibility in mouse embryonic stem cells and neural progenitor cells. Nature Genetics, 2017, 49, 377-386.	9.4	76
340	The transcriptional regulator Aire binds to and activates super-enhancers. Nature Immunology, 2017, 18, 263-273.	7.0	130
341	Sequencing thousands of single-cell genomes with combinatorial indexing. Nature Methods, 2017, 14, 302-308.	9.0	251
342	Single-cell epigenomic variability reveals functional cancer heterogeneity. Genome Biology, 2017, 18, 15.	3.8	92
343	Cooperative Binding of Transcription Factors Orchestrates Reprogramming. Cell, 2017, 168, 442-459.e20.	13.5	432
344	How best to identify chromosomal interactions: a comparison of approaches. Nature Methods, 2017, 14, 125-134.	9.0	124
345	Understanding Human Autoimmunity and Autoinflammation Through Transcriptomics. Annual Review of Immunology, 2017, 35, 337-370.	9.5	69
346	Immunobiology of Long Noncoding RNAs. Annual Review of Immunology, 2017, 35, 177-198.	9.5	395

#	Article	IF	Citations
347	Decreased STARD10 Expression Is Associated with Defective Insulin Secretion in Humans and Mice. American Journal of Human Genetics, 2017, 100, 238-256.	2.6	60
348	Assay for Transposaseâ€Accessible Chromatin Using Sequencing (ATACâ€seq) Data Analysis. Current Protocols in Human Genetics, 2017, 92, 20.4.1-20.4.13.	3.5	9
349	MLL-AF4 Spreading Identifies Binding Sites that Are Distinct from Super-Enhancers and that Govern Sensitivity to DOT1L Inhibition in Leukemia. Cell Reports, 2017, 18, 482-495.	2.9	69
350	Genome-wide identification of regulatory elements in Sertoli cells. Development (Cambridge), 2017, 144, 720-730.	1.2	36
351	Regulatory elements in molecular networks. Wiley Interdisciplinary Reviews: Systems Biology and Medicine, 2017, 9, e1374.	6.6	23
352	High-throughput automated microfluidic sample preparation for accurate microbial genomics. Nature Communications, 2017, 8, 13919.	5.8	81
353	Decoding transcriptional states in cancer. Current Opinion in Genetics and Development, 2017, 43, 82-92.	1.5	7
354	CpG Island Hypermethylation Mediated by DNMT3A Is a Consequence of AML Progression. Cell, 2017, 168, 801-816.e13.	13.5	177
355	Myotonic dystrophy type 1 patient-derived iPSCs for the investigation of CTG repeat instability. Scientific Reports, 2017, 7, 42522.	1.6	34
356	OTX2 Activity at Distal Regulatory Elements Shapes the Chromatin Landscape of Group 3 Medulloblastoma. Cancer Discovery, 2017, 7, 288-301.	7.7	53
357	Epigenetic characteristics of the mitotic chromosome in 1D and 3D. Critical Reviews in Biochemistry and Molecular Biology, 2017, 52, 185-204.	2.3	25
358	Topologically associated domains: a successful scaffold for the evolution of gene regulation in animals. Wiley Interdisciplinary Reviews: Developmental Biology, 2017, 6, e265.	5.9	75
359	Non-coding genetic variation in cancer. Current Opinion in Systems Biology, 2017, 1, 9-15.	1.3	42
360	High constitutive activity of a broad panel of housekeeping and tissue-specific cis-regulatory elements depends on a subset of ETS proteins. Genes and Development, 2017, 31, 399-412.	2.7	48
361	Cell Type-Specific Epigenomic Analysis Reveals a Uniquely Closed Chromatin Architecture in Mouse Rod Photoreceptors. Scientific Reports, 2017, 7, 43184.	1.6	71
362	Epigenetics of Atherosclerosis: Emerging Mechanisms and Methods. Trends in Molecular Medicine, 2017, 23, 332-347.	3.5	163
363	Epigenetic Regulation: A New Frontier for Biomedical Engineers. Annual Review of Biomedical Engineering, 2017, 19, 195-219.	5.7	135
364	Exhaustion-associated regulatory regions in CD8 ⁺ tumor-infiltrating T cells. Proceedings of the National Academy of Sciences of the United States of America, 2017, 114, E2776-E2785.	3.3	242

#	Article	IF	Citations
365	Genome-wide chromatin accessibility, DNA methylation and gene expression analysis of histone deacetylase inhibition in triple-negative breast cancer. Genomics Data, 2017, 12, 14-16.	1.3	17
366	Essential role for the transcription factor Bhlhe41 in regulating the development, self-renewal and BCR repertoire of B-1a cells. Nature Immunology, 2017, 18, 442-455.	7.0	103
367	TOP2 synergizes with BAF chromatin remodeling for both resolution and formation of facultative heterochromatin. Nature Structural and Molecular Biology, 2017, 24, 344-352.	3.6	66
368	Resolving Heart Regeneration by Replacement Histone Profiling. Developmental Cell, 2017, 40, 392-404.e5.	3.1	98
369	Critical role of IRF1 and BATF in forming chromatin landscape during type 1 regulatory cell differentiation. Nature Immunology, 2017, 18, 412-421.	7.0	103
370	Neuronal activity modifies the chromatin accessibility landscape in the adult brain. Nature Neuroscience, 2017, 20, 476-483.	7.1	218
371	Dnmt3a restrains mast cell inflammatory responses. Proceedings of the National Academy of Sciences of the United States of America, 2017, 114, E1490-E1499.	3.3	108
372	Functional characterisation of cis-regulatory elements governing dynamic Eomes expression in the early mouse embryo. Development (Cambridge), 2017, 144, 1249-1260.	1.2	32
373	Cutting Edge: Chromatin Accessibility Programs CD8 T Cell Memory. Journal of Immunology, 2017, 198, 2238-2243.	0.4	68
374	Maintenance of macrophage transcriptional programs and intestinal homeostasis by epigenetic reader SP140. Science Immunology, 2017, 2, .	5.6	54
375	Epigenomics of human CD8 T cell differentiation and aging. Science Immunology, 2017, 2, .	5.6	181
376	HLA-G: At the Interface of Maternalâ€“Fetal Tolerance. Trends in Immunology, 2017, 38, 272-286.	2.9	212
377	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.	3.3	78
378	Genetic regulatory signatures underlying islet gene expression and type 2 diabetes. Proceedings of the National Academy of Sciences of the United States of America, 2017, 114, 2301-2306.	3.3	189
379	Flicr , a long noncoding RNA, modulates Foxp3 expression and autoimmunity. Proceedings of the National Academy of Sciences of the United States of America, 2017, 114, E3472-E3480.	3.3	141
380	Chromosomal dynamics predicted by an elastic network model explains genome-wide accessibility and long-range couplings. Nucleic Acids Research, 2017, 45, 3663-3673.	6.5	24
381	Gene Regulatory Elements, Major Drivers of Human Disease. Annual Review of Genomics and Human Genetics, 2017, 18, 45-63.	2.5	115
382	Ploidy-dependent changes in the epigenome of symbiotic cells correlate with specific patterns of gene expression. Proceedings of the National Academy of Sciences of the United States of America, 2017, 114, 4543-4548.	3.3	50

#	Article	IF	Citations
383	Epithelial-Mesenchymal Micro-niches Govern Stem Cell Lineage Choices. Cell, 2017, 169, 483-496.e13.	13.5	209
384	Single-cell whole-genome analyses by Linear Amplification via Transposon Insertion (LIANTI). Science, 2017, 356, 189-194.	6.0	303
385	Sequential Response to Multiple Developmental Network Circuits Encoded in an Intronic cis-Regulatory Module of Sea Urchin hox11/13b. Cell Reports, 2017, 19, 364-374.	2.9	19
386	Stem Cell Lineage Infidelity Drives Wound Repair and Cancer. Cell, 2017, 169, 636-650.e14.	13.5	255
387	EBF2 transcriptionally regulates brown adipogenesis via the histone reader DPF3 and the BAF chromatin remodeling complex. Genes and Development, 2017, 31, 660-673.	2.7	64
388	Gene and Variant Annotation for Mendelian Disorders in the Era of Advanced Sequencing Technologies. Annual Review of Genomics and Human Genetics, 2017, 18, 229-256.	2.5	37
389	Inference of cell type specific regulatory networks on mammalian lineages. Current Opinion in Systems Biology, 2017, 2, 130-139.	1.3	16
390	Vitamin A mediates conversion of monocyte-derived macrophages into tissue-resident macrophages during alternative activation. Nature Immunology, 2017, 18, 642-653.	7.0	131
391	Biotagging of Specific Cell Populations in Zebrafish Reveals Gene Regulatory Logic Encoded in the Nuclear Transcriptome. Cell Reports, 2017, 19, 425-440.	2.9	43
392	A tiling-deletion-based genetic screen for cis-regulatory element identification in mammalian cells. Nature Methods, 2017, 14, 629-635.	9.0	217
393	ORIO (Online Resource for Integrative Omics): a web-based platform for rapid integration of next generation sequencing data. Nucleic Acids Research, 2017, 45, 5678-5690.	6.5	11
394	Metabolic and Epigenetic Coordination of T Cell and Macrophage Immunity. Immunity, 2017, 46, 714-729.	6.6	234
395	Genomic Characterization of Murine Monocytes Reveals C/EBPÎ² Transcription Factor Dependence of Ly6C â^' Cells. Immunity, 2017, 46, 849-862.e7.	6.6	233
396	Single-cell regulome data analysis by SCRAT. Bioinformatics, 2017, 33, 2930-2932.	1.8	47
397	Combining Genetic and Developmental Methods to Study Musculoskeletal Evolution in Primates. , 2017, , 175-204.		1
398	Conserved roles of mouse DUX and human DUX4 in activating cleavage-stage genes and MERVL/HERVL retrotransposons. Nature Genetics, 2017, 49, 925-934.	9.4	545
399	The Dynamic Epigenetic Landscape of the Retina During Development, Reprogramming, and Tumorigenesis. Neuron, 2017, 94, 550-568.e10.	3.8	222
400	Elevated FOXG1 and SOX2 in glioblastoma enforces neural stem cell identity through transcriptional control of cell cycle and epigenetic regulators. Genes and Development, 2017, 31, 757-773.	2.7	102

#	Article	IF	Citations
401	Donâ€™t Stop Re-healinâ€™! Cancer as an Ongoing Stem Cell Affair. Cell, 2017, 169, 563-565.	13.5	6
402	Mocap: large-scale inference of transcription factor binding sites from chromatin accessibility. Nucleic Acids Research, 2017, 45, 4315-4329.	6.5	30
403	Impact of cytosine methylation on DNA binding specificities of human transcription factors. Science, 2017, 356, .	6.0	912
404	Mll3 and Mll4 Facilitate Enhancer RNA Synthesis and Transcription from Promoters Independently of H3K4 Monomethylation. Molecular Cell, 2017, 66, 568-576.e4.	4.5	322
405	KAT-Independent Gene Regulation by Tip60 Promotes ESC Self-Renewal but Not Pluripotency. Cell Reports, 2017, 19, 671-679.	2.9	29
406	Independent evolution of genomic characters during major metazoan transitions. Developmental Biology, 2017, 427, 179-192.	0.9	30
407	Chromatin Accessibility Landscape of Cutaneous T Cell Lymphoma and Dynamic Response to HDAC Inhibitors. Cancer Cell, 2017, 32, 27-41.e4.	7.7	136
408	Transcriptional and epigenetic regulation of T cell hyporesponsiveness. Journal of Leukocyte Biology, 2017, 102, 601-615.	1.5	39
409	Microfluidics as a Strategic Player to Decipher Single-Cell Omics?. Trends in Biotechnology, 2017, 35, 713-727.	4.9	27
410	DNase I SIM: A Simplified In-Nucleus Method for DNase I Hypersensitive Site Sequencing. Methods in Molecular Biology, 2017, 1629, 141-154.	0.4	1
411	The E-Id Protein Axis Specifies Adaptive Lymphoid Cell Identity and Suppresses Thymic Innate Lymphoid Cell Development. Immunity, 2017, 46, 818-834.e4.	6.6	73
412	Chromatin states define tumour-specific T cell dysfunction and reprogramming. Nature, 2017, 545, 452-456.	13.7	643
413	Genetic advances in systemic lupus erythematosus: an update. Current Opinion in Rheumatology, 2017, 29, 423-433.	2.0	112
415	ASXL2 is essential for haematopoiesis and acts as a haploinsufficient tumour suppressor in leukemia. Nature Communications, 2017, 8, 15429.	5.8	55
416	Perspectives on Gene Regulatory Network Evolution. Trends in Genetics, 2017, 33, 436-447.	2.9	66
417	Bioinformatics Tools for Genome-Wide Epigenetic Research. Advances in Experimental Medicine and Biology, 2017, 978, 489-512.	0.8	43
418	Dynamic chromatin technologies: from individual molecules to epigenomic regulation in cells. Nature Reviews Genetics, 2017, 18, 457-472.	7.7	60
419	Emerging Chemistry Strategies for Engineering Native Chromatin. Journal of the American Chemical Society, 2017, 139, 9090-9096.	6.6	25

#	Article	IF	Citations
420	Dynamic Reorganization of Chromatin Accessibility Signatures during Dedifferentiation of Secretory Precursors into Lgr5+ Intestinal Stem Cells. Cell Stem Cell, 2017, 21, 65-77.e5.	5.2	190
421	Rare cell variability and drug-induced reprogramming as a mode of cancer drug resistance. Nature, 2017, 546, 431-435.	13.7	938
422	Hyperactivation of HUSH complex function by Charcotâ€“Marieâ€“Tooth disease mutation in MORC2. Nature Genetics, 2017, 49, 1035-1044.	9.4	105
423	Modeling gene regulation from paired expression and chromatin accessibility data. Proceedings of the National Academy of Sciences of the United States of America, 2017, 114, E4914-E4923.	3.3	167
424	Genome-Wide Identification of Basic Helixâ€“Loopâ€“Helix and NF-1 Motifs Underlying GR Binding Sites in Male Rat Hippocampus. Endocrinology, 2017, 158, 1486-1501.	1.4	24
425	Understanding nucleosome dynamics and their links to gene expression and DNA replication. Nature Reviews Molecular Cell Biology, 2017, 18, 548-562.	16.1	380
426	Bivariate Genomic Footprinting Detects Changes in Transcription Factor Activity. Cell Reports, 2017, 19, 1710-1722.	2.9	94
427	Reducing mitochondrial reads in ATAC-seq using CRISPR/Cas9. Scientific Reports, 2017, 7, 2451.	1.6	51
428	Associating cellular epigenetic models with human phenotypes. Nature Reviews Genetics, 2017, 18, 441-451.	7.7	257
429	Clonally stable VÎ² allelic choice instructs IgÎ² repertoire. Nature Communications, 2017, 8, 15575.	5.8	17
430	PHF6 regulates phenotypic plasticity through chromatin organization within lineage-specific genes. Genes and Development, 2017, 31, 973-989.	2.7	50
431	Widespread changes in nucleosome accessibility without changes in nucleosome occupancy during a rapid transcriptional induction. Genes and Development, 2017, 31, 451-462.	2.7	90
432	PI3K pathway regulates ER-dependent transcription in breast cancer through the epigenetic regulator KMT2D. Science, 2017, 355, 1324-1330.	6.0	217
433	Interplay between genetic and epigenetic mechanisms in rheumatoid arthritis. Epigenomics, 2017, 9, 493-504.	1.0	23
434	Transcription factorâ€“DNA binding: beyond binding site motifs. Current Opinion in Genetics and Development, 2017, 43, 110-119.	1.5	245
435	Open chromatin profiling of human postmortem brain infers functional roles for non-coding schizophrenia loci. Human Molecular Genetics, 2017, 26, 1942-1951.	1.4	69
436	LncFunNet: an integrated computational framework for identification of functional long noncoding RNAs in mouse skeletal muscle cells. Nucleic Acids Research, 2017, 45, e108-e108.	6.5	43
437	The DDR at telomeres lacking intact shelterin does not require substantial chromatin decompaction. Genes and Development, 2017, 31, 578-589.	2.7	54

#	Article	IF	Citations
438	Long Noncoding RNA MANTIS Facilitates Endothelial Angiogenic Function. Circulation, 2017, 136, 65-79.	1.6	196
439	Dynamic Gene Regulatory Networks of Human Myeloid Differentiation. Cell Systems, 2017, 4, 416-429.e3.	2.9	105
440	Gene bivalency at Polycomb domains regulates cranial neural crest positional identity. Science, 2017, 355, .	6.0	112
441	Epigenetic landscapes reveal transcription factors that regulate CD8+ T cell differentiation. Nature Immunology, 2017, 18, 573-582.	7.0	193
442	Microfluidics for genome-wide studies involving next generation sequencing. Biomicrofluidics, 2017, 11, 021501.	1.2	29
443	Engineered Split-TET2 Enzyme for Inducible Epigenetic Remodeling. Journal of the American Chemical Society, 2017, 139, 4659-4662.	6.6	19
444	BTBD18 Regulates a Subset of piRNA-Generating Loci through Transcription Elongation in Mice. Developmental Cell, 2017, 40, 453-466.e5.	3.1	30
445	Molecular endocrinology of vitamin D on the epigenome level. Molecular and Cellular Endocrinology, 2017, 453, 14-21.	1.6	70
446	Chd7 is indispensable for mammalian brain development through activation of a neuronal differentiation programme. Nature Communications, 2017, 8, 14758.	5.8	118
447	Variable chromatin structure revealed by in situ spatially correlated DNA cleavage mapping. Nature, 2017, 541, 237-241.	13.7	132
448	Cdx is crucial for the timing mechanism driving colinear Hox activation and defines a trunk segment in the Hox cluster topology. Developmental Biology, 2017, 422, 146-154.	0.9	65
449	A Multi-step Transcriptional and Chromatin State Cascade Underlies Motor Neuron Programming from Embryonic Stem Cells. Cell Stem Cell, 2017, 20, 205-217.e8.	5.2	86
450	Genome-Wide Insights into the Development and Function of Thermogenic Adipocytes. Trends in Endocrinology and Metabolism, 2017, 28, 104-120.	3.1	29
451	Dynamics of BAFâ€“Polycomb complex opposition on heterochromatin in normal and oncogenic states. Nature Genetics, 2017, 49, 213-222.	9.4	220
452	Transcriptional programs that control expression of the autoimmune regulator gene Aire. Nature Immunology, 2017, 18, 161-172.	7.0	81
453	DNA sequencing technologies: 2006â€“2016. Nature Protocols, 2017, 12, 213-218.	5.5	266
454	Guidance of regulatory T cell development by Satb1-dependent super-enhancer establishment. Nature Immunology, 2017, 18, 173-183.	7.0	300
455	Deep homology in the age of next-generation sequencing. Philosophical Transactions of the Royal Society B: Biological Sciences, 2017, 372, 20150475.	1.8	36

#	Article	IF	Citations
456	The histone demethylase UTX regulates the lineage-specific epigenetic program of invariant natural killer T cells. Nature Immunology, 2017, 18, 184-195.	7.0	56
457	Comparative analyses of super-enhancers reveal conserved elements in vertebrate genomes. Genome Research, 2017, 27, 259-268.	2.4	39
458	Plant NF-Y transcription factors: Key players in plant-microbe interactions, root development and adaptation to stress. Biochimica Et Biophysica Acta - Gene Regulatory Mechanisms, 2017, 1860, 645-654.	0.9	70
459	Mammalian Transcription Factor Networks: Recent Advances in Interrogating Biological Complexity. Cell Systems, 2017, 5, 319-331.	2.9	54
460	Histone H1 depletion triggers an interferon response in cancer cells via activation of heterochromatic repeats. Nucleic Acids Research, 2017, 45, 11622-11642.	6.5	46
461	Concise Review: Epigenetic Regulation of Hematopoiesis: Biological Insights and Therapeutic Applications. Stem Cells Translational Medicine, 2017, 6, 2106-2114.	1.6	26
462	Genetic and epigenetic determinants of inter-individual variability in responses to toxicants. Current Opinion in Toxicology, 2017, 6, 50-59.	2.6	11
463	Singleâ€Assay Profiling of Nucleosome Occupancy and Chromatin Accessibility. Current Protocols in Molecular Biology, 2017, 120, 21.34.1-21.34.18.	2.9	10
464	The BRAIN Initiative Cell Census Consortium: Lessons Learned toward Generating a Comprehensive Brain Cell Atlas. Neuron, 2017, 96, 542-557.	3.8	235
465	TGF-Î²-Induced Quiescence Mediates Chemoresistance of Tumor-Propagating Cells in Squamous Cell Carcinoma. Cell Stem Cell, 2017, 21, 650-664.e8.	5.2	119
466	A dynamic interplay of enhancer elements regulates Klf4 expression in naÃ¯ve pluripotency. Genes and Development, 2017, 31, 1795-1808.	2.7	49
467	Chromatin and Single-Cell RNA-Seq Profiling Reveal Dynamic Signaling and Metabolic Transitions during Human Spermatogonial Stem Cell Development. Cell Stem Cell, 2017, 21, 533-546.e6.	5.2	200
468	DMS-Seq for InÂVivo Genome-wide Mapping of Protein-DNA Interactions and Nucleosome Centers. Cell Reports, 2017, 21, 289-300.	2.9	13
469	Enhancer connectome in primary human cells identifies target genes of disease-associated DNA elements. Nature Genetics, 2017, 49, 1602-1612.	9.4	419
470	Tim-3 signaling in peripheral NK cells promotes maternal-fetal immune tolerance and alleviates pregnancy loss. Science Signaling, 2017, 10, .	1.6	82
471	Priming of lineage-specifying genes by Bcl11b is required for lineage choice in post-selection thymocytes. Nature Communications, 2017, 8, 702.	5.8	41
472	Mechanistic insights in X-chromosome inactivation. Philosophical Transactions of the Royal Society B: Biological Sciences, 2017, 372, 20160356.	1.8	59
473	Rapid Chromatin Switch in the Direct Reprogramming of Fibroblasts to Neurons. Cell Reports, 2017, 20, 3236-3247.	2.9	121

#	Article	IF	Citations
474	A Specific ChREBP and PPARÎ± Cross-Talk Is Required for the Glucose-Mediated FGF21 Response. Cell Reports, 2017, 21, 403-416.	2.9	99
475	Genome-wide mapping of DNase I hypersensitive sites in rare cell populations using single-cell DNase sequencing. Nature Protocols, 2017, 12, 2342-2354.	5.5	41
476	Online resources for studies of genome biology and epigenetics. Current Opinion in Toxicology, 2017, 6, 34-41.	2.6	0
477	The three-dimensional genome: regulating gene expression during pluripotency and development. Development (Cambridge), 2017, 144, 3646-3658.	1.2	96
478	Inflammatory memory sensitizes skin epithelial stem cells to tissue damage. Nature, 2017, 550, 475-480.	13.7	440
479	ILC1 Confer Early Host Protection at Initial Sites of Viral Infection. Cell, 2017, 171, 795-808.e12.	13.5	352
480	A shared Runx1-bound Zbtb16 enhancer directs innate and innate-like lymphoid lineage development. Nature Communications, 2017, 8, 863.	5.8	54
481	Genome-wide prediction of DNase I hypersensitivity using gene expression. Nature Communications, 2017, 8, 1038.	5.8	34
482	Rif1 promotes a repressive chromatin state to safeguard against endogenous retrovirus activation. Nucleic Acids Research, 2017, 45, 12723-12738.	6.5	49
484	Cancer-Specific Retargeting of BAF Complexes by a Prion-like Domain. Cell, 2017, 171, 163-178.e19.	13.5	350
485	The Short Isoform of BRD4 Promotes HIV-1 Latency by Engaging Repressive SWI/SNF Chromatin-Remodeling Complexes. Molecular Cell, 2017, 67, 1001-1012.e6.	4.5	99
486	Quantitative analysis of chromatin accessibility in mouse embryonic fibroblasts. Biochemical and Biophysical Research Communications, 2017, 493, 814-820.	1.0	4
487	Type I interferons and the cytokine TNF cooperatively reprogram the macrophage epigenome to promote inflammatory activation. Nature Immunology, 2017, 18, 1104-1116.	7.0	204
488	Membrane and genomic DNA dual-targeting of citrus flavonoid naringenin against Staphylococcus aureus. Integrative Biology (United Kingdom), 2017, 9, 820-829.	0.6	36
489	5-hydroxymethylcytosine accumulation in postmitotic neurons results in functional demethylation of expressed genes. Proceedings of the National Academy of Sciences of the United States of America, 2017, 114, E7812-E7821.	3.3	122
490	Fate mapping of human glioblastoma reveals an invariant stem cell hierarchy. Nature, 2017, 549, 227-232.	13.7	321
491	Concise Review: Mechanisms of Quiescent Hair Follicle Stem Cell Regulation. Stem Cells, 2017, 35, 2323-2330.	1.4	52
492	Global Inhibition with Specific Activation: How p53 and MYC Redistribute the Transcriptome in the DNA Double-Strand Break Response. Molecular Cell, 2017, 67, 1013-1025.e9.	4.5	55

#	Article	IF	Citations
493	Integration of Kinase and Calcium Signaling at the Level of Chromatin Underlies Inducible Gene Activation in T Cells. Journal of Immunology, 2017, 199, 2652-2667.	0.4	51
494	The IRF4 Gene Regulatory Module Functions as a Read-Write Integrator to Dynamically Coordinate TÂHelper Cell Fate. Immunity, 2017, 47, 481-497.e7.	6.6	104
495	Epigenetic restriction of extraembryonic lineages mirrors the somatic transition to cancer. Nature, 2017, 549, 543-547.	13.7	146
496	Profiling of Singleâ€€Cell Transcriptomes. Current Protocols in Mouse Biology, 2017, 7, 145-175.	1.2	16
497	The chromatin accessibility signature of human immune aging stems from CD8+ T cells. Journal of Experimental Medicine, 2017, 214, 3123-3144.	4.2	150
498	Nup153 Interacts with Sox2 to Enable Bimodal Gene Regulation and Maintenance of Neural Progenitor Cells. Cell Stem Cell, 2017, 21, 618-634.e7.	5.2	97
499	Mbd3/NuRD controls lymphoid cell fate and inhibits tumorigenesis by repressing a B cell transcriptional program. Journal of Experimental Medicine, 2017, 214, 3085-3104.	4.2	21
500	Sasquatch: predicting the impact of regulatory SNPs on transcription factor binding from cell- and tissue-specific DNase footprints. Genome Research, 2017, 27, 1730-1742.	2.4	33
501	DNA and Histone Modifications in Cancer Diagnosis. Cancer Drug Discovery and Development, 2017, , 533-584.	0.2	0
502	Non-coding Transcription Instructs Chromatin Folding and Compartmentalization to Dictate Enhancer-Promoter Communication and T Cell Fate. Cell, 2017, 171, 103-119.e18.	13.5	251
503	Alpha TC1 and Beta-TC-6 genomic profiling uncovers both shared and distinct transcriptional regulatory features with their primary islet counterparts. Scientific Reports, 2017, 7, 11959.	1.6	41
504	The Hox proteins Ubx and AbdA collaborate with the transcription pausing factor M1<scp>BP</scp> to regulate gene transcription. EMBO Journal, 2017, 36, 2887-2906.	3.5	29
505	MicroRNAs Induce a Permissive Chromatin Environment that Enables Neuronal Subtype-Specific Reprogramming of Adult Human Fibroblasts. Cell Stem Cell, 2017, 21, 332-348.e9.	5.2	112
506	Open Sesame: Open Chromatin Regions Shed Light onto Non-coding Risk Variants. Cell Stem Cell, 2017, 21, 285-287.	5.2	5
507	Mapping genome-wide transcription-factor binding sites using DAP-seq. Nature Protocols, 2017, 12, 1659-1672.	5.5	330
508	Immunogenomic approaches to understand the function of immune disease variants. Immunology, 2017, 152, 527-535.	2.0	5
509	p53 regulates enhancer accessibility and activity in response to DNA damage. Nucleic Acids Research, 2017, 45, 9889-9900.	6.5	61
510	Multicellular Transcriptional Analysis of Mammalian Heart Regeneration. Circulation, 2017, 136, 1123-1139.	1.6	222

#	Article	IF	Citations
511	Robust Identification of Developmentally Active Endothelial Enhancers in Zebrafish Using FANS-Assisted ATAC-Seq. Cell Reports, 2017, 20, 709-720.	2.9	62
512	At the base of colinear Hox gene expression: cis -features and trans -factors orchestrating the initial phase of Hox cluster activation. Developmental Biology, 2017, 428, 293-299.	0.9	29
513	Tissue-specific CTCFâ€“cohesin-mediated chromatin architecture delimits enhancer interactions and function in vivo. Nature Cell Biology, 2017, 19, 952-961.	4.6	179
514	CRISPR/Cas9-Mediated Scanning for Regulatory Elements Required for HPRT1 Expression via Thousands of Large, Programmed Genomic Deletions. American Journal of Human Genetics, 2017, 101, 192-205.	2.6	133
515	ASCL1 Reorganizes Chromatin to Direct Neuronal Fate and Suppress Tumorigenicity of Glioblastoma Stem Cells. Cell Stem Cell, 2017, 21, 209-224.e7.	5.2	150
516	Fusion of Regionally Specified hPSC-Derived Organoids Models Human Brain Development and Interneuron Migration. Cell Stem Cell, 2017, 21, 383-398.e7.	5.2	508
517	Mechanisms of Type 2 Diabetes Risk Loci. Current Diabetes Reports, 2017, 17, 72.	1.7	39
518	Enhancer Reprogramming Promotes Pancreatic Cancer Metastasis. Cell, 2017, 170, 875-888.e20.	13.5	339
519	UROPA: a tool for Universal RObust Peak Annotation. Scientific Reports, 2017, 7, 2593.	1.6	45
520	Prediction of Chromatin Accessibility in Gene-Regulatory Regions from Transcriptomics Data. Scientific Reports, 2017, 7, 4660.	1.6	6
521	Mapping the chromatin landscape and Blimp1 transcriptional targets that regulate trophoblast differentiation. Scientific Reports, 2017, 7, 6793.	1.6	15
522	Deacetylase activity of histone deacetylase 3 is required for productive VDJ recombination and B-cell development. Proceedings of the National Academy of Sciences of the United States of America, 2017, 114, 8608-8613.	3.3	22
523	Towards <scp>CRISPR</scp>/Cas crops â€“ bringing together genomics and genome editing. New Phytologist, 2017, 216, 682-698.	3.5	235
524	Repression of Stress-Induced LINE-1 Expression Protects Cancer Cell Subpopulations from Lethal Drug Exposure. Cancer Cell, 2017, 32, 221-237.e13.	7.7	177
525	Epigenetic effects of environmental chemicals: Insights from zebrafish. Current Opinion in Toxicology, 2017, 6, 26-33.	2.6	24
526	BLIMP1 Induces Transient Metastatic Heterogeneity in Pancreatic Cancer. Cancer Discovery, 2017, 7, 1184-1199.	7.7	53
527	Interferon-Î³ Represses M2 Gene Expression in Human Macrophages by Disassembling Enhancers Bound by the Transcription Factor MAF. Immunity, 2017, 47, 235-250.e4.	6.6	153
528	Integrated Analysis of Biopsies from Inflammatory Bowel Disease Patients Identifies SAA1 as a Link Between Mucosal Microbes with TH17 and TH22 Cells. Inflammatory Bowel Diseases, 2017, 23, 1544-1554.	0.9	31

#	Article	IF	Citations
529	Antagonistic Activities of Sox2 and Brachyury Control the Fate Choice of Neuro-Mesodermal Progenitors. Developmental Cell, 2017, 42, 514-526.e7.	3.1	139
530	Comprehensive single-cell transcriptional profiling of a multicellular organism. Science, 2017, 357, 661-667.	6.0	1,067
531	Open Chromatin Profiling in hiPSC-Derived Neurons Prioritizes Functional Noncoding Psychiatric Risk Variants and Highlights Neurodevelopmental Loci. Cell Stem Cell, 2017, 21, 305-318.e8.	5.2	106
532	Stochastics of Cellular Differentiation Explained by Epigenetics: The Case of Tâ€Cell Differentiation and Functional Plasticity. Scandinavian Journal of Immunology, 2017, 86, 184-195.	1.3	8
533	The interplay of epigenetic marks during stem cell differentiation and development. Nature Reviews Genetics, 2017, 18, 643-658.	7.7	414
534	NFIA co-localizes with PPARÎ³ and transcriptionally controls the brown fat gene program. Nature Cell Biology, 2017, 19, 1081-1092.	4.6	73
535	Characterization of noncoding regulatory DNA in the human genome. Nature Biotechnology, 2017, 35, 732-746.	9.4	79
536	Origin and differentiation of human memory CD8 T cells after vaccination. Nature, 2017, 552, 362-367.	13.7	412
537	Ancestral perinatal obesogen exposure results in a transgenerational thrifty phenotype in mice. Nature Communications, 2017, 8, 2012.	5.8	116
538	Convergence of BMI1 and CHD7 on ERK Signaling in Medulloblastoma. Cell Reports, 2017, 21, 2772-2784.	2.9	31
539	3D Chromatin Architecture of Large Plant Genomes Determined by Local A/B Compartments. Molecular Plant, 2017, 10, 1497-1509.	3.9	234
540	Chromatin Accessibility Dynamics during iPSC Reprogramming. Cell Stem Cell, 2017, 21, 819-833.e6.	5.2	180
541	Transient and Permanent Reconfiguration of Chromatin and Transcription Factor Occupancy Drive Reprogramming. Cell Stem Cell, 2017, 21, 834-845.e6.	5.2	95
542	Challenges and recommendations for epigenomics in precision health. Nature Biotechnology, 2017, 35, 1128-1132.	9.4	19
543	hnRNPK Recruits PCGF3/5-PRC1 to the Xist RNA B-Repeat to Establish Polycomb-Mediated Chromosomal Silencing. Molecular Cell, 2017, 68, 955-969.e10.	4.5	255
544	Leveraging advances in biology to design biomaterials. Nature Materials, 2017, 16, 1178-1185.	13.3	97
545	Transcription pausing regulates mouse embryonic stem cell differentiation. Stem Cell Research, 2017, 25, 250-255.	0.3	16
546	Constitutively Active SMAD2/3 Are Broad-Scope Potentiators of Transcription-Factor-Mediated Cellular Reprogramming. Cell Stem Cell, 2017, 21, 791-805.e9.	5.2	35

#	Article	IF	Citations
547	Aberrant Activation of a Gastrointestinal Transcriptional Circuit in Prostate Cancer Mediates Castration Resistance. Cancer Cell, 2017, 32, 792-806.e7.	7.7	61
548	Harnessing BET Inhibitor Sensitivity Reveals AMIGO2 as a Melanoma Survival Gene. Molecular Cell, 2017, 68, 731-744.e9.	4.5	90
549	Mapping Genome-wide Accessible Chromatin in Primary Human T Lymphocytes by ATAC-Seq. Journal of Visualized Experiments, 2017, , .	0.2	8
550	Chromatin accessibility dynamics reveal novel functional enhancers in C. elegans. Genome Research, 2017, 27, 2096-2107.	2.4	142
551	The Aryl Hydrocarbon Receptor Preferentially Marks and Promotes Gut Regulatory T Cells. Cell Reports, 2017, 21, 2277-2290.	2.9	130
552	Advancing towards a global mammalian gene regulation model through single-cell analysis and synthetic biology. Current Opinion in Biomedical Engineering, 2017, 4, 174-193.	1.8	7
553	Comparative genome analysis of programmed DNA elimination in nematodes. Genome Research, 2017, 27, 2001-2014.	2.4	94
554	A cross-species approach to identify transcriptional regulators exemplified for Dnajc22 and Hnf4a. Scientific Reports, 2017, 7, 4056.	1.6	3
555	MUC-king with HIF May Rewire Pyrimidine Biosynthesis and Curb Gemcitabine Resistance in Pancreatic Cancer. Cancer Cell, 2017, 32, 3-5.	7.7	7
556	HDAC Inhibitors Finally Open Up: Chromatin Accessibility Signatures of CTCL. Cancer Cell, 2017, 32, 1-3.	7.7	8
557	Platelet function is modified by common sequence variation in megakaryocyte super enhancers. Nature Communications, 2017, 8, 16058.	5.8	50
558	Muscle Stem Cells Undergo Extensive Clonal Drift during Tissue Growth via Meox1-Mediated Induction of G2 Cell-Cycle Arrest. Cell Stem Cell, 2017, 21, 107-119.e6.	5.2	62
559	Genome-wide Mapping of the Nucleosome Landscape by Micrococcal Nuclease and Chemical Mapping. Trends in Genetics, 2017, 33, 495-507.	2.9	34
560	Transcriptional determination and functional specificity of myeloid cells: making sense of diversity. Nature Reviews Immunology, 2017, 17, 595-607.	10.6	75
561	Omics approaches to study gene regulatory networks for development in echinoderms. Briefings in Functional Genomics, 2017, 16, 299-308.	1.3	12
562	Functional Annotation of All Salmonid Genomes (FAASG): an international initiative supporting future salmonid research, conservation and aquaculture. BMC Genomics, 2017, 18, 484.	1.2	99
563	NicE-seq: high resolution open chromatin profiling. Genome Biology, 2017, 18, 122.	3.8	45
564	Epimetheus - a multi-profile normalizer for epigenomic sequencing data. BMC Bioinformatics, 2017, 18, 259.	1.2	5

#	Article	IF	Citations
565	Modular combinatorial binding among human trans-acting factors reveals direct and indirect factor binding. BMC Genomics, 2017, 18, 45.	1.2	27
566	The Arabidopsis SWI/SNF protein BAF60 mediates seedling growth control by modulating DNA accessibility. Genome Biology, 2017, 18, 114.	3.8	53
567	Dosage compensation and sex-specific epigenetic landscape of the X chromosome in the pea aphid. Epigenetics and Chromatin, 2017, 10, 30.	1.8	34
568	Genome-Wide Temporal Profiling of Transcriptome and Open Chromatin of Early Cardiomyocyte Differentiation Derived From hiPSCs and hESCs. Circulation Research, 2017, 121, 376-391.	2.0	118
569	Assay for Transposase-Accessible Chromatin with High-Throughput Sequencing (ATAC-Seq) Protocol for Zebrafish Embryos. Methods in Molecular Biology, 2017, 1507, 59-66.	0.4	16
570	The Cartography of <scp>UV</scp>â€induced <scp>DNA</scp> Damage Formation and <scp>DNA</scp> Repair. Photochemistry and Photobiology, 2017, 93, 199-206.	1.3	26
571	DNA methylation and chromatin accessibility profiling of mouse and human fetal germ cells. Cell Research, 2017, 27, 165-183.	5.7	102
573	Computational Approaches for Mining GRO-Seq Data to Identify and Characterize Active Enhancers. Methods in Molecular Biology, 2017, 1468, 121-138.	0.4	27
574	Striatal H3K27 Acetylation Linked to Glutamatergic Gene Dysregulation in Human Heroin Abusers Holds Promise as Therapeutic Target. Biological Psychiatry, 2017, 81, 585-594.	0.7	77
575	TET proteins regulate the lineage specification and TCR-mediated expansion of iNKT cells. Nature Immunology, 2017, 18, 45-53.	7.0	108
576	Cistrome Data Browser: a data portal for ChIP-Seq and chromatin accessibility data in human and mouse. Nucleic Acids Research, 2017, 45, D658-D662.	6.5	451
577	Cell-Type-Specific Chromatin States Differentially Prime Squamous Cell Carcinoma Tumor-Initiating Cells for Epithelial to Mesenchymal Transition. Cell Stem Cell, 2017, 20, 191-204.e5.	5.2	170
578	Origin and evolution of the metazoan non-coding regulatory genome. Developmental Biology, 2017, 427, 193-202.	0.9	42
579	A novel method for predicting activity of cis-regulatory modules, based on a diverse training set. Bioinformatics, 2017, 33, 1-7.	1.8	56
580	Denoising genome-wide histone ChIP-seq with convolutional neural networks. Bioinformatics, 2017, 33, i225-i233.	1.8	48
581	A c-Myb mutant causes deregulated differentiation due to impaired histone binding and abrogated pioneer factor function. Nucleic Acids Research, 2017, 45, 7681-7696.	6.5	28
582	AP-1 Transcription Factors and the BAF Complex Mediate Signal-Dependent Enhancer Selection. Molecular Cell, 2017, 68, 1067-1082.e12.	4.5	328
583	Pathways to understanding the genomic aetiology of osteoarthritis. Human Molecular Genetics, 2017, 26, R193-R201.	1.4	38

#	Article	IF	Citations
584	Transcription factor-dependent â€˜anti-repressiveâ€™ mammalian enhancers exclude H3K27me3 from extended genomic domains. Genes and Development, 2017, 31, 2391-2404.	2.7	34
585	Developmental plasticity. Evolution, Medicine and Public Health, 2017, 2017, 162-175.	1.1	78
586	Correcting nucleotide-specific biases in high-throughput sequencing data. BMC Bioinformatics, 2017, 18, 357.	1.2	18
587	qPCR-based characterization of DNA fragmentation efficiency of Tn5 transposomes. Biology Methods and Protocols, 2017, 2, bpx001.	1.0	5
588	Functional assessment of human enhancer activities using whole-genome STARR-sequencing. Genome Biology, 2017, 18, 219.	3.8	94
589	An improved ATAC-seq protocol reduces background and enables interrogation of frozen tissues. Nature Methods, 2017, 14, 959-962.	9.0	1,653
590	Combining ATAC-seq with nuclei sorting for discovery of cis-regulatory regions in plant genomes. Nucleic Acids Research, 2017, 45, e41-e41.	6.5	231
591	How Do Plants and Phytohormones Accomplish Heterophylly, Leaf Phenotypic Plasticity, in Response to Environmental Cues. Frontiers in Plant Science, 2017, 8, 1717.	1.7	58
592	The Scope of Big Data in One Medicine: Unprecedented Opportunities and Challenges. Frontiers in Veterinary Science, 2017, 4, 194.	0.9	55
593	Identification of DNAâ€“protein Binding Sites through Multi-Scale Local Average Blocks on Sequence Information. Molecules, 2017, 22, 2079.	1.7	32
594	Molecular Techniques for DNA Methylation Studies. , 2017, , 103-139.		5
595	Microdevices for Non-Invasive Detection of Bladder Cancer. Chemosensors, 2017, 5, 30.	1.8	8
596	Gene Regulatory Network Rewiring in the Immune Cells Associated with Cancer. Genes, 2017, 8, 308.	1.0	12
597	Epigenomics of Alzheimerâ€™s Disease. , 2017, , 227-278.		2
598	Mouse Models of Human GWAS Hits for Obesity and Diabetes in the Post Genomic Era: Time for Reevaluation. Frontiers in Endocrinology, 2017, 8, 11.	1.5	9
599	Frontiers in Toxicogenomics in the Twenty-First Centuryâ€”the Grand Challenge: To Understand How the Genome and Epigenome Interact with the Toxic Environment at the Single-Cell, Whole-Organism, and Multi-Generational Level. Frontiers in Genetics, 2017, 8, 173.	1.1	6
600	T Cell Receptor and Cytokine Signaling Can Function at Different Stages to Establish and Maintain Transcriptional Memory and Enable T Helper Cell Differentiation. Frontiers in Immunology, 2017, 8, 204.	2.2	25
601	â€œMulti-Omicsâ€•Analyses of the Development and Function of Natural Killer Cells. Frontiers in Immunology, 2017, 8, 1095.	2.2	20

#	Article	IF	Citations
602	Layer-specific chromatin accessibility landscapes reveal regulatory networks in adult mouse visual cortex. ELife, 2017, 6, .	2.8	73
603	The pioneer factor OCT4 requires the chromatin remodeller BRG1 to support gene regulatory element function in mouse embryonic stem cells. ELife, 2017, 6, .	2.8	215
604	The formation of the light-sensing compartment of cone photoreceptors coincides with a transcriptional switch. ELife, 2017, 6, .	2.8	28
605	A map of human PRDM9 binding provides evidence for novel behaviors of PRDM9 and other zinc-finger proteins in meiosis. ELife, 2017, 6, .	2.8	80
606	Chromatin accessibility underlies synthetic lethality of SWI/SNF subunits in ARID1A-mutant cancers. ELife, 2017, 6, .	2.8	138
607	Krox20 hindbrain regulation incorporates multiple modes of cooperation between cis-acting elements. PLoS Genetics, 2017, 13, e1006903.	1.5	18
608	Pax7 remodels the chromatin landscape in skeletal muscle stem cells. PLoS ONE, 2017, 12, e0176190.	1.1	40
609	Identification of breast cancer associated variants that modulate transcription factor binding. PLoS Genetics, 2017, 13, e1006761.	1.5	37
610	Limb-Enhancer Genie: An accessible resource of accurate enhancer predictions in the developing limb. PLoS Computational Biology, 2017, 13, e1005720.	1.5	17
611	Open chromatin profiling identifies AP1 as a transcriptional regulator in oesophageal adenocarcinoma. PLoS Genetics, 2017, 13, e1006879.	1.5	41
612	Environmental perturbations lead to extensive directional shifts in RNA processing. PLoS Genetics, 2017, 13, e1006995.	1.5	25
613	Using omics approaches to understand pulmonary diseases. Respiratory Research, 2017, 18, 149.	1.4	90
614	Chromatin status and transcription factor binding to gonadotropin promoters in gonadotrope cell lines. Reproductive Biology and Endocrinology, 2017, 15, 86.	1.4	8
615	Topological organization and dynamic regulation of human tRNA genes during macrophage differentiation. Genome Biology, 2017, 18, 180.	3.8	27
616	McEnhancer: predicting gene expression via semi-supervised assignment of enhancers to target genes. Genome Biology, 2017, 18, 199.	3.8	27
617	Hypomethylated domain-enriched DNA motifs prepattern the accessible nucleosome organization in teleosts. Epigenetics and Chromatin, 2017, 10, 44.	1.8	11
618	Using singleâ€cell multiple omics approaches to resolve tumor heterogeneity. Clinical and Translational Medicine, 2017, 6, 46.	1.7	73
619	Assessing the model transferability for prediction of transcription factor binding sites based on chromatin accessibility. BMC Bioinformatics, 2017, 18, 355.	1.2	22

#	Article	IF	Citations
620	Epigenetic mechanisms underlying maternal diabetes-associated risk of congenital heart disease. JCI Insight, 2017, 2, .	2.3	59
621	HMCan-diff: a method to detect changes in histone modifications in cells with different genetic characteristics. Nucleic Acids Research, 2017, 45, gkw1319.	6.5	8
622	Beyond mCG. , 2017, , 81-94.		0
623	Stimulation of functional neuronal regeneration from MÃ¼ller glia in adult mice. Nature, 2017, 548, 103-107.	13.7	423
624	Epithelial-mesenchymal transition is predetermined by the epigenetic state of the skin tumor cell of origin. Stem Cell Investigation, 2017, 4, 37-37.	1.3	0
625	Strategies for the acquisition of transcriptional and epigenetic information in single cells. Journal of Thoracic Disease, 2017, 9, S9-S16.	0.6	16
626	Lineage-Determining Transcription Factor TCF-1 Initiates the Epigenetic Identity of T Cells. Immunity, 2018, 48, 243-257.e10.	6.6	164
627	Proliferation of Regulatory DNA Elements Derived from Transposable Elements in the Maize Genome. Plant Physiology, 2018, 176, 2789-2803.	2.3	71
628	The IL-4/STAT6/PPARÎ³ signaling axis is driving the expansion of the RXR heterodimer cistrome, providing complex ligand responsiveness in macrophages. Nucleic Acids Research, 2018, 46, 4425-4439.	6.5	47
629	Changes in chromatin accessibility between Arabidopsis stem cells and mesophyll cells illuminate cell typeâ€specific transcription factor networks. Plant Journal, 2018, 94, 215-231.	2.8	110
630	Functional genomics and assays of regulatory activity detect mechanisms at loci for lipid traits and coronary artery disease. Current Opinion in Genetics and Development, 2018, 50, 52-59.	1.5	5
631	Fine-Resolution Mapping of TF Binding and Chromatin Interactions. Cell Reports, 2018, 22, 2797-2807.	2.9	46
632	Pioneer transcription factors shape the epigenetic landscape. Journal of Biological Chemistry, 2018, 293, 13795-13804.	1.6	184
633	Assessing sufficiency and necessity of enhancer activities for gene expression and the mechanisms of transcription activation. Genes and Development, 2018, 32, 202-223.	2.7	171
634	Nascent Induced Pluripotent Stem Cells Efficiently Generate Entirely iPSC-Derived Mice while Expressing Differentiation-Associated Genes. Cell Reports, 2018, 22, 876-884.	2.9	12
635	Intrinsic DNA binding properties demonstrated for lineage-specifying basic helix-loop-helix transcription factors. Genome Research, 2018, 28, 484-496.	2.4	31
636	The SS18-SSX Oncoprotein Hijacks KDM2B-PRC1.1 to Drive Synovial Sarcoma. Cancer Cell, 2018, 33, 527-541.e8.	7.7	99
637	Transcript-indexed ATAC-seq for precision immune profiling. Nature Medicine, 2018, 24, 580-590.	15.2	124

#	Article	IF	Citations
638	Functional Assays to Screen and Dissect Genomic Hits. Circulation Genomic and Precision Medicine, 2018, 11, e002178.	1.6	18
639	An optimized FAIRE procedure for low cell numbers in yeast. Yeast, 2018, 35, 507-512.	0.8	4
640	Topological Arrangement of Cardiac Fibroblasts Regulates Cellular Plasticity. Circulation Research, 2018, 123, 73-85.	2.0	42
641	Computational Methods for Assessing Chromatin Hierarchy. Computational and Structural Biotechnology Journal, 2018, 16, 43-53.	1.9	22
642	TFAP2C regulates transcription in human naive pluripotency by opening enhancers. Nature Cell Biology, 2018, 20, 553-564.	4.6	134
643	CD4 Helper and CD8 Cytotoxic T Cell Differentiation. Annual Review of Immunology, 2018, 36, 579-601.	9.5	151
644	Epigenomics. Circulation Research, 2018, 122, 1191-1199.	2.0	80
645	Orientation-dependent Dxz4 contacts shape the 3D structure of the inactive X chromosome. Nature Communications, 2018, 9, 1445.	5.8	63
646	c-Maf controls immune responses by regulating disease-specific gene networks and repressing IL-2 in CD4+ T cells. Nature Immunology, 2018, 19, 497-507.	7.0	118
647	Theoretical and Applied Epigenetics in Plants. , 2018, , 265-286.		0
648	The Transcription Factor Runx3 Establishes Chromatin Accessibility of cis-Regulatory Landscapes that Drive Memory Cytotoxic T Lymphocyte Formation. Immunity, 2018, 48, 659-674.e6.	6.6	129
649	GoldiRunx and Remembering Cytotoxic Memory. Immunity, 2018, 48, 614-615.	6.6	1
650	Using Barcoded HIV Ensembles (Bâ€HIVE) for Single Provirus Transcriptomics. Current Protocols in Molecular Biology, 2018, 122, e56.	2.9	10
651	Global H3.3 dynamic deposition defines its bimodal role in cell fate transition. Nature Communications, 2018, 9, 1537.	5.8	49
652	Pluripotency factors functionally premark cell-type-restricted enhancers in ES cells. Nature, 2018, 556, 510-514.	13.7	42
653	c-Maf in CD4+ T cells: itâ€™s all about context. Nature Immunology, 2018, 19, 429-431.	7.0	5
654	Research in Computational Molecular Biology. Lecture Notes in Computer Science, 2018, , .	1.0	0
655	KLRG1+ Effector CD8+ T Cells Lose KLRG1, Differentiate into All Memory T Cell Lineages, and Convey Enhanced Protective Immunity. Immunity, 2018, 48, 716-729.e8.	6.6	300

#	Article	IF	Citations
656	How do we measure the epigenome(s)?. Multiple Sclerosis Journal, 2018, 24, 446-448.	1.4	0
657	Identification of chromatinâ€accessible domains in nonâ€alcoholic steatohepatitisâ€derived hepatocellular carcinoma. Molecular Carcinogenesis, 2018, 57, 978-987.	1.3	22
658	Chromatin Accessibility Dynamics during Chemical Induction of Pluripotency. Cell Stem Cell, 2018, 22, 529-542.e5.	5.2	75
659	A Beginnerâ€™s Guide to Analysis of RNA Sequencing Data. American Journal of Respiratory Cell and Molecular Biology, 2018, 59, 145-157.	1.4	78
660	A Common Type 2 Diabetes Risk Variant Potentiates Activity of an Evolutionarily Conserved Islet Stretch Enhancer and Increases C2CD4A and C2CD4B Expression. American Journal of Human Genetics, 2018, 102, 620-635.	2.6	47
661	Open chromatin dynamics reveals stage-specific transcriptional networks in hiPSC-based neurodevelopmental model. Stem Cell Research, 2018, 29, 88-98.	0.3	18
662	Applied RNA Bioscience. , 2018, , .		1
663	ATAC-Seq analysis reveals a widespread decrease of chromatin accessibility in age-related macular degeneration. Nature Communications, 2018, 9, 1364.	5.8	124
664	Global dynamics of stage-specific transcription factor binding during thymocyte development. Scientific Reports, 2018, 8, 5605.	1.6	13
665	Targeted in situ genome-wide profiling with high efficiency for low cell numbers. Nature Protocols, 2018, 13, 1006-1019.	5.5	572
666	Chromatin Accessibility-Based Characterization of the Gene Regulatory Network Underlying Plasmodium falciparum Blood-Stage Development. Cell Host and Microbe, 2018, 23, 557-569.e9.	5.1	135
667	SLFN11 Blocks Stressed Replication Forks Independently of ATR. Molecular Cell, 2018, 69, 371-384.e6.	4.5	177
668	Intratumor heterogeneity in epigenetic patterns. Seminars in Cancer Biology, 2018, 51, 12-21.	4.3	49
669	Visualizing transcription factor dynamics in living cells. Journal of Cell Biology, 2018, 217, 1181-1191.	2.3	159
670	Decoding the dynamic DNA methylation and hydroxymethylation landscapes in endodermal lineage intermediates during pancreatic differentiation of hESC. Nucleic Acids Research, 2018, 46, 2883-2900.	6.5	66
671	Comparative Analysis of Immune Cells Reveals a Conserved Regulatory Lexicon. Cell Systems, 2018, 6, 381-394.e7.	2.9	19
672	Single-nucleus analysis of accessible chromatin in developing mouse forebrain reveals cell-type-specific transcriptional regulation. Nature Neuroscience, 2018, 21, 432-439.	7.1	290
673	Shared genetic effects on chromatin and gene expression indicate a role for enhancer priming in immune response. Nature Genetics, 2018, 50, 424-431.	9.4	253

#	Article	IF	Citations
674	Epigenetic control of CD8+ T cell differentiation. Nature Reviews Immunology, 2018, 18, 340-356.	10.6	334
675	BRD4 Profiling Identifies Critical Chronic Lymphocytic Leukemia Oncogenic Circuits and Reveals Sensitivity to PLX51107, a Novel Structurally Distinct BET Inhibitor. Cancer Discovery, 2018, 8, 458-477.	7.7	101
676	From Genotype to Phenotype. Circulation Genomic and Precision Medicine, 2018, 11, .	1.6	16
677	Dynamic motif occupancy (DynaMO) analysis identifies transcription factors and their binding sites driving dynamic biological processes. Nucleic Acids Research, 2018, 46, e2-e2.	6.5	11
678	The Transcription Factor STAT6 Mediates Direct Repression of Inflammatory Enhancers and Limits Activation of Alternatively Polarized Macrophages. Immunity, 2018, 48, 75-90.e6.	6.6	185
679	Regulation of embryonic haematopoietic multipotency by EZH1. Nature, 2018, 553, 506-510.	13.7	70
680	Dot1 regulates nucleosome dynamics by its inherent histone chaperone activity in yeast. Nature Communications, 2018, 9, 240.	5.8	30
681	Analysis of rat cardiac myocytes and fibroblasts identifies combinatorial enhancer organization and transcription factor families. Journal of Molecular and Cellular Cardiology, 2018, 116, 91-105.	0.9	13
682	Transcriptional regulation of macrophage cholesterol efflux and atherogenesis by a long noncoding RNA. Nature Medicine, 2018, 24, 304-312.	15.2	171
683	Genomic tools for behavioural ecologists to understand repeatable individual differences in behaviour. Nature Ecology and Evolution, 2018, 2, 944-955.	3.4	97
684	Epigenetics, microbiota, and intraocular inflammation: New paradigms of immune regulation in the eye. Progress in Retinal and Eye Research, 2018, 64, 84-95.	7.3	46
685	Genetic determinants and epigenetic effects of pioneer-factor occupancy. Nature Genetics, 2018, 50, 250-258.	9.4	139
686	Pioneer factor Pax7 deploys a stable enhancer repertoire for specification of cell fate. Nature Genetics, 2018, 50, 259-269.	9.4	133
687	Microbiome Influences Prenatal and Adult Microglia in a Sex-Specific Manner. Cell, 2018, 172, 500-516.e16.	13.5	563
688	The yeast stands alone: the future of protein biologic production. Current Opinion in Biotechnology, 2018, 53, 50-58.	3.3	56
689	Nuclear receptors in cancer â€" uncovering new and evolving roles through genomic analysis. Nature Reviews Genetics, 2018, 19, 160-174.	7.7	74
690	BCG Educates Hematopoietic Stem Cells to Generate Protective Innate Immunity against Tuberculosis. Cell, 2018, 172, 176-190.e19.	13.5	802
691	Temporal Layering of Signaling Effectors Drives Chromatin Remodeling during Hair Follicle Stem Cell Lineage Progression. Cell Stem Cell, 2018, 22, 398-413.e7.	5.2	85

#	Article	IF	Citations
692	EZH2 Represses the B Cell Transcriptional Program and Regulates Antibody-Secreting Cell Metabolism and Antibody Production. Journal of Immunology, 2018, 200, 1039-1052.	0.4	99
693	Therapeutic targeting of ependymoma as informed by oncogenic enhancer profiling. Nature, 2018, 553, 101-105.	13.7	170
694	Analysis of chromatin accessibility in decidualizing human endometrial stromal cells. FASEB Journal, 2018, 32, 2467-2477.	0.2	32
695	Dynamic reorganization of open chromatin underlies diverse transcriptomes during spermatogenesis. Nucleic Acids Research, 2018, 46, 593-608.	6.5	100
696	Transcription factors orchestrate dynamic interplay between genome topology and gene regulation during cell reprogramming. Nature Genetics, 2018, 50, 238-249.	9.4	295
697	Rapid chromatin repression by Aire provides precise control of immune tolerance. Nature Immunology, 2018, 19, 162-172.	7.0	69
698	Complex Relationships between Chromatin Accessibility, Sequence Divergence, and Gene Expression in Arabidopsis thaliana. Molecular Biology and Evolution, 2018, 35, 837-854.	3.5	33
699	Lymphocytes eject interferogenic mitochondrial DNA webs in response to CpG and non-CpG oligodeoxynucleotides of class C. Proceedings of the National Academy of Sciences of the United States of America, 2018, 115, E478-E487.	3.3	100
700	The Dynamic Landscape of Open Chromatin during Human Cortical Neurogenesis. Cell, 2018, 172, 289-304.e18.	13.5	281
701	A major chromatin regulator determines resistance of tumor cells to T cellâ€“mediated killing. Science, 2018, 359, 770-775.	6.0	641
702	Long Noncoding RNA Discovery in Cardiovascular Disease. Circulation Research, 2018, 122, 155-166.	2.0	224
703	Enhanced JBrowse plugins for epigenomics data visualization. BMC Bioinformatics, 2018, 19, 159.	1.2	20
704	Towards a map of cis-regulatory sequences in the human genome. Nucleic Acids Research, 2018, 46, 5395-5409.	6.5	20
705	Chromatin analysis in human early development reveals epigenetic transition during ZGA. Nature, 2018, 557, 256-260.	13.7	241
706	Integrated Single-Cell Analysis Maps the Continuous Regulatory Landscape of Human Hematopoietic Differentiation. Cell, 2018, 173, 1535-1548.e16.	13.5	545
707	ATAC Primer Tool for targeted analysis of accessible chromatin. Nature Methods, 2018, 15, 304-305.	9.0	14
708	Bcl11b is essential for licensing Th2 differentiation during helminth infection and allergic asthma. Nature Communications, 2018, 9, 1679.	5.8	27
709	Assessing transcriptional network changes accompanying cell differentiation. Plant Journal, 2018, 94, 213-214.	2.8	0

#	Article	IF	Citations
710	Plasma cell differentiation is controlled by multiple cell division-coupled epigenetic programs. Nature Communications, 2018, 9, 1698.	5.8	93
711	Chromatin reprogramming in breast cancer. Endocrine-Related Cancer, 2018, 25, R385-R404.	1.6	17
713	Assay for Transposase Accessible Chromatin (ATAC-Seq) to Chart the Open Chromatin Landscape of Human Pancreatic Islets. Methods in Molecular Biology, 2018, 1766, 197-208.	0.4	10
714	Defining Regulatory Elements in the Human Genome Using Nucleosome Occupancy and Methylome Sequencing (NOMe-Seq). Methods in Molecular Biology, 2018, 1766, 209-229.	0.4	12
715	Evolutionary emergence of the rac3b / rfng / sgca regulatory cluster refined mechanisms for hindbrain boundaries formation. Proceedings of the National Academy of Sciences of the United States of America, 2018, 115, E3731-E3740.	3.3	26
716	Applications of Single-Cell Sequencing for Multiomics. Methods in Molecular Biology, 2018, 1754, 327-374.	0.4	18
717	Insights of Acute Lymphoblastic Leukemia with Development of Genomic Investigation. Methods in Molecular Biology, 2018, 1754, 387-413.	0.4	1
718	ERRÎ³ Preserves Brown Fat Innate Thermogenic Activity. Cell Reports, 2018, 22, 2849-2859.	2.9	30
719	A High-Throughput Mutational Scan of an Intrinsically Disordered Acidic Transcriptional Activation Domain. Cell Systems, 2018, 6, 444-455.e6.	2.9	135
720	Reshaping of the Dendritic Cell Chromatin Landscape and Interferon Pathways during HIV Infection. Cell Host and Microbe, 2018, 23, 366-381.e9.	5.1	34
721	Tagmentation on Microbeads: Restore Long-Range DNA Sequence Information Using Next Generation Sequencing with Library Prepared by Surface-Immobilized Transposomes. ACS Applied Materials & Interfaces, 2018, 10, 11539-11545.	4.0	8
722	The cis-regulatory dynamics of embryonic development at single-cell resolution. Nature, 2018, 555, 538-542.	13.7	323
723	Atrx inactivation drives disease-defining phenotypes in glioma cells of origin through global epigenomic remodeling. Nature Communications, 2018, 9, 1057.	5.8	66
724	GATA3 zinc finger 2 mutations reprogram the breast cancer transcriptional network. Nature Communications, 2018, 9, 1059.	5.8	72
725	Designer epigenome modifiers enable robust and sustained gene silencing in clinically relevant human cells. Nucleic Acids Research, 2018, 46, 4456-4468.	6.5	63
726	Genome-Wide Mapping of DNA Accessibility and Binding Sites for CREB and C/EBPÎ² in Vasopressin-Sensitive Collecting Duct Cells. Journal of the American Society of Nephrology: JASN, 2018, 29, 1490-1500.	3.0	29
727	Comprehensive, high-resolution binding energy landscapes reveal context dependencies of transcription factor binding. Proceedings of the National Academy of Sciences of the United States of America, 2018, 115, E3702-E3711.	3.3	69
728	Genome-Wide Association Studies and Heritability Estimation in the Functional Genomics Era. Population Genomics, 2018, , 361-425.	0.2	6

#	Article	IF	Citations
729	Chromium disrupts chromatin organization and CTCF access to its cognate sites in promoters of differentially expressed genes. Epigenetics, 2018, 13, 363-375.	1.3	21
730	Aging Epigenetics. , 2018, , 3-32.		7
731	A long range distal enhancer controls temporal fine-tuning of PAX6 expression in neuronal precursors. Developmental Biology, 2018, 436, 94-107.	0.9	5
732	The impact of single-cell RNA sequencing on understanding the functional organization of the immune system. Briefings in Functional Genomics, 2018, 17, 265-272.	1.3	30
733	esATAC: an easy-to-use systematic pipeline for ATAC-seq data analysis. Bioinformatics, 2018, 34, 2664-2665.	1.8	50
734	Clinical and Genomic Crosstalk between Glucocorticoid Receptor and Estrogen Receptor Î± In Endometrial Cancer. Cell Reports, 2018, 22, 2995-3005.	2.9	52
735	Universal correction of enzymatic sequence bias reveals molecular signatures of protein/DNA interactions. Nucleic Acids Research, 2018, 46, e9-e9.	6.5	39
736	Transcriptional Regulation in Prostate Cancer. Cold Spring Harbor Perspectives in Medicine, 2018, 8, a030437.	2.9	57
737	Dynamic enhancer function in the chromatin context. Wiley Interdisciplinary Reviews: Systems Biology and Medicine, 2018, 10, e1390.	6.6	18
738	The impact of epigenomic nextâ€generation sequencing approaches on our understanding of neuropsychiatric disorders. Clinical Genetics, 2018, 93, 467-480.	1.0	11
739	Profiling Developmentally and Environmentally Controlled Chromatin Reprogramming. Methods in Molecular Biology, 2018, 1675, 3-30.	0.4	1
740	Identification of Open Chromatin Regions in Plant Genomes Using ATAC-Seq. Methods in Molecular Biology, 2018, 1675, 183-201.	0.4	114
741	CD4+CD28+KIR+CD11ahi T cells correlate with disease activity and are characterized by a pro-inflammatory epigenetic and transcriptional profile in lupus patients. Journal of Autoimmunity, 2018, 86, 19-28.	3.0	21
742	Epigenetic regulation of gene expression in cancer: techniques, resources and analysis. Briefings in Functional Genomics, 2018, 17, 49-63.	1.3	111
743	MyD88-dependent dendritic and epithelial cell crosstalk orchestrates immune responses to allergens. Mucosal Immunology, 2018, 11, 796-810.	2.7	18
744	Single cell epigenome sequencing technologies. Molecular Aspects of Medicine, 2018, 59, 62-69.	2.7	30
746	Impact of DNA methylation programming on normal and pre-leukemic hematopoiesis. Seminars in Cancer Biology, 2018, 51, 89-100.	4.3	21
747	Argonaute Proteins. Methods in Molecular Biology, 2018, , .	0.4	2

#	Article	IF	Citations
748	Profiling Open Chromatin Structure in theÂOvarian Somatic Cells Using ATAC-seq. Methods in Molecular Biology, 2018, 1680, 165-177.	0.4	4
749	Lighting the shadows: methods that expose nuclear and cytoplasmic gene regulatory control. Current Opinion in Biotechnology, 2018, 49, 29-34.	3.3	8
750	Genomic Approaches to Hematology. , 2018, , 25-36.		0
751	FOXF1 Defines the Core-Regulatory Circuitry in Gastrointestinal Stromal Tumor. Cancer Discovery, 2018, 8, 234-251.	7.7	49
752	Complexity and conservation of regulatory landscapes underlie evolutionary resilience of mammalian gene expression. Nature Ecology and Evolution, 2018, 2, 152-163.	3.4	131
753	Dominant-negative SMARCA4 mutants alter the accessibility landscape of tissue-unrestricted enhancers. Nature Structural and Molecular Biology, 2018, 25, 61-72.	3.6	140
754	Integrative single-cell analysis of transcriptional and epigenetic states in the human adult brain. Nature Biotechnology, 2018, 36, 70-80.	9.4	762
755	Molecular and functional variation in iPSC-derived sensory neurons. Nature Genetics, 2018, 50, 54-61.	9.4	191
756	Profiling of Accessible Chromatin Regions across Multiple Plant Species and Cell Types Reveals Common Gene Regulatory Principles and New Control Modules. Plant Cell, 2018, 30, 15-36.	3.1	226
757	IL-10 Signaling Remodels Adipose Chromatin Architecture to Limit Thermogenesis and Energy Expenditure. Cell, 2018, 172, 218-233.e17.	13.5	142
758	Nudt21 Controls Cell Fate by Connecting Alternative Polyadenylation to Chromatin Signaling. Cell, 2018, 172, 106-120.e21.	13.5	123
759	Epigenome in Early Mammalian Development: Inheritance, Reprogramming and Establishment. Trends in Cell Biology, 2018, 28, 237-253.	3.6	158
760	STAT4 and T-bet control follicular helper T cell development in viral infections. Journal of Experimental Medicine, 2018, 215, 337-355.	4.2	89
761	Impact of regulatory variation across human iPSCs and differentiated cells. Genome Research, 2018, 28, 122-131.	2.4	114
762	Gain of function of ASXL1 truncating protein in the pathogenesis of myeloid malignancies. Blood, 2018, 131, 328-341.	0.6	133
763	Multilayer epigenetic analysis reveals novel transcription factor networks in CD8 T cells. Cellular and Molecular Immunology, 2018, 15, 199-202.	4.8	3
764	Epigenetic germline inheritance in mammals: looking to the past to understand the future. Genes, Brain and Behavior, 2018, 17, e12407.	1.1	48
765	rPCMP: robust p-value combination by multiple partitions with applications to ATAC-seq data. BMC Systems Biology, 2018, 12, 141.	3.0	0

#	Article	IF	Citations
766	HOX genes in normal, engineered and malignant hematopoiesis. International Journal of Developmental Biology, 2018, 62, 847-856.	0.3	23
767	Epigenetic and Transcriptional Regulation in the Induction, Maintenance, Heterogeneity, and Recall-Response of Effector and Memory Th2 Cells. Frontiers in Immunology, 2018, 9, 2929.	2.2	23
768	Recent advances in functional genome analysis. F1000Research, 2018, 7, 1968.	0.8	16
769	Nucleosome Positioning and Its Role in Gene Regulation in Yeast. , 2018, , .		1
770	TGFÎ² Imprinting During Activation Promotes Natural Killer Cell Cytokine Hypersecretion. Cancers, 2018, 10, 423.	1.7	38
771	Phenotype loss is associated with widespread divergence of the gene regulatory landscape in evolution. Nature Communications, 2018, 9, 4737.	5.8	51
772	A CHAF1B-Dependent Molecular Switch in Hematopoiesis and Leukemia Pathogenesis. Cancer Cell, 2018, 34, 707-723.e7.	7.7	68
773	Cytokinin modulates context-dependent chromatin accessibility through the type-B response regulators. Nature Plants, 2018, 4, 1102-1111.	4.7	44
775	Genetic variant at coronary artery disease and ischemic stroke locus 1p32.2 regulates endothelial responses to hemodynamics. Proceedings of the National Academy of Sciences of the United States of America, 2018, 115, E11349-E11358.	3.3	58
776	Single cell RNA-seq and ATAC-seq analysis of cardiac progenitor cell transition states and lineage settlement. Nature Communications, 2018, 9, 4877.	5.8	174
777	Loss of G9a preserves mutation patterns but increases chromatin accessibility, genomic instability and aggressiveness in skin tumours. Nature Cell Biology, 2018, 20, 1400-1409.	4.6	35
778	Warm up, cool down, and tearing apart in NK cell memory. Cellular and Molecular Immunology, 2018, 15, 1095-1097.	4.8	14
779	Differential open chromatin profile and transcriptomic signature define depot-specific human subcutaneous preadipocytes: primary outcomes. Clinical Epigenetics, 2018, 10, 148.	1.8	20
780	Parkinson-Associated SNCA Enhancer Variants Revealed by Open Chromatin in Mouse Dopamine Neurons. American Journal of Human Genetics, 2018, 103, 874-892.	2.6	30
781	Enhancer Architecture and Essential Core Regulatory Circuitry of Chronic Lymphocytic Leukemia. Cancer Cell, 2018, 34, 982-995.e7.	7.7	101
782	Amphioxus functional genomics and the origins of vertebrate gene regulation. Nature, 2018, 564, 64-70.	13.7	224
783	Transcriptome analyses of reprogrammed feather / scale chimeric explants revealed co-expressed epithelial gene networks during organ specification. BMC Genomics, 2018, 19, 780.	1.2	7
784	Aryl Hydrocarbon Receptor Signaling Cell Intrinsically Inhibits Intestinal Group 2 Innate Lymphoid Cell Function. Immunity, 2018, 49, 915-928.e5.	6.6	149

#	Article	IF	Citations
785	Simultaneous Profiling of DNA Accessibility and Gene Expression Dynamics with ATAC-Seq and RNA-Seq. Methods in Molecular Biology, 2018, 1819, 317-333.	0.4	18
786	Improved reference genome of Aedes aegypti informs arbovirus vector control. Nature, 2018, 563, 501-507.	13.7	426
787	Retinoic acid and BMP4 cooperate with p63 to alter chromatin dynamics during surface epithelial commitment. Nature Genetics, 2018, 50, 1658-1665.	9.4	47
788	Human retinoic acidâ€“regulated CD161+ regulatory T cells support wound repair in intestinal mucosa. Nature Immunology, 2018, 19, 1403-1414.	7.0	86
789	The Scalloped and Nerfin-1 Transcription Factors Cooperate to Maintain Neuronal Cell Fate. Cell Reports, 2018, 25, 1561-1576.e7.	2.9	31
790	33rd Annual Meeting & Pre-Conference Programs of the Society for Immunotherapy of Cancer (SITC 2018). , 2018, 6, 115.		24
791	Transcriptional and Epigenetic Regulation of Effector and Memory CD8 T Cell Differentiation. Frontiers in Immunology, 2018, 9, 2826.	2.2	112
792	The TFAP2C-Regulated OCT4 Naive Enhancer Is Involved in Human Germline Formation. Cell Reports, 2018, 25, 3591-3602.e5.	2.9	60
793	A rapid and robust method for single cell chromatin accessibility profiling. Nature Communications, 2018, 9, 5345.	5.8	188
794	An empirical Bayes test for allelic-imbalance detection in ChIP-seq. Biostatistics, 2018, 19, 546-561.	0.9	6
795	High-resolution genome-wide functional dissection of transcriptional regulatory regions and nucleotides in human. Nature Communications, 2018, 9, 5380.	5.8	117
796	Enhanced astrocyte responses are driven by a genetic risk allele associated with multiple sclerosis. Nature Communications, 2018, 9, 5337.	5.8	54
797	LXR Suppresses Inflammatory Gene Expression and Neutrophil Migration through cis-Repression and Cholesterol Efflux. Cell Reports, 2018, 25, 3774-3785.e4.	2.9	64
798	Regulatory chromatin landscape in Arabidopsis thaliana roots uncovered by coupling INTACT and ATAC-seq. Plant Methods, 2018, 14, 113.	1.9	45
799	Interleukin 2 modulates thymic-derived regulatory T cell epigenetic landscape. Nature Communications, 2018, 9, 5368.	5.8	26
800	Chromatin accessibility identifies diversity in mesenchymal stem cells from different tissue origins. Scientific Reports, 2018, 8, 17765.	1.6	29
801	Genomic and regulatory characteristics of significant transcription factors in colorectal cancer metastasis. Scientific Reports, 2018, 8, 17836.	1.6	20
802	Neuron-specific signatures in the chromosomal connectome associated with schizophrenia risk. Science, 2018, 362, .	6.0	162

#	Article	IF	Citations
803	Genomeâ€Wide Maps of Transcription Regulatory Elements and Transcription Enhancers in Development and Disease. , 2018, 9, 439-455.		12
804	Chromatin Accessibility and Interactions in the Transcriptional Regulation of T Cells. Frontiers in Immunology, 2018, 9, 2738.	2.2	36
805	Engrafted parenchymal brain macrophages differ from microglia in transcriptome, chromatin landscape and response to challenge. Nature Communications, 2018, 9, 5206.	5.8	166
806	Binding of HMGN proteins to cell specific enhancers stabilizes cell identity. Nature Communications, 2018, 9, 5240.	5.8	32
807	Genetic accommodation and the role of ancestral plasticity in the evolution of insect eusociality. Journal of Experimental Biology, 2018, 221, .	0.8	20
808	Agnostic detection of genomic alterations by holistic DNA structural interrogation. PLoS ONE, 2018, 13, e0208054.	1.1	1
809	From Pioneer to Repressor: Bimodal foxd3 Activity Dynamically Remodels Neural Crest Regulatory Landscape InÂVivo. Developmental Cell, 2018, 47, 608-628.e6.	3.1	92
810	Honey bee Royalactin unlocks conserved pluripotency pathway in mammals. Nature Communications, 2018, 9, 5078.	5.8	22
811	Megadomains and superloops form dynamically but are dispensable for X-chromosome inactivation and gene escape. Nature Communications, 2018, 9, 5004.	5.8	46
812	Comprehensively Profiling the Chromatin Architecture of Tissue Restricted Antigen Expression in Thymic Epithelial Cells Over Development. Frontiers in Immunology, 2018, 9, 2120.	2.2	17
813	High-saltâ€“recovered sequences are associated with the active chromosomal compartment and with large ribonucleoprotein complexes including nuclear bodies. Genome Research, 2018, 28, 1733-1746.	2.4	11
814	Advanced model systems and tools for basic and translational human immunology. Genome Medicine, 2018, 10, 73.	3.6	68
815	Nondestructive, base-resolution sequencing of 5-hydroxymethylcytosine using a DNA deaminase. Nature Biotechnology, 2018, 36, 1083-1090.	9.4	154
816	Enhancer and superâ€enhancer: Positive regulators in gene transcription. Animal Models and Experimental Medicine, 2018, 1, 169-179.	1.3	49
817	BRWD1 orchestrates epigenetic landscape of late B lymphopoiesis. Nature Communications, 2018, 9, 3888.	5.8	24
818	High-throughput characterization of genetic effects on DNAâ€“protein binding and gene transcription. Genome Research, 2018, 28, 1701-1708.	2.4	34
819	Transcriptional and epigenomic landscapes of CNS and non-CNS vascular endothelial cells. ELife, 2018, 7, .	2.8	180
820	Single-cell RNA-seq reveals dynamic transcriptome profiling in human early neural differentiation. GigaScience, 2018, 7, .	3.3	18

#	Article	IF	Citations
821	Young genes have distinct gene structure, epigenetic profiles, and transcriptional regulation. Genome Research, 2018, 28, 1675-1687.	2.4	57
822	Integrative Omics for Interactomes. , 2018, , 39-49.		3
823	Analysis of chromatin accessibility uncovers TEAD1 as a regulator of migration in human glioblastoma. Nature Communications, 2018, 9, 4020.	5.8	64
824	Synthetic Biology. , 2018, , .		2
825	Stage-Specific Transcription Factors Drive Astrogliogenesis by Remodeling Gene Regulatory Landscapes. Cell Stem Cell, 2018, 23, 557-571.e8.	5.2	79
826	Reprogramming normal human epithelial tissues to a common, lethal neuroendocrine cancer lineage. Science, 2018, 362, 91-95.	6.0	217
827	The methylome of the marbled crayfish links gene body methylation to stable expression of poorly accessible genes. Epigenetics and Chromatin, 2018, 11, 57.	1.8	56
828	Determinants of promoter and enhancer transcription directionality in metazoans. Nature Communications, 2018, 9, 4472.	5.8	22
829	Joint single-cell DNA accessibility and protein epitope profiling reveals environmental regulation of epigenomic heterogeneity. Nature Communications, 2018, 9, 4590.	5.8	76
830	Mechanoresponsive stem cells acquire neural crest fate in jaw regeneration. Nature, 2018, 563, 514-521.	13.7	121
831	Targeting CDK9 Reactivates Epigenetically Silenced Genes in Cancer. Cell, 2018, 175, 1244-1258.e26.	13.5	182
832	Regulation of Neuroregeneration by Long Noncoding RNAs. Molecular Cell, 2018, 72, 553-567.e5.	4.5	83
833	The chromatin accessibility landscape of primary human cancers. Science, 2018, 362, .	6.0	781
834	Bioinformatics: Sequences, Structures, Phylogeny. , 2018, , .		0
835	The adult human testis transcriptional cell atlas. Cell Research, 2018, 28, 1141-1157.	5.7	426
836	Current Trends of Microfluidic Single-Cell Technologies. International Journal of Molecular Sciences, 2018, 19, 3143.	1.8	63
837	Epigenetics and Chromatin Remodeling. , 2018, , 557-591.		0
838	The Nuclear Receptor PPARÎ³ Controls Progressive Macrophage Polarization as a Ligand-Insensitive Epigenomic Ratchet of Transcriptional Memory. Immunity, 2018, 49, 615-626.e6.	6.6	128

#	Article	IF	Citations
839	Computational Epigenomics and Its Application in Regulatory Genomics. , 2018, , 115-139.		0
840	Nervous System Regionalization Entails Axial Allocation before Neural Differentiation. Cell, 2018, 175, 1105-1118.e17.	13.5	128
841	Polymer Simulations of Heteromorphic Chromatin Predict the 3D Folding of Complex Genomic Loci. Molecular Cell, 2018, 72, 786-797.e11.	4.5	131
842	A neural network based model effectively predicts enhancers from clinical ATAC-seq samples. Scientific Reports, 2018, 8, 16048.	1.6	23
843	Distinct Regulation of Th17 and Th1 Cell Differentiation by Glutaminase-Dependent Metabolism. Cell, 2018, 175, 1780-1795.e19.	13.5	445
844	Chromatin run-on and sequencing maps the transcriptional regulatory landscape of glioblastoma multiforme. Nature Genetics, 2018, 50, 1553-1564.	9.4	108
845	The â€œcomputable eggâ€: Myth or useful concept?. Current Opinion in Systems Biology, 2018, 11, 91-97.	1.3	2
846	Med23 serves as a gatekeeper of the myeloid potential of hematopoietic stem cells. Nature Communications, 2018, 9, 3746.	5.8	5
847	A Chromatin Basis for Cell Lineage and Disease Risk in the Human Pancreas. Cell Systems, 2018, 7, 310-322.e4.	2.9	38
848	Fine-mapping and functional studies highlight potential causal variants for rheumatoid arthritis and type 1 diabetes. Nature Genetics, 2018, 50, 1366-1374.	9.4	122
849	Epigenetic mechanisms regulating T-cell responses. Journal of Allergy and Clinical Immunology, 2018, 142, 728-743.	1.5	100
850	Type 2 Diabetesâ€“Associated Genetic Variants Regulate Chromatin Accessibility in Human Islets. Diabetes, 2018, 67, 2466-2477.	0.3	44
851	Genome organization and chromatin analysis identify transcriptional downregulation of insulin-like growth factor signaling as a hallmark of aging in developing B cells. Genome Biology, 2018, 19, 126.	3.8	29
852	Insights and Implications of Genome-Wide Association Studies of Height. Journal of Clinical Endocrinology and Metabolism, 2018, 103, 3155-3168.	1.8	31
853	Epigenetic Regulation of Skin Development and Regeneration. Pancreatic Islet Biology, 2018, , .	0.1	0
854	Enhancer-Promoter Interactions and Their Role in theÂControl of Epidermal Differentiation. Contributions To Management Science, 2018, , 231-262.	0.4	0
855	Intertumoral Heterogeneity in SCLC Is Influenced by the Cell Type of Origin. Cancer Discovery, 2018, 8, 1316-1331.	7.7	123
857	The Histone Demethylase LSD1 Regulates B Cell Proliferation and Plasmablast Differentiation. Journal of Immunology, 2018, 201, 2799-2811.	0.4	43

#	Article	IF	Citations
858	Identification of the Human Skeletal Stem Cell. Cell, 2018, 175, 43-56.e21.	13.5	425
859	Necroptosis microenvironment directs lineage commitment in liver cancer. Nature, 2018, 562, 69-75.	13.7	283
860	A microfluidic device for isolating intact chromosomes from single mammalian cells and probing their folding stability by controlling solution conditions. Scientific Reports, 2018, 8, 13684.	1.6	8
861	Single Cell and Open Chromatin Analysis Reveals Molecular Origin of Epidermal Cells of the Skin. Developmental Cell, 2018, 47, 21-37.e5.	3.1	56
862	Transcription Factors Drive Tet2-Mediated Enhancer Demethylation to Reprogram Cell Fate. Cell Stem Cell, 2018, 23, 727-741.e9.	5.2	156
863	Differential IL-2 expression defines developmental fates of follicular versus nonfollicular helper T cells. Science, 2018, 361, .	6.0	173
864	Histone H4K20 methylation mediated chromatin compaction threshold ensures genome integrity by limiting DNA replication licensing. Nature Communications, 2018, 9, 3704.	5.8	83
865	Molecular diversification of regulatory T cells in nonlymphoid tissues. Science Immunology, 2018, 3, .	5.6	123
866	High-throughput chromatin accessibility profiling at single-cell resolution. Nature Communications, 2018, 9, 3647.	5.8	124
867	Mutant NPM1 Maintains the Leukemic State through HOX Expression. Cancer Cell, 2018, 34, 499-512.e9.	7.7	209
868	TET mediated epigenetic regulation of iNKT cell lineage fate choice and function. Molecular Immunology, 2018, 101, 564-573.	1.0	6
869	Epioncogene Networks: Identification of Epigenomic and Transcriptomic Cooperation by Multi-omics Integration of ChIP-Seq and RNA-Seq Data. RNA Technologies, 2018, , 129-151.	0.2	1
870	Polycomb repressive complex 1 shapes the nucleosome landscape but not accessibility at target genes. Genome Research, 2018, 28, 1494-1507.	2.4	72
871	Pioneering, chromatin remodeling, and epigenetic constraint in early T-cell gene regulation by SPI1 (PU.1). Genome Research, 2018, 28, 1508-1519.	2.4	56
872	Joint profiling of chromatin accessibility and gene expression in thousands of single cells. Science, 2018, 361, 1380-1385.	6.0	683
873	Gene regulatory network architecture in different developmental contexts influences the genetic basis of morphological evolution. PLoS Genetics, 2018, 14, e1007375.	1.5	38
874	Postnatal DNA demethylation and its role in tissue maturation. Nature Communications, 2018, 9, 2040.	5.8	56
875	Transcription Factor IRF8 Orchestrates the Adaptive Natural Killer Cell Response. Immunity, 2018, 48, 1172-1182.e6.	6.6	100

#	Article	IF	Citations
876	Inherited DNA methylation primes the establishment of accessible chromatin during genome activation. Genome Research, 2018, 28, 998-1007.	2.4	54
877	Rare-Variant Studies to Complement Genome-Wide Association Studies. Annual Review of Genomics and Human Genetics, 2018, 19, 97-112.	2.5	34
878	EchinoBase: Tools for Echinoderm Genome Analyses. Methods in Molecular Biology, 2018, 1757, 349-369.	0.4	31
879	Reprogramming of Chromatin Accessibility in Somatic Cell Nuclear Transfer Is DNA Replication Independent. Cell Reports, 2018, 23, 1939-1947.	2.9	30
880	Analysis of ChIP-Seq and RNA-Seq Data with BioWardrobe. Methods in Molecular Biology, 2018, 1783, 343-360.	0.4	11
881	Analysis of Genetically Diverse Macrophages Reveals Local and Domain-wide Mechanisms that Control Transcription Factor Binding and Function. Cell, 2018, 173, 1796-1809.e17.	13.5	165
882	Advances of DNase-seq for mapping active gene regulatory elements across the genome in animals. Gene, 2018, 667, 83-94.	1.0	20
883	Gene Expression Analysis. Methods in Molecular Biology, 2018, , .	0.4	3
884	B cell activation and plasma cell differentiation are inhibited by de novo DNA methylation. Nature Communications, 2018, 9, 1900.	5.8	94
885	Activity-dependent neuroprotective protein recruits HP1 and CHD4 to control lineage-specifying genes. Nature, 2018, 557, 739-743.	13.7	169
886	3D genome and its disorganization in diseases. Cell Biology and Toxicology, 2018, 34, 351-365.	2.4	41
887	Disruption of TET2 promotes the therapeutic efficacy of CD19-targeted T cells. Nature, 2018, 558, 307-312.	13.7	574
888	Long genes linked to autism spectrum disorders harbor broad enhancer-like chromatin domains. Genome Research, 2018, 28, 933-942.	2.4	40
889	The SS18-SSX Fusion Oncoprotein Hijacks BAF Complex Targeting and Function to Drive Synovial Sarcoma. Cancer Cell, 2018, 33, 1128-1141.e7.	7.7	169
890	Cnidarian Cell Type Diversity and Regulation Revealed by Whole-Organism Single-Cell RNA-Seq. Cell, 2018, 173, 1520-1534.e20.	13.5	284
891	Formaldehyde-assisted Isolation of Regulatory Elements to Measure Chromatin Accessibility in Mammalian Cells. Journal of Visualized Experiments, 2018, , .	0.2	15
892	Molecular and Cellular Biology of the Right Heart. , 2018, , 57-89.		1
893	Apoptotic cellâ€“induced AhR activity is required for immunological tolerance and suppression of systemic lupus erythematosus in mice and humans. Nature Immunology, 2018, 19, 571-582.	7.0	137

#	Article	IF	Citations
894	Distinct macrophage populations direct inflammatory versus physiological changes in adipose tissue. Proceedings of the National Academy of Sciences of the United States of America, 2018, 115, E5096-E5105.	3.3	280
895	Comprehensive epigenetic landscape of rheumatoid arthritis fibroblast-like synoviocytes. Nature Communications, 2018, 9, 1921.	5.8	119
896	Size-tagged preferred ends in maternal plasma DNA shed light on the production mechanism and show utility in noninvasive prenatal testing. Proceedings of the National Academy of Sciences of the United States of America, 2018, 115, E5106-E5114.	3.3	107
897	Genomics and Epigenomics of Congenital Heart Defects: Expert Review and Lessons Learned in Africa. OMICS A Journal of Integrative Biology, 2018, 22, 301-321.	1.0	18
898	Integrating ChIP-seq with other functional genomics data. Briefings in Functional Genomics, 2018, 17, 104-115.	1.3	63
899	Genome-scale identification of transcription factors that mediate an inflammatory network during breast cellular transformation. Nature Communications, 2018, 9, 2068.	5.8	24
900	A Muscle-Specific Enhancer RNA Mediates Cohesin Recruitment and Regulates Transcription In trans. Molecular Cell, 2018, 71, 129-141.e8.	4.5	126
901	ERÎ± promotes murine hematopoietic regeneration through the Ire1Î±-mediated unfolded protein response. ELife, 2018, 7, .	2.8	39
902	Integration of human pancreatic islet genomic data refines regulatory mechanisms at Type 2 Diabetes susceptibility loci. ELife, 2018, 7, .	2.8	103
903	Chromatin-associated RNA sequencing (ChAR-seq) maps genome-wide RNA-to-DNA contacts. ELife, 2018, 7, .	2.8	121
904	Tumor Cell-Intrinsic Factors Underlie Heterogeneity of Immune Cell Infiltration and Response to Immunotherapy. Immunity, 2018, 49, 178-193.e7.	6.6	502
905	An atlas of chromatin accessibility in the adult human brain. Genome Research, 2018, 28, 1243-1252.	2.4	170
906	Mouse medulloblastoma driven by CRISPR activation of cellular Myc. Scientific Reports, 2018, 8, 8733.	1.6	17
907	Epigenetics of T cell aging. Journal of Leukocyte Biology, 2018, 104, 691-699.	1.5	46
908	Type 2 Immunity. Methods in Molecular Biology, 2018, , .	0.4	1
909	CBFÎ²-SMMHC Inhibition Triggers Apoptosis by Disrupting MYC Chromatin Dynamics in Acute Myeloid Leukemia. Cell, 2018, 174, 172-186.e21.	13.5	68
910	Recovering Gene Interactions from Single-Cell Data Using Data Diffusion. Cell, 2018, 174, 716-729.e27.	13.5	1,197
911	The Tumor Suppressor ARID1A Controls Global Transcription via Pausing of RNA Polymerase II. Cell Reports, 2018, 23, 3933-3945.	2.9	83

#	Article	IF	Citations
912	Interactions between genetic variation and cellular environment in skeletal muscle gene expression. PLoS ONE, 2018, 13, e0195788.	1.1	18
913	A stable mode of bookmarking by TBP recruits RNA polymerase II to mitotic chromosomes. ELife, 2018, 7, .	2.8	92
914	A workflow for simplified analysis of ATAC-cap-seq data in R. GigaScience, 2018, 7, .	3.3	6
915	Uhrf1 regulates active transcriptional marks at bivalent domains in pluripotent stem cells through Setd1a. Nature Communications, 2018, 9, 2583.	5.8	35
916	DMSâ€seq for In Vivo Genomeâ€Wide Mapping of Proteinâ€DNA Interactions and Nucleosome Centers. Current Protocols in Molecular Biology, 2018, 123, e60.	2.9	7
917	CATaDa reveals global remodelling of chromatin accessibility during stem cell differentiation in vivo. ELife, 2018, 7, .	2.8	67
918	Library Preparation for ATAC-Sequencing of Mouse CD4+ T Cells Isolated from the Lung and Lymph Nodes After Helminth Infection. Methods in Molecular Biology, 2018, 1799, 327-340.	0.4	3
919	Single-cell epigenetics â€“ Chromatin modification atlas unveiled by mass cytometry. Clinical Immunology, 2018, 196, 40-48.	1.4	29
920	Inference of Developmental Gene Regulatory Networks Beyond Classical Model Systems: New Approaches in the Post-genomic Era. Integrative and Comparative Biology, 2018, 58, 640-653.	0.9	13
921	Direct Conversion of Mouse Fibroblasts into Neural Stem Cells by Chemical Cocktail Requires Stepwise Activation of Growth Factors and Nup210. Cell Reports, 2018, 24, 1355-1362.e3.	2.9	20
923	A Single-Cell Atlas of InÂVivo Mammalian Chromatin Accessibility. Cell, 2018, 174, 1309-1324.e18.	13.5	620
924	FACT Sets a Barrier for Cell Fate Reprogramming in Caenorhabditis elegans and Human Cells. Developmental Cell, 2018, 46, 611-626.e12.	3.1	89
925	Cicero Predicts cis-Regulatory DNA Interactions from Single-Cell Chromatin Accessibility Data. Molecular Cell, 2018, 71, 858-871.e8.	4.5	572
926	Emerging Principles of Gene Expression Programs and Their Regulation. Molecular Cell, 2018, 71, 389-397.	4.5	101
927	Age Alters Chromatin Structure and Expression of SUMO Proteins under Stress Conditions in Human Adipose-Derived Stem Cells. Scientific Reports, 2018, 8, 11502.	1.6	17
928	Application of MNase-Seq in the Global Mapping of Nucleosome Positioning in Plants. Methods in Molecular Biology, 2018, 1830, 353-366.	0.4	6
929	Epigenetic control of innate and adaptive immune memory. Nature Immunology, 2018, 19, 963-972.	7.0	217
930	The SUMO protease SENP1 and the chromatin remodeler CHD3 interact and jointly affect chromatin accessibility and gene expression. Journal of Biological Chemistry, 2018, 293, 15439-15454.	1.6	14

#	Article	IF	Citations
931	Evaluation of chromatin accessibility in prefrontal cortex of individuals with schizophrenia. Nature Communications, 2018, 9, 3121.	5.8	141
932	Canonical PRC2 function is essential for mammary gland development and affects chromatin compaction in mammary organoids. PLoS Biology, 2018, 16, e2004986.	2.6	10
933	The hackers teaching old DNA sequencers new tricks. Nature, 2018, 559, 643-645.	13.7	8
935	Genome-Scale Oscillations in DNA Methylation during Exit from Pluripotency. Cell Systems, 2018, 7, 63-76.e12.	2.9	70
936	A droplet microfluidic platform for efficient enzymatic chromatin digestion enables robust determination of nucleosome positioning. Lab on A Chip, 2018, 18, 2583-2592.	3.1	13
937	Genome-Wide Mapping of DNase I Hypersensitive Sites in Tomato. Methods in Molecular Biology, 2018, 1830, 367-379.	0.4	2
938	Pioneer Factors in Animals and Plantsâ€"Colonizing Chromatin for Gene Regulation. Molecules, 2018, 23, 1914.	1.7	18
939	ATAC2GRN: optimized ATAC-seq and DNase1-seq pipelines for rapid and accurate genome regulatory network inference. BMC Genomics, 2018, 19, 563.	1.2	19
940	Establishment of regulatory elements during erythro-megakaryopoiesis identifies hematopoietic lineage-commitment points. Epigenetics and Chromatin, 2018, 11, 22.	1.8	49
941	Bioinformatic Analysis of Nucleosome and Histone Variant Positioning. Methods in Molecular Biology, 2018, 1832, 185-203.	0.4	1
942	Regulatory Architecture of the LÎ²T2 Gonadotrope Cell Underlying the Response to Gonadotropin-Releasing Hormone. Frontiers in Endocrinology, 2018, 9, 34.	1.5	15
943	Brain-Resident Microglia and Blood-Borne Macrophages Orchestrate Central Nervous System Inflammation in Neurodegenerative Disorders and Brain Cancer. Frontiers in Immunology, 2018, 9, 697.	2.2	164
944	Bioinformatics of Epigenomic Data Generated From Next-Generation Sequencing. , 2018, , 65-106.		4
945	Diversity matters: combinatorial information coding by GABAA receptor subunits during spatial learning and its allosteric modulation. Cellular Signalling, 2018, 50, 142-159.	1.7	5
946	The Peripheral and Intratumoral Immune Cell Landscape in Cancer Patients: A Proxy for Tumor Biology and a Tool for Outcome Prediction. Biomedicines, 2018, 6, 25.	1.4	19
947	Different chromatin and DNA sequence characteristics define glucocorticoid receptor binding sites that are blocked or not blocked by coregulator Hic-5. PLoS ONE, 2018, 13, e0196965.	1.1	8
948	Genetic determinants of co-accessible chromatin regions in activated T cells across humans. Nature Genetics, 2018, 50, 1140-1150.	9.4	139
949	NKX3-1 is required for induced pluripotent stem cell reprogramming and can replace OCT4 in mouse and human iPSC induction. Nature Cell Biology, 2018, 20, 900-908.	4.6	37

#	Article	IF	Citations
950	Single-cell mapping of the thymic stroma identifies IL-25-producing tuft epithelial cells. Nature, 2018, 559, 622-626.	13.7	235
951	GIVE: portable genome browsers for personal websites. Genome Biology, 2018, 19, 92.	3.8	15
952	Arid1a restrains Kras-dependent changes in acinar cell identity. ELife, 2018, 7, .	2.8	39
953	TCR signal strength controls thymic differentiation of iNKT cell subsets. Nature Communications, 2018, 9, 2650.	5.8	79
954	Single-Cell Multi-omics: An Engine for New Quantitative Models of Gene Regulation. Trends in Genetics, 2018, 34, 653-665.	2.9	86
955	Chromatin Accessibility Impacts Transcriptional Reprogramming in Oocytes. Cell Reports, 2018, 24, 304-311.	2.9	50
956	GRHL2-Dependent Enhancer Switching Maintains a Pluripotent Stem Cell Transcriptional Subnetwork after Exit from Naive Pluripotency. Cell Stem Cell, 2018, 23, 226-238.e4.	5.2	87
957	Prospective Isolation of Poised iPSC Intermediates Reveals Principles of Cellular Reprogramming. Cell Stem Cell, 2018, 23, 289-305.e5.	5.2	60
958	Epigenetic regulation in development: is the mouse a good model for the human?. Human Reproduction Update, 2018, 24, 556-576.	5.2	99
959	A common pattern of DNase I footprinting throughout the human mtDNA unveils clues for a chromatin-like organization. Genome Research, 2018, 28, 1158-1168.	2.4	15
960	OX40 Costimulation Inhibits Foxp3 Expression and Treg Induction via BATF3-Dependent and Independent Mechanisms. Cell Reports, 2018, 24, 607-618.	2.9	79
961	Characterization of the accessible genome in the human malaria parasite Plasmodium falciparum. Nucleic Acids Research, 2018, 46, 9414-9431.	6.5	50
962	Single Copy Transgene Integration in a Transcriptionally Active Site for Recombinant Protein Synthesis. Biotechnology Journal, 2018, 13, e1800226.	1.8	24
963	Functional Dissection of the Enhancer Repertoire in Human Embryonic Stem Cells. Cell Stem Cell, 2018, 23, 276-288.e8.	5.2	151
964	Direct reprogramming of fibroblasts into neural stem cells by single non-neural progenitor transcription factor Ptf1a. Nature Communications, 2018, 9, 2865.	5.8	72
965	Zbtb7a is a transducer for the control of promoter accessibility by NF-kappa B and multiple other transcription factors. PLoS Biology, 2018, 16, e2004526.	2.6	39
966	Single-Cell (Multi)omics Technologies. Annual Review of Genomics and Human Genetics, 2018, 19, 15-41.	2.5	149
967	Transcription start site profiling uncovers divergent transcription and enhancer-associated RNAs in Drosophila melanogaster. BMC Genomics, 2018, 19, 157.	1.2	34

#	Article	IF	Citations
968	The start of a human life program. Journal of Genetics and Genomics, 2018, 45, 183-184.	1.7	0
969	TrawlerWeb: an online de novo motif discovery tool for next-generation sequencing datasets. BMC Genomics, 2018, 19, 238.	1.2	12
970	Genetic risk for Alzheimerâ€™s disease is concentrated in specific macrophage and microglial transcriptional networks. Genome Medicine, 2018, 10, 14.	3.6	83
971	Thinking BIG rheumatology: how to make functional genomics data work for you. Arthritis Research and Therapy, 2018, 20, 29.	1.6	4
972	UTX-mediated enhancer and chromatin remodeling suppresses myeloid leukemogenesis through noncatalytic inverse regulation of ETS and GATA programs. Nature Genetics, 2018, 50, 883-894.	9.4	117
973	Vitamin D Switches BAF Complexes to Protect Î² Cells. Cell, 2018, 173, 1135-1149.e15.	13.5	162
974	Translating GWAS in rheumatic disease: approaches to establishing mechanism and function for genetic associations with ankylosing spondylitis. Briefings in Functional Genomics, 2018, 17, 308-318.	1.3	6
975	Enhancer Logic and Mechanics in Development and Disease. Trends in Cell Biology, 2018, 28, 608-630.	3.6	146
976	Allele-specific control of replication timing and genome organization during development. Genome Research, 2018, 28, 800-811.	2.4	63
977	SALP, a new single-stranded DNA library preparation method especially useful for the high-throughput characterization of chromatin openness states. BMC Genomics, 2018, 19, 143.	1.2	20
978	ATACseqQC: a Bioconductor package for post-alignment quality assessment of ATAC-seq data. BMC Genomics, 2018, 19, 169.	1.2	153
979	NOTCH-mediated non-cell autonomous regulation of chromatin structure during senescence. Nature Communications, 2018, 9, 1840.	5.8	57
980	Vitamin D and Chromatin. , 2018, , 217-225.		0
981	Selective gene dependencies in MYCN-amplified neuroblastoma include the core transcriptional regulatory circuitry. Nature Genetics, 2018, 50, 1240-1246.	9.4	199
982	Control of inducible gene expression links cohesin to hematopoietic progenitor self-renewal and differentiation. Nature Immunology, 2018, 19, 932-941.	7.0	175
983	Patterns of chromatin accessibility along the anterior-posterior axis in the early Drosophila embryo. PLoS Genetics, 2018, 14, e1007367.	1.5	38
984	GUAVA: A Graphical User Interface for the Analysis and Visualization of ATAC-seq Data. Frontiers in Genetics, 2018, 9, 250.	1.1	15
985	ChromTime: modeling spatio-temporal dynamics of chromatin marks. Genome Biology, 2018, 19, 109.	3.8	10

#	Article	IF	Citations
986	Cooperation, cis-interactions, versatility and evolutionary plasticity of multiple cis-acting elements underlie krox20 hindbrain regulation. PLoS Genetics, 2018, 14, e1007581.	1.5	21
987	Polycomb complexes associate with enhancers and promote oncogenic transcriptional programs in cancer through multiple mechanisms. Nature Communications, 2018, 9, 3377.	5.8	112
988	Differential analysis of chromatin accessibility and histone modifications for predicting mouse developmental enhancers. Nucleic Acids Research, 2018, 46, 11184-11201.	6.5	36
989	JunB defines functional and structural integrity of the epidermo-pilosebaceous unit in the skin. Nature Communications, 2018, 9, 3425.	5.8	26
990	Endocrine lineage biases arise in temporally distinct endocrine progenitors during pancreatic morphogenesis. Nature Communications, 2018, 9, 3356.	5.8	67
991	Human cardiac cis-regulatory elements, their cognate transcription factors, and regulatory DNA sequence variants. Genome Research, 2018, 28, 1577-1588.	2.4	25
992	Combinatorial Smad2/3 Activities Downstream of Nodal Signaling Maintain Embryonic/Extra-Embryonic Cell Identities during Lineage Priming. Cell Reports, 2018, 24, 1977-1985.e7.	2.9	31
993	Lamin B1 mapping reveals the existence of dynamic and functional euchromatin lamin B1 domains. Nature Communications, 2018, 9, 3420.	5.8	66
994	Trac-looping measures genome structure and chromatin accessibility. Nature Methods, 2018, 15, 741-747.	9.0	74
995	Enhancer Activity Requires CBP/P300 Bromodomain-Dependent Histone H3K27 Acetylation. Cell Reports, 2018, 24, 1722-1729.	2.9	231
996	Sex Hormones Regulate Innate Immune Cells and Promote Sex Differences in Respiratory Virus Infection. Frontiers in Immunology, 2018, 9, 1653.	2.2	123
997	TRPS1 shapes YAP/TEAD-dependent transcription in breast cancer cells. Nature Communications, 2018, 9, 3115.	5.8	58
998	Whole-genome bisulfite sequencing with improved accuracy and cost. Genome Research, 2018, 28, 1364-1371.	2.4	64
999	Epigenetic Reprogramming with Antisense Oligonucleotides Enhances the Effectiveness of Androgen Receptor Inhibition in Castration-Resistant Prostate Cancer. Cancer Research, 2018, 78, 5731-5740.	0.4	40
1000	Foxd1 is required for terminal differentiation of anterior hypothalamic neuronal subtypes. Developmental Biology, 2018, 439, 102-111.	0.9	28
1001	The transcription factor Grainy head primes epithelial enhancers for spatiotemporal activation by displacing nucleosomes. Nature Genetics, 2018, 50, 1011-1020.	9.4	122
1002	Comprehensive comparative analysis of 5â€²-end RNA-sequencing methods. Nature Methods, 2018, 15, 505-511.	9.0	90
1003	Gastrointestinal stromal tumor enhancers support a transcription factor network predictive of clinical outcome. Proceedings of the National Academy of Sciences of the United States of America, 2018, 115, E5746-E5755.	3.3	20

#	Article	IF	Citations
1004	TCR Transgenic Mice Reveal Stepwise, Multi-site Acquisition of the Distinctive Fat-Treg Phenotype. Cell, 2018, 174, 285-299.e12.	13.5	165
1005	Sex reversal following deletion of a single distal enhancer of Sox9. Science, 2018, 360, 1469-1473.	6.0	189
1006	Transcriptomic immune profiling of ovarian cancers in paraneoplastic cerebellar degeneration associated with anti-Yo antibodies. British Journal of Cancer, 2018, 119, 105-113.	2.9	15
1007	HSV-1-induced disruption of transcription termination resembles a cellular stress response but selectively increases chromatin accessibility downstream of genes. PLoS Pathogens, 2018, 14, e1006954.	2.1	71
1008	Analyzing Circulating Tumor Cells One at a Time. Trends in Cell Biology, 2018, 28, 764-775.	3.6	37
1009	SETBP1 induces transcription of a network of development genes by acting as an epigenetic hub. Nature Communications, 2018, 9, 2192.	5.8	66
1010	From Identification to Function: Current Strategies to Prioritise and Follow-Up GWAS Results. Methods in Molecular Biology, 2018, 1793, 259-275.	0.4	2
1011	An integrated global regulatory network of hematopoietic precursor cell self-renewal and differentiation. Integrative Biology (United Kingdom), 2018, 10, 390-405.	0.6	4
1012	A noncanonical PPARÎ³/RXRÎ±-binding sequence regulates leptin expression in response to changes in adipose tissue mass. Proceedings of the National Academy of Sciences of the United States of America, 2018, 115, E6039-E6047.	3.3	27
1013	Spt6 Association with RNA Polymerase II Directs mRNA Turnover During Transcription. Molecular Cell, 2018, 70, 1054-1066.e4.	4.5	38
1014	Transcriptional regulatory control of mammalian nephron progenitors revealed by multi-factor cistromic analysis and genetic studies. PLoS Genetics, 2018, 14, e1007181.	1.5	40
1015	Dual Requirement of CHD8 for Chromatin Landscape Establishment and Histone Methyltransferase Recruitment to Promote CNS Myelination and Repair. Developmental Cell, 2018, 45, 753-768.e8.	3.1	112
1016	Transcription Factor PU.1 Represses and Activates Gene Expression in Early T Cells by Redirecting Partner Transcription Factor Binding. Immunity, 2018, 48, 1119-1134.e7.	6.6	83
1017	Mammary molecular portraits reveal lineage-specific features and progenitor cell vulnerabilities. Journal of Cell Biology, 2018, 217, 2951-2974.	2.3	35
1018	Contribution of noncoding pathogenic variants to RPGRIP1-mediated inherited retinal degeneration. Genetics in Medicine, 2019, 21, 694-704.	1.1	27
1019	Assay for Transposase-Accessible Chromatin-Sequencing Using Xenopus Embryos. Cold Spring Harbor Protocols, 2019, 2019, pdb.prot098327.	0.2	10
1020	Genome-Wide Scanning of Gene Expression. , 2019, , 452-462.		0
1021	ATAC-pipe: general analysis of genome-wide chromatin accessibility. Briefings in Bioinformatics, 2019, 20, 1934-1943.	3.2	25

#	Article	IF	Citations
1022	Chromatin regulation in complex brain disorders. Current Opinion in Behavioral Sciences, 2019, 25, 57-65.	2.0	20
1023	Mapping histone modifications in low cell number and single cells using antibody-guided chromatin tagmentation (ACT-seq). Nature Communications, 2019, 10, 3747.	5.8	111
1024	PAX8 activates metabolic genes via enhancer elements in Renal Cell Carcinoma. Nature Communications, 2019, 10, 3739.	5.8	49
1025	PAX5 is part of a functional transcription factor network targeted in lymphoid leukemia. PLoS Genetics, 2019, 15, e1008280.	1.5	33
1026	ARID1A and PI3-kinase pathway mutations in the endometrium drive epithelial transdifferentiation and collective invasion. Nature Communications, 2019, 10, 3554.	5.8	96
1027	Genetic Variation in Long-Range Enhancers. Current Topics in Behavioral Neurosciences, 2019, 42, 35-50.	0.8	2
1028	Blood stem cell-forming haemogenic endothelium in zebrafish derives from arterial endothelium. Nature Communications, 2019, 10, 3577.	5.8	37
1029	Quantitative modelling predicts the impact of DNA methylation on RNA polymerase II traffic. Proceedings of the National Academy of Sciences of the United States of America, 2019, 116, 14995-15000.	3.3	42
1030	Biochemical analysis of nucleosome targeting by Tn5 transposase. Open Biology, 2019, 9, 190116.	1.5	14
1031	Detect accessible chromatin using ATAC-sequencing, from principle to applications. Hereditas, 2019, 156, 29.	0.5	49
1032	Beyond the Exome: The Non-coding Genome and Enhancers in Neurodevelopmental Disorders and Malformations of Cortical Development. Frontiers in Cellular Neuroscience, 2019, 13, 352.	1.8	53
1033	Cryptic activation of an Irf8 enhancer governs cDC1 fate specification. Nature Immunology, 2019, 20, 1161-1173.	7.0	100
1034	BindSpace decodes transcription factor binding signals by large-scale sequence embedding. Nature Methods, 2019, 16, 858-861.	9.0	28
1035	HNF4 factors control chromatin accessibility and are redundantly required for maturation of the fetal intestine. Development (Cambridge), 2019, 146, .	1.2	22
1036	A 50 year history of technologies that drove discovery in eukaryotic transcription regulation. Nature Structural and Molecular Biology, 2019, 26, 777-782.	3.6	30
1037	Interconversion between Tumorigenic and Differentiated States in Acute Myeloid Leukemia. Cell Stem Cell, 2019, 25, 258-272.e9.	5.2	60
1038	Dissection of acute stimulus-inducible nucleosome remodeling in mammalian cells. Genes and Development, 2019, 33, 1159-1174.	2.7	27
1039	Pluripotency reprogramming by competent and incompetent POU factors uncovers temporal dependency for Oct4 and Sox2. Nature Communications, 2019, 10, 3477.	5.8	60

#	Article	IF	Citations
1040	C/EBPÎ± mediates the growth inhibitory effect of progestins on breast cancer cells. EMBO Journal, 2019, 38, e101426.	3.5	15
1041	Functional genetic variants can mediate their regulatory effects through alteration of transcription factor binding. Nature Communications, 2019, 10, 3472.	5.8	39
1042	Massively parallel single-cell chromatin landscapes of human immune cell development and intratumoral T cell exhaustion. Nature Biotechnology, 2019, 37, 925-936.	9.4	622
1043	The role of chromatin dynamics under global warming response in the symbiotic coral model Aiptasia. Communications Biology, 2019, 2, 282.	2.0	24
1044	KDM2 proteins constrain transcription from CpG island gene promoters independently of their histone demethylase activity. Nucleic Acids Research, 2019, 47, 9005-9023.	6.5	26
1045	Biased gene retention during diploidization in Brassica linked to three-dimensional genome organization. Nature Plants, 2019, 5, 822-832.	4.7	52
1046	Slc6a8-Mediated Creatine Uptake and Accumulation Reprogram Macrophage Polarization via Regulating Cytokine Responses. Immunity, 2019, 51, 272-284.e7.	6.6	121
1047	Global prediction of chromatin accessibility using small-cell-number and single-cell RNA-seq. Nucleic Acids Research, 2019, 47, e121-e121.	6.5	24
1048	Chromatin Remodeling in Response to BRCA2-Crisis. Cell Reports, 2019, 28, 2182-2193.e6.	2.9	6
1049	Activation of PDGF pathway links LMNA mutation to dilated cardiomyopathy. Nature, 2019, 572, 335-340.	13.7	136
1050	Chromatin Profiles of Chromosomally Integrated Human Herpesvirus-6A. Frontiers in Microbiology, 2019, 10, 1408.	1.5	22
1051	Integrating regulatory DNA sequence and gene expression to predict genome-wide chromatin accessibility across cellular contexts. Bioinformatics, 2019, 35, i108-i116.	1.8	54
1052	Cloudy with a Chance of Insights: Context Dependent Gene Regulation and Implications for Evolutionary Studies. Genes, 2019, 10, 492.	1.0	21
1053	Single-Cell Epigenomics: Technology and Applications. , 2019, , 215-229.		10
1054	Pioneer and repressive functions of p63 during zebrafish embryonic ectoderm specification. Nature Communications, 2019, 10, 3049.	5.8	39
1055	SET Domainâ€“Containing Protein 4 Epigenetically Controls Breast Cancer Stem Cell Quiescence. Cancer Research, 2019, 79, 4729-4743.	0.4	41
1056	Chemical genomics reveals histone deacetylases are required for core regulatory transcription. Nature Communications, 2019, 10, 3004.	5.8	107
1057	Matrix stiffness induces a tumorigenic phenotype in mammary epithelium through changes in chromatin accessibility. Nature Biomedical Engineering, 2019, 3, 1009-1019.	11.6	135

#	Article	IF	Citations
1058	Study of database application for human open chromatin regions from ATAC-seq. AIP Conference Proceedings, 2019, , .	0.3	1
1059	Epigenetic Regulation at the Interplay Between Gut Microbiota and Host Metabolism. Frontiers in Genetics, 2019, 10, 638.	1.1	116
1060	Low-Affinity Binding Sites and the Transcription Factor Specificity Paradox in Eukaryotes. Annual Review of Cell and Developmental Biology, 2019, 35, 357-379.	4.0	144
1061	FOXA2 Is Required for Enhancer Priming during Pancreatic Differentiation. Cell Reports, 2019, 28, 382-393.e7.	2.9	111
1062	From insects to mammals: regulation of genome architecture in neural development. Current Opinion in Neurobiology, 2019, 59, 146-156.	2.0	3
1063	A Single-Cell Transcriptomic Atlas of Human Neocortical Development during Mid-gestation. Neuron, 2019, 103, 785-801.e8.	3.8	361
1064	Satb1 integrates DNA binding site geometry and torsional stress to differentially target nucleosome-dense regions. Nature Communications, 2019, 10, 3221.	5.8	33
1065	Super-enhancers: critical roles and therapeutic targets in hematologic malignancies. Journal of Hematology and Oncology, 2019, 12, 77.	6.9	69
1066	GemC1 is a critical switch for neural stem cell generation in the postnatal brain. Glia, 2019, 67, 2360-2373.	2.5	23
1067	Genomeâ€Wide Measurement and Computational Analysis of Transcription Factor Binding and Chromatin Accessibility in Lymphocytes. Current Protocols in Immunology, 2019, 126, e84.	3.6	0
1068	Single-cell lineage tracing by endogenous mutations enriched in transposase accessible mitochondrial DNA. ELife, 2019, 8, .	2.8	93
1069	Microfluidic epigenomic mapping technologies for precision medicine. Lab on A Chip, 2019, 19, 2630-2650.	3.1	11
1070	Therapeutic Ligands Antagonize Estrogen Receptor Function by Impairing Its Mobility. Cell, 2019, 178, 949-963.e18.	13.5	131
1071	IFN-Î³ selectively suppresses a subset of TLR4-activated genes and enhancers to potentiate macrophage activation. Nature Communications, 2019, 10, 3320.	5.8	71
1072	A Mutation in Histone H2B Represents a New Class of Oncogenic Driver. Cancer Discovery, 2019, 9, 1438-1451.	7.7	65
1073	Vitamin Câ€“dependent lysine demethylase 6 (KDM6)-mediated demethylation promotes a chromatin state that supports the endothelial-to-hematopoietic transition. Journal of Biological Chemistry, 2019, 294, 13657-13670.	1.6	35
1074	Genome-wide discovery of the daily transcriptome, DNA regulatory elements and transcription factor occupancy in the monarch butterfly brain. PLoS Genetics, 2019, 15, e1008265.	1.5	26
1075	Arabidopsis SWR1-associated protein methyl-CpG-binding domain 9 is required for histone H2A.Z deposition. Nature Communications, 2019, 10, 3352.	5.8	60

#	Article	IF	Citations
1076	Pre-marked chromatin and transcription factor co-binding shape the pioneering activity of Foxa2. Nucleic Acids Research, 2019, 47, 9069-9086.	6.5	65
1077	An integrative genomic analysis of the Longshanks selection experiment for longer limbs in mice. ELife, 2019, 8, .	2.8	58
1078	Functional dissection of the Sox9â€“Kcnj2 locus identifies nonessential and instructive roles of TAD architecture. Nature Genetics, 2019, 51, 1263-1271.	9.4	223
1079	Epigenetic Regulation Of Axon Regeneration and Glial Activation in Injury Responses. Frontiers in Genetics, 2019, 10, 640.	1.1	25
1080	Interplay between FACT subunit SPT16 and TRIM33 can remodel chromatin at macrophage distal regulatory elements. Epigenetics and Chromatin, 2019, 12, 46.	1.8	7
1081	The Magnitude of IFN-Î³ Responses Is Fine-Tuned by DNA Architecture and the Non-coding Transcript of Ifng-as1. Molecular Cell, 2019, 75, 1229-1242.e5.	4.5	58
1082	Estrogen-independent molecular actions of mutant estrogen receptor 1 in endometrial cancer. Genome Research, 2019, 29, 1429-1441.	2.4	27
1083	Epigenomics and Single-Cell Sequencing Define a Developmental Hierarchy in Langerhans Cell Histiocytosis. Cancer Discovery, 2019, 9, 1406-1421.	7.7	42
1084	Human pancreatic islet three-dimensional chromatin architecture provides insights into the genetics of type 2 diabetes. Nature Genetics, 2019, 51, 1137-1148.	9.4	208
1085	Avian Genomics in Animal Breeding and the End of the Model Organism. , 2019, , 21-67.		3
1086	DOT1L inhibition reveals a distinct subset of enhancers dependent on H3K79 methylation. Nature Communications, 2019, 10, 2803.	5.8	99
1087	Rate-oriented trans-omics: integration of multiple omic data on the basis of reaction kinetics. Current Opinion in Systems Biology, 2019, 15, 109-120.	1.3	9
1088	Chromatin organization in the female mouse brain fluctuates across the oestrous cycle. Nature Communications, 2019, 10, 2851.	5.8	68
1089	Epigenetic programming underpins B cell dysfunction in human SLE. Nature Immunology, 2019, 20, 1071-1082.	7.0	142
1090	Single cell RNA-Seq reveals pre-cDCs fate determined by transcription factor combinatorial dose. BMC Molecular and Cell Biology, 2019, 20, 20.	1.0	18
1091	Long-read sequencing unveils IGH-DUX4 translocation into the silenced IGH allele in B-cell acute lymphoblastic leukemia. Nature Communications, 2019, 10, 2789.	5.8	14
1092	TOX transcriptionally and epigenetically programs CD8+ T cell exhaustion. Nature, 2019, 571, 211-218.	13.7	934
1093	Mouse cytomegalovirus-experienced ILC1s acquire a memory response dependent on the viral glycoprotein m12. Nature Immunology, 2019, 20, 1004-1011.	7.0	75

#	Article	IF	Citations
1094	Chromatin Architecture as an Essential Determinant of Dendritic Cell Function. Frontiers in Immunology, 2019, 10, 1119.	2.2	14
1095	Characterization of Transcriptional Regulatory Networks that Promote and Restrict Identities and Functions of Intestinal Innate Lymphoid Cells. Immunity, 2019, 51, 185-197.e6.	6.6	72
1096	Pioneer Factor-Nucleosome Binding Events during Differentiation Are Motif Encoded. Molecular Cell, 2019, 75, 562-575.e5.	4.5	98
1097	HAT1 Coordinates Histone Production and Acetylation via H4 Promoter Binding. Molecular Cell, 2019, 75, 711-724.e5.	4.5	55
1098	Context-Specific Transcription Factor Functions Regulate Epigenomic and Transcriptional Dynamics during Cardiac Reprogramming. Cell Stem Cell, 2019, 25, 87-102.e9.	5.2	89
1099	Conserved NPPB + Border Zone Switches From MEF2- to AP-1â€“Driven Gene Program. Circulation, 2019, 140, 864-879.	1.6	70
1100	Mapping chromatin modifications at the single cell level. Development (Cambridge), 2019, 146, .	1.2	38
1101	Identification of an Intronic Regulatory Element Necessary for Tissue-Specific Expression of Foxn1 in Thymic Epithelial Cells. Journal of Immunology, 2019, 203, 686-695.	0.4	17
1102	Genomic architecture of Shh dependent cochlear morphogenesis. Development (Cambridge), 2019, 146, .	1.2	19
1103	Identification and Massively Parallel Characterization of Regulatory Elements Driving Neural Induction. Cell Stem Cell, 2019, 25, 713-727.e10.	5.2	76
1104	Reconstruction of the Global Neural Crest Gene Regulatory Network InÂVivo. Developmental Cell, 2019, 51, 255-276.e7.	3.1	108
1105	Going low to reach high: Smallâ€scale ChIPâ€seq maps new terrain. Wiley Interdisciplinary Reviews: Systems Biology and Medicine, 2020, 12, e1465.	6.6	8
1106	IRF2 is a master regulator of human keratinocyte stem cell fate. Nature Communications, 2019, 10, 4676.	5.8	25
1107	Understanding P. falciparum Asymptomatic Infections: A Proposition for a Transcriptomic Approach. Frontiers in Immunology, 2019, 10, 2398.	2.2	27
1108	A genome-wide assessment of the ancestral neural crest gene regulatory network. Nature Communications, 2019, 10, 4689.	5.8	46
1109	Transcriptional Atlas of Intestinal Immune Cells Reveals that Neuropeptide Î±-CGRP Modulates Group 2 Innate Lymphoid Cell Responses. Immunity, 2019, 51, 696-708.e9.	6.6	154
1110	Jump ahead with a twist: DNA acrobatics drive transposition forward. Current Opinion in Structural Biology, 2019, 59, 168-177.	2.6	12
1111	Cellular reprogramming for successful CNS axon regeneration is driven by a temporally changing cast of transcription factors. Scientific Reports, 2019, 9, 14198.	1.6	28

#	Article	IF	Citations
1112	Dynamic enhancers control skeletal muscle identity and reprogramming. PLoS Biology, 2019, 17, e3000467.	2.6	34
1113	SCALE method for single-cell ATAC-seq analysis via latent feature extraction. Nature Communications, 2019, 10, 4576.	5.8	162
1114	Inference of transcription factor binding from cell-free DNA enables tumor subtype prediction and early detection. Nature Communications, 2019, 10, 4666.	5.8	146
1115	Signal Integration and Transcriptional Regulation of the Inflammatory Response Mediated by the GM-/M-CSF Signaling Axis in Human Monocytes. Cell Reports, 2019, 29, 860-872.e5.	2.9	29
1116	Data Integration in Poplar: â€˜Omics Layers and Integration Strategies. Frontiers in Genetics, 2019, 10, 874.	1.1	15
1117	The impact of proinflammatory cytokines on the Î²-cell regulatory landscape provides insights into the genetics of type 1 diabetes. Nature Genetics, 2019, 51, 1588-1595.	9.4	117
1118	Identification and dynamic quantification of regulatory elements using total RNA. Genome Research, 2019, 29, 1836-1846.	2.4	102
1119	Omics Approaches to Understanding Muscle Biology. , 2019, , .		3
1120	Developmental Evolution: Downsizing Wings in the Flightless Emu. Current Biology, 2019, 29, R1131-R1133.	1.8	2
1121	Regulation of CHD2 expression by the Chaserr long noncoding RNA gene is essential for viability. Nature Communications, 2019, 10, 5092.	5.8	71
1122	A Breath of Fresh Air: Opening up the Lung Cancer Genome. Cancer Research, 2019, 79, 4808-4810.	0.4	0
1123	Intron 1â€“Mediated Regulation of EGFR Expression in EGFR-Dependent Malignancies Is Mediated by AP-1 and BET Proteins. Molecular Cancer Research, 2019, 17, 2208-2220.	1.5	10
1124	Batf Pioneers the Reorganization of Chromatin in Developing Effector T Cells via Ets1-Dependent Recruitment of Ctcf. Cell Reports, 2019, 29, 1203-1220.e7.	2.9	63
1125	Long-range Pitx2c enhancerâ€“promoter interactions prevent predisposition to atrial fibrillation. Proceedings of the National Academy of Sciences of the United States of America, 2019, 116, 22692-22698.	3.3	46
1126	<scp>ATRX</scp> loss induces telomere dysfunction and necessitates induction of alternative lengthening of telomeres during human cell immortalization. EMBO Journal, 2019, 38, e96659.	3.5	71
1127	Histone modifications and their regulatory roles in plant development and environmental memory. Journal of Genetics and Genomics, 2019, 46, 467-476.	1.7	76
1128	Absolute nucleosome occupancy map for the Saccharomyces cerevisiae genome. Genome Research, 2019, 29, 1996-2009.	2.4	71
1129	Chromatin dynamics enable transcriptional rhythms in the cnidarian Nematostella vectensis. PLoS Genetics, 2019, 15, e1008397.	1.5	9

#	Article	IF	Citations
1130	B4GALT1 Is a New Candidate to Maintain the Stemness of Lung Cancer Stem Cells. Journal of Clinical Medicine, 2019, 8, 1928.	1.0	13
1131	ANISEED 2019: 4D exploration of genetic data for an extended range of tunicates. Nucleic Acids Research, 2020, 48, D668-D675.	6.5	30
1132	Genome-wide CRISPR Screens in T Helper Cells Reveal Pervasive Crosstalk between Activation and Differentiation. Cell, 2019, 176, 882-896.e18.	13.5	135
1133	Shox2 regulates osteogenic differentiation and pattern formation during hard palate development in mice. Journal of Biological Chemistry, 2019, 294, 18294-18305.	1.6	17
1134	Enhancer Dysfunction in 3D Genome and Disease. Cells, 2019, 8, 1281.	1.8	15
1135	Coordinate regulation ofELF5andEHFat the chr11p13 CF modifier region. Journal of Cellular and Molecular Medicine, 2019, 23, 7726-7740.	1.6	12
1136	Complex Phenotypes: Mechanisms Underlying Variation in Human Stature. Current Osteoporosis Reports, 2019, 17, 301-323.	1.5	11
1137	Pioneer and nonpioneer factor cooperation drives lineage specific chromatin opening. Nature Communications, 2019, 10, 3807.	5.8	100
1138	Bcl11b prevents catastrophic autoimmunity by controlling multiple aspects of a regulatory T cell gene expression program. Science Advances, 2019, 5, eaaw0706.	4.7	15
1139	Identification of a pituitary ERÎ±-activated enhancer triggering the expression of Nr5a1, the earliest gonadotrope lineage-specific transcription factor. Epigenetics and Chromatin, 2019, 12, 48.	1.8	12
1140	IL-2 production by self-reactive CD4 thymocytes scales regulatory T cell generation in the thymus. Journal of Experimental Medicine, 2019, 216, 2466-2478.	4.2	62
1141	Bhlhe40 and Bhlhe41 transcription factors regulate alveolar macrophage selfâ€renewal and identity. EMBO Journal, 2019, 38, e101233.	3.5	68
1142	Antiâ€“B-cell Maturation Antigen Chimeric Antigen Receptor T cell Function against Multiple Myeloma Is Enhanced in the Presence of Lenalidomide. Molecular Cancer Therapeutics, 2019, 18, 2246-2257.	1.9	61
1143	The ChAHP Complex Counteracts Chromatin Looping at CTCF Sites that Emerged from SINE Expansions in Mouse. Cell, 2019, 178, 1437-1451.e14.	13.5	118
1145	Broad Heterochromatic Domains Open in Gonocyte Development Prior to De Novo DNA Methylation. Developmental Cell, 2019, 51, 21-34.e5.	3.1	26
1146	Immediate and deferred epigenomic signatures of in vivo neuronal activation in mouse hippocampus. Nature Neuroscience, 2019, 22, 1718-1730.	7.1	114
1147	Engineered triple inhibitory receptor resistance improves anti-tumor CAR-T cell performance via CD56. Nature Communications, 2019, 10, 4109.	5.8	72
1148	A Unique Epigenomic Landscape Defines Human Erythropoiesis. Cell Reports, 2019, 28, 2996-3009.e7.	2.9	41

#	Article	IF	Citations
1149	CUT&RUNTools: a flexible pipeline for CUT&RUN processing and footprint analysis. Genome Biology, 2019, 20, 192.	3.8	83
1150	Tet inactivation disrupts YY1 binding and long-range chromatin interactions during embryonic heart development. Nature Communications, 2019, 10, 4297.	5.8	44
1151	A mass spectrometry-based assay using metabolic labeling to rapidly monitor chromatin accessibility of modified histone proteins. Scientific Reports, 2019, 9, 13613.	1.6	32
1152	Evolutionary flexibility in flooding response circuitry in angiosperms. Science, 2019, 365, 1291-1295.	6.0	101
1153	Mitochondrial Reprogramming Underlies Resistance to BCL-2 Inhibition in Lymphoid Malignancies. Cancer Cell, 2019, 36, 369-384.e13.	7.7	224
1154	Maternal pluripotency factors initiate extensive chromatin remodelling to predefine first response to inductive signals. Nature Communications, 2019, 10, 4269.	5.8	45
1155	Î±-Ketoglutarate links p53 to cell fate during tumour suppression. Nature, 2019, 573, 595-599.	13.7	187
1156	Integrative analysis from the epigenome to translatome uncovers patterns of dominant nuclear regulation during transient stress. Plant Cell, 2019, 31, tpc.00463.2019.	3.1	53
1157	A systematic sequencing-based approach for microbial contaminant detection and functional inference. BMC Biology, 2019, 17, 72.	1.7	13
1158	The BACH1â€“HMOX1 Regulatory Axis Is Indispensable for Proper Macrophage Subtype Specification and Skeletal Muscle Regeneration. Journal of Immunology, 2019, 203, 1532-1547.	0.4	22
1159	Mapping the Lineage Relationship between CXCR5+ and CXCR5â^' CD4+ T Cells in HIV-Infected Human Lymph Nodes. Cell Reports, 2019, 28, 3047-3060.e7.	2.9	17
1160	Nucleosome Dynamics: a new tool for the dynamic analysis of nucleosome positioning. Nucleic Acids Research, 2019, 47, 9511-9523.	6.5	12
1161	Evolution, Origin of Life, Concepts and Methods. , 2019, , .		4
1162	Identifying clusters of cis-regulatory elements underpinning TAD structures and lineage-specific regulatory networks. Genome Research, 2019, 29, 1733-1743.	2.4	19
1163	Phosphoinositide 3-Kinase Signaling Can Modulate MHC Class I and II Expression. Molecular Cancer Research, 2019, 17, 2395-2409.	1.5	36
1164	EvoChromo: towards a synthesis of chromatin biology and evolution. Development (Cambridge), 2019, 146, .	1.2	16
1165	The RIPK4â€“IRF6 signalling axis safeguards epidermal differentiation and barrier function. Nature, 2019, 574, 249-253.	13.7	51
1166	EpiSAFARI: sensitive detection of valleys in epigenetic signals for enhancing annotations of functional elements. Bioinformatics, 2020, 36, 1014-1021.	1.8	1

#	Article	IF	Citations
1167	CommonMind Consortium provides transcriptomic and epigenomic data for Schizophrenia and Bipolar Disorder. Scientific Data, 2019, 6, 180.	2.4	149
1168	Comparing Sensory Organs to Define the Path for Hair Cell Regeneration. Annual Review of Cell and Developmental Biology, 2019, 35, 567-589.	4.0	26
1169	Adipose Tissue Gene Expression Associations Reveal Hundreds of Candidate Genes for Cardiometabolic Traits. American Journal of Human Genetics, 2019, 105, 773-787.	2.6	45
1170	Dynamic Incorporation of Histone H3 Variants into Chromatin Is Essential for Acquisition of Aggressive Traits and Metastatic Colonization. Cancer Cell, 2019, 36, 402-417.e13.	7.7	69
1171	Chromatin-informed inference of transcriptional programs in gynecologic and basal breast cancers. Nature Communications, 2019, 10, 4369.	5.8	18
1172	The RNA Helicase DDX6 Controls Cellular Plasticity by Modulating P-Body Homeostasis. Cell Stem Cell, 2019, 25, 622-638.e13.	5.2	82
1173	Liver-Derived Signals Sequentially Reprogram Myeloid Enhancers to Initiate and Maintain Kupffer Cell Identity. Immunity, 2019, 51, 655-670.e8.	6.6	234
1174	Mitochondrial calcium exchange links metabolism with the epigenome to control cellular differentiation. Nature Communications, 2019, 10, 4509.	5.8	93
1175	Unique and assay specific features of NOMe-, ATAC- and DNase I-seq data. Nucleic Acids Research, 2019, 47, 10580-10596.	6.5	31
1176	LSD1 Cooperates with Noncanonical NF-Î¹B Signaling to Regulate Marginal Zone B Cell Development. Journal of Immunology, 2019, 203, 1867-1881.	0.4	12
1177	Smarcb1 maintains the cellular identity and the chromatin landscapes of mouse embryonic stem cells. Biochemical and Biophysical Research Communications, 2019, 519, 705-713.	1.0	4
1178	Ikaros prevents autoimmunity by controlling anergy and Toll-like receptor signaling in B cells. Nature Immunology, 2019, 20, 1517-1529.	7.0	52
1179	CD103hi Treg cells constrain lung fibrosis induced by CD103lo tissue-resident pathogenic CD4 T cells. Nature Immunology, 2019, 20, 1469-1480.	7.0	80
1180	Epigenomic signatures underpin the axonal regenerative ability of dorsal root ganglia sensory neurons. Nature Neuroscience, 2019, 22, 1913-1924.	7.1	71
1181	Functional interpretation of genetic variants using deep learning predicts impact on chromatin accessibility and histone modification. Nucleic Acids Research, 2019, 47, 10597-10611.	6.5	39
1182	Genome-wide analysis of chromatin accessibility using ATAC-seq. Methods in Cell Biology, 2019, 151, 219-235.	0.5	50
1183	Building Transcription Factor Binding Site Models to Understand Gene Regulation in Plants. Molecular Plant, 2019, 12, 743-763.	3.9	71
1184	An integrated chromatin accessibility and transcriptome landscape of human pre-implantation embryos. Nature Communications, 2019, 10, 364.	5.8	82

#	Article	IF	Citations
1185	Small-molecule targeting of brachyury transcription factor addiction in chordoma. Nature Medicine, 2019, 25, 292-300.	15.2	120
1186	High Quality ATAC-Seq Data Recovered from Cryopreserved Breast Cell Lines and Tissue. Scientific Reports, 2019, 9, 516.	1.6	26
1187	From Genotype to Phenotype: Through Chromatin. Genes, 2019, 10, 76.	1.0	31
1188	Combined chemosensitivity and chromatin profiling prioritizes drug combinations in CLL. Nature Chemical Biology, 2019, 15, 232-240.	3.9	34
1189	Deconvolution of single-cell multi-omics layers reveals regulatory heterogeneity. Nature Communications, 2019, 10, 470.	5.8	156
1190	Leveraging chromatin accessibility for transcriptional regulatory network inference in T Helper 17 Cells. Genome Research, 2019, 29, 449-463.	2.4	87
1191	Using ATAC-seq and RNA-seq to increase resolution in GRN connectivity. Methods in Cell Biology, 2019, 151, 115-126.	0.5	19
1192	TFAP2C- and p63-Dependent Networks Sequentially Rearrange Chromatin Landscapes to Drive Human Epidermal Lineage Commitment. Cell Stem Cell, 2019, 24, 271-284.e8.	5.2	76
1193	De Novo PITX1 Expression Controls Bi-Stable Transcriptional Circuits to Govern Self-Renewal and Differentiation in Squamous Cell Carcinoma. Cell Stem Cell, 2019, 24, 390-404.e8.	5.2	31
1194	Mitotic chromosome binding predicts transcription factor properties in interphase. Nature Communications, 2019, 10, 487.	5.8	77
1195	The role of systems biology approaches in determining molecular signatures for the development of more effective vaccines. Expert Review of Vaccines, 2019, 18, 253-267.	2.0	18
1196	Revolutionizing Cancer Immunology: The Power of Next-Generation Sequencing Technologies. Cancer Immunology Research, 2019, 7, 168-173.	1.6	10
1197	High-throughput ChIPmentation: freely scalable, single day ChIPseq data generation from very low cell-numbers. BMC Genomics, 2019, 20, 59.	1.2	30
1198	Chromatin accessibility and the regulatory epigenome. Nature Reviews Genetics, 2019, 20, 207-220.	7.7	1,112
1199	The cis-Regulatory Atlas of the Mouse Immune System. Cell, 2019, 176, 897-912.e20.	13.5	315
1200	Encounters across networks: Windows into principles of genomic regulation. Marine Genomics, 2019, 44, 3-12.	0.4	3
1201	Multi-study inference of regulatory networks for more accurate models of gene regulation. PLoS Computational Biology, 2019, 15, e1006591.	1.5	67
1202	SMARCA4 loss is synthetic lethal with CDK4/6 inhibition in non-small cell lung cancer. Nature Communications, 2019, 10, 557.	5.8	125

#	Article	IF	Citations
1203	Genomic Enhancers in Brain Health and Disease. Genes, 2019, 10, 43.	1.0	53
1204	ATAC-seq reveals alterations in open chromatin in pancreatic islets from subjects with type 2 diabetes. Scientific Reports, 2019, 9, 7785.	1.6	51
1205	Development of circulating CD4⁺ Tâ€cell memory. Immunology and Cell Biology, 2019, 97, 617-624.	1.0	12
1206	The Open Chromatin Landscape of Nonâ€“Small Cell Lung Carcinoma. Cancer Research, 2019, 79, 4840-4854.	0.4	24
1207	Cold stress induces enhanced chromatin accessibility and bivalent histone modifications H3K4me3 and H3K27me3 of active genes in potato. Genome Biology, 2019, 20, 123.	3.8	119
1208	Open Chromatin Profiling in Adipose Tissue Marks Genomic Regions with Functional Roles in Cardiometabolic Traits. G3: Genes, Genomes, Genetics, 2019, 9, 2521-2533.	0.8	19
1209	Single-Cell Sequencing in Precision Medicine. Cancer Treatment and Research, 2019, 178, 237-252.	0.2	19
1210	What functional genomics has taught us about transcriptional regulation in malaria parasites. Briefings in Functional Genomics, 2019, 18, 290-301.	1.3	23
1211	Epigenetic activation and memory at a TGFB2 enhancer in systemic sclerosis. Science Translational Medicine, 2019, 11, .	5.8	47
1212	Accelerating Climate Resilient Plant Breeding by Applying Next-Generation Artificial Intelligence. Trends in Biotechnology, 2019, 37, 1217-1235.	4.9	134
1213	Epigenetic signature of PD-1+ TCF1+ CD8 T cells that act as resource cells during chronic viral infection and respond to PD-1 blockade. Proceedings of the National Academy of Sciences of the United States of America, 2019, 116, 14113-14118.	3.3	157
1214	HMMRATAC: a Hidden Markov ModeleR for ATAC-seq. Nucleic Acids Research, 2019, 47, e91-e91.	6.5	67
1215	Emerging Roles of p53 Related lncRNAs in Cancer Progression: A Systematic Review. International Journal of Biological Sciences, 2019, 15, 1287-1298.	2.6	51
1216	Droplet-based combinatorial indexing for massive-scale single-cell chromatin accessibility. Nature Biotechnology, 2019, 37, 916-924.	9.4	315
1217	Glucose Metabolism Drives Histone Acetylation Landscape Transitions that Dictate Muscle Stem Cell Function. Cell Reports, 2019, 27, 3939-3955.e6.	2.9	94
1218	refTSS: A Reference Data Set for Human and Mouse Transcription Start Sites. Journal of Molecular Biology, 2019, 431, 2407-2422.	2.0	72
1219	Distinct structural classes of activating FOXA1 alterations in advanced prostate cancer. Nature, 2019, 571, 413-418.	13.7	192
1220	Nonhistone human chromatin protein PC4 is critical for genomic integrity and negatively regulates autophagy. FEBS Journal, 2019, 286, 4422-4442.	2.2	15

#	Article	IF	Citations
1221	XL-DNase-seq: improved footprinting of dynamic transcription factors. Epigenetics and Chromatin, 2019, 12, 30.	1.8	9
1222	Robust hematopoietic specification requires the ubiquitous Sp1 and Sp3 transcription factors. Epigenetics and Chromatin, 2019, 12, 33.	1.8	21
1223	Dedifferentiation by adenovirus E1A due to inactivation of Hippo pathway effectors YAP and TAZ. Genes and Development, 2019, 33, 828-843.	2.7	25
1224	Mendelian Randomization Analysis Reveals a Causal Influence of Circulating Sclerostin Levels on Bone Mineral Density and Fractures. Journal of Bone and Mineral Research, 2019, 34, 1824-1836.	3.1	24
1225	Heterogeneity and fate choice: T cell exhaustion in cancer and chronic infections. Current Opinion in Immunology, 2019, 58, 98-103.	2.4	83
1226	2-hydroxyglutarate inhibits MyoD-mediated differentiation by preventing H3K9 demethylation. Proceedings of the National Academy of Sciences of the United States of America, 2019, 116, 12851-12856.	3.3	28
1227	The Poly(C) Motif in the Proximal Promoter Region of the D Site-Binding Protein Gene (Dbp) Drives Its High-Amplitude Oscillation. Molecular and Cellular Biology, 2019, 39, .	1.1	6
1228	Transcriptional States and Chromatin Accessibility Underlying Human Erythropoiesis. Cell Reports, 2019, 27, 3228-3240.e7.	2.9	122
1229	Lens differentiation is characterized by stage-specific changes in chromatin accessibility correlating with differentiation state-specific gene expression. Developmental Biology, 2019, 453, 86-104.	0.9	16
1230	TCF-1 limits the formation of Tc17 cells via repression of the MAFâ€“RORÎ³t axis. Journal of Experimental Medicine, 2019, 216, 1682-1699.	4.2	48
1231	Crunch: integrated processing and modeling of ChIP-seq data in terms of regulatory motifs. Genome Research, 2019, 29, 1164-1177.	2.4	7
1232	Phosphorylation of histone H3.3 at serine 31 promotes p300 activity and enhancer acetylation. Nature Genetics, 2019, 51, 941-946.	9.4	110
1233	Chromatin modification and remodeling in schizophrenia. , 2019, , 303-330.		1
1234	A guide to visualizing the spatial epigenome with superâ€resolution microscopy. FEBS Journal, 2019, 286, 3095-3109.	2.2	18
1235	NOMePlot: analysis of DNA methylation and nucleosome occupancy at the single molecule. Scientific Reports, 2019, 9, 8140.	1.6	3
1236	Sox7Regulates Lineage Decisions in Cardiovascular Progenitor Cells. Stem Cells and Development, 2019, 28, 1089-1103.	1.1	13
1237	Endodermal Maternal Transcription Factors Establish Super-Enhancers during Zygotic Genome Activation. Cell Reports, 2019, 27, 2962-2977.e5.	2.9	31
1238	methyl-ATAC-seq measures DNA methylation at accessible chromatin. Genome Research, 2019, 29, 969-977.	2.4	32

#	Article	IF	Citations
1239	Functional impacts of non-coding RNA processing on enhancer activity and target gene expression. Journal of Molecular Cell Biology, 2019, 11, 868-879.	1.5	15
1240	BarkBase: Epigenomic Annotation of Canine Genomes. Genes, 2019, 10, 433.	1.0	25
1241	Epidermal stem cell lineages. Advances in Stem Cells and Their Niches, 2019, 3, 31-72.	0.1	1
1242	Reverse geneâ€“environment interaction approach to identify variants influencing body-mass index in humans. Nature Metabolism, 2019, 1, 630-642.	5.1	14
1243	KLRG1 and NKp46 discriminate subpopulations of human CD117+CRTH2â^' ILCs biased toward ILC2 or ILC3. Journal of Experimental Medicine, 2019, 216, 1762-1776.	4.2	93
1244	Transcription Restart Establishes Chromatin Accessibility after DNA Replication. Molecular Cell, 2019, 75, 284-297.e6.	4.5	62
1245	Decomposing Cell Identity for Transfer Learning across Cellular Measurements, Platforms, Tissues, and Species. Cell Systems, 2019, 8, 395-411.e8.	2.9	121
1246	An ATAC-seq atlas of chromatin accessibility in mouse tissues. Scientific Data, 2019, 6, 65.	2.4	89
1247	Hand2 Selectively Reorganizes Chromatin Accessibility to Induce Pacemaker-like Transcriptional Reprogramming. Cell Reports, 2019, 27, 2354-2369.e7.	2.9	23
1248	Probing the Tumor Suppressor Function of BAP1 in CRISPR-Engineered Human Liver Organoids. Cell Stem Cell, 2019, 24, 927-943.e6.	5.2	136
1249	Zfp281 Shapes the Transcriptome of Trophoblast Stem Cells and Is Essential for Placental Development. Cell Reports, 2019, 27, 1742-1754.e6.	2.9	34
1250	Pancreatic islet chromatin accessibility and conformation reveals distal enhancer networks of type 2 diabetes risk. Nature Communications, 2019, 10, 2078.	5.8	82
1251	Genetic Insights Into Smooth Muscle Cell Contributions to Coronary Artery Disease. Arteriosclerosis, Thrombosis, and Vascular Biology, 2019, 39, 1006-1017.	1.1	26
1252	Fate-Mapping of GM-CSF Expression Identifies a Discrete Subset of Inflammation-Driving T Helper Cells Regulated by Cytokines IL-23 and IL-1Î². Immunity, 2019, 50, 1289-1304.e6.	6.6	163
1253	Multiple SCN5A variant enhancers modulate its cardiac gene expression and the QT interval. Proceedings of the National Academy of Sciences of the United States of America, 2019, 116, 10636-10645.	3.3	22
1254	Causal Gene Regulatory Network Modeling and Genomics: Second-Generation Challenges. Journal of Computational Biology, 2019, 26, 703-718.	0.8	17
1255	Single-cell technologies â€" studying rheumatic diseases one cell at a time. Nature Reviews Rheumatology, 2019, 15, 340-354.	3.5	30
1256	Ikaros tumor suppressor function includes induction of active enhancers and super-enhancers along with pioneering activity. Leukemia, 2019, 33, 2720-2731.	3.3	32

#	Article	IF	Citations
1257	Profiling of chromatin accessibility and identification of general cis-regulatory mechanisms that control two ocular lens differentiation pathways. Epigenetics and Chromatin, 2019, 12, 27.	1.8	34
1258	Proneural factors Ascl1 and Neurog2 contribute to neuronal subtype identities by establishing distinct chromatin landscapes. Nature Neuroscience, 2019, 22, 897-908.	7.1	99
1259	Role of H3K9me3 heterochromatin in cell identity establishment and maintenance. Current Opinion in Genetics and Development, 2019, 55, 1-10.	1.5	177
1260	Genome-wide strategies reveal target genes of Npas4l associated with vascular development in zebrafish. Development (Cambridge), 2019, 146, .	1.2	29
1261	Long Non-Coding RNAs and the Innate Immune Response. Non-coding RNA, 2019, 5, 34.	1.3	75
1262	Multiple myeloma immunoglobulin lambda translocations portend poor prognosis. Nature Communications, 2019, 10, 1911.	5.8	109
1263	PAD2-Mediated Citrullination Contributes to Efficient Oligodendrocyte Differentiation and Myelination. Cell Reports, 2019, 27, 1090-1102.e10.	2.9	59
1264	Hominoid-Specific Transposable Elements and KZFPs Facilitate Human Embryonic Genome Activation and Control Transcription in Naive Human ESCs. Cell Stem Cell, 2019, 24, 724-735.e5.	5.2	208
1265	Chronic heavy drinking drives distinct transcriptional and epigenetic changes in splenic macrophages. EBioMedicine, 2019, 43, 594-606.	2.7	17
1266	Specific chromatin changes mark lateral organ founder cells in the Arabidopsis inflorescence meristem. Journal of Experimental Botany, 2019, 70, 3867-3879.	2.4	17
1267	Chromatin three-dimensional interactions mediate genetic effects on gene expression. Science, 2019, 364, .	6.0	163
1268	p63 establishes epithelial enhancers at critical craniofacial development genes. Science Advances, 2019, 5, eaaw0946.	4.7	36
1269	CUT&Tag for efficient epigenomic profiling of small samples and single cells. Nature Communications, 2019, 10, 1930.	5.8	1,101
1270	Epigenomic profiling of retinal progenitors reveals LHX2 is required for developmental regulation of open chromatin. Communications Biology, 2019, 2, 142.	2.0	36
1271	ONECUT transcription factors induce neuronal characteristics and remodel chromatin accessibility. Nucleic Acids Research, 2019, 47, 5587-5602.	6.5	40
1272	Epigenetic modulation of a hardwired 3D chromatin landscape in two naive states of pluripotency. Nature Cell Biology, 2019, 21, 568-578.	4.6	55
1273	Loss of Nuclear TDP-43 Is Associated with Decondensation of LINE Retrotransposons. Cell Reports, 2019, 27, 1409-1421.e6.	2.9	137
1274	Measuring sequencer size bias using REcount: a novel method for highly accurate Illumina sequencing-based quantification. Genome Biology, 2019, 20, 85.	3.8	29

#	Article	IF	Citations
1275	Inhibition of MYC by the SMARCB1 tumor suppressor. Nature Communications, 2019, 10, 2014.	5.8	57
1276	RUNX represses Pmp22 to drive neurofibromagenesis. Science Advances, 2019, 5, eaau8389.	4.7	11
1277	Mammalian SWI/SNF collaborates with a polycomb-associated protein to regulate male germ line transcription in the mouse. Development (Cambridge), 2019, 146, .	1.2	29
1278	Maintenance of CTCF- and Transcription Factor-Mediated Interactions from the Gametes to the Early Mouse Embryo. Molecular Cell, 2019, 75, 154-171.e5.	4.5	81
1279	Single-Cell RNA-Sequencing-Based CRISPRi Screening Resolves Molecular Drivers of Early Human Endoderm Development. Cell Reports, 2019, 27, 708-718.e10.	2.9	81
1280	MAPS: Model-based analysis of long-range chromatin interactions from PLAC-seq and HiChIP experiments. PLoS Computational Biology, 2019, 15, e1006982.	1.5	94
1281	Development of a high efficient promoter finding method based on transient transfection. Gene: X, 2019, 2, 100008.	2.3	3
1282	Mammalian ISWI and SWI/SNF selectively mediate binding of distinct transcription factors. Nature, 2019, 569, 136-140.	13.7	169
1283	Direct Induction of the Three Pre-implantation Blastocyst Cell Types from Fibroblasts. Cell Stem Cell, 2019, 24, 983-994.e7.	5.2	47
1284	Pioneering function of Isl1 in the epigenetic control of cardiomyocyte cell fate. Cell Research, 2019, 29, 486-501.	5.7	72
1285	OVOL2 induces mesenchymal-to-epithelial transition in fibroblasts and enhances cell-state reprogramming towards epithelial lineages. Scientific Reports, 2019, 9, 6490.	1.6	38
1286	TET enzymes augment activation-induced deaminase (AID) expression via 5-hydroxymethylcytosine modifications at the Aicda superenhancer. Science Immunology, 2019, 4, .	5.6	65
1287	Gene activation precedes DNA demethylation in response to infection in human dendritic cells. Proceedings of the National Academy of Sciences of the United States of America, 2019, 116, 6938-6943.	3.3	127
1288	ATAC-seq Assay with Low Mitochondrial DNA Contamination from Primary Human CD4+ T Lymphocytes. Journal of Visualized Experiments, 2019, , .	0.2	9
1289	Epigenetic Changes Induced by Bacteroides fragilis Toxin. Infection and Immunity, 2019, 87, .	1.0	43
1290	High-Resolution Mapping of the Escherichia coli Chromosome Reveals Positions of High and Low Transcription. Cell Systems, 2019, 8, 212-225.e9.	2.9	79
1291	Integrated epigenomic profiling reveals endogenous retrovirus reactivation in renal cell carcinoma. EBioMedicine, 2019, 41, 427-442.	2.7	26
1292	Subtle changes in chromatin loop contact propensity are associated with differential gene regulation and expression. Nature Communications, 2019, 10, 1054.	5.8	100

#	Article	IF	Citations
1293	ARNT2 Tunes Activity-Dependent Gene Expression through NCoR2-Mediated Repression and NPAS4-Mediated Activation. Neuron, 2019, 102, 390-406.e9.	3.8	35
1294	Large-Scale, Quantitative Protein Assays on a High-Throughput DNA Sequencing Chip. Molecular Cell, 2019, 73, 1075-1082.e4.	4.5	42
1295	Identification of transcription factor binding sites using ATAC-seq. Genome Biology, 2019, 20, 45.	3.8	346
1296	Time-dependent Pax3-mediated chromatin remodeling and cooperation with Six4 and Tead2 specify the skeletal myogenic lineage in developing mesoderm. PLoS Biology, 2019, 17, e3000153.	2.6	23
1297	Leveraging technological innovations to investigate evolutionary transitions to eusociality. Current Opinion in Insect Science, 2019, 34, 27-32.	2.2	2
1298	Bcor loss perturbs myeloid differentiation and promotes leukaemogenesis. Nature Communications, 2019, 10, 1347.	5.8	41
1299	Safeguard function of PU.1 shapes the inflammatory epigenome of neutrophils. Nature Immunology, 2019, 20, 546-558.	7.0	40
1300	Gene regulation and the architecture of complex human traits in the genomics era. Current Opinion in Psychology, 2019, 27, 93-97.	2.5	0
1301	Nucleoporin Seh1 Interacts with Olig2/Brd7 to Promote Oligodendrocyte Differentiation and Myelination. Neuron, 2019, 102, 587-601.e7.	3.8	63
1302	Mechanisms of Action of Hematopoietic Transcription Factor PU.1 in Initiation of T-Cell Development. Frontiers in Immunology, 2019, 10, 228.	2.2	58
1303	Systems immunology: Integrating multi-omics data to infer regulatory networks and hidden drivers of immunity. Current Opinion in Systems Biology, 2019, 15, 19-29.	1.3	32
1304	Acoel genome reveals the regulatory landscape of whole-body regeneration. Science, 2019, 363, .	6.0	125
1305	A master regulator of regeneration. Science, 2019, 363, 1152-1153.	6.0	0
1306	Mechanosensing and Mechanoregulation of Endothelial Cell Functions. , 2019, 9, 873-904.		115
1307	Bromodomain inhibition of the coactivators CBP/EP300 facilitate cellular reprogramming. Nature Chemical Biology, 2019, 15, 519-528.	3.9	67
1308	cisTopic: cis-regulatory topic modeling on single-cell ATAC-seq data. Nature Methods, 2019, 16, 397-400.	9.0	322
1309	Genomic and epigenomic mapping of leptin-responsive neuronal populations involved in body weight regulation. Nature Metabolism, 2019, 1, 475-484.	5.1	17
1310	Single Molecule and Single Cell Sequencing. Advances in Experimental Medicine and Biology, 2019, , .	0.8	7

#	Article	IF	Citations
1311	Rbpj expression in regulatory T cells is critical for restraining TH2 responses. Nature Communications, 2019, 10, 1621.	5.8	41
1312	ATAC-seq reveals regional differences in enhancer accessibility during the establishment of spatial coordinates in the Drosophila blastoderm. Genome Research, 2019, 29, 771-783.	2.4	49
1313	MKL1-actin pathway restricts chromatin accessibility and prevents mature pluripotency activation. Nature Communications, 2019, 10, 1695.	5.8	31
1314	An Informative Approach to Single-Cell Sequencing Analysis. Advances in Experimental Medicine and Biology, 2019, 1129, 81-96.	0.8	3
1315	Chromatin fiber structural motifs as regulatory hubs of genome function?. Essays in Biochemistry, 2019, 63, 123-132.	2.1	4
1316	The histone chaperone CAF-1 cooperates with the DNA methyltransferases to maintain Cd4 silencing in cytotoxic T cells. Genes and Development, 2019, 33, 669-683.	2.7	27
1317	PAN-INTACT enables direct isolation of lineage-specific nuclei from fibrous tissues. PLoS ONE, 2019, 14, e0214677.	1.1	8
1318	Engineering a haematopoietic stem cell niche by revitalizing mesenchymal stromal cells. Nature Cell Biology, 2019, 21, 560-567.	4.6	74
1319	A reinforcing HNF4â€“SMAD4 feed-forward module stabilizes enterocyte identity. Nature Genetics, 2019, 51, 777-785.	9.4	110
1320	Modeling the Pathological Long-Range Regulatory Effects of Human Structural Variation with Patient-Specific hiPSCs. Cell Stem Cell, 2019, 24, 736-752.e12.	5.2	90
1321	Comparison of genotoxic versus nongenotoxic stabilization of p53 provides insight into parallel stress-responsive transcriptional networks. Cell Cycle, 2019, 18, 809-823.	1.3	11
1322	Sequential conditioning-stimulation reveals distinct gene- and stimulus-specific effects of Type I and II IFN on human macrophage functions. Scientific Reports, 2019, 9, 5288.	1.6	26
1323	Atheroprotective Flow Upregulates ITPR3 (Inositol 1,4,5-Trisphosphate Receptor 3) in Vascular Endothelium via KLF4 (KrÃ¼ppel-Like Factor 4)-Mediated Histone Modifications. Arteriosclerosis, Thrombosis, and Vascular Biology, 2019, 39, 902-914.	1.1	45
1324	Predicting enhancers in mammalian genomes using supervised hidden Markov models. BMC Bioinformatics, 2019, 20, 157.	1.2	12
1325	Genetic compensation triggered by mutant mRNA degradation. Nature, 2019, 568, 193-197.	13.7	734
1326	Efficient and unique cobarcoding of second-generation sequencing reads from long DNA molecules enabling cost-effective and accurate sequencing, haplotyping, and de novo assembly. Genome Research, 2019, 29, 798-808.	2.4	176
1327	Profiling of Pluripotency Factors in Single Cells and Early Embryos. Cell, 2019, 177, 1319-1329.e11.	13.5	150
1328	PI3K Inhibition Activates SGK1 via a Feedback Loop to Promote Chromatin-Based Regulation of ER-Dependent Gene Expression. Cell Reports, 2019, 27, 294-306.e5.	2.9	49

#	Article	IF	Citations
1329	Convergent regulatory evolution and loss of flight in paleognathous birds. Science, 2019, 364, 74-78.	6.0	189
1330	TET2 binding to enhancers facilitates transcription factor recruitment in hematopoietic cells. Genome Research, 2019, 29, 564-575.	2.4	66
1331	Generation of Whole Genome Bisulfite Sequencing Libraries from Very Low DNA Input. Methods in Molecular Biology, 2019, 1956, 229-248.	0.4	1
1332	Diverse Genome Topologies Characterize Dosage Compensation across Species. Trends in Genetics, 2019, 35, 308-315.	2.9	16
1333	Reproducible inference of transcription factor footprints in ATAC-seq and DNase-seq datasets using protocol-specific bias modeling. Genome Biology, 2019, 20, 42.	3.8	73
1334	Combined analysis of dissimilar promoter accessibility and gene expression profiles identifies tissue-specific genes and actively repressed networks. Epigenetics and Chromatin, 2019, 12, 16.	1.8	61
1335	Epigenetic control of early dendritic cell lineage specification by the transcription factor IRF8 in mice. Blood, 2019, 133, 1803-1813.	0.6	42
1336	Oncogenic Notch Promotes Long-Range Regulatory Interactions within Hyperconnected 3D Cliques. Molecular Cell, 2019, 73, 1174-1190.e12.	4.5	83
1338	HDAC6 selective inhibition of melanoma patient T-cells augments anti-tumor characteristics. , 2019, 7, 33.		62
1339	Determination of local chromatin interactions using a combined CRISPR and peroxidase APEX2 system. Nucleic Acids Research, 2019, 47, e52-e52.	6.5	37
1340	Orientation-aware plasma cell-free DNA fragmentation analysis in open chromatin regions informs tissue of origin. Genome Research, 2019, 29, 418-427.	2.4	159
1341	Dynamics of cardiomyocyte transcriptome and chromatin landscape demarcates key events of heart development. Genome Research, 2019, 29, 506-519.	2.4	21
1342	NR4A transcription factors limit CAR T cell function in solid tumours. Nature, 2019, 567, 530-534.	13.7	519
1343	High Sensitivity Profiling of Chromatin Structure by MNase-SSP. Cell Reports, 2019, 26, 2465-2476.e4.	2.9	31
1344	Subsets of exhausted CD8+ T cells differentially mediate tumor control and respond to checkpoint blockade. Nature Immunology, 2019, 20, 326-336.	7.0	1,148
1345	c-Maf-dependent Treg cell control of intestinal TH17 cells and IgA establishes hostâ€“microbiota homeostasis. Nature Immunology, 2019, 20, 471-481.	7.0	138
1346	Hemi-methylated CpG sites connect Dnmt1-knockdown-induced and Tet1-induced DNA demethylation during somatic cell reprogramming. Cell Discovery, 2019, 5, 11.	3.1	10
1347	The single-cell transcriptional landscape of mammalian organogenesis. Nature, 2019, 566, 496-502.	13.7	2,292

#	Article	IF	Citations
1348	Chromatin organization modulates the origin of heritable structural variations in human genome. Nucleic Acids Research, 2019, 47, 2766-2777.	6.5	12
1349	Genomic annotation of disease-associated variants reveals shared functional contexts. Diabetologia, 2019, 62, 735-743.	2.9	5
1350	Integrated Functional Genomic Analysis Enables Annotation of Kidney Genome-Wide Association Study Loci. Journal of the American Society of Nephrology: JASN, 2019, 30, 421-441.	3.0	27
1351	Preprocessing and Computational Analysis of Single-Cell Epigenomic Datasets. Methods in Molecular Biology, 2019, 1935, 187-202.	0.4	2
1352	Blimp1 Prevents Methylation of Foxp3 and Loss of Regulatory T Cell Identity at Sites of Inflammation. Cell Reports, 2019, 26, 1854-1868.e5.	2.9	91
1353	YAP Partially Reprograms Chromatin Accessibility to Directly Induce Adult Cardiogenesis InÂVivo. Developmental Cell, 2019, 48, 765-779.e7.	3.1	171
1354	The genetics and epigenetics of animal migration and orientation: birds, butterflies and beyond. Journal of Experimental Biology, 2019, 222, .	0.8	93
1355	Interpreting Coronary Artery Disease Risk Through Geneâ€“Environment Interactions in Gene Regulation. Genetics, 2019, 213, 651-663.	1.2	20
1356	The application of single-cell sequencing technology in the diagnosis and treatment of hepatocellular carcinoma. Annals of Translational Medicine, 2019, 7, 790-790.	0.7	11
1357	Chromatin occupancy and epigenetic analysis reveal new insights into the function of the GATA1 N terminus in erythropoiesis. Blood, 2019, 134, 1619-1631.	0.6	34
1358	Recapitulation-like developmental transitions of chromatin accessibility in vertebrates. Zoological Letters, 2019, 5, 33.	0.7	24
1359	An Approach for Prediction of Enhancers Based on the Bayesian Model. , 2019, , .		0
1360	Sleepâ€“wake-driven and circadian contributions to daily rhythms in gene expression and chromatin accessibility in the murine cortex. Proceedings of the National Academy of Sciences of the United States of America, 2019, 116, 25773-25783.	3.3	66
1361	Widespread long-range cis-regulatory elements in the maize genome. Nature Plants, 2019, 5, 1237-1249.	4.7	250
1362	The prevalence, evolution and chromatin signatures of plant regulatory elements. Nature Plants, 2019, 5, 1250-1259.	4.7	219
1363	Parallel evolution of ancient, pleiotropic enhancers underlies butterfly wing pattern mimicry. Proceedings of the National Academy of Sciences of the United States of America, 2019, 116, 24174-24183.	3.3	102
1364	Intercalation of small molecules into DNA in chromatin is primarily controlled by superhelical constraint. PLoS ONE, 2019, 14, e0224936.	1.1	10
1365	Technological advances in studying epigenetics biomarkers of prognostic potential for clinical research. , 2019, , 45-83.		1

#	Article	IF	Citations
1366	The changing paradigm of intron retention: regulation, ramifications and recipes. Nucleic Acids Research, 2019, 47, 11497-11513.	6.5	90
1367	GATA3-Controlled Nucleosome Eviction Drives MYC Enhancer Activity in T-cell Development and Leukemia. Cancer Discovery, 2019, 9, 1774-1791.	7.7	27
1368	Cooperativity of co-factor NR2F2 with Pioneer Factors GATA3, FOXA1 in promoting ERÎ± function. Theranostics, 2019, 9, 6501-6516.	4.6	25
1369	Transcription Factor T-bet in B Cells Modulates Germinal Center Polarization and Antibody Affinity Maturation in Response to Malaria. Cell Reports, 2019, 29, 2257-2269.e6.	2.9	36
1370	Endogenous fluctuations of <scp>OCT</scp> 4 and <scp>SOX</scp> 2 bias pluripotent cell fate decisions. Molecular Systems Biology, 2019, 15, e9002.	3.2	39
1371	Chromatin accessibility and transcription dynamics during in vitro astrocyte differentiation of Huntingtonâ€™s Disease Monkey pluripotent stem cells. Epigenetics and Chromatin, 2019, 12, 67.	1.8	10
1372	Characterization of cancer omics and drug perturbations in panels of lung cancer cells. Scientific Reports, 2019, 9, 19529.	1.6	13
1373	Multi-species annotation of transcriptome and chromatin structure in domesticated animals. BMC Biology, 2019, 17, 108.	1.7	109
1374	<scp>FOXA</scp> 2 controls the cis â€regulatory networks of pancreatic cancer cells in a differentiation gradeâ€specific manner. EMBO Journal, 2019, 38, e102161.	3.5	30
1375	Identification of four novel associations for B-cell acute lymphoblastic leukaemia risk. Nature Communications, 2019, 10, 5348.	5.8	58
1376	MLLT3 governs human haematopoietic stem-cell self-renewal and engraftment. Nature, 2019, 576, 281-286.	13.7	94
1377	Histone hyperacetylation disrupts core gene regulatory architecture in rhabdomyosarcoma. Nature Genetics, 2019, 51, 1714-1722.	9.4	113
1378	Pancreatic Islet Transcriptional Enhancers and Diabetes. Current Diabetes Reports, 2019, 19, 145.	1.7	11
1379	Gcn5-Mediated Histone Acetylation Governs Nucleosome Dynamics in Spermiogenesis. Developmental Cell, 2019, 51, 745-758.e6.	3.1	47
1380	Transcriptome and chromatin accessibility in porcine intestinal epithelial cells upon Zearalenone exposure. Scientific Data, 2019, 6, 298.	2.4	7
1381	Genome-wide histone modification profiling of inner cell mass and trophectoderm of bovine blastocysts by RAT-ChIP. PLoS ONE, 2019, 14, e0225801.	1.1	8
1382	Transcriptional control by enhancers and enhancer RNAs. Transcription, 2019, 10, 171-186.	1.7	49
1383	Quantification of Differential Transcription Factor Activity and Multiomics-Based Classification into Activators and Repressors: diffTF. Cell Reports, 2019, 29, 3147-3159.e12.	2.9	84

#	Article	IF	Citations
1384	Helios enhances the preferential differentiation of human fetal CD4 ⁺ naÃ¯ve T cells into regulatory T cells. Science Immunology, 2019, 4, .	5.6	31
1385	Epigenetics and the dynamics of chromatin during adenovirus infections. FEBS Letters, 2019, 593, 3551-3570.	1.3	25
1386	Transcription factor Znf2 coordinates with the chromatin remodeling SWI/SNF complex to regulate cryptococcal cellular differentiation. Communications Biology, 2019, 2, 412.	2.0	19
1387	Understanding and measuring human Bâ€cell tolerance and its breakdown in autoimmune disease. Immunological Reviews, 2019, 292, 76-89.	2.8	34
1388	EpiMethylTag: simultaneous detection of ATAC-seq or ChIP-seq signals with DNA methylation. Genome Biology, 2019, 20, 248.	3.8	27
1389	Eomes and Brachyury control pluripotency exit and germ-layer segregation by changing the chromatin state. Nature Cell Biology, 2019, 21, 1518-1531.	4.6	81
1390	Early chromatin shaping predetermines multipotent vagal neural crest into neural, neuronal and mesenchymal lineages. Nature Cell Biology, 2019, 21, 1504-1517.	4.6	41
1391	Phase separation of YAP reorganizes genome topology for long-term YAP target gene expression. Nature Cell Biology, 2019, 21, 1578-1589.	4.6	237
1392	c-Jun overexpression in CAR T cells induces exhaustion resistance. Nature, 2019, 576, 293-300.	13.7	480
1393	An ultra high-throughput method for single-cell joint analysis of open chromatin and transcriptome. Nature Structural and Molecular Biology, 2019, 26, 1063-1070.	3.6	239
1394	Gut Microbiota Has a Widespread and Modifiable Effect on Host Gene Regulation. MSystems, 2019, 4, .	1.7	74
1395	Exploring Mammalian Genome within Phase-Separated Nuclear Bodies: Experimental Methods and Implications for Gene Expression. Genes, 2019, 10, 1049.	1.0	15
1396	The role of noncoding mutations in blood cancers. DMM Disease Models and Mechanisms, 2019, 12, .	1.2	9
1397	PRDM1 controls the sequential activation of neural, neural crest and sensory progenitor determinants. Development (Cambridge), 2019, 146, .	1.2	11
1398	Toll-like Receptor Signaling Rewires Macrophage Metabolism and Promotes Histone Acetylation via ATP-Citrate Lyase. Immunity, 2019, 51, 997-1011.e7.	6.6	216
1399	MLL-AF9 initiates transformation from fast-proliferating myeloid progenitors. Nature Communications, 2019, 10, 5767.	5.8	41
1400	Mutant IDH1 confers resistance to energy stress in normal biliary cells through PFKP-induced aerobic glycolysis and AMPK activation. Scientific Reports, 2019, 9, 18859.	1.6	18
1401	Spatial Genome Re-organization between Fetal and Adult Hematopoietic Stem Cells. Cell Reports, 2019, 29, 4200-4211.e7.	2.9	46

#	Article	IF	Citations
1402	NSD2 overexpression drives clustered chromatin and transcriptional changes in a subset of insulated domains. Nature Communications, 2019, 10, 4843.	5.8	57
1403	Organoid single-cell genomic atlas uncovers human-specific features of brain development. Nature, 2019, 574, 418-422.	13.7	496
1404	High-throughput sequencing of the transcriptome and chromatin accessibility in the same cell. Nature Biotechnology, 2019, 37, 1452-1457.	9.4	550
1405	Allele-specific NKX2-5 binding underlies multiple genetic associations with human electrocardiographic traits. Nature Genetics, 2019, 51, 1506-1517.	9.4	35
1406	Landscape of stimulation-responsive chromatin across diverse human immune cells. Nature Genetics, 2019, 51, 1494-1505.	9.4	196
1407	PTPN2 regulates the generation of exhausted CD8+ T cell subpopulations and restrains tumor immunity. Nature Immunology, 2019, 20, 1335-1347.	7.0	142
1408	Fibroblastic reticular cells enhance T cell metabolism and survival via epigenetic remodeling. Nature Immunology, 2019, 20, 1668-1680.	7.0	53
1409	Functional genomic approaches to elucidate the role of enhancers during development. Wiley Interdisciplinary Reviews: Systems Biology and Medicine, 2019, 12, e1467.	6.6	19
1410	Targeting REGNASE-1 programs long-lived effector T cells for cancer therapy. Nature, 2019, 576, 471-476.	13.7	251
1411	A cis -element within the ARF locus mediates repression of p16 ^{INK4A} expression via long-range chromatin interactions. Proceedings of the National Academy of Sciences of the United States of America, 2019, 116, 26644-26652.	3.3	16
1412	GCN2 drives macrophage and MDSC function and immunosuppression in the tumor microenvironment. Science Immunology, 2019, 4, .	5.6	85
1413	ARID1A, a SWI/SNF subunit, is critical to acinar cell homeostasis and regeneration and is a barrier to transformation and epithelial-mesenchymal transition in the pancreas. Gut, 2019, 68, 1245-1258.	6.1	58
1414	Environmental influences on RNA processing: Biochemical, molecular and genetic regulators of cellular response. Wiley Interdisciplinary Reviews RNA, 2019, 10, e1503.	3.2	31
1415	Epigenetic regulation of renal development. Seminars in Cell and Developmental Biology, 2019, 91, 111-118.	2.3	12
1416	Transcriptional Programs and Regeneration Enhancers Underlying Heart Regeneration. Journal of Cardiovascular Development and Disease, 2019, 6, 2.	0.8	7
1417	Metabolic heterogeneity underlies reciprocal fates of TH17 cell stemness and plasticity. Nature, 2019, 565, 101-105.	13.7	141
1418	Integrative Approaches for Inference of Genome-Scale Gene Regulatory Networks. Methods in Molecular Biology, 2019, 1883, 161-194.	0.4	3
1419	Smc3 is required for mouse embryonic and adult hematopoiesis. Experimental Hematology, 2019, 70, 70-84.e6.	0.2	12

#	Article	IF	Citations
1420	Epigenome-wide study uncovers large-scale changes in histone acetylation driven by tau pathology in aging and Alzheimerâ€™s human brains. Nature Neuroscience, 2019, 22, 37-46.	7.1	188
1421	Factor cooperation for chromosome discrimination inDrosophila. Nucleic Acids Research, 2019, 47, 1706-1724.	6.5	30
1422	Laundry detergents and detergent residue after rinsing directly disrupt tight junction barrier integrity in human bronchial epithelial cells. Journal of Allergy and Clinical Immunology, 2019, 143, 1892-1903.	1.5	96
1423	Gonadal supporting cells acquire sex-specific chromatin landscapes during mammalian sex determination. Developmental Biology, 2019, 446, 168-179.	0.9	37
1424	An atlas of genetic influences on osteoporosis in humans and mice. Nature Genetics, 2019, 51, 258-266.	9.4	557
1425	An upstream enhancer regulates Gpihbp1 expression in a tissue-specific manner. Journal of Lipid Research, 2019, 60, 869-879.	2.0	7
1426	Cell Specificity of Human Regulatory Annotations and Their Genetic Effects on Gene Expression. Genetics, 2019, 211, 549-562.	1.2	16
1427	Transposable elements are regulated by context-specific patterns of chromatin marks in mouse embryonic stem cells. Nature Communications, 2019, 10, 34.	5.8	104
1428	Coupled Single-Cell CRISPR Screening and Epigenomic Profiling Reveals Causal Gene Regulatory Networks. Cell, 2019, 176, 361-376.e17.	13.5	215
1429	Identification of regulatory elements from nascent transcription using dREG. Genome Research, 2019, 29, 293-303.	2.4	85
1430	The evolution and patterning of male gametophyte development. Current Topics in Developmental Biology, 2019, 131, 257-298.	1.0	56
1431	The biology of the cell â€“ insights from mass cytometry. FEBS Journal, 2019, 286, 1514-1522.	2.2	20
1432	Integrated Epigenetic Mapping of Human and Mouse Salivary Gene Regulation. Journal of Dental Research, 2019, 98, 209-217.	2.5	12
1433	A CD4+ T cell population expanded in lupus blood provides B cell help through interleukin-10 and succinate. Nature Medicine, 2019, 25, 75-81.	15.2	189
1434	Identification of Genomic Alterations Through Multilevel DNA Structural Analysis. Methods in Molecular Biology, 2019, 1896, 191-201.	0.4	0
1435	Prospects of pan-genomics in barley. Theoretical and Applied Genetics, 2019, 132, 785-796.	1.8	38
1436	The Impact of Next-Generation Sequencing on Cancer Genomics: From Discovery to Clinic. Cold Spring Harbor Perspectives in Medicine, 2019, 9, a036269.	2.9	43
1437	BiFET: sequencing <u>Bi</u>as-free transcription factor <u>F</u>ootprint <u>E</u>nrichment <u>T</u>est. Nucleic Acids Research, 2019, 47, e11-e11.	6.5	9

#	Article	IF	Citations
1438	Functional Annotation of Animal Genomes (FAANG): Current Achievements and Roadmap. Annual Review of Animal Biosciences, 2019, 7, 65-88.	3.6	172
1439	Computational prediction of gene regulatory networks in plant growth and development. Current Opinion in Plant Biology, 2019, 47, 96-105.	3.5	66
1440	Genome-Wide Regulatory Adaptation Shapes Population-Level Genomic Landscapes inHeliconius. Molecular Biology and Evolution, 2019, 36, 159-173.	3.5	49
1441	Transcriptional control of natural killer cell differentiation. Immunology, 2019, 156, 111-119.	2.0	15
1442	IKZF2 Drives Leukemia Stem Cell Self-Renewal and Inhibits Myeloid Differentiation. Cell Stem Cell, 2019, 24, 153-165.e7.	5.2	66
1443	Chromatin Accessibility as a Strategy to Detect Changes Associated With Development, Disease, and Exposure and Susceptibility to Chemical Toxins. , 2019, , 85-103.		3
1444	Novel Bioinformatics Methods for Toxicoepigenetics. , 2019, , 265-288.		11
1445	Environmental Control of Astrocyte Pathogenic Activities in CNS Inflammation. Cell, 2019, 176, 581-596.e18.	13.5	150
1446	Multiomic Profiling Identifies cis-Regulatory Networks Underlying Human Pancreatic Î² Cell Identity and Function. Cell Reports, 2019, 26, 788-801.e6.	2.9	68
1447	Evolution of embryonic cis-regulatory landscapes between divergent Phallusia and Ciona ascidians. Developmental Biology, 2019, 448, 71-87.	0.9	29
1448	CTCF sites display cell cycleâ€“dependent dynamics in factor binding and nucleosome positioning. Genome Research, 2019, 29, 236-249.	2.4	104
1449	Transcription factor activity and nucleosome organization in mitosis. Genome Research, 2019, 29, 250-260.	2.4	84
1450	Linking Enhancer to Epigenetics: New Way to Think About Human Diseases. , 2019, , 145-163.		0
1451	Approaches for the study of epigenetic modifications in the inner ear and related tissues. Hearing Research, 2019, 376, 69-85.	0.9	6
1452	Retinoic Acid Receptor Alpha Represses a Th9 Transcriptional and Epigenomic Program to Reduce Allergic Pathology. Immunity, 2019, 50, 106-120.e10.	6.6	54
1453	Accurate prediction of cell type-specific transcription factor binding. Genome Biology, 2019, 20, 9.	3.8	82
1454	Classifying cells with Scasat, a single-cell ATAC-seq analysis tool. Nucleic Acids Research, 2019, 47, e10-e10.	6.5	60
1455	Genome-wide chromatin accessibility and transcriptome profiling show minimal epigenome changes and coordinated transcriptional dysregulation of hedgehog signaling in Danforthâ€™s short tail mice. Human Molecular Genetics, 2019, 28, 736-750.	1.4	7

#	Article	IF	Citations
1456	Tissue Regeneration Enhancer Elements: A Way to Unlock Endogenous Healing Power. Developmental Dynamics, 2019, 248, 34-42.	0.8	26
1457	Identification of Novel Loci Associated With Hip Shape: A Meta-Analysis of Genomewide Association Studies. Journal of Bone and Mineral Research, 2019, 34, 241-251.	3.1	47
1458	A chromatin integration labelling method enables epigenomic profiling with lower input. Nature Cell Biology, 2019, 21, 287-296.	4.6	121
1459	Social status alters chromatin accessibility and the gene regulatory response to glucocorticoid stimulation in rhesus macaques. Proceedings of the National Academy of Sciences of the United States of America, 2019, 116, 1219-1228.	3.3	71
1460	Gene Regulatory Networks. Methods in Molecular Biology, 2019, , .	0.4	41
1461	SWI/SNF remains localized to chromatin in the presence of SCHLAP1. Nature Genetics, 2019, 51, 26-29.	9.4	28
1462	Differential viral accessibility (DIVA) identifies alterations in chromatin architecture through large-scale mapping of lentiviral integration sites. Nature Protocols, 2019, 14, 153-170.	5.5	7
1463	Precocious expression of Blimp1 in B cells causes autoimmune disease with increased selfâ€reactive plasma cells. EMBO Journal, 2019, 38, 1-19.	3.5	165
1464	Epigenomic drivers of immune dysfunction in aging. Aging Cell, 2019, 18, e12878.	3.0	60
1465	Machine learning for integrating data in biology and medicine: Principles, practice, and opportunities. Information Fusion, 2019, 50, 71-91.	11.7	340
1466	Corticosteroid Receptors in the Brain: Transcriptional Mechanisms for Specificity and Context-Dependent Effects. Cellular and Molecular Neurobiology, 2019, 39, 539-549.	1.7	45
1467	Epigenetics in Insects: Genome Regulation and the Generation of Phenotypic Diversity. Annual Review of Entomology, 2019, 64, 185-203.	5.7	137
1468	Regulation of Astrocyte Functions in Multiple Sclerosis. Cold Spring Harbor Perspectives in Medicine, 2019, 9, a029009.	2.9	69
1469	Biological annotation of genetic loci associated with intelligence in a meta-analysis of 87,740 individuals. Molecular Psychiatry, 2019, 24, 182-197.	4.1	47
1470	Signatures of sex: Sex differences in gene expression in the vertebrate brain. Wiley Interdisciplinary Reviews: Developmental Biology, 2020, 9, e348.	5.9	48
1471	Transcription factorsâ€“DNA interactions in rice: identification and verification. Briefings in Bioinformatics, 2020, 21, 946-956.	3.2	19
1472	Chromatin dynamics underlying the precise regeneration of a vertebrate limb â€“ Epigenetic regulation and cellular memory. Seminars in Cell and Developmental Biology, 2020, 97, 16-25.	2.3	8
1473	The histone methyltransferase EZH2 primes the early differentiation of follicular helper T cells during acute viral infection. Cellular and Molecular Immunology, 2020, 17, 247-260.	4.8	38

#	Article	IF	Citations
1474	MACPET: model-based analysis for ChIA-PET. Biostatistics, 2020, 21, 625-639.	0.9	2
1475	ID1 Mediates Escape from TGFÎ² Tumor Suppression in Pancreatic Cancer. Cancer Discovery, 2020, 10, 142-157.	7.7	59
1476	PTEN in Chromatin Remodeling. Cold Spring Harbor Perspectives in Medicine, 2020, 10, a036160.	2.9	15
1477	AP-1 activity induced by co-stimulation is required for chromatin opening during T cell activation. Journal of Experimental Medicine, 2020, 217, .	4.2	80
1478	Quantitative assessment of effective regurgitant orifice: impact on risk stratification, and cut-off for severe and torrential tricuspid regurgitation grade. European Heart Journal Cardiovascular Imaging, 2020, 21, 768-776.	0.5	46
1479	Single Cell Omics: From Assay Design to Biomedical Application. Biotechnology Journal, 2020, 15, e1900262.	1.8	34
1480	Mechanistic homeostasis of vitamin D metabolism in the kidney through reciprocal modulation of Cyp27b1 and Cyp24a1 expression. Journal of Steroid Biochemistry and Molecular Biology, 2020, 196, 105500.	1.2	47
1481	hnRNPU/TrkB Defines a Chromatin Accessibility Checkpoint for Liver Injury and Nonalcoholic Steatohepatitis Pathogenesis. Hepatology, 2020, 71, 1228-1246.	3.6	27
1482	Inherited variants at 3q13.33 and 3p24.1 are associated with risk of diffuse large B-cell lymphoma and implicate immune pathways. Human Molecular Genetics, 2020, 29, 70-79.	1.4	17
1483	Sperm RNA: Quo vadis?. Seminars in Cell and Developmental Biology, 2020, 97, 123-130.	2.3	25
1484	Global changes in chromatin accessibility and transcription following ATRX inactivation in human cancer cells. FEBS Letters, 2020, 594, 67-78.	1.3	15
1485	DNA Methylation in Epidermal Differentiation, Aging, and Cancer. Journal of Investigative Dermatology, 2020, 140, 38-47.	0.3	54
1486	LOXL2-mediated H3K4 oxidation reduces chromatin accessibility in triple-negative breast cancer cells. Oncogene, 2020, 39, 79-121.	2.6	28
1487	Regulatory annotation of genomic intervals based on tissue-specific expression QTLs. Bioinformatics, 2020, 36, 690-697.	1.8	9
1488	Reactivation of super-enhancers by KLF4 in human Head and Neck Squamous Cell Carcinoma. Oncogene, 2020, 39, 262-277.	2.6	15
1489	Life-long epigenetic programming of cortical architecture by maternal â€˜Westernâ€™ diet during pregnancy. Molecular Psychiatry, 2020, 25, 22-36.	4.1	28
1490	The Dynamic Chromatin Architecture of the Regenerating Liver. Cellular and Molecular Gastroenterology and Hepatology, 2020, 9, 121-143.	2.3	37
1491	High-mobility group nucleosomal binding domain 2 protects against microcephaly by maintaining global chromatin accessibility during corticogenesis. Journal of Biological Chemistry, 2020, 295, 468-480.	1.6	10

#	Article	IF	Citations
1492	Segregation, linkage, GWAS, and sequencing. , 2020, , 7-23.		0
1493	Circulating Tumor Cells Exhibit Metastatic Tropism and Reveal Brain Metastasis Drivers. Cancer Discovery, 2020, 10, 86-103.	7.7	100
1494	The transcription factor GATA10 regulates fertility conversion of a twoâ€line hybrid tms5 mutant rice via the modulation of Ub_{L40} expression. Journal of Integrative Plant Biology, 2020, 62, 1034-1056.	4.1	16
1495	Dynamic transcriptome, accessible genome, and PGR cistrome profiles in the human myometrium. FASEB Journal, 2020, 34, 2252-2268.	0.2	13
1496	Understanding epigenomics based on the rice model. Theoretical and Applied Genetics, 2020, 133, 1345-1363.	1.8	17
1497	Transdifferentiation of Mouse Embryonic Fibroblasts into Dopaminergic Neurons Reactivates LINE-1 Repetitive Elements. Stem Cell Reports, 2020, 14, 60-74.	2.3	16
1498	Epigenetics Analysis and Integrated Analysis of Multiomics Data, Including Epigenetic Data, Using Artificial Intelligence in the Era of Precision Medicine. Biomolecules, 2020, 10, 62.	1.8	61
1499	Epidermal autonomous VEGFA/Flt1/Nrp1 functions mediate psoriasis-like disease. Science Advances, 2020, 6, eaax5849.	4.7	37
1500	Chromatin interactome mapping at 139 independent breast cancer risk signals. Genome Biology, 2020, 21, 8.	3.8	27
1501	Integration of ATAC-Seq and RNA-Seq Identifies Key Genes in Light-Induced Primordia Formation of Sparassis latifolia. International Journal of Molecular Sciences, 2020, 21, 185.	1.8	21
1502	Osteoarthritis year in review 2019: genetics, genomics and epigenetics. Osteoarthritis and Cartilage, 2020, 28, 275-284.	0.6	81
1503	Single-cell ATAC-Seq in human pancreatic islets and deep learning upscaling of rare cells reveals cell-specific type 2 diabetes regulatory signatures. Molecular Metabolism, 2020, 32, 109-121.	3.0	103
1504	Gene regulatory networks STARR-ing B cells. Nature Immunology, 2020, 21, 110-112.	7.0	0
1505	Lessons from eRNAs: understanding transcriptional regulation through the lens of nascent RNAs. Transcription, 2020, 11, 3-18.	1.7	13
1506	A Conserved Noncoding Locus Regulates Random Monoallelic Xist Expression across a Topological Boundary. Molecular Cell, 2020, 77, 352-367.e8.	4.5	48
1507	Precursors for Nonlymphoid-Tissue Treg Cells Reside in Secondary Lymphoid Organs and Are Programmed by the Transcription Factor BATF. Immunity, 2020, 52, 295-312.e11.	6.6	140
1508	Genome-wide profiling of nucleosome position and chromatin accessibility in single cells using scMNase-seq. Nature Protocols, 2020, 15, 68-85.	5.5	17
1509	An intrinsic role of IL-33 in Treg cellâ€“mediated tumor immunoevasion. Nature Immunology, 2020, 21, 75-85.	7.0	82

#	Article	IF	Citations
1510	Circadian Entrainment Triggers Maturation of Human InÂVitro Islets. Cell Stem Cell, 2020, 26, 108-122.e10.	5.2	127
1511	The developmental transcriptome for Lytechinus variegatus exhibits temporally punctuated gene expression changes. Developmental Biology, 2020, 460, 139-154.	0.9	16
1512	Protect-seq: genome-wide profiling of nuclease inaccessible domains reveals physical properties of chromatin. Nucleic Acids Research, 2020, 48, e16-e16.	6.5	10
1513	Cephalopod Biology: At the Intersection Between Genomic and Organismal Novelties. Annual Review of Animal Biosciences, 2020, 8, 71-90.	3.6	30
1514	Prostate cancer research: The next generation; report from the 2019 Coffeyâ€Holden Prostate Cancer Academy Meeting. Prostate, 2020, 80, 113-132.	1.2	25
1515	A method for assessing histone surface accessibility genome-wide. Methods, 2020, 184, 61-69.	1.9	3
1516	TFIIIC Binding to Alu Elements Controls Gene Expression via Chromatin Looping and Histone Acetylation. Molecular Cell, 2020, 77, 475-487.e11.	4.5	65
1517	Global Co-transcriptional Splicing in Arabidopsis and the Correlation with Splicing Regulation in Mature RNAs. Molecular Plant, 2020, 13, 266-277.	3.9	36
1518	Genomic methods in profiling DNA accessibility and factor localization. Chromosome Research, 2020, 28, 69-85.	1.0	71
1519	Systematic integration of GATA transcription factors and epigenomes via IDEAS paints the regulatory landscape of hematopoietic cells. IUBMB Life, 2020, 72, 27-38.	1.5	8
1520	KrÃ¼ppel-like Factor 5 Regulates Stemness, Lineage Specification, and Regeneration of Intestinal Epithelial Stem Cells. Cellular and Molecular Gastroenterology and Hepatology, 2020, 9, 587-609.	2.3	26
1521	RNA-seq and ChIP-seq as Complementary Approaches for Comprehension of Plant Transcriptional Regulatory Mechanism. International Journal of Molecular Sciences, 2020, 21, 167.	1.8	24
1522	Distinct contributions of DNA methylation and histone acetylation to the genomic occupancy of transcription factors. Genome Research, 2020, 30, 1393-1406.	2.4	41
1523	ATAC-Seq Identifies Chromatin Landscapes Linked to the Regulation of Oxidative Stress in the Human Fungal Pathogen Candida albicans. Journal of Fungi (Basel, Switzerland), 2020, 6, 182.	1.5	13
1524	Loss of Extreme Long-Range Enhancers in Human Neural Crest Drives a Craniofacial Disorder. Cell Stem Cell, 2020, 27, 765-783.e14.	5.2	101
1525	STAT3â€“BDNFâ€“TrkB signalling promotes alveolar epithelial regeneration after lung injury. Nature Cell Biology, 2020, 22, 1197-1210.	4.6	71
1526	UTX/KDM6A suppresses AP-1 and a gliogenesis program during neural differentiation of human pluripotent stem cells. Epigenetics and Chromatin, 2020, 13, 38.	1.8	5
1527	Impact of Sustained Transforming Growth Factor-Î² Receptor Inhibition on Chromatin Accessibility and Gene Expression in Cultured Human Endometrial MSC. Frontiers in Cell and Developmental Biology, 2020, 8, 567610.	1.8	15

#	Article	IF	Citations
1528	tagHi-C Reveals 3D Chromatin Architecture Dynamics during Mouse Hematopoiesis. Cell Reports, 2020, 32, 108206.	2.9	43
1529	Epigenomic technologies for precision oncology. Seminars in Cancer Biology, 2022, 84, 60-68.	4.3	6
1530	Universal NicE-seq for high-resolution accessible chromatin profiling for formaldehyde-fixed and FFPE tissues. Clinical Epigenetics, 2020, 12, 143.	1.8	12
1531	CHD7 promotes neural progenitor differentiation in embryonic stem cells via altered chromatin accessibility and nascent gene expression. Scientific Reports, 2020, 10, 17445.	1.6	23
1532	The transcription factor EGR2 is the molecular linchpin connecting STAT6 activation to the late, stable epigenomic program of alternative macrophage polarization. Genes and Development, 2020, 34, 1474-1492.	2.7	38
1533	Chromatin Landscape Underpinning Human Dendritic Cell Heterogeneity. Cell Reports, 2020, 32, 108180.	2.9	18
1534	Co-option of Neutrophil Fates by Tissue Environments. Cell, 2020, 183, 1282-1297.e18.	13.5	246
1535	BRD4 (Bromodomain-Containing Protein 4) Interacts with GATA4 (GATA Binding Protein 4) to Govern Mitochondrial Homeostasis in Adult Cardiomyocytes. Circulation, 2020, 142, 2338-2355.	1.6	31
1536	The human malaria parasite genome is configured into thousands of coexpressed linear regulatory units. Journal of Genetics and Genomics, 2020, 47, 513-521.	1.7	2
1537	The lysine demethylase KDM4A controls the cell-cycle expression of replicative canonical histone genes. Biochimica Et Biophysica Acta - Gene Regulatory Mechanisms, 2020, 1863, 194624.	0.9	7
1539	AP-1 and TGFÃŸ cooperativity drives non-canonical Hedgehog signaling in resistant basal cell carcinoma. Nature Communications, 2020, 11, 5079.	5.8	47
1540	In vivo mRNA display enables large-scale proteomics by next generation sequencing. Proceedings of the National Academy of Sciences of the United States of America, 2020, 117, 26710-26718.	3.3	9
1541	Two subsets of stem-like CD8+ memory T cell progenitors with distinct fate commitments in humans. Nature Immunology, 2020, 21, 1552-1562.	7.0	167
1542	Genome-Wide Analysis Identifies an Essential Human TBX3 Pacemaker Enhancer. Circulation Research, 2020, 127, 1522-1535.	2.0	22
1543	Interleukin-10 Prevents Pathological Microglia Hyperactivation following Peripheral Endotoxin Challenge. Immunity, 2020, 53, 1033-1049.e7.	6.6	93
1544	A comparative analysis of chromatin accessibility in cattle, pig, and mouse tissues. BMC Genomics, 2020, 21, 698.	1.2	43
1545	ATAC-Seq Reveals an Isl1 Enhancer That Regulates Sinoatrial Node Development and Function. Circulation Research, 2020, 127, 1502-1518.	2.0	35
1546	Rapid Enhancer Remodeling and Transcription Factor Repurposing Enable High Magnitude Gene Induction upon Acute Activation of NK Cells. Immunity, 2020, 53, 745-758.e4.	6.6	46

#	Article	IF	Citations
1547	Mapping the epigenomic and transcriptomic interplay during memory formation and recall in the hippocampal engram ensemble. Nature Neuroscience, 2020, 23, 1606-1617.	7.1	89
1548	Cis-regulatory units of grass genomes identified by their DNA methylation. Proceedings of the National Academy of Sciences of the United States of America, 2020, 117, 25198-25199.	3.3	2
1549	Prostate cancer reactivates developmental epigenomic programs during metastatic progression. Nature Genetics, 2020, 52, 790-799.	9.4	174
1550	Myocardial infarction accelerates breast cancer via innate immune reprogramming. Nature Medicine, 2020, 26, 1452-1458.	15.2	138
1551	Behavior-related gene regulatory networks: A new level of organization in the brain. Proceedings of the National Academy of Sciences of the United States of America, 2020, 117, 23270-23279.	3.3	52
1552	The endocannabinoid anandamide has an anti-inflammatory effect on CCL2 expression in vascular smooth muscle cells. Basic Research in Cardiology, 2020, 115, 34.	2.5	15
1553	Analysis of accessible chromatin landscape in the inner cell mass and trophectoderm of human blastocysts. Molecular Human Reproduction, 2020, 26, 702-711.	1.3	5
1554	Alternative Activation of Macrophages Is Accompanied by Chromatin Remodeling Associated with Lineage-Dependent DNA Shape Features Flanking PU.1 Motifs. Journal of Immunology, 2020, 205, 1070-1083.	0.4	7
1555	Plasma Cell Fate Is Orchestrated by Elaborate Changes in Genome Compartmentalization and Inter-chromosomal Hubs. Cell Reports, 2020, 31, 107470.	2.9	14
1556	Attenuated Epigenetic Suppression of Muscle Stem Cell Necroptosis Is Required for Efficient Regeneration of Dystrophic Muscles. Cell Reports, 2020, 31, 107652.	2.9	19
1557	A Genome-wide CRISPR Screen Reveals a Role for the Non-canonical Nucleosome-Remodeling BAF Complex in Foxp3 Expression and Regulatory T Cell Function. Immunity, 2020, 53, 143-157.e8.	6.6	62
1558	T-box transcription factor 3 governs a transcriptional program for the function of the mouse atrioventricular conduction system. Proceedings of the National Academy of Sciences of the United States of America, 2020, 117, 18617-18626.	3.3	19
1559	Monitoring genome-wide chromatin accessibility by formaldehyde-assisted isolation of regulatory elements sequencing (FAIRE-seq). , 2020, , 353-369.		1
1560	ATAC-seq method applied to embryonic germ cells and neural stem cells from mouse: Practical tips and modifications. , 2020, , 371-386.		2
1561	Recent advances in computational-based approaches in epigenetics studies. , 2020, , 569-590.		1
1562	Transcriptomic and epigenomic dynamics associated with development of human iPSC-derived GABAergic interneurons. Human Molecular Genetics, 2020, 29, 2579-2595.	1.4	3
1563	Tumors induce de novo steroid biosynthesis in T cells to evade immunity. Nature Communications, 2020, 11, 3588.	5.8	54
1564	Identification and requirements of enhancers that direct gene expression during zebrafish fin regeneration. Development (Cambridge), 2020, 147, .	1.2	39

#	Article	IF	Citations
1565	Analysis of singleâ€€cell RNAseq identifies transitional states of T cells associated with hepatocellular carcinoma. Clinical and Translational Medicine, 2020, 10, e133.	1.7	17
1566	Networks of transcription factors. , 2020, , 137-155.		3
1567	Protein Prenylation Drives Discrete Signaling Programs for the Differentiation and Maintenance of Effector Treg Cells. Cell Metabolism, 2020, 32, 996-1011.e7.	7.2	28
1568	Chromatin accessibility landscapes of skin cells in systemic sclerosis nominate dendritic cells in disease pathogenesis. Nature Communications, 2020, 11, 5843.	5.8	22
1569	Altered transcriptional and chromatin responses to rhinovirus in bronchial epithelial cells from adults with asthma. Communications Biology, 2020, 3, 678.	2.0	13
1570	NGS-Integrator: An efficient tool for combining multiple NGS data tracks using minimum Bayesâ€™ factors. BMC Genomics, 2020, 21, 806.	1.2	3
1571	Differential abilities to engage inaccessible chromatin diversify vertebrate HOX binding patterns. Development (Cambridge), 2020, 147, .	1.2	34
1572	Distinct Age-Related Epigenetic Signatures in CD4 and CD8 T Cells. Frontiers in Immunology, 2020, 11, 585168.	2.2	46
1573	Common variants in signaling transcription-factor-binding sites drive phenotypic variability in red blood cell traits. Nature Genetics, 2020, 52, 1333-1345.	9.4	24
1574	Requisite Chromatin Remodeling for Myeloid and Erythroid Lineage Differentiation from Erythromyeloid Progenitors. Cell Reports, 2020, 33, 108395.	2.9	6
1575	An Integrated Epigenomic and Transcriptomic Map of Mouse and Human Î±Î² T Cell Development. Immunity, 2020, 53, 1182-1201.e8.	6.6	49
1576	Genomic retargeting of p53 and CTCF is associated with transcriptional changes during oncogenic HRas-induced transformation. Communications Biology, 2020, 3, 696.	2.0	4
1577	A map of cis-regulatory elements and 3D genome structures in zebrafish. Nature, 2020, 588, 337-343.	13.7	80
1578	Simultaneous profiling of chromatin accessibility and methylation on human cell lines with nanopore sequencing. Nature Methods, 2020, 17, 1191-1199.	9.0	133
1579	Genomic profiling of T-cell activation suggests increased sensitivity of memory T cells to CD28 costimulation. Genes and Immunity, 2020, 21, 390-408.	2.2	17
1580	The Transcription Factor Foxp3 Shapes Regulatory T Cell Identity by Tuning the Activity of trans-Acting Intermediaries. Immunity, 2020, 53, 971-984.e5.	6.6	60
1581	BMP signaling: at the gate between activated melanocyte stem cells and differentiation. Genes and Development, 2020, 34, 1713-1734.	2.7	35
1582	Dedifferentiation and neuronal repression define familial Alzheimerâ€™s disease. Science Advances, 2020, 6, .	4.7	44

#	Article	IF	Citations
1583	Interrogating Host Antiviral Environments Driven by Nuclear DNA Sensing: A Multiomic Perspective. Biomolecules, 2020, 10, 1591.	1.8	7
1584	TGFÎ² promotes widespread enhancer chromatin opening and operates on genomic regulatory domains. Nature Communications, 2020, 11, 6196.	5.8	21
1585	A developmental stage specific network approach for studying dynamic transcription factor-microRNA co-regulation during craniofacial development. Development (Cambridge), 2020, 147, .	1.2	17
1586	RNA sequencing: new technologies and applications in cancer research. Journal of Hematology and Oncology, 2020, 13, 166.	6.9	229
1587	Chromatin Structure and Function in Mosquitoes. Frontiers in Genetics, 2020, 11, 602949.	1.1	9
1588	A Customizable Analysis Flow in Integrative Multi-Omics. Biomolecules, 2020, 10, 1606.	1.8	14
1589	Tn5 Transposase Applied in Genomics Research. International Journal of Molecular Sciences, 2020, 21, 8329.	1.8	23
1590	A human cell atlas of fetal gene expression. Science, 2020, 370, .	6.0	436
1591	Bibliometric Analysis of ATAC-Seq and Its Use in Cancer Biology via Nucleic Acid Detection. Frontiers in Medicine, 2020, 7, 584728.	1.2	14
1592	Engineering of Î±-PD-1 antibody-expressing long-lived plasma cells by CRISPR/Cas9-mediated targeted gene integration. Cell Death and Disease, 2020, 11, 973.	2.7	20
1593	ATAC-seq with unique molecular identifiers improves quantification and footprinting. Communications Biology, 2020, 3, 675.	2.0	21
1594	The Clusters of Transcription Factors NFATC2, STAT5, GATA2, AP1, RUNX1 and EGR2 Binding Sites at the Induced Il13 Enhancers Mediate Il13 Gene Transcription in Response to Antigenic Stimulation. Journal of Immunology, 2020, 205, 3311-3318.	0.4	4
1595	Advances in Chromatin and Chromosome Research: Perspectives from Multiple Fields. Molecular Cell, 2020, 79, 881-901.	4.5	42
1596	Identifying Improved Sites for Heterologous Gene Integration Using ATAC-seq. ACS Synthetic Biology, 2020, 9, 2515-2524.	1.9	13
1597	Integrative analyses of single-cell transcriptome and regulome using MAESTRO. Genome Biology, 2020, 21, 198.	3.8	126
1598	Tousled-Like Kinases Suppress Innate Immune Signaling Triggered by Alternative Lengthening of Telomeres. Cell Reports, 2020, 32, 107983.	2.9	23
1599	Decoding the plant genome: From epigenome to 3D organization. Journal of Genetics and Genomics, 2020, 47, 425-435.	1.7	8
1600	Visualization and Sequencing of Accessible Chromatin Reveals Cell Cycle and Post-HDAC inhibitor Treatment Dynamics. Journal of Molecular Biology, 2020, 432, 5304-5321.	2.0	8

#	Article	IF	Citations
1601	Chromatin accessibility landscape of pediatric Tâ€lymphoblastic leukemia and human Tâ€cell precursors. EMBO Molecular Medicine, 2020, 12, e12104.	3.3	13
1602	Integrative Omics Analyses Reveal Epigenetic Memory in Diabetic Renal Cells Regulating Genes Associated With Kidney Dysfunction. Diabetes, 2020, 69, 2490-2502.	0.3	11
1603	Network Approaches for Dissecting the Immune System. IScience, 2020, 23, 101354.	1.9	28
1604	Ancestral and derived transcriptional enhancers share regulatory sequence and a pleiotropic site affecting chromatin accessibility. Proceedings of the National Academy of Sciences of the United States of America, 2020, 117, 20636-20644.	3.3	18
1605	Self-Reporting Transposons Enable SimultaneousÂReadout of Gene Expression and TranscriptionÂFactor Binding in Single Cells. Cell, 2020, 182, 992-1008.e21.	13.5	54
1606	Differential contribution of p300 and CBP to regulatory element acetylation in mESCs. BMC Molecular and Cell Biology, 2020, 21, 55.	1.0	44
1607	Assessment of the epigenetic nature of chromosomal proteins during DNA replication and mitosis. , 2020, , 447-476.		0
1608	Single-cell epigenomics: Methods and translation. , 2020, , 525-535.		0
1609	Epigenomic State Transitions Characterize Tumor Progression in Mouse Lung Adenocarcinoma. Cancer Cell, 2020, 38, 212-228.e13.	7.7	140
1610	Unraveling the Complexity of the Cancer Microenvironment With Multidimensional Genomic and Cytometric Technologies. Frontiers in Oncology, 2020, 10, 1254.	1.3	45
1611	Discovering How Heme Controls Genome Function Through Heme-omics. Cell Reports, 2020, 31, 107832.	2.9	21
1612	Stem Cell Determinant SOX9 Promotes Lineage Plasticity and Progression in Basal-like Breast Cancer. Cell Reports, 2020, 31, 107742.	2.9	34
1613	An atlas of dynamic chromatin landscapes in mouse fetal development. Nature, 2020, 583, 744-751.	13.7	257
1614	Spatiotemporal DNA methylome dynamics of the developing mouse fetus. Nature, 2020, 583, 752-759.	13.7	84
1615	Landscape of cohesin-mediated chromatin loops in the human genome. Nature, 2020, 583, 737-743.	13.7	134
1616	Expanded encyclopaedias of DNA elements in the human and mouse genomes. Nature, 2020, 583, 699-710.	13.7	1,252
1617	Networkâ€based approaches for understanding gene regulation and function in plants. Plant Journal, 2020, 104, 302-317.	2.8	35
1618	Dissecting Murine Muscle Stem Cell Aging through Regeneration Using Integrative Genomic Analysis. Cell Reports, 2020, 32, 107964.	2.9	49

#	Article	IF	Citations
1619	Human fetal microglia acquire homeostatic immune-sensing properties early in development. Science, 2020, 369, 530-537.	6.0	104
1620	Cross-species analysis of enhancer logic using deep learning. Genome Research, 2020, 30, 1815-1834.	2.4	65
1621	Improving plant gene regulatory network inference by integrative analysis of multi-omics and high resolution data sets. Current Opinion in Systems Biology, 2020, 22, 8-15.	1.3	10
1622	Chromatin Accessibility Dynamics and a Hierarchical Transcriptional Regulatory Network Structure for Plant Somatic Embryogenesis. Developmental Cell, 2020, 54, 742-757.e8.	3.1	88
1623	JMJD5 couples with CDK9 to release the paused RNA polymerase II. Proceedings of the National Academy of Sciences of the United States of America, 2020, 117, 19888-19895.	3.3	8
1624	Chronic lymphocytic leukemia (CLL) risk is mediated by multiple enhancer variants within CLL risk loci. Human Molecular Genetics, 2020, 29, 2761-2774.	1.4	6
1625	Interactions With Histone H3 & Tools to Study Them. Frontiers in Cell and Developmental Biology, 2020, 8, 701.	1.8	17
1626	Endogenous Retrovirus-Derived lncRNA BANCR Promotes Cardiomyocyte Migration in Humans and Non-human Primates. Developmental Cell, 2020, 54, 694-709.e9.	3.1	37
1627	Sustained Activation of AMPK Enhances Differentiation of Human iPSC-Derived Cardiomyocytes via Sirtuin Activation. Stem Cell Reports, 2020, 15, 498-514.	2.3	16
1628	Monarch Butterfly Migration Moving into the Genetic Era. Trends in Genetics, 2020, 36, 689-701.	2.9	21
1629	EED-mediated histone methylation is critical for CNS myelination and remyelination by inhibiting WNT, BMP, and senescence pathways. Science Advances, 2020, 6, eaaz6477.	4.7	29
1630	Integrating single-cell RNA-sequencing and functional assays to decipher mammary cell states and lineage hierarchies. Npj Breast Cancer, 2020, 6, 32.	2.3	8
1631	G-quadruplex structures bind to EZ-Tn5 transposase. Biochimie, 2020, 177, 190-197.	1.3	2
1632	Altered 3D chromatin structure permits inversional recombination at the IgH locus. Science Advances, 2020, 6, eaaz8850.	4.7	13
1634	Unique Epigenetic Programming Distinguishes Regenerative Spermatogonial Stem Cells in the Developing Mouse Testis. IScience, 2020, 23, 101596.	1.9	22
1635	Activation of Clustered IFNÎ³ Target Genes Drives Cohesin-Controlled Transcriptional Memory. Molecular Cell, 2020, 80, 396-409.e6.	4.5	32
1636	FoxO maintains a genuine muscle stem-cell quiescent state until geriatric age. Nature Cell Biology, 2020, 22, 1307-1318.	4.6	96
1637	Single-cell epigenomic analyses implicate candidate causal variants at inherited risk loci for Alzheimerâ€™s and Parkinsonâ€™s diseases. Nature Genetics, 2020, 52, 1158-1168.	9.4	217

#	Article	IF	Citations
1638	Molecular evolution of gland cell types and chemical interactions in animals. Journal of Experimental Biology, 2020, 223, .	0.8	29
1639	How to study enhancers in non-traditional insect models. Journal of Experimental Biology, 2020, 223, .	0.8	5
1640	Distinctive regulatory architectures of germline-active and somatic genes in C. elegans. Genome Research, 2020, 30, 1752-1765.	2.4	32
1641	Chromatin Potential Identified by Shared Single-Cell Profiling of RNA and Chromatin. Cell, 2020, 183, 1103-1116.e20.	13.5	600
1642	G9a Plays Distinct Roles in Maintaining DNA Methylation, Retrotransposon Silencing, and Chromatin Looping. Cell Reports, 2020, 33, 108315.	2.9	43
1643	Probing infectious disease by single-cell RNA sequencing: Progresses and perspectives. Computational and Structural Biotechnology Journal, 2020, 18, 2962-2971.	1.9	32
1644	Genome-wide identification of accessible chromatin regions in bumblebee by ATAC-seq. Scientific Data, 2020, 7, 367.	2.4	2
1645	Deletion of Histone Methyltransferase G9a Suppresses Mutant Kras-driven Pancreatic Carcinogenesis. Cancer Genomics and Proteomics, 2020, 17, 695-705.	1.0	9
1646	Genome-wide chromatin accessibility is restricted by ANP32E. Nature Communications, 2020, 11, 5063.	5.8	29
1647	Trained Immunity-Promoting Nanobiologic Therapy Suppresses Tumor Growth and Potentiates Checkpoint Inhibition. Cell, 2020, 183, 786-801.e19.	13.5	101
1648	Globally altered epigenetic landscape and delayed osteogenic differentiation in H3.3-G34W-mutant giant cell tumor of bone. Nature Communications, 2020, 11, 5414.	5.8	31
1649	Alternative Enhancer Usage and Targeted Polycomb Marking Hallmark Promoter Choice during T Cell Differentiation. Cell Reports, 2020, 32, 108048.	2.9	13
1650	Pairwise Stimulations of Pathogen-Sensing Pathways Predict Immune Responses to Multi-adjuvant Combinations. Cell Systems, 2020, 11, 495-508.e10.	2.9	22
1651	Functional interactions between Mi-2Î² and AP1 complexes control response and recovery from skin barrier disruption. Journal of Experimental Medicine, 2020, 217, .	4.2	10
1652	BACH2 drives quiescence and maintenance of resting Treg cells to promote homeostasis and cancer immunosuppression. Journal of Experimental Medicine, 2020, 217, .	4.2	47
1653	Efficient chromatin profiling of H3K4me3 modification in cotton using CUT&Tag. Plant Methods, 2020, 16, 120.	1.9	31
1654	The transcription factor E2A activates multiple enhancers that drive Rag expression in developing T and B cells. Science Immunology, 2020, 5, .	5.6	41
1655	Pioneer Transcription Factors Initiating Gene Network Changes. Annual Review of Genetics, 2020, 54, 367-385.	3.2	247

#	Article	IF	Citations
1656	Single-Cell Analysis of Neonatal HSC Ontogeny Reveals Gradual and Uncoordinated Transcriptional Reprogramming that Begins before Birth. Cell Stem Cell, 2020, 27, 732-747.e7.	5.2	53
1657	The prospects of singleâ€cell analysis in autoimmunity. Scandinavian Journal of Immunology, 2020, 92, e12964.	1.3	2
1658	FOXA1 Mutations Reveal Distinct Chromatin Profiles and Influence Therapeutic Response in Breast Cancer. Cancer Cell, 2020, 38, 534-550.e9.	7.7	67
1659	YTHDF2/3 Are Required for Somatic Reprogramming through Different RNA Deadenylation Pathways. Cell Reports, 2020, 32, 108120.	2.9	44
1660	Designing custom CRISPR libraries for hypothesis-driven drug target discovery. Computational and Structural Biotechnology Journal, 2020, 18, 2237-2246.	1.9	10
1661	Illuminating the noncoding genome in cancer. Nature Cancer, 2020, 1, 864-872.	5.7	37
1662	Transcription factor expression defines subclasses of developing projection neurons highly similar to single-cell RNA-seq subtypes. Proceedings of the National Academy of Sciences of the United States of America, 2020, 117, 25074-25084.	3.3	23
1663	Revisiting 3D chromatin architecture in cancer development and progression. Nucleic Acids Research, 2020, 48, 10632-10647.	6.5	22
1664	Evolution of vertebrate gill covers via shifts in an ancient Pou3f3 enhancer. Proceedings of the National Academy of Sciences of the United States of America, 2020, 117, 24876-24884.	3.3	19
1665	CHD8 dosage regulates transcription in pluripotency and early murine neural differentiation. Proceedings of the National Academy of Sciences of the United States of America, 2020, 117, 22331-22340.	3.3	27
1666	Molecular Insights Into Regulatory T-Cell Adaptation to Self, Environment, and Host Tissues: Plasticity or Loss of Function in Autoimmune Disease. Frontiers in Immunology, 2020, 11, 1269.	2.2	14
1667	ATAC-seq footprinting unravels kinetics of transcription factor binding during zygotic genome activation. Nature Communications, 2020, 11, 4267.	5.8	318
1668	regSNPs-ASB: A Computational Framework for Identifying Allele-Specific Transcription Factor Binding From ATAC-seq Data. Frontiers in Bioengineering and Biotechnology, 2020, 8, 886.	2.0	5
1669	What Have Advances in Transcriptomic Technologies Taught us About Human White Matter Pathologies?. Frontiers in Cellular Neuroscience, 2020, 14, 238.	1.8	8
1671	Hyperacetylated chromatin domains mark cell type-specific genes and suggest distinct modes of enhancer function. Nature Communications, 2020, 11, 4544.	5.8	12
1672	Cancer-specific CTCF binding facilitates oncogenic transcriptional dysregulation. Genome Biology, 2020, 21, 247.	3.8	70
1673	Chromatin accessibility mapping of the striatum identifies tyrosine kinase FYN as a therapeutic target for heroin use disorder. Nature Communications, 2020, 11, 4634.	5.8	21
1674	ReprogrammingÂroadmap reveals route toÂhuman induced trophoblast stem cells. Nature, 2020, 586, 101-107.	13.7	131

#	Article	IF	Citations
1675	VDRâ€“SOX2 signaling promotes colorectal cancer stemness and malignancy in an acidic microenvironment. Signal Transduction and Targeted Therapy, 2020, 5, 183.	7.1	30
1676	Efficient low-cost chromatin profiling with CUT&Tag. Nature Protocols, 2020, 15, 3264-3283.	5.5	181
1677	Early programming of CD8 ⁺ T cell response by the orphan nuclear receptor NR4A3. Proceedings of the National Academy of Sciences of the United States of America, 2020, 117, 24392-24402.	3.3	20
1678	In Vivo Reporter Assays Uncover Changes in Enhancer Activity Caused by Type 2 Diabetesâ€“Associated Single Nucleotide Polymorphisms. Diabetes, 2020, 69, 2794-2805.	0.3	4
1679	ARID1a Associates with Lymphoid-Restricted Transcription Factors and Has an Essential Role in T Cell Development. Journal of Immunology, 2020, 205, 1419-1432.	0.4	15
1680	Next steps in the identification of gene targets for type 1 diabetes. Diabetologia, 2020, 63, 2260-2269.	2.9	12
1681	Chronic cortisol exposure in early development leads to neuroendocrine dysregulation in adulthood. BMC Research Notes, 2020, 13, 366.	0.6	8
1682	Identifying proteins bound to native mitotic ESC chromosomes reveals chromatin repressors are important for compaction. Nature Communications, 2020, 11, 4118.	5.8	26
1683	Phf21b imprints the spatiotemporal epigenetic switch essential for neural stem cell differentiation. Genes and Development, 2020, 34, 1190-1209.	2.7	9
1684	Cytoplasmic Citrate Flux Modulates the Immune Stimulatory NKG2D Ligand MICA in Cancer Cells. Frontiers in Immunology, 2020, 11, 1968.	2.2	11
1685	E proteins orchestrate dynamic transcriptional cascades implicated in the suppression of the differentiation of group 2 innate lymphoid cells. Journal of Biological Chemistry, 2020, 295, 14866-14877.	1.6	10
1686	Early precursor T cells establish and propagate T cell exhaustion in chronic infection. Nature Immunology, 2020, 21, 1256-1266.	7.0	160
1687	SAMMY-seq reveals early alteration of heterochromatin and deregulation of bivalent genes in Hutchinson-Gilford Progeria Syndrome. Nature Communications, 2020, 11, 6274.	5.8	22
1688	Experimental and computational technologies to dissect the kidney at the single-cell level. Nephrology Dialysis Transplantation, 2022, 37, 628-637.	0.4	6
1689	A Review About Transcription Factor Binding Sites Prediction Based on Deep Learning. IEEE Access, 2020, 8, 219256-219274.	2.6	16
1690	Creation of bladder assembloids mimicking tissue regeneration and cancer. Nature, 2020, 588, 664-669.	13.7	133
1691	Predicting transcription factor binding in single cells through deep learning. Science Advances, 2020, 6, .	4.7	41
1692	Human T-bet Governs Innate and Innate-like Adaptive IFN-Î³ Immunity against Mycobacteria. Cell, 2020, 183, 1826-1847.e31.	13.5	83

#	Article	IF	Citations
1693	The Identity of Human Tissue-Emigrant CD8+ T Cells. Cell, 2020, 183, 1946-1961.e15.	13.5	58
1694	The Master Regulator Protein BAZ2B Can Reprogram Human Hematopoietic Lineage-Committed Progenitors into a Multipotent State. Cell Reports, 2020, 33, 108474.	2.9	19
1695	A long noncoding RNA, LncMyoD , modulates chromatin accessibility to regulate muscle stem cell myogenic lineage progression. Proceedings of the National Academy of Sciences of the United States of America, 2020, 117, 32464-32475.	3.3	32
1696	Che-1/AATF-induced transcriptionally active chromatin promotes cell proliferation in multiple myeloma. Blood Advances, 2020, 4, 5616-5630.	2.5	10
1697	Common schizophrenia risk variants are enriched in open chromatin regions of human glutamatergic neurons. Nature Communications, 2020, 11, 5581.	5.8	53
1698	Lineage-Resolved Enhancer and Promoter Usage during a Time Course of Embryogenesis. Developmental Cell, 2020, 55, 648-664.e9.	3.1	47
1699	An Organoid Biobank of Neuroendocrine Neoplasms Enables Genotype-Phenotype Mapping. Cell, 2020, 183, 1420-1435.e21.	13.5	111
1700	Repetitive Elements Trigger RIG-I-like Receptor Signaling that Regulates the Emergence of Hematopoietic Stem and Progenitor Cells. Immunity, 2020, 53, 934-951.e9.	6.6	43
1701	Profiling chromatin regulatory landscape: insights into the development of ChIP-seq and ATAC-seq. Molecular Biomedicine, 2020, 1, 9.	1.7	34
1702	Molecular structures and mechanisms of DNA break processing in mouse meiosis. Genes and Development, 2020, 34, 806-818.	2.7	46
1703	AP-1 Contributes to Chromatin Accessibility to Promote Sarcomere Disassembly and Cardiomyocyte Protrusion During Zebrafish Heart Regeneration. Circulation Research, 2020, 126, 1760-1778.	2.0	87
1704	Epigenetic Changes During Human Thyroid Cell Differentiation. Thyroid, 2020, 30, 1666-1675.	2.4	7
1705	Prenet: Predictive network from ATAC-SEQ data. Journal of Bioinformatics and Computational Biology, 2020, 18, 2040003.	0.3	2
1706	Integrated single-cell and bulk gene expression and ATAC-seq reveals heterogeneity and early changes in pathways associated with resistance to cetuximab in HNSCC-sensitive cell lines. British Journal of Cancer, 2020, 123, 101-113.	2.9	38
1707	Unique properties of a subset of human pluripotent stem cells with high capacity for self-renewal. Nature Communications, 2020, 11, 2420.	5.8	29
1708	MEDEA: analysis of transcription factor binding motifs in accessible chromatin. Genome Research, 2020, 30, 736-748.	2.4	8
1709	Bâ€cell lymphoma 2 family genes show a molecular pattern of spatiotemporal heterogeneity in gynaecologic and breast cancer. Cell Proliferation, 2020, 53, e12826.	2.4	6
1710	Protection from DNA re-methylation by transcription factors in primordial germ cells and pre-implantation embryos can explain trans-generational epigenetic inheritance. Genome Biology, 2020, 21, 118.	3.8	43

#	Article	IF	Citations
1711	HOX13-dependent chromatin accessibility underlies the transition towards the digit development program. Nature Communications, 2020, 11, 2491.	5.8	40
1712	Chromatin Regulator CHD1 Remodels the Immunosuppressive Tumor Microenvironment in PTEN-Deficient Prostate Cancer. Cancer Discovery, 2020, 10, 1374-1387.	7.7	60
1713	Cistrome Data Browser and Toolkit: analyzing human and mouse genomic data using compendia of ChIPâ€seq and chromatin accessibility data. Quantitative Biology, 2020, 8, 267-276.	0.3	11
1714	NFI transcription factors provide chromatin access to maintain stem cell identity while preventing unintended lineage fate choices. Nature Cell Biology, 2020, 22, 640-650.	4.6	52
1715	The Promises and the Challenges of Integrating Multi-Omics and Systems Biology in Comparative Stress Biology. Integrative and Comparative Biology, 2020, 60, 89-97.	0.9	13
1716	Functional genomics analysis of human colon organoids identifies key transcription factors. Physiological Genomics, 2020, 52, 234-244.	1.0	16
1717	Matrix factorization and transfer learning uncover regulatory biology across multiple single-cell ATAC-seq data sets. Nucleic Acids Research, 2020, 48, e68-e68.	6.5	8
1718	A distal enhancer at risk locus 11q13.5 promotes suppression of colitis by Treg cells. Nature, 2020, 583, 447-452.	13.7	40
1719	APEC: an accesson-based method for single-cell chromatin accessibility analysis. Genome Biology, 2020, 21, 116.	3.8	12
1720	Dynamics of the 4D genome during in vivo lineage specification and differentiation. Nature Communications, 2020, 11, 2722.	5.8	79
1721	Organ of Corti size is governed by Yap/Tead-mediated progenitor self-renewal. Proceedings of the National Academy of Sciences of the United States of America, 2020, 117, 13552-13561.	3.3	36
1722	Regulatory sharing between estrogen receptor Î± bound enhancers. Nucleic Acids Research, 2020, 48, 6597-6610.	6.5	7
1723	Epigenetics and imprinting in assisted reproduction. , 2020, , 69-87.		0
1724	Recent advances and future perspectives in vector-omics. Current Opinion in Insect Science, 2020, 40, 94-103.	2.2	6
1725	Enhancer evolution in chordates: Lessons from functional analyses of cephalochordate cisâ€regulatory modules. Development Growth and Differentiation, 2020, 62, 279-300.	0.6	4
1726	Seq-ing answers: Current data integration approaches to uncover mechanisms of transcriptional regulation. Computational and Structural Biotechnology Journal, 2020, 18, 1330-1341.	1.9	16
1727	Folding Keratin Gene Clusters during Skin Regional Specification. Developmental Cell, 2020, 53, 561-576.e9.	3.1	18
1728	Inactivation of Arid1a in the endometrium is associated with endometrioid tumorigenesis through transcriptional reprogramming. Nature Communications, 2020, 11, 2717.	5.8	45

#	Article	IF	Citations
1729	CRISPR Screens Identify Essential Cell Growth Mediators in BRAF Inhibitor-resistant Melanoma. Genomics, Proteomics and Bioinformatics, 2020, 18, 26-40.	3.0	14
1730	BAF60a deficiency uncouples chromatin accessibility and cold sensitivity from white fat browning. Nature Communications, 2020, 11, 2379.	5.8	20
1731	From GWAS to Function: Using Functional Genomics to Identify the Mechanisms Underlying Complex Diseases. Frontiers in Genetics, 2020, 11, 424.	1.1	335
1732	Investigating Human Mitochondrial Genomes in Single Cells. Genes, 2020, 11, 534.	1.0	8
1733	Identification of Plant Enhancers and Their Constituent Elements by STARR-seq in Tobacco Leaves. Plant Cell, 2020, 32, 2120-2131.	3.1	53
1734	Inhibition of Glycolysis in Pathogenic TH17 Cells through Targeting a miR-21â€“Peli1â€“c-Rel Pathway Prevents Autoimmunity. Journal of Immunology, 2020, 204, 3160-3170.	0.4	17
1735	Single-cell genomic analysis of human cerebral organoids. Methods in Cell Biology, 2020, 159, 229-256.	0.5	14
1736	All-in-one sequencing: an improved library preparation method for cost-effective and high-throughput next-generation sequencing. Plant Methods, 2020, 16, 74.	1.9	10
1737	Analysis of putative cis-regulatory elements regulating blood pressure variation. Human Molecular Genetics, 2020, 29, 1922-1932.	1.4	7
1738	Genome-Wide Characterization of DNase I-Hypersensitive Sites and Cold Response Regulatory Landscapes in Grasses. Plant Cell, 2020, 32, 2457-2473.	3.1	29
1739	Glucocorticoid regulates mesenchymal cell differentiation required for perinatal lung morphogenesis and function. American Journal of Physiology - Lung Cellular and Molecular Physiology, 2020, 319, L239-L255.	1.3	19
1740	The Gossypium longicalyx Genome as a Resource for Cotton Breeding and Evolution. G3: Genes, Genomes, Genetics, 2020, 10, 1457-1467.	0.8	32
1741	Single-cell ATAC sequencing analysis: From data preprocessing to hypothesis generation. Computational and Structural Biotechnology Journal, 2020, 18, 1429-1439.	1.9	91
1742	An Erg-driven transcriptional program controls B cell lymphopoiesis. Nature Communications, 2020, 11, 3013.	5.8	29
1743	The Number of Transcription Factors at an Enhancer Determines Switch-like Gene Expression. Cell Reports, 2020, 31, 107724.	2.9	25
1744	Functional genomics of parental care of insects. Hormones and Behavior, 2020, 122, 104756.	1.0	5
1745	Translational Opportunities for Microfluidic Technologies to Enable Precision Epigenomics. Analytical Chemistry, 2020, 92, 7989-7997.	3.2	8
1746	Homeostatic Cytokines Drive Epigenetic Reprogramming of Activated T Cells into a â€œNaive-Memoryâ€• Phenotype. IScience, 2020, 23, 100989.	1.9	15

#	Article	IF	Citations
1747	Reduced chromatin accessibility underlies gene expression differences in homologous chromosome arms of diploid Aegilops tauschii and hexaploid wheat. GigaScience, 2020, 9, .	3.3	23
1748	Targeting Nuclear NOTCH2 by Gliotoxin Recovers a Tumor-Suppressor NOTCH3 Activity in CLL. Cells, 2020, 9, 1484.	1.8	7
1749	Intergenerationally Maintained Histone H4 Lysine 16 Acetylation Is Instructive for Future Gene Activation. Cell, 2020, 182, 127-144.e23.	13.5	57
1750	SIRT7 antagonizes human stem cell aging as a heterochromatin stabilizer. Protein and Cell, 2020, 11, 483-504.	4.8	85
1751	Genomic resources for dissecting the role of non-protein coding variation in gene-environment interactions. Toxicology, 2020, 441, 152505.	2.0	2
1752	Integrative computational epigenomics to build data-driven gene regulation hypotheses. GigaScience, 2020, 9, .	3.3	13
1753	Genomic Rewiring of SOX2 Chromatin Interaction Network during Differentiation of ESCs to Postmitotic Neurons. Cell Systems, 2020, 10, 480-494.e8.	2.9	25
1754	Hematopoietic stem and progenitor cell-restricted Cdx2 expression induces transformation to myelodysplasia and acute leukemia. Nature Communications, 2020, 11, 3021.	5.8	15
1755	3D genome architecture coordinates trans and cis regulation of differentially expressed ear and tassel genes in maize. Genome Biology, 2020, 21, 143.	3.8	60
1756	Establishment of chromatin accessibility by the conserved transcription factor Grainy head is developmentally regulated. Development (Cambridge), 2020, 147, .	1.2	16
1757	Prediabetes Induced by a Single Autoimmune B Cell Clone. Frontiers in Immunology, 2020, 11, 1073.	2.2	3
1758	Epigenetic biomarkers and preterm birth. Environmental Epigenetics, 2020, 6, dvaa005.	0.9	19
1759	Fat Distribution in Women Is Associated With Depot-Specific Transcriptomic Signatures and Chromatin Structure. Journal of the Endocrine Society, 2020, 4, bvaa042.	0.1	11
1760	AP-1 imprints a reversible transcriptional programme of senescent cells. Nature Cell Biology, 2020, 22, 842-855.	4.6	114
1761	CTCF is dispensable for immune cell transdifferentiation but facilitates an acute inflammatory response. Nature Genetics, 2020, 52, 655-661.	9.4	98
1762	Dynamic chromatin accessibility profiling reveals changes in host genome organization in response to baculovirus infection. PLoS Pathogens, 2020, 16, e1008633.	2.1	12
1763	Unravelling the complex genetics of common kidney diseases: from variants to mechanisms. Nature Reviews Nephrology, 2020, 16, 628-640.	4.1	33
1764	Understanding immune system development: An epigenetic perspective. , 2020, , 39-76.		1

#	Article	IF	Citations
1765	Advances in single-cell epigenomics of the immune system. , 2020, , 185-216.		1
1766	Dysregulation of BRD4 Function Underlies the Functional Abnormalities of MeCP2 Mutant Neurons. Molecular Cell, 2020, 79, 84-98.e9.	4.5	53
1767	Complexities of Understanding Function from CKD-Associated DNA Variants. Clinical Journal of the American Society of Nephrology: CJASN, 2020, 15, 1028-1040.	2.2	1
1768	Machine learning and deep learning for the advancement of epigenomics. , 2020, , 217-237.		0
1769	Dissecting the early steps of MLL induced leukaemogenic transformation using a mouse model of AML. Nature Communications, 2020, 11, 1407.	5.8	13
1770	The histone methyltransferase Setd8 alters the chromatin landscape and regulates the expression of key transcription factors during erythroid differentiation. Epigenetics and Chromatin, 2020, 13, 16.	1.8	17
1771	Characterization of functional transposable element enhancers in acute myeloid leukemia. Science China Life Sciences, 2020, 63, 675-687.	2.3	7
1772	Chromatin-remodeling links metabolic signaling to gene expression. Molecular Metabolism, 2020, 38, 100973.	3.0	37
1773	A molecular network regulating the proinflammatory phenotype of human memory T lymphocytes. Nature Immunology, 2020, 21, 388-399.	7.0	56
1774	3D ATAC-PALM: super-resolution imaging of the accessible genome. Nature Methods, 2020, 17, 430-436.	9.0	62
1775	Global Regulation of the Histone Mark H3K36me2 Underlies Epithelial Plasticity and Metastatic Progression. Cancer Discovery, 2020, 10, 854-871.	7.7	54
1776	Integrating Peak Colocalization and Motif Enrichment Analysis for the Discovery of Genome-Wide Regulatory Modules and Transcription Factor Recruitment Rules. Frontiers in Genetics, 2020, 11, 72.	1.1	6
1777	An integrative view of the regulatory and transcriptional landscapes in mouse hematopoiesis. Genome Research, 2020, 30, 472-484.	2.4	38
1778	Transcription and Beyond: Delineating FOXG1 Function in Cortical Development and Disorders. Frontiers in Cellular Neuroscience, 2020, 14, 35.	1.8	46
1779	Long-lived T follicular helper cells retain plasticity and help sustain humoral immunity. Science Immunology, 2020, 5, .	5.6	78
1780	Developmental Transcriptional Enhancers: A Subtle Interplay between Accessibility and Activity. BioEssays, 2020, 42, e1900188.	1.2	18
1781	A key control point in the T cell response to chronic infection and neoplasia: FOXO1. Current Opinion in Immunology, 2020, 63, 51-60.	2.4	7
1782	Prioritizing disease and trait causal variants at the TNFAIP3 locus using functional and genomic features. Nature Communications, 2020, 11, 1237.	5.8	38

#	Article	IF	Citations
1783	Specific subfamilies of transposable elements contribute to different domains of T lymphocyte enhancers. Proceedings of the National Academy of Sciences of the United States of America, 2020, 117, 7905-7916.	3.3	46
1784	ATACing DNA Methylation during Differentiation. Molecular Cell, 2020, 77, 1159-1161.	4.5	4
1785	Evaluating Enhancer Function and Transcription. Annual Review of Biochemistry, 2020, 89, 213-234.	5.0	123
1786	Cis-regulatory analysis of Onecut1 expression in fate-restricted retinal progenitor cells. Neural Development, 2020, 15, 5.	1.1	13
1787	Capturing functional epigenomes for insight into metabolic diseases. Molecular Metabolism, 2020, 38, 100936.	3.0	9
1788	Chromatyping: Reconstructing Nucleosome Profiles from NOMe Sequencing Data. Journal of Computational Biology, 2020, 27, 330-341.	0.8	0
1789	Time course regulatory analysis based on paired expression and chromatin accessibility data. Genome Research, 2020, 30, 622-634.	2.4	35
1790	Characterization of the chromatin accessibility in an Alzheimerâ€™s disease (AD) mouse model. Alzheimer's Research and Therapy, 2020, 12, 29.	3.0	29
1791	Chromatin Remodeling and Immediate Early Gene Activation by SLFN11 in Response to Replication Stress. Cell Reports, 2020, 30, 4137-4151.e6.	2.9	48
1792	Exploring 3D chromatin contacts in gene regulation: The evolution of approaches for the identification of functional enhancer-promoter interaction. Computational and Structural Biotechnology Journal, 2020, 18, 558-570.	1.9	37
1793	Environmental Pressures on Transgenerational Epigenetic Inheritance. , 2020, , 97-122.		0
1794	Evolutionary Selection and Constraint on Human Knee Chondrocyte Regulation Impacts Osteoarthritis Risk. Cell, 2020, 181, 362-381.e28.	13.5	64
1795	Quantification, Dynamic Visualization, and Validation of Bias in ATAC-Seq Data with ataqv. Cell Systems, 2020, 10, 298-306.e4.	2.9	53
1796	Transposable elements contribute to the genomic response to insecticides in Drosophila melanogaster. Philosophical Transactions of the Royal Society B: Biological Sciences, 2020, 375, 20190341.	1.8	27
1797	Pro-neuronal activity of Myod1 due to promiscuous binding to neuronal genes. Nature Cell Biology, 2020, 22, 401-411.	4.6	38
1798	BET protein inhibitor JQ1 downregulates chromatin accessibility and suppresses metastasis of gastric cancer via inactivating RUNX2/NID1 signaling. Oncogenesis, 2020, 9, 33.	2.1	59
1799	Smarcad1 mediates microbiota-induced inflammation in mouse and coordinates gene expression in the intestinal epithelium. Genome Biology, 2020, 21, 64.	3.8	13
1800	Invited Review: The role and contribution of transcriptional enhancers in brain cancer. Neuropathology and Applied Neurobiology, 2020, 46, 48-56.	1.8	3

#	Article	IF	Citations
1801	A laminâ€like protein OsNMCP1 regulates drought resistance and root growth through chromatin accessibility modulation by interacting with a chromatin remodeller OsSWI3C in rice. New Phytologist, 2020, 227, 65-83.	3.5	20
1802	Genome-Scale CRISPR Screening in Human Intestinal Organoids Identifies Drivers of TGF-Î² Resistance. Cell Stem Cell, 2020, 26, 431-440.e8.	5.2	103
1803	Epigenetic basis for monocyte dysfunction in patients with severe alcoholic hepatitis. Journal of Hepatology, 2020, 73, 303-314.	1.8	24
1804	Chromatin accessibility and histone acetylation in the regulation of competence in early development. Developmental Biology, 2020, 462, 20-35.	0.9	29
1805	Graph embedding and unsupervised learning predict genomic sub-compartments from HiC chromatin interaction data. Nature Communications, 2020, 11, 1173.	5.8	40
1806	Induced pluripotent stem cells as models of human neurodevelopmental disorders. , 2020, , 99-127.		0
1807	An Activity-Mediated Transition in Transcription in Early Postnatal Neurons. Neuron, 2020, 107, 874-890.e8.	3.8	41
1808	Perspectives on somatic reprogramming: spotlighting epigenetic regulation and cellular heterogeneity. Current Opinion in Genetics and Development, 2020, 64, 21-25.	1.5	5
1809	Dynamic transcriptional and chromatin accessibility landscape of medaka embryogenesis. Genome Research, 2020, 30, 924-937.	2.4	24
1810	Cancer and HIV-1 Infection: Patterns of Chronic Antigen Exposure. Frontiers in Immunology, 2020, 11, 1350.	2.2	13
1811	Structural cells are key regulators of organ-specific immune responses. Nature, 2020, 583, 296-302.	13.7	292
1812	Wapl repression by Pax5 promotes V gene recombination by Igh loop extrusion. Nature, 2020, 584, 142-147.	13.7	79
1813	Gene regulatory networks controlling neuronal development. , 2020, , 699-730.		0
1814	Human neurogenesis. , 2020, , 751-767.		0
1815	HiCoP, a simple and robust method for detecting interactions of regulatory regions. Epigenetics and Chromatin, 2020, 13, 27.	1.8	9
1816	TP63, SOX2, and KLF5 Establish a Core Regulatory Circuitry That Controls Epigenetic and Transcription Patterns in Esophageal Squamous Cell Carcinoma Cell Lines. Gastroenterology, 2020, 159, 1311-1327.e19.	0.6	92
1817	Identification of human CD4 ⁺ T cell populations with distinct antitumor activity. Science Advances, 2020, 6, .	4.7	27
1818	lentiMPRA and MPRAflow for high-throughput functional characterization of gene regulatory elements. Nature Protocols, 2020, 15, 2387-2412.	5.5	65

#	Article	IF	Citations
1819	Regulatory noncoding RNAs and the major histocompatibility complex. Human Immunology, 2021, 82, 532-540.	1.2	7
1820	Epigenetic and Transcriptional Networks Underlying Atrial Fibrillation. Circulation Research, 2020, 127, 34-50.	2.0	48
1821	Single-molecule regulatory architectures captured by chromatin fiber sequencing. Science, 2020, 368, 1449-1454.	6.0	106
1822	Chromatin accessibility and transcriptome landscapes of Monomorium pharaonis brain. Scientific Data, 2020, 7, 217.	2.4	10
1823	Genome-wide studies reveal the essential and opposite roles of ARID1A in controlling human cardiogenesis and neurogenesis from pluripotent stem cells. Genome Biology, 2020, 21, 169.	3.8	28
1824	Analytical Approaches for ATACâ€seq Data Analysis. Current Protocols in Human Genetics, 2020, 106, e101.	3.5	14
1825	Mapping effector genes at lupus GWAS loci using promoter Capture-C in follicular helper T cells. Nature Communications, 2020, 11, 3294.	5.8	44
1826	Single-cell ATAC-seq signal extraction and enhancement with SCATE. Genome Biology, 2020, 21, 161.	3.8	34
1827	Dynamics in protein translation sustaining T cell preparedness. Nature Immunology, 2020, 21, 927-937.	7.0	120
1828	TRACE: transcription factor footprinting using chromatin accessibility data and DNA sequence. Genome Research, 2020, 30, 1040-1046.	2.4	12
1829	Epigenetic regulation of intestinal stem cell differentiation. American Journal of Physiology - Renal Physiology, 2020, 319, G189-G196.	1.6	11
1830	The regulatory landscape of early maize inflorescence development. Genome Biology, 2020, 21, 165.	3.8	32
1831	Prospective isolation of radiation induced erythroid stress progenitors reveals unique transcriptomic and epigenetic signatures enabling increased erythroid output. Haematologica, 2020, 105, 2561-2571.	1.7	8
1832	Prospects and challenges of multi-omics data integration in toxicology. Archives of Toxicology, 2020, 94, 371-388.	1.9	142
1833	Lisa: inferring transcriptional regulators through integrative modeling of public chromatin accessibility and ChIP-seq data. Genome Biology, 2020, 21, 32.	3.8	161
1834	An inferred fitness consequence map of the rice genome. Nature Plants, 2020, 6, 119-130.	4.7	20
1835	Assaying Chromatin Accessibility Using ATAC-Seq in Invertebrate Chordate Embryos. Frontiers in Cell and Developmental Biology, 2020, 7, 372.	1.8	12
1836	Regeneration enhancers: A clue to reactivation of developmental genes. Development Growth and Differentiation, 2020, 62, 343-354.	0.6	20

#	Article	IF	Citations
1837	Sex-specific adipose tissue imprinting of regulatory T cells. Nature, 2020, 579, 581-585.	13.7	141
1838	Joint profiling of chromatin accessibility and CAR-T integration site analysis at population and single-cell levels. Proceedings of the National Academy of Sciences of the United States of America, 2020, 117, 5442-5452.	3.3	34
1839	What animals can teach us about evolution, the human genome, and human disease. Upsala Journal of Medical Sciences, 2020, 125, 1-9.	0.4	12
1840	Pioneering meiotic recombination. Genes and Development, 2020, 34, 395-397.	2.7	1
1841	Deletion of a conserved Gata2 enhancer impairs haemogenic endothelium programming and adult Zebrafish haematopoiesis. Communications Biology, 2020, 3, 71.	2.0	26
1842	HIV-1-induced cytokines deplete homeostatic innate lymphoid cells and expand TCF7-dependent memory NK cells. Nature Immunology, 2020, 21, 274-286.	7.0	60
1843	EBF1-deficient bone marrow stroma elicits persistent changes in HSC potential. Nature Immunology, 2020, 21, 261-273.	7.0	30
1844	ATM Paradoxically Promotes Oncogenic Transformation via Transcriptional Reprogramming. Cancer Research, 2020, 80, 1669-1680.	0.4	7
1845	Sex differences in spiders: from phenotype to genomics. Development Genes and Evolution, 2020, 230, 155-172.	0.4	21
1846	Mechanisms and Functions of Chromosome Compartmentalization. Trends in Biochemical Sciences, 2020, 45, 385-396.	3.7	159
1847	Identification of universal and cell-type specific p53 DNA binding. BMC Molecular and Cell Biology, 2020, 21, 5.	1.0	14
1848	Chromatin accessibility analysis reveals regulatory dynamics of developing human retina and hiPSC-derived retinal organoids. Science Advances, 2020, 6, eaay5247.	4.7	47
1849	Pubertal adversity alters chromatin dynamics and stress circuitry in the pregnant brain. Neuropsychopharmacology, 2020, 45, 1263-1271.	2.8	17
1850	Chromatin interaction analyses elucidate the roles of PRC2-bound silencers in mouse development. Nature Genetics, 2020, 52, 264-272.	9.4	104
1851	S3norm: simultaneous normalization of sequencing depth and signal-to-noise ratio in epigenomic data. Nucleic Acids Research, 2020, 48, e43-e43.	6.5	31
1852	Role of cell-type specific nucleosome positioning in inducible activation of mammalian promoters. Nature Communications, 2020, 11, 1075.	5.8	24
1853	Coordination of germ layer lineage choice by TET1 during primed pluripotency. Genes and Development, 2020, 34, 598-618.	2.7	7
1854	Regenerating zebrafish fin epigenome is characterized by stable lineage-specific DNA methylation and dynamic chromatin accessibility. Genome Biology, 2020, 21, 52.	3.8	44

#	Article	IF	Citations
1855	TOPORS, a tumor suppressor protein, contributes to the maintenance of higher-order chromatin architecture. Biochimica Et Biophysica Acta - Gene Regulatory Mechanisms, 2020, 1863, 194518.	0.9	8
1856	Considerations in the analysis of plant chromatin accessibility data. Current Opinion in Plant Biology, 2020, 54, 69-78.	3.5	15
1857	Long-range single-molecule mapping of chromatin accessibility in eukaryotes. Nature Methods, 2020, 17, 319-327.	9.0	93
1858	Formaldehyde-assisted isolation of regulatory DNA elements from Arabidopsis leaves. Nature Protocols, 2020, 15, 713-733.	5.5	7
1859	ETV4 Is Necessary for Estrogen Signaling and Growth in Endometrial Cancer Cells. Cancer Research, 2020, 80, 1234-1245.	0.4	39
1860	Genetic Variation in Type 1 Diabetes Reconfigures the 3D Chromatin Organization of T Cells and Alters Gene Expression. Immunity, 2020, 52, 257-274.e11.	6.6	42
1861	Inhibition of methyltransferase activity of enhancer of zeste 2 leads to enhanced lipid accumulation and altered chromatin status in zebrafish. Epigenetics and Chromatin, 2020, 13, 5.	1.8	7
1862	Sphingosine 1-Phosphate Receptor Signaling Establishes AP-1 Gradients to Allow for Retinal Endothelial Cell Specialization. Developmental Cell, 2020, 52, 779-793.e7.	3.1	38
1863	ARID1A determines luminal identity and therapeutic response in estrogen-receptor-positive breast cancer. Nature Genetics, 2020, 52, 198-207.	9.4	140
1864	Decoding the development of the human hippocampus. Nature, 2020, 577, 531-536.	13.7	141
1865	Chromatin accessibility established by Pou5f3, Sox19b and Nanog primes genes for activity during zebrafish genome activation. PLoS Genetics, 2020, 16, e1008546.	1.5	59
1866	Widespread Transcriptional Scanning in the Testis Modulates Gene Evolution Rates. Cell, 2020, 180, 248-262.e21.	13.5	111
1867	A Comprehensive Map of the Monocyte-Derived Dendritic Cell Transcriptional Network Engaged upon Innate Sensing of HIV. Cell Reports, 2020, 30, 914-931.e9.	2.9	15
1868	YAP/TAZ direct commitment and maturation of lymph node fibroblastic reticular cells. Nature Communications, 2020, 11, 519.	5.8	35
1869	From Genetic Association to Molecular Mechanisms for Islet-cell Dysfunction in Type 2 Diabetes. Journal of Molecular Biology, 2020, 432, 1551-1578.	2.0	27
1870	Human iPSC-derived Down syndrome astrocytes display genome-wide perturbations in gene expression, an altered adhesion profile, and increased cellular dynamics. Human Molecular Genetics, 2020, 29, 785-802.	1.4	30
1871	IL-1 Transcriptional Responses to Lipopolysaccharides Are Regulated by a Complex of RNA Binding Proteins. Journal of Immunology, 2020, 204, 1334-1344.	0.4	12
1872	Environmental cues regulate epigenetic reprogramming of airway-resident memory CD8+ T cells. Nature Immunology, 2020, 21, 309-320.	7.0	72

#	Article	IF	Citations
1873	ModHMM: A Modular Supra-Bayesian Genome Segmentation Method. Journal of Computational Biology, 2020, 27, 442-457.	0.8	6
1874	Transcriptomic and open chromatin atlas of high-resolution anatomical regions in the rhesus macaque brain. Nature Communications, 2020, 11, 474.	5.8	32
1875	Towards a comprehensive catalogue of validated and target-linked human enhancers. Nature Reviews Genetics, 2020, 21, 292-310.	7.7	229
1876	ATAC-Me Captures Prolonged DNA Methylation of Dynamic Chromatin Accessibility Loci during Cell Fate Transitions. Molecular Cell, 2020, 77, 1350-1364.e6.	4.5	47
1877	RNA sequencing by direct tagmentation of RNA/DNA hybrids. Proceedings of the National Academy of Sciences of the United States of America, 2020, 117, 2886-2893.	3.3	86
1878	Impaired Death Receptor Signaling in Leukemia Causes Antigen-Independent Resistance by Inducing CAR T-cell Dysfunction. Cancer Discovery, 2020, 10, 552-567.	7.7	184
1879	HELLS and PRDM9 form a pioneer complex to open chromatin at meiotic recombination hot spots. Genes and Development, 2020, 34, 398-412.	2.7	51
1880	Chromatin mapping and single-cell immune profiling define the temporal dynamics of ibrutinib response in CLL. Nature Communications, 2020, 11, 577.	5.8	69
1881	Modeling the effect of prolonged ethanol exposure on global gene expression and chromatin accessibility in normal 3D colon organoids. PLoS ONE, 2020, 15, e0227116.	1.1	22
1882	Unraveling the Hierarchy of cis and trans Factors That Determine the DNA Binding by Peroxisome Proliferator-Activated Receptor Î³. Molecular and Cellular Biology, 2020, 40, .	1.1	5
1883	From reads to insight: a hitchhikerâ€™s guide to ATAC-seq data analysis. Genome Biology, 2020, 21, 22.	3.8	268
1884	Genome-wide MNase hypersensitivity assay unveils distinct classes of open chromatin associated with H3K27me3 and DNA methylation in Arabidopsis thaliana. Genome Biology, 2020, 21, 24.	3.8	35
1885	ORSO (Online Resource for Social Omics): A data-driven social network connecting scientists to genomics datasets. PLoS Computational Biology, 2020, 16, e1007571.	1.5	2
1886	Sexual-dimorphism in human immune system aging. Nature Communications, 2020, 11, 751.	5.8	316
1887	Liver gene regulatory networks: Contributing factors to nonalcoholic fatty liver disease. Wiley Interdisciplinary Reviews: Systems Biology and Medicine, 2020, 12, e1480.	6.6	1
1888	DUX-miR-344-ZMYM2-Mediated Activation of MERVL LTRs Induces a Totipotent 2C-like State. Cell Stem Cell, 2020, 26, 234-250.e7.	5.2	99
1889	Wheat chromatin architecture is organized in genome territories and transcription factories. Genome Biology, 2020, 21, 104.	3.8	99
1890	Hypoxiaâ€induced alterations of transcriptome and chromatin accessibility in <scp>HL</scp>â€1 cells. IUBMB Life, 2020, 72, 1737-1746.	1.5	13

#	Article	IF	Citations
1891	Niche-Specific Reprogramming of Epigenetic Landscapes Drives Myeloid Cell Diversity in Nonalcoholic Steatohepatitis. Immunity, 2020, 52, 1057-1074.e7.	6.6	248
1892	Genomic Profiling by ALaP-Seq Reveals Transcriptional Regulation by PML Bodies through DNMT3A Exclusion. Molecular Cell, 2020, 78, 493-505.e8.	4.5	31
1893	ZBTB1 Regulates Asparagine Synthesis and Leukemia Cell Response to L-Asparaginase. Cell Metabolism, 2020, 31, 852-861.e6.	7.2	40
1894	Functional Genomics of the Pediatric Obese Asthma Phenotype Reveal Enrichment of Rho-GTPase Pathways. American Journal of Respiratory and Critical Care Medicine, 2020, 202, 259-274.	2.5	17
1895	Missing heritability in Parkinsonâ€™s disease: the emerging role of non-coding genetic variation. Journal of Neural Transmission, 2020, 127, 729-748.	1.4	27
1896	Gene Regulatory and Expression Differences between Mouse and Pig Limb Buds Provide Insights into the Evolutionary Emergence of Artiodactyl Traits. Cell Reports, 2020, 31, 107490.	2.9	19
1897	RXRs control serous macrophage neonatal expansion and identity and contribute to ovarian cancer progression. Nature Communications, 2020, 11, 1655.	5.8	39
1898	Interplay between genetics and epigenetics in osteoarthritis. Nature Reviews Rheumatology, 2020, 16, 268-281.	3.5	91
1899	Spt5-mediated enhancer transcription directly couples enhancer activation with physical promoter interaction. Nature Genetics, 2020, 52, 505-515.	9.4	62
1900	Kethoxal-assisted single-stranded DNA sequencing captures global transcription dynamics and enhancer activity in situ. Nature Methods, 2020, 17, 515-523.	9.0	64
1901	Systematic alteration of ATAC-seq for profiling open chromatin in cryopreserved nuclei preparations from livestock tissues. Scientific Reports, 2020, 10, 5230.	1.6	26
1902	Mapping the cis -regulatory architecture of the human retina reveals noncoding genetic variation in disease. Proceedings of the National Academy of Sciences of the United States of America, 2020, 117, 9001-9012.	3.3	72
1903	H2A.Z is dispensable for both basal and activated transcription in post-mitotic mouse muscles. Nucleic Acids Research, 2020, 48, 4601-4613.	6.5	18
1904	Developmental regulation of cell type-specific transcription by novel promoter-proximal sequence elements. Genes and Development, 2020, 34, 663-677.	2.7	23
1905	Dynamics of the Transcriptome and Accessible Chromatin Landscapes During Early Goose Ovarian Development. Frontiers in Cell and Developmental Biology, 2020, 8, 196.	1.8	13
1906	Single Cell Analysis in Vascular Biology. Frontiers in Cardiovascular Medicine, 2020, 7, 42.	1.1	51
1907	Discrete functional and mechanistic roles of chromodomain Y-like 2 (CDYL2) transcript variants in breast cancer growth and metastasis. Theranostics, 2020, 10, 5242-5258.	4.6	14
1908	IKZF3/Aiolos Is Associated with but Not Sufficient for the Expression of IL-10 by CD4+ T Cells. Journal of Immunology, 2020, 204, 2940-2948.	0.4	13

#	Article	IF	Citations
1909	Absolute Quantification of Transcription Factors Reveals Principles of Gene Regulation in Erythropoiesis. Molecular Cell, 2020, 78, 960-974.e11.	4.5	83
1910	Genomics Methods for Xenopus Embryos and Tissues. Cold Spring Harbor Protocols, 2020, 2020, pdb.top097915.	0.2	2
1911	Circulating Tumor Cells in Breast Cancer Metastatic Disease. Advances in Experimental Medicine and Biology, 2020, , .	0.8	2
1912	Integration of ATAC-seq and RNA-seq Unravels Chromatin Accessibility during Sex Reversal in Orange-Spotted Grouper (Epinephelus coioides). International Journal of Molecular Sciences, 2020, 21, 2800.	1.8	15
1913	MYC Controls the Epstein-Barr Virus Lytic Switch. Molecular Cell, 2020, 78, 653-669.e8.	4.5	67
1914	Profiling Cell Signaling Networks at Single-cell Resolution. Molecular and Cellular Proteomics, 2020, 19, 744-756.	2.5	39
1915	DolphinNext: a distributed data processing platform for high throughput genomics. BMC Genomics, 2020, 21, 310.	1.2	66
1916	The Biochemistry of Retinoid Signaling III. Sub-Cellular Biochemistry, 2020, , .	1.0	0
1917	Advances and challenges in epigenomic single-cell sequencing applications. Current Opinion in Chemical Biology, 2020, 57, 17-26.	2.8	13
1918	IL-33-PU.1 Transcriptome Reprogramming Drives Functional State Transition and Clearance Activity of Microglia in Alzheimerâ€™s Disease. Cell Reports, 2020, 31, 107530.	2.9	65
1919	Loss of the neural-specific BAF subunit ACTL6B relieves repression of early response genes and causes recessive autism. Proceedings of the National Academy of Sciences of the United States of America, 2020, 117, 10055-10066.	3.3	34
1920	Release of promoterâ€“proximal paused Pol II in response to histone deacetylase inhibition. Nucleic Acids Research, 2020, 48, 4877-4890.	6.5	32
1921	Modeling glioblastoma invasion using human brain organoids and single-cell transcriptomics. Neuro-Oncology, 2020, 22, 1138-1149.	0.6	75
1922	High-dimensional immune-profiling in cancer: implications for immunotherapy. , 2020, 8, e000363.		49
1923	ATAC-seq normalization method can significantly affect differential accessibility analysis and interpretation. Epigenetics and Chromatin, 2020, 13, 22.	1.8	49
1924	Deconstructing cerebellar development cell by cell. PLoS Genetics, 2020, 16, e1008630.	1.5	32
1925	Combined Cohesinâ€“RUNX1 Deficiency Synergistically Perturbs Chromatin Looping and Causes Myelodysplastic Syndromes. Cancer Discovery, 2020, 10, 836-853.	7.7	51
1926	Characterization of epigenetic and transcriptional landscape in infantile hemangiomas with ATAC-seq and RNA-seq. Epigenomics, 2020, 12, 893-905.	1.0	11

#	Article	IF	Citations
1927	H3K79me2/3 controls enhancerâ€“promoter interactions and activation of the pan-cancer stem cell marker PROM1/CD133 in MLL-AF4 leukemia cells. Leukemia, 2021, 35, 90-106.	3.3	35
1928	Epigenetic Modifications in Schizophrenia and Related Disorders: Molecular Scars of Environmental Exposures and Source of Phenotypic Variability. Biological Psychiatry, 2021, 89, 215-226.	0.7	89
1929	YAP1 Withdrawal in Hepatoblastoma Drives Therapeutic Differentiation of Tumor Cells to Functional Hepatocyteâ€Like Cells. Hepatology, 2021, 73, 1011-1027.	3.6	10
1930	Epigenetic and Transcriptional Control of the Epidermal Growth Factor Receptor Regulates the Tumor Immune Microenvironment in Pancreatic Cancer. Cancer Discovery, 2021, 11, 736-753.	7.7	73
1931	Genetically Defined Syngeneic Mouse Models of Ovarian Cancer as Tools for the Discovery of Combination Immunotherapy. Cancer Discovery, 2021, 11, 384-407.	7.7	64
1932	Plasmablasts derive from CD23â€“ activated B cells after the extinction of IL-4/STAT6 signaling and IRF4 induction. Blood, 2021, 137, 1166-1180.	0.6	18
1933	Dynamic chromatin accessibility landscape changes following interleukin-1 stimulation. Epigenetics, 2021, 16, 106-119.	1.3	8
1934	The Power of Singleâ€Cell Analysis for the Study of Liver Pathobiology. Hepatology, 2021, 73, 437-448.	3.6	19
1935	Massively parallel single-cell mitochondrial DNA genotyping and chromatin profiling. Nature Biotechnology, 2021, 39, 451-461.	9.4	150
1936	Stabilization of heterochromatin by CLOCK promotes stem cell rejuvenation and cartilage regeneration. Cell Research, 2021, 31, 187-205.	5.7	67
1937	Parsing the Functional Impact of Noncoding Genetic Variants in the Brain Epigenome. Biological Psychiatry, 2021, 89, 65-75.	0.7	8
1938	Mechanisms underlying the control of dynamic regulatory element activity and chromatin accessibility during metamorphosis. Current Opinion in Insect Science, 2021, 43, 21-28.	2.2	11
1939	Spirits in the Material World: Enhancer RNAs in Transcriptional Regulation. Trends in Biochemical Sciences, 2021, 46, 138-153.	3.7	39
1940	Isolation of Highly Purified and Viable Retinal Endothelial Cells. Journal of Vascular Research, 2021, 58, 49-57.	0.6	8
1941	Network Effects of the 15q13.3 Microdeletion on the Transcriptome and Epigenome in Human-Induced Neurons. Biological Psychiatry, 2021, 89, 497-509.	0.7	17
1942	Chromatin Proteomics to Study Epigenetics â€” Challenges and Opportunities. Molecular and Cellular Proteomics, 2021, 20, 100056.	2.5	14
1944	Epigenetic Signatures and Plasticity of Intestinal and Other Stem Cells. Annual Review of Physiology, 2021, 83, 405-427.	5.6	6
1945	Understanding tumour cell heterogeneity and its implication for immunotherapy in liver cancer using single-cell analysis. Journal of Hepatology, 2021, 74, 700-715.	1.8	60

#	Article	IF	Citations
1946	Capture of Mouse and Human Stem Cells with Features of Formative Pluripotency. Cell Stem Cell, 2021, 28, 453-471.e8.	5.2	151
1947	Nuclear receptors: Key regulators of somatic cell functions in the ovulatory process. Molecular Aspects of Medicine, 2021, 78, 100937.	2.7	25
1948	Roadmap to a plasma cell: Epigenetic and transcriptional cues that guide B cell differentiation. Immunological Reviews, 2021, 300, 54-64.	2.8	12
1949	Epigenetic principles underlying epileptogenesis and epilepsy syndromes. Neurobiology of Disease, 2021, 148, 105179.	2.1	20
1950	CDK4/6 inhibition reprograms the breast cancer enhancer landscape by stimulating AP-1 transcriptional activity. Nature Cancer, 2021, 2, 34-48.	5.7	48
1951	Chromatin accessibility in canine stromal cells and its implications for canine somatic cell reprogramming. Stem Cells Translational Medicine, 2021, 10, 441-454.	1.6	6
1952	The Transition from Quiescent to Activated States in Human Hematopoietic Stem Cells Is Governed by Dynamic 3D Genome Reorganization. Cell Stem Cell, 2021, 28, 488-501.e10.	5.2	51
1953	GTRD: an integrated view of transcription regulation. Nucleic Acids Research, 2021, 49, D104-D111.	6.5	137
1954	The epigenetic basis of cellular heterogeneity. Nature Reviews Genetics, 2021, 22, 235-250.	7.7	163
1955	Conservative route to genome compaction in a miniature annelid. Nature Ecology and Evolution, 2021, 5, 231-242.	3.4	51
1956	Altered chromatin landscape in circulating T follicular helper and regulatory cells following grass pollen subcutaneous and sublingual immunotherapy. Journal of Allergy and Clinical Immunology, 2021, 147, 663-676.	1.5	34
1957	Deciphering the Identity of Renin Cells in Health and Disease. Trends in Molecular Medicine, 2021, 27, 280-292.	3.5	11
1958	Mutant Kras co-opts a proto-oncogenic enhancer network in inflammation-induced metaplastic progenitor cells to initiate pancreatic cancer. Nature Cancer, 2021, 2, 49-65.	5.7	54
1959	Super enhancers define regulatory subtypes and cell identity in neuroblastoma. Nature Cancer, 2021, 2, 114-128.	5.7	73
1960	The Evolutionary History of Common Genetic Variants Influencing Human Cortical Surface Area. Cerebral Cortex, 2021, 31, 1873-1887.	1.6	21
1961	A Tumor Suppressor Enhancer ofPTENin T-cell Development and Leukemia. Blood Cancer Discovery, 2021, 2, 92-109.	2.6	15
1962	Understanding the epigenetic landscape and cellular architecture of childhood brain tumors. Neurochemistry International, 2021, 144, 104940.	1.9	2
1963	SWI/SNF Complex Mutations Promote Thyroid Tumor Progression and Insensitivity to Redifferentiation Therapies. Cancer Discovery, 2021, 11, 1158-1175.	7.7	57

#	Article	IF	Citations
1964	Systems biology in cardiovascular disease: a multiomics approach. Nature Reviews Cardiology, 2021, 18, 313-330.	6.1	134
1965	Integration of the Transcriptome and Genome-Wide Landscape of BRD2 and BRD4 Binding Motifs Identifies Key Superenhancer Genes and Reveals the Mechanism of Bet Inhibitor Action in Rheumatoid Arthritis Synovial Fibroblasts. Journal of Immunology, 2021, 206, 422-431.	0.4	23
1966	Cis-acting variation is common across regulatory layers but is often buffered during embryonic development. Genome Research, 2021, 31, 211-224.	2.4	19
1967	Genomeâ€wide prediction of chromatin accessibility based on gene expression. Wiley Interdisciplinary Reviews: Computational Statistics, 2021, 13, e1544.	2.1	5
1968	Genomic Mechanisms Governing Mineral Homeostasis and the Regulation and Maintenance of Vitamin D Metabolism. JBMR Plus, 2021, 5, e10433.	1.3	13
1969	Highâ€resolution threeâ€dimensional chromatin profiling of the Chinese hamster ovary cell genome. Biotechnology and Bioengineering, 2021, 118, 784-796.	1.7	5
1970	ATACdb: a comprehensive human chromatin accessibility database. Nucleic Acids Research, 2021, 49, D55-D64.	6.5	27
1971	Capturing Chromosome Conformation. Methods in Molecular Biology, 2021, , .	0.4	1
1972	Transcriptional enhancers: from prediction to functional assessment on a genome-wide scale. Genome, 2021, 64, 426-448.	0.9	12
1975	Deciphering the multifaceted roles of TET proteins in Tâ€cell lineage specification and malignant transformation. Immunological Reviews, 2021, 300, 22-36.	2.8	9
1976	Multiple Modes of Regulation Control Dynamic Transcription Patterns During the Mitosis-G1 Transition. SSRN Electronic Journal, 0, , .	0.4	0
1977	Optimization and Validation of CAR Transduction into Human Primary NK Cells Using CRISPR and AAV. SSRN Electronic Journal, 0, , .	0.4	1
1978	Chromatin accessibility maps provide evidence of multilineage gene priming in hematopoietic stem cells. Epigenetics and Chromatin, 2021, 14, 2.	1.8	20
1979	Histone modifications, DNA methylation, and the epigenetic code of alcohol use disorder. International Review of Neurobiology, 2021, 156, 1-62.	0.9	21
1980	Genomic Footprinting Analyses from DNase-seq Data to Construct Gene Regulatory Networks. Methods in Molecular Biology, 2021, 2328, 25-46.	0.4	1
1981	Chromatin accessibility profiling provides insights into larval cuticle color and adult longevity in butterflies. Zoological Research, 2021, 42, 614-619.	0.9	5
1982	Next Generation Imaging Techniques to Define Immune Topographies in Solid Tumors. Frontiers in Immunology, 2020, 11, 604967.	2.2	12
1983	Single-cell chromatin accessibility profiling of glioblastoma identifies an invasive cancer stem cell population associated with lower survival. ELife, 2021, 10, .	2.8	45

#	Article	IF	Citations
1987	ATAC-seq and psychiatric disorders. , 2021, , 143-162.		0
1988	A multi-omics approach to Epstein-Barr virus immortalization of B-cells reveals EBNA1 chromatin pioneering activities targeting nucleotide metabolism. PLoS Pathogens, 2021, 17, e1009208.	2.1	21
1990	Principles of epigenetics and DNA methylation. , 2021, , 3-26.		0
1992	TSLP-Driven Chromatin Remodeling and Trained Systemic Immunity after Neonatal Respiratory Viral Infection. Journal of Immunology, 2021, 206, 1315-1328.	0.4	12
1995	The Study of Proteinâ€“DNA Interactions in CD4+ T-Cells Using ChIPmentation. Methods in Molecular Biology, 2021, 2285, 201-216.	0.4	0
1996	Induction of spontaneous human neocentromere formation and long-term maturation. Journal of Cell Biology, 2021, 220, .	2.3	27
1997	EGR1 is a gatekeeper of inflammatory enhancers in human macrophages. Science Advances, 2021, 7, .	4.7	67
1998	Core transcription regulatory circuitry orchestrates corneal epithelial homeostasis. Nature Communications, 2021, 12, 420.	5.8	32
1999	The T-box transcription factor Eomesodermin governs haemogenic competence of yolk sac mesodermal progenitors. Nature Cell Biology, 2021, 23, 61-74.	4.6	10
2000	The elevated transcription of ADAM19 by the oncohistone H2BE76K contributes to oncogenic properties in breast cancer. Journal of Biological Chemistry, 2021, 296, 100374.	1.6	17
2001	Epigenetic reprogramming rewires transcription during the alternation of generations in Arabidopsis. ELife, 2021, 10, .	2.8	55
2002	Coordinated Gene Expression and Chromatin Regulation during Hydra Head Regeneration. Genome Biology and Evolution, 2021, 13, .	1.1	12
2004	Perspective on Beyond Statistical Significance: Finding Meaningful Effects. Complex Psychiatry, 2021, 7, 1-8.	1.3	3
2005	Loss of FOXC1 contributes to the corneal epithelial fate switch and pathogenesis. Signal Transduction and Targeted Therapy, 2021, 6, 5.	7.1	12
2006	The developmental hourglass model and recapitulation: An attempt to integrate the two models. Journal of Experimental Zoology Part B: Molecular and Developmental Evolution, 2022, 338, 76-86.	0.6	10
2007	Postnatal Arx transcriptional activity regulates functional properties of PV interneurons. IScience, 2021, 24, 101999.	1.9	7
2008	F-Seq2: improving the feature density based peak caller with dynamic statistics. NAR Genomics and Bioinformatics, 2021, 3, lqab012.	1.5	6
2009	Nonlinear relationship between chromatin accessibility and estradiol-regulated gene expression. Oncogene, 2021, 40, 1332-1346.	2.6	12

#	Article	IF	Citations
2010	Foxc1 establishes enhancer accessibility for craniofacial cartilage differentiation. ELife, 2021, 10, .	2.8	24
2011	Falco: high-speed FastQC emulation for quality control of sequencing data. F1000Research, 2019, 8, 1874.	0.8	112
2013	FOXO1 constrains activation and regulates senescence in CD8 TÂcells. Cell Reports, 2021, 34, 108674.	2.9	40
2014	In vivo base editing rescues Hutchinsonâ€“Gilford progeria syndrome in mice. Nature, 2021, 589, 608-614.	13.7	275
2016	Single-Cell Technologies in Parkinson×³s Disease. , 2021, , 15-30.		0
2017	An optimised method for intact nuclei isolation from diatoms. Scientific Reports, 2021, 11, 1681.	1.6	7
2018	Inferring time series chromatin states for promoter-enhancer pairs based on Hi-C data. BMC Genomics, 2021, 22, 84.	1.2	3
2020	Variation in Pleiotropic Hub Gene Expression Is Associated with Interspecific Differences in Head Shape and Eye Size in Drosophila. Molecular Biology and Evolution, 2021, 38, 1924-1942.	3.5	14
2022	DNAVec: Pre-Trained Word Vector Representation of Genomic DNA Sequences. Hans Journal of Biomedicine, 2021, 11, 121-128.	0.0	0
2023	Measuring Chromatin Accessibility:. Methods in Molecular Biology, 2021, 2351, 105-121.	0.4	1
2024	Multi-level remodelling of chromatin underlying activation of human T cells. Scientific Reports, 2021, 11, 528.	1.6	26
2025	The regulatory genome of the malaria vector Anopheles gambiae: integrating chromatin accessibility and gene expression. NAR Genomics and Bioinformatics, 2021, 3, lqaa113.	1.5	12
2026	Multi-omic Analysis of Developing Human Retina and Organoids Reveals Cell-Specific Cis-Regulatory Elements and Mechanisms of Non-Coding Genetic Disease Risk. SSRN Electronic Journal, 0, , .	0.4	1
2027	Transcriptionally active enhancers in human cancer cells. Molecular Systems Biology, 2021, 17, e9873.	3.2	28
2028	SLE non-coding genetic risk variant determines the epigenetic dysfunction of an immune cell specific enhancer that controls disease-critical microRNA expression. Nature Communications, 2021, 12, 135.	5.8	48
2029	ATAC-Seq-based Identification of Extrachromosomal Circular DNA in Mammalian Cells and Its Validation Using Inverse PCR and FISH. Bio-protocol, 2021, 11, e4003.	0.2	8
2030	Prototypical oncogene family Myc defines unappreciated distinct lineage states of small cell lung cancer. Science Advances, 2021, 7, .	4.7	40
2031	Single cell transcriptomics and epigenomics methods provide high resolution genomics profiling of brain disorders. , 2021, , 175-196.		0

#	Article	IF	Citations
2032	Dynamic Chromatin State Profiling Reveals Regulatory Principle of Pluripotency During Shoot Regeneration. SSRN Electronic Journal, 0, , .	0.4	1
2033	Single-cell profiling of the human decidual immune microenvironment in patients with recurrent pregnancy loss. Cell Discovery, 2021, 7, 1.	3.1	152
2036	Kmt2c mutations enhance HSC self-renewal capacity and convey a selective advantage after chemotherapy. Cell Reports, 2021, 34, 108751.	2.9	13
2038	Chromatin Accessibility Is Associated with Artemisinin Biosynthesis Regulation in Artemisia annua. Molecules, 2021, 26, 1194.	1.7	3
2039	Chromatin information content landscapes inform transcription factor and DNA interactions. Nature Communications, 2021, 12, 1307.	5.8	19
2040	CD4+â€‰T cells from children with active juvenile idiopathic arthritis show altered chromatin features associated with transcriptional abnormalities. Scientific Reports, 2021, 11, 4011.	1.6	5
2042	Reactivation of the pluripotency program precedes formation of the cranial neural crest. Science, 2021, 371, .	6.0	84
2043	Single Cell Omics for Musculoskeletal Research. Current Osteoporosis Reports, 2021, 19, 131-140.	1.5	10
2044	Environmental enrichment influences novelty reactivity, novelty preference, and anxiety via distinct genetic mechanisms in C57BL/6J and DBA/2J mice. Scientific Reports, 2021, 11, 3928.	1.6	10
2045	New tools for â€˜ZEBRA-FISHINGâ€™. Briefings in Functional Genomics, 2021, , .	1.3	0
2048	Chromatin architecture reveals cell type-specific target genes for kidney disease risk variants. BMC Biology, 2021, 19, 38.	1.7	12
2049	Profiling Chromatin Accessibility at Single-cell Resolution. Genomics, Proteomics and Bioinformatics, 2021, 19, 172-190.	3.0	18
2050	A Non-stop identity complex (NIC) supervises enterocyte identity and protects from premature aging. ELife, 2021, 10, .	2.8	6
2054	Conserved Epigenetic Programming and Enhanced Heme Metabolism Drive Memory B Cell Reactivation. Journal of Immunology, 2021, 206, 1493-1504.	0.4	15
2055	Developmental hourglass and heterochronic shifts in fin and limb development. ELife, 2021, 10, .	2.8	10
2057	Pancreatic progenitor epigenome maps prioritize type 2 diabetes risk genes with roles in development. ELife, 2021, 10, .	2.8	15
2058	Cross-species examination of X-chromosome inactivation highlights domains of escape from silencing. Epigenetics and Chromatin, 2021, 14, 12.	1.8	23
2059	ATF3 drives senescence by reconstructing accessible chromatin profiles. Aging Cell, 2021, 20, e13315.	3.0	38

#	Article	IF	Citations
2060	Role of Transposable Elements in Gene Regulation in the Human Genome. Life, 2021, 11, 118.	1.1	31
2061	DNABERT: pre-trained Bidirectional Encoder Representations from Transformers model for DNA-language in genome. Bioinformatics, 2021, 37, 2112-2120.	1.8	282
2063	SOX17 integrates HOXA and arterial programs in hemogenic endothelium to drive definitive lympho-myeloid hematopoiesis. Cell Reports, 2021, 34, 108758.	2.9	27
2064	TATA and paused promoters active in differentiated tissues have distinct expression characteristics. Molecular Systems Biology, 2021, 17, e9866.	3.2	20
2066	A unique bipartite Polycomb signature regulates stimulus-response transcription during development. Nature Genetics, 2021, 53, 379-391.	9.4	16
2067	SUMOylation regulates the protein network and chromatin accessibility at glucocorticoid receptor-binding sites. Nucleic Acids Research, 2021, 49, 1951-1971.	6.5	23
2068	Dynamic effects of genetic variation on gene expression revealed following hypoxic stress in cardiomyocytes. ELife, 2021, 10, .	2.8	41
2069	Stem cell quiescence: the challenging path to activation. Development (Cambridge), 2021, 148, .	1.2	54
2070	Dissecting the response to photoperiod at the cell-type level. Plant Cell, 2021, 33, 1083-1084.	3.1	0
2071	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, .	2.8	32
2072	Chromatin accessibility of circulating CD8+ T cells predicts treatment response to PD-1 blockade in patients with gastric cancer. Nature Communications, 2021, 12, 975.	5.8	26
2073	Metformin Reduces Histone H3K4me3 at the Promoter Regions of Positive Cell Cycle Regulatory Genes in Lung Cancer Cells. Cancers, 2021, 13, 739.	1.7	14
2074	Characterising open chromatin in chick embryos identifies cis-regulatory elements important for paraxial mesoderm formation and axis extension. Nature Communications, 2021, 12, 1157.	5.8	8
2077	RAD: a web application to identify region associated differentially expressed genes. Bioinformatics, 2021, 37, 2741-2743.	1.8	11
2078	Joint profiling of histone modifications and transcriptome in single cells from mouse brain. Nature Methods, 2021, 18, 283-292.	9.0	171
2079	Comprehensive analysis of single cell ATAC-seq data with SnapATAC. Nature Communications, 2021, 12, 1337.	5.8	253
2080	In situ genome sequencing resolves DNA sequence and structure in intact biological samples. Science, 2021, 371, .	6.0	141
2081	p53 is a central regulator driving neurodegeneration caused by C9orf72 poly(PR). Cell, 2021, 184, 689-708.e20.	13.5	104

#	Article	IF	Citations
2085	ELF3 activated by a superenhancer and an autoregulatory feedback loop is required for high-level HLA-C expression on extravillous trophoblasts. Proceedings of the National Academy of Sciences of the United States of America, 2021, 118, .	3.3	10
2086	Persistence of self-reactive CD8+ T cells in the CNS requires TOX-dependent chromatin remodeling. Nature Communications, 2021, 12, 1009.	5.8	19
2088	Filtering the Junk: Assigning Function to the Mosquito Non-Coding Genome. Insects, 2021, 12, 186.	1.0	7
2089	Annotation of chromatin states in 66 complete mouse epigenomes during development. Communications Biology, 2021, 4, 239.	2.0	34
2090	Multi-Dimensional Gene Regulation in Innate and Adaptive Lymphocytes: A View From Regulomes. Frontiers in Immunology, 2021, 12, 655590.	2.2	12
2092	Unraveling the cartography of the cancer ecosystem. Genome Biology, 2021, 22, 87.	3.8	4
2093	Scientific and technological approaches to improve SCNT efficiency in farm animals and pets. Reproduction, 2021, 162, F33-F43.	1.1	5
2094	Identification and characterization of conserved noncoding cis-regulatory elements that impact Mecp2 expression and neurological functions. Genes and Development, 2021, 35, 489-494.	2.7	4
2095	Stepwise chromatin and transcriptional acquisition of an intraepithelial lymphocyte program. Nature Immunology, 2021, 22, 449-459.	7.0	29
2099	Cell type-specific chromatin accessibility analysis in the mouse and human brain. Epigenetics, 2022, 17, 202-219.	1.3	13
2100	Transcriptome and chromatin landscape of iNKT cells are shaped by subset differentiation and antigen exposure. Nature Communications, 2021, 12, 1446.	5.8	21
2101	Dual DNA and protein tagging of open chromatin unveils dynamics of epigenomic landscapes in leukemia. Nature Methods, 2021, 18, 293-302.	9.0	9
2102	An ATAC-seq Dataset Uncovers the Regulatory Landscape During Axolotl Limb Regeneration. Frontiers in Cell and Developmental Biology, 2021, 9, 651145.	1.8	10
2103	The Cranial Neural Crest in a Multiomics Era. Frontiers in Physiology, 2021, 12, 634440.	1.3	10
2104	Chromatin Accessibility Identifies Regulatory Elements Predictive of Gene Expression and Disease Outcome in Multiple Myeloma. Clinical Cancer Research, 2021, 27, 3178-3189.	3.2	15
2105	Genetic control of retinal ganglion cell genesis. Cellular and Molecular Life Sciences, 2021, 78, 4417-4433.	2.4	16
2106	MAP3K2-regulated intestinal stromal cells define a distinct stem cell niche. Nature, 2021, 592, 606-610.	13.7	53
2107	Evidence for additive and synergistic action of mammalian enhancers during cell fate determination. ELife, 2021, 10, .	2.8	64

#	Article	IF	Citations
2108	Time-resolved single-cell analysis of Brca1 associated mammary tumourigenesis reveals aberrant differentiation of luminal progenitors. Nature Communications, 2021, 12, 1502.	5.8	34
2112	Runx proteins and transcriptional mechanisms that govern memory CD8 T cell development. Immunological Reviews, 2021, 300, 100-124.	2.8	13
2113	GAF is essential for zygotic genome activation and chromatin accessibility in the early Drosophila embryo. ELife, 2021, 10, .	2.8	75
2114	Advances in bulk and single-cell multi-omics approaches for systems biology and precision medicine. Briefings in Bioinformatics, 2021, 22, .	3.2	31
2116	Integration of Alzheimerâ€™s disease genetics and myeloid genomics identifies disease risk regulatory elements and genes. Nature Communications, 2021, 12, 1610.	5.8	118
2117	Generic injuries are sufficient to induce ectopic Wnt organizers in Hydra. ELife, 2021, 10, .	2.8	24
2121	Identification of Stemness-Related Genes for Cervical Squamous Cell Carcinoma and Endocervical Adenocarcinoma by Integrated Bioinformatics Analysis. Frontiers in Cell and Developmental Biology, 2021, 9, 642724.	1.8	6
2122	Creb5 establishes the competence for Prg4 expression in articular cartilage. Communications Biology, 2021, 4, 332.	2.0	30
2124	Epstein-Barr virus inactivates the transcriptome and disrupts the chromatin architecture of its host cell in the first phase of lytic reactivation. Nucleic Acids Research, 2021, 49, 3217-3241.	6.5	16
2125	Epigenetic regulation of nitrogen and phosphorus responses in plants. Journal of Plant Physiology, 2021, 258-259, 153363.	1.6	13
2126	Investigating the molecular guts of endoderm formation using zebrafish. Briefings in Functional Genomics, 2021, , .	1.3	2
2127	Androgen and glucocorticoid receptor direct distinct transcriptional programs by receptor-specific and shared DNA binding sites. Nucleic Acids Research, 2021, 49, 3856-3875.	6.5	17
2128	hnRNP K supports the maintenance of RORÎ³ circadian rhythm through ERK signaling. FASEB Journal, 2021, 35, e21507.	0.2	3
2129	Intestinal-epithelial LSD1 controls goblet cell maturation and effector responses required for gut immunity to bacterial and helminth infection. PLoS Pathogens, 2021, 17, e1009476.	2.1	13
2130	Heart Enhancers: Development and Disease Control at a Distance. Frontiers in Genetics, 2021, 12, 642975.	1.1	4
2131	Germ cell differentiation requires Tdrd7-dependent chromatin and transcriptome reprogramming marked by germ plasm relocalization. Developmental Cell, 2021, 56, 641-656.e5.	3.1	18
2132	InÂvivo CRISPR screening reveals nutrient signaling processes underpinning CD8+ TÂcell fate decisions. Cell, 2021, 184, 1245-1261.e21.	13.5	68
2133	EZH2 inhibition activates a dsRNAâ€“STINGâ€“interferon stress axis that potentiates response to PD-1 checkpoint blockade in prostate cancer. Nature Cancer, 2021, 2, 444-456.	5.7	118

#	Article	IF	Citations
2135	Single-Cell Toolkits Opening a New Era for Cell Engineering. Molecules and Cells, 2021, 44, 127-135.	1.0	11
2139	PRDM16 regulates a temporal transcriptional program to promote progression of cortical neural progenitors. Development (Cambridge), 2021, 148, .	1.2	5
2140	Protocol for assay of transposase accessible chromatin sequencing in non-model species. STAR Protocols, 2021, 2, 100341.	0.5	6
2142	Enhancers predominantly regulate gene expression during differentiation via transcription initiation. Molecular Cell, 2021, 81, 983-997.e7.	4.5	27
2143	A single nucleotide polymorphism variant located in the cisâ€regulatory region of the ABCG2 gene is associated with mallard egg colour. Molecular Ecology, 2021, 30, 1477-1491.	2.0	22
2144	InÂvivo CD8+ TÂcell CRISPR screening reveals control by Fli1 in infection and cancer. Cell, 2021, 184, 1262-1280.e22.	13.5	107
2145	Climate-driven flyway changes and memory-based long-distance migration. Nature, 2021, 591, 259-264.	13.7	49
2146	Nucleosome Positioning and Spacing: From Mechanism to Function. Journal of Molecular Biology, 2021, 433, 166847.	2.0	26
2147	Targeted molecular profiling of rare olfactory sensory neurons identifies fate, wiring, and functional determinants. ELife, 2021, 10, .	2.8	6
2148	Generating fragment density plots in R/Bioconductor with VplotR. Journal of Open Source Software, 2021, 6, 3009.	2.0	2
2149	Functional annotations of three domestic animal genomes provide vital resources for comparative and agricultural research. Nature Communications, 2021, 12, 1821.	5.8	105
2150	DNA mechanics and its biological impact. Journal of Molecular Biology, 2021, 433, 166861.	2.0	31
2151	Neuronal enhancers are hotspots for DNA single-strand break repair. Nature, 2021, 593, 440-444.	13.7	126
2152	IRF1 governs the differential interferon-stimulated gene responses in human monocytes and macrophages by regulating chromatin accessibility. Cell Reports, 2021, 34, 108891.	2.9	46
2153	Chromatin accessibility of kidney tubular cells under stress reveals key transcription factor mediating acute and chronic kidney disease. FEBS Journal, 2021, 288, 5446-5458.	2.2	1
2155	Molecular and computational approaches to map regulatory elements in 3D chromatin structure. Epigenetics and Chromatin, 2021, 14, 14.	1.8	9
2156	Profiling chromatin accessibility in pediatric acute lymphoblastic leukemia identifies subtype-specific chromatin landscapes and gene regulatory networks. Leukemia, 2021, 35, 3078-3091.	3.3	15
2158	Deep learning-based enhancement of epigenomics data with AtacWorks. Nature Communications, 2021, 12, 1507.	5.8	33

#	Article	IF	Citations
2159	Pan-cancer chromatin analysis of the human vtRNA genes uncovers their association with cancer biology. F1000Research, 2021, 10, 182.	0.8	3
2160	From Hi-C Contact Map to Three-Dimensional Organization of Interphase Human Chromosomes. Physical Review X, 2021, 11, .	2.8	12
2161	Drosophila Fezf functions as a transcriptional repressor to direct layer-specific synaptic connectivity in the fly visual system. Proceedings of the National Academy of Sciences of the United States of America, 2021, 118, .	3.3	14
2163	Scrt1, a transcriptional regulator of Î²-cell proliferation identified by differential chromatin accessibility during islet maturation. Scientific Reports, 2021, 11, 8800.	1.6	6
2164	Accessible chromatin reveals regulatory mechanisms underlying cell fate decisions during early embryogenesis. Scientific Reports, 2021, 11, 7896.	1.6	3
2165	Cell Fate Decisions in the Wake of Histone H3 Deposition. Frontiers in Cell and Developmental Biology, 2021, 9, 654915.	1.8	6
2166	Locus-Specific Genomic DNA Purification Using the CRISPR System: Methods and Applications. CRISPR Journal, 2021, 4, 290-300.	1.4	4
2167	IDO1 Expression in Ovarian Cancer Induces PD-1 in T Cells via Aryl Hydrocarbon Receptor Activation. Frontiers in Immunology, 2021, 12, 678999.	2.2	40
2168	Mapping Astrocyte Transcriptional Signatures in Response to Neuroactive Compounds. International Journal of Molecular Sciences, 2021, 22, 3975.	1.8	12
2169	Comprehensive characterization of tissue-specific chromatin accessibility in L2 Caenorhabditis elegans nematodes. Genome Research, 2021, 31, 1952-1969.	2.4	8
2170	Renin Cells, the Kidney, and Hypertension. Circulation Research, 2021, 128, 887-907.	2.0	25
2171	Sharing biological data: why, when, and how. FEBS Letters, 2021, 595, 847-863.	1.3	26
2172	E2A-regulated epigenetic landscape promotes memory CD8 T cell differentiation. Proceedings of the National Academy of Sciences of the United States of America, 2021, 118, .	3.3	21
2173	A comprehensive transcriptome signature of murine hematopoietic stem cell aging. Blood, 2021, 138, 439-451.	0.6	52
2174	Single-cell chromatin accessibility landscape identifies tissue repair program in human regulatory TÂcells. Immunity, 2021, 54, 702-720.e17.	6.6	78
2175	Cas9 deactivation with photocleavable guide RNAs. Molecular Cell, 2021, 81, 1553-1565.e8.	4.5	30
2176	Transcription factor chromatin profiling genome-wide using uliCUT&RUN in single cells and individual blastocysts. Nature Protocols, 2021, 16, 2633-2666.	5.5	23
2177	Logic and lineage impacts on functional transcription factor deployment for T-cell fate commitment. Biophysical Journal, 2021, 120, 4162-4181.	0.2	9

#	Article	IF	Citations
2179	Enhancement and Imputation of Peak Signal Enables Accurate Cell-Type Classification in scATAC-seq. Frontiers in Genetics, 2021, 12, 658352.	1.1	2
2180	The Stochastic Genome and Its Role in Gene Expression. Cold Spring Harbor Perspectives in Biology, 2021, 13, a040386.	2.3	18
2181	Profiling the genetic determinants of chromatin accessibility with scalable single-cell CRISPR screens. Nature Biotechnology, 2021, 39, 1270-1277.	9.4	43
2182	Genomic Features of Open Chromatin Regions (OCRs) in Wild Soybean and Their Effects on Gene Expressions. Genes, 2021, 12, 640.	1.0	9
2183	B cell-specific XIST complex enforces X-inactivation and restrains atypical B cells. Cell, 2021, 184, 1790-1803.e17.	13.5	105
2184	Rapid and Low-Input Profiling of Histone Marks in Plants Using Nucleus CUT&Tag. Frontiers in Plant Science, 2021, 12, 634679.	1.7	17
2185	Fish-Ing for Enhancers in the Heart. International Journal of Molecular Sciences, 2021, 22, 3914.	1.8	5
2187	B1a and B2 cells are characterized by distinct CpG modification states at DNMT3A-maintained enhancers. Nature Communications, 2021, 12, 2208.	5.8	14
2189	Sequence deeper without sequencing more: Bayesian resolution of ambiguously mapped reads. PLoS Computational Biology, 2021, 17, e1008926.	1.5	8
2190	Importance of clonal hematopoiesis in heart failure. Trends in Cardiovascular Medicine, 2022, 32, 198-203.	2.3	7
2191	Kdm6b Regulates the Generation of Effector CD8+ T Cells by Inducing Chromatin Accessibility in Effector-Associated Genes. Journal of Immunology, 2021, 206, 2170-2183.	0.4	18
2192	Variants That Differentiate Wolf and Dog Populations Are Enriched in Regulatory Elements. Genome Biology and Evolution, 2021, 13, .	1.1	4
2193	Myod1 and GR coordinate myofiber-specific transcriptional enhancers. Nucleic Acids Research, 2021, 49, 4472-4492.	6.5	18
2194	Stress-induced transcriptional memory accelerates promoter-proximal pause release and decelerates termination over mitotic divisions. Molecular Cell, 2021, 81, 1715-1731.e6.	4.5	28
2195	KrÃ¼ppel-like factor 1 is a core cardiomyogenic trigger in zebrafish. Science, 2021, 372, 201-205.	6.0	32
2196	DNA hypomethylating agents increase activation and cytolytic activity of CD8+ TÂcells. Molecular Cell, 2021, 81, 1469-1483.e8.	4.5	52
2197	Accurate prediction ofcis-regulatory modules reveals a prevalent regulatory genome of humans. NAR Genomics and Bioinformatics, 2021, 3, lqab052.	1.5	21
2198	Donor cell memory confers a metastable state of directly converted cells. Cell Stem Cell, 2021, 28, 1291-1306.e10.	5.2	5

#	Article	IF	Citations
2202	Chd8 regulates X chromosome inactivation in mouse through fine-tuning control of Xist expression. Communications Biology, 2021, 4, 485.	2.0	10
2203	Morphological and genomic shifts in mole-rat â€˜queensâ€™ increase fecundity but reduce skeletal integrity. ELife, 2021, 10, .	2.8	8
2204	Profile of Howard Y. Chang. Proceedings of the National Academy of Sciences of the United States of America, 2021, 118, e2104246118.	3.3	0
2205	Chromatin accessibility landscapes of immune cells in rheumatoid arthritis nominate monocytes in disease pathogenesis. BMC Biology, 2021, 19, 79.	1.7	5
2206	H3K27ac bookmarking promotes rapid post-mitotic activation of the pluripotent stem cell program without impacting 3D chromatin reorganization. Molecular Cell, 2021, 81, 1732-1748.e8.	4.5	60
2207	A unique histone 3 lysine 14 chromatin signature underlies tissue-specific gene regulation. Molecular Cell, 2021, 81, 1766-1780.e10.	4.5	17
2208	Subtype-associated epigenomic landscape and 3D genome structure in bladder cancer. Genome Biology, 2021, 22, 105.	3.8	29
2210	Single-cell transcriptome atlas and chromatin accessibility landscape reveal differentiation trajectories in the rice root. Nature Communications, 2021, 12, 2053.	5.8	107
2211	Transient rest restores functionality in exhausted CAR-T cells through epigenetic remodeling. Science, 2021, 372, .	6.0	297
2212	Multi-omic profiling of pituitary thyrotropic cells and progenitors. BMC Biology, 2021, 19, 76.	1.7	5
2214	Transcriptional circuitry atlas of genetic diverse unstimulated murine and human macrophages define disparity in population-wide innate immunity. Scientific Reports, 2021, 11, 7373.	1.6	7
2215	RA3 is a reference-guided approach for epigenetic characterization of single cells. Nature Communications, 2021, 12, 2177.	5.8	31
2216	Multiple interactions of the oncoprotein transcription factor MYC with the SWI/SNF chromatin remodeler. Oncogene, 2021, 40, 3593-3609.	2.6	14
2218	Single-suture craniosynostosis and the epigenome: current evidence and a review of epigenetic principles. Neurosurgical Focus, 2021, 50, E10.	1.0	7
2221	Hemodynamic Forces Regulate Cardiac Regeneration-Responsive Enhancer Activity during Ventricle Regeneration. International Journal of Molecular Sciences, 2021, 22, 3945.	1.8	7
2222	EVI1 activates tumor-promoting transcriptional enhancers in pancreatic cancer. NAR Cancer, 2021, 3, zcab023.	1.6	10
2223	A Transcription Start Site Map in Human Pancreatic Islets Reveals Functional Regulatory Signatures. Diabetes, 2021, 70, 1581-1591.	0.3	7
2224	Cis-regulatory dissection of cone development reveals a broad role for Otx2 and Oc transcription factors. Development (Cambridge), 2021, 148, .	1.2	9

#	Article	IF	Citations
2226	Mapping the regulatory landscape of auditory hair cells from single-cell multi-omics data. Genome Research, 2021, 31, 1885-1899.	2.4	16
2227	Barcoded viral tracing of single-cell interactions in central nervous system inflammation. Science, 2021, 372, .	6.0	127
2228	Deconvoluting global cytokine signaling networks in natural killer cells. Nature Immunology, 2021, 22, 627-638.	7.0	31
2229	Surface antigen-guided CRISPR screens identify regulators of myeloid leukemia differentiation. Cell Stem Cell, 2021, 28, 718-731.e6.	5.2	38
2230	Structural alteration of the nucleus for the reprogramming of gene expression. FEBS Journal, 2022, 289, 7221-7233.	2.2	5
2232	Selective sweep for an enhancer involucrin allele identifies skin barrier adaptation out of Africa. Nature Communications, 2021, 12, 2557.	5.8	5
2235	Yap regulates skeletal muscle fatty acid oxidation and adiposity in metabolic disease. Nature Communications, 2021, 12, 2887.	5.8	18
2236	Stability of DNA methylation and chromatin accessibility in structurally diverse maize genomes. G3: Genes, Genomes, Genetics, 2021, 11, .	0.8	3
2237	Core-binding factor leukemia hijacks the T-cellâ€“prone PU.1 antisense promoter. Blood, 2021, 138, 1345-1358.	0.6	12
2238	Single-nucleotide-level mapping of DNA regulatory elements that control fetal hemoglobin expression. Nature Genetics, 2021, 53, 869-880.	9.4	37
2239	Genomic Characterization of Cisplatin Response Uncovers Priming of Cisplatin-Induced Genes in a Resistant Cell Line. International Journal of Molecular Sciences, 2021, 22, 5814.	1.8	8
2240	A distal Foxp3 enhancer enables interleukin-2 dependent thymic Treg cell lineage commitment for robust immune tolerance. Immunity, 2021, 54, 931-946.e11.	6.6	46
2241	The iNKT-dependent butterfly effect in HCT. Blood, 2021, 138, 821-822.	0.6	0
2242	Integrated Analysis of Whole Genome and Epigenome Data Using Machine Learning Technology: Toward the Establishment of Precision Oncology. Frontiers in Oncology, 2021, 11, 666937.	1.3	25
2243	A latent subset of human hematopoietic stem cells resists regenerative stress to preserve stemness. Nature Immunology, 2021, 22, 723-734.	7.0	26
2245	Chromatin accessibility in neuropsychiatric disorders. Neurobiology of Learning and Memory, 2021, 181, 107438.	1.0	2
2246	Aged hematopoietic stem cells are refractory to bloodborne systemic rejuvenation interventions. Journal of Experimental Medicine, 2021, 218, .	4.2	48
2247	Epigenomic profiling of primate lymphoblastoid cell lines reveals the evolutionary patterns of epigenetic activities in gene regulatory architectures. Nature Communications, 2021, 12, 3116.	5.8	19

#	Article	IF	Citations
2248	Integrative single-cell analysis of allele-specific copy number alterations and chromatin accessibility in cancer. Nature Biotechnology, 2021, 39, 1259-1269.	9.4	31
2249	Deregulation of enhancer structure, function, and dynamics in acute lymphoblastic leukemia. Trends in Immunology, 2021, 42, 418-431.	2.9	4
2251	Repression of endogenous retroviruses prevents antiviral immune response and is required for mammary gland development. Cell Stem Cell, 2021, 28, 1790-1804.e8.	5.2	10
2252	The SMC5/6 complex compacts and silences unintegrated HIV-1 DNA and is antagonized by Vpr. Cell Host and Microbe, 2021, 29, 792-805.e6.	5.1	49
2254	The Chromatin Accessibility Landscape of Adult Rat. Frontiers in Genetics, 2021, 12, 651604.	1.1	1
2255	Epigenetic silencing by SETDB1 suppresses tumour intrinsic immunogenicity. Nature, 2021, 595, 309-314.	13.7	181
2256	Cell-type-specific effects of genetic variation on chromatin accessibility during human neuronal differentiation. Nature Neuroscience, 2021, 24, 941-953.	7.1	47
2258	Role of epigenetics in unicellular to multicellular transition in Dictyostelium. Genome Biology, 2021, 22, 134.	3.8	12
2259	Environmental Enrichment Induces Epigenomic and Genome Organization Changes Relevant for Cognition. Frontiers in Molecular Neuroscience, 2021, 14, 664912.	1.4	12
2261	Validation of protein arginine methyltransferase 5 (PRMT5) as a candidate therapeutic target in the spontaneous canine model of non-Hodgkin lymphoma. PLoS ONE, 2021, 16, e0250839.	1.1	6
2263	Epigenetic Reprogramming of Host and Viral Genes by Human Cytomegalovirus Infection in Kasumi-3 Myeloid Progenitor Cells at Early Times Postinfection. Journal of Virology, 2021, 95, .	1.5	5
2265	Neuronal genes deregulated in Cornelia de Lange Syndrome respond to removal and re-expression of cohesin. Nature Communications, 2021, 12, 2919.	5.8	18
2266	Tissue-Resident Memory T Cells in Antifungal Immunity. Frontiers in Immunology, 2021, 12, 693055.	2.2	4
2267	Low Replicative Stress Triggers Cell-Type Specific Inheritable Advanced Replication Timing. International Journal of Molecular Sciences, 2021, 22, 4959.	1.8	3
2268	CTCF looping is established during gastrulation in medaka embryos. Genome Research, 2021, 31, 968-980.	2.4	37
2269	Cross-tissue organization of the fibroblast lineage. Nature, 2021, 593, 575-579.	13.7	463
2270	Pancreatic cancer prognosis is predicted by an ATAC-array technology for assessing chromatin accessibility. Nature Communications, 2021, 12, 3044.	5.8	19
2271	Exposure to sevoflurane results in changes of transcription factor occupancy in sperm and inheritance of autismâ€. Biology of Reproduction, 2021, 105, 705-719.	1.2	12

#	Article	IF	Citations
2272	Chromatin accessibility and translational landscapes of tea plants under chilling stress. Horticulture Research, 2021, 8, 96.	2.9	28
2273	Genetic and epigenetic features of promoters with ubiquitous chromatin accessibility support ubiquitous transcription of cell-essential genes. Nucleic Acids Research, 2021, 49, 5705-5725.	6.5	10
2276	Ectopic targeting of CG DNA methylation in Arabidopsis with the bacterial SssI methyltransferase. Nature Communications, 2021, 12, 3130.	5.8	20
2278	Molecular analysis of the erythroid phenotype of a patient with BCL11A haploinsufficiency. Blood Advances, 2021, 5, 2339-2349.	2.5	7
2279	Tutorial: practical considerations for tissue clearing and imaging. Nature Protocols, 2021, 16, 2732-2748.	5.5	51
2281	Evidence from oyster suggests an ancient role for Pdx in regulating insulin gene expression in animals. Nature Communications, 2021, 12, 3117.	5.8	10
2282	PlantDeepSEA, a deep learning-based web service to predict the regulatory effects of genomic variants in plants. Nucleic Acids Research, 2021, 49, W523-W529.	6.5	20
2284	Epigenetic Modulation of Radiation-Induced Diacylglycerol Kinase Alpha Expression Prevents Pro-Fibrotic Fibroblast Response. Cancers, 2021, 13, 2455.	1.7	8
2286	PKM2-dependent metabolic skewing of hepatic Th17 cells regulates pathogenesis of non-alcoholic fatty liver disease. Cell Metabolism, 2021, 33, 1187-1204.e9.	7.2	60
2287	Selective Requirement of MYB for Oncogenic Hyperactivation of a Translocated Enhancer in Leukemia. Cancer Discovery, 2021, 11, 2868-2883.	7.7	25
2289	AKR1C2 and AKR1C3 expression in adipose tissue: Association with body fat distribution and regulatory variants. Molecular and Cellular Endocrinology, 2021, 527, 111220.	1.6	11
2290	Integrated transcriptomics and epigenomics reveal chamber-specific and species-specific characteristics of human and mouse hearts. PLoS Biology, 2021, 19, e3001229.	2.6	5
2291	Stable Epigenetic Programming of Effector and Central Memory CD4 T Cells Occurs Within 7 Days of Antigen Exposure In Vivo. Frontiers in Immunology, 2021, 12, 642807.	2.2	4
2292	B Lymphocyte Specification Is Preceded by Extensive Epigenetic Priming in Multipotent Progenitors. Journal of Immunology, 2021, 206, 2700-2713.	0.4	6
2294	In vivo tissue-specific chromatin profiling in Drosophila melanogaster using GFP-tagged nuclei. Genetics, 2021, 218, .	1.2	14
2295	INTACT vs. FANS for Cell-Type-Specific Nuclei Sorting: A Comprehensive Qualitative and Quantitative Comparison. International Journal of Molecular Sciences, 2021, 22, 5335.	1.8	12
2296	OpenAnnotate: a web server to annotate the chromatin accessibility of genomic regions. Nucleic Acids Research, 2021, 49, W483-W490.	6.5	17
2297	The Chromatin Accessibility Landscape of Peripheral Blood Mononuclear Cells in Patients With Systemic Lupus Erythematosus at Single-Cell Resolution. Frontiers in Immunology, 2021, 12, 641886.	2.2	6

#	Article	IF	Citations
2298	Robust single-cell discovery of RNA targets of RNA-binding proteins and ribosomes. Nature Methods, 2021, 18, 507-519.	9.0	77
2299	High-throughput single-cell chromatin accessibility CRISPR screens enable unbiased identification of regulatory networks in cancer. Nature Communications, 2021, 12, 2969.	5.8	73
2300	Antigen-driven EGR2 expression is required for exhausted CD8+ T cell stability and maintenance. Nature Communications, 2021, 12, 2782.	5.8	20
2301	Extracellular signal-regulated kinase mediates chromatin rewiring and lineage transformation in lung cancer. ELife, 2021, 10, .	2.8	16
2302	Embeddings of genomic region sets capture rich biological associations in lower dimensions. Bioinformatics, 2021, 37, 4299-4306.	1.8	9
2303	Epigenetic Features of HIV-Induced T-Cell Exhaustion Persist Despite Early Antiretroviral Therapy. Frontiers in Immunology, 2021, 12, 647688.	2.2	19
2304	Skin and gut imprinted helper T cell subsets exhibit distinct functional phenotypes in central nervous system autoimmunity. Nature Immunology, 2021, 22, 880-892.	7.0	34
2307	Transcriptional Control of Cell Fate Determination in Antigen-Experienced CD8 T Cells. Cold Spring Harbor Perspectives in Biology, 2022, 14, a037945.	2.3	4
2309	STAG2 loss rewires oncogenic and developmental programs to promote metastasis in Ewing sarcoma. Cancer Cell, 2021, 39, 827-844.e10.	7.7	49
2311	The FLI portion of EWS/FLI contributes a transcriptional regulatory function that is distinct and separable from its DNA-binding function in Ewing sarcoma. Oncogene, 2021, 40, 4759-4769.	2.6	14
2312	HIRA stabilizes skeletal muscle lineage identity. Nature Communications, 2021, 12, 3450.	5.8	17
2313	Applications of single-cell sequencing in cancer research: progress and perspectives. Journal of Hematology and Oncology, 2021, 14, 91.	6.9	172
2315	Toward genomic selection in Pinus taeda: Integrating resources to support array design in a complex conifer genome. Applications in Plant Sciences, 2021, 9, e11439.	0.8	19
2316	Multi-omics analysis of intertumoral heterogeneity within medulloblastoma uncharted-pathway subtypes. Brain Tumor Pathology, 2021, 38, 234-242.	1.1	4
2317	ATRX promotes heterochromatin formation to protect cells from G-quadruplex DNA-mediated stress. Nature Communications, 2021, 12, 3887.	5.8	49
2318	Leveraging Novel Integrated Single-Cell Analyses to Define HIV-1 Latency Reversal. Viruses, 2021, 13, 1197.	1.5	3
2319	Learning the Regulatory Code of Gene Expression. Frontiers in Molecular Biosciences, 2021, 8, 673363.	1.6	17
2320	Melatonin enhances nitrogen metabolism and haustorium development in hemiparasite Santalum album Linn.. Environmental and Experimental Botany, 2021, 186, 104460.	2.0	10

#	Article	IF	Citations
2322	Chromatin accessibility profiling in Neurospora crassa reveals molecular features associated with accessible and inaccessible chromatin. BMC Genomics, 2021, 22, 459.	1.2	13
2323	A gain-of-function single nucleotide variant creates a new promoter which acts as an orientation-dependent enhancer-blocker. Nature Communications, 2021, 12, 3806.	5.8	18
2325	Long-read RNA sequencing reveals widespread sex-specific alternative splicing in threespine stickleback fish. Genome Research, 2021, 31, 1486-1497.	2.4	23
2326	High throughput screening identifies SOX2 as a super pioneer factor that inhibits DNA methylation maintenance at its binding sites. Nature Communications, 2021, 12, 3337.	5.8	31
2328	Impact of Interleukin 10 Deficiency on Intestinal Epithelium Responses to Inflammatory Signals. Frontiers in Immunology, 2021, 12, 690817.	2.2	13
2329	Melanoma dedifferentiation induced by IFN-Î³ epigenetic remodeling in response to antiâ€“PD-1 therapy. Journal of Clinical Investigation, 2021, 131, .	3.9	35
2330	Applications of Single-Cell Omics in Tumor Immunology. Frontiers in Immunology, 2021, 12, 697412.	2.2	21
2331	Sequential CRISPR gene editing in human iPSCs charts the clonal evolution of myeloid leukemia and identifies early disease targets. Cell Stem Cell, 2021, 28, 1074-1089.e7.	5.2	37
2333	Breast tumor stiffness instructs bone metastasis via maintenance of mechanical conditioning. Cell Reports, 2021, 35, 109293.	2.9	29
2334	mTOR Driven Gene Transcription Is Required for Cholesterol Production in Neurons of the Developing Cerebral Cortex. International Journal of Molecular Sciences, 2021, 22, 6034.	1.8	11
2335	Tissue-resident macrophages provide a pro-tumorigenic niche to early NSCLC cells. Nature, 2021, 595, 578-584.	13.7	284
2336	Alternative splicing is a developmental switch for hTERT expression. Molecular Cell, 2021, 81, 2349-2360.e6.	4.5	19
2337	Coordination of two enhancers drives expression of olfactory trace amine-associated receptors. Nature Communications, 2021, 12, 3798.	5.8	8
2339	A microRNA expression and regulatory element activity atlas of the mouse immune system. Nature Immunology, 2021, 22, 914-927.	7.0	19
2340	Current Methodological Challenges of Single-Cell and Single-Nucleus RNA-Sequencing in Glomerular Diseases. Journal of the American Society of Nephrology: JASN, 2021, 32, 1838-1852.	3.0	21
2341	Mapping chromatin accessibility and active regulatory elements reveals pathological mechanisms in human gliomas. Nature Communications, 2021, 12, 3621.	5.8	22
2342	Negative correlation of single-cell PAX3:FOXO1 expression with tumorigenicity in rhabdomyosarcoma. Life Science Alliance, 2021, 4, e202001002.	1.3	4
2343	Dissociation of chick embryonic tissue for FACS and preparation of isolated cells for genome-wide downstream assays. STAR Protocols, 2021, 2, 100414.	0.5	2

#	Article	IF	Citations
2344	Probing Chromatin Compaction and Its Epigenetic States in situ With Single-Molecule Localization-Based Super-Resolution Microscopy. Frontiers in Cell and Developmental Biology, 2021, 9, 653077.	1.8	5
2345	Epigenetic regulation in medulloblastoma pathogenesis revealed by genetically engineered mouse models. Cancer Science, 2021, 112, 2948-2957.	1.7	4
2346	Reduction of lamin B receptor levels by miR-340-5p disrupts chromatin, promotes cell senescence and enhances senolysis. Nucleic Acids Research, 2021, 49, 7389-7405.	6.5	14
2347	Genome editing to define the function of risk loci and variants in rheumatic disease. Nature Reviews Rheumatology, 2021, 17, 462-474.	3.5	9
2348	The epigenetics of keloids. Experimental Dermatology, 2021, 30, 1099-1114.	1.4	17
2350	Methods of massive parallel reporter assays for investigation of enhancers. Vavilovskii Zhurnal Genetiki I Selektsii, 2021, 25, 344-355.	0.4	2
2353	DNA repair in neurons and its possible link to the epigenetic machinery at enhancers. Epigenomics, 2021, 13, 913-917.	1.0	1
2354	Protocol for single-cell ATAC sequencing using combinatorial indexing in mouse lung adenocarcinoma. STAR Protocols, 2021, 2, 100583.	0.5	9
2355	Runx1 shapes the chromatin landscape via a cascade of direct and indirect targets. PLoS Genetics, 2021, 17, e1009574.	1.5	19
2357	BMI1 maintains the Treg epigenomic landscape to prevent inflammatory bowel disease. Journal of Clinical Investigation, 2021, 131, .	3.9	10
2359	Chromatin accessibility changes at intergenic regions are associated with ovarian cancer drug resistance. Clinical Epigenetics, 2021, 13, 122.	1.8	7
2363	Single-cell chromatin accessibility landscape of human umbilical cord blood in trisomy 18 syndrome. Human Genomics, 2021, 15, 40.	1.4	2
2364	Pan-cancer chromatin analysis of the human vtRNA genes uncovers their association with cancer biology. F1000Research, 2021, 10, 182.	0.8	8
2365	Extrachromosomal circular DNA: a new potential role in cancer progression. Journal of Translational Medicine, 2021, 19, 257.	1.8	36
2366	Tumors exploit FTO-mediated regulation of glycolytic metabolism to evade immune surveillance. Cell Metabolism, 2021, 33, 1221-1233.e11.	7.2	138
2367	Foxp3 enhancers synergize to maximize regulatory T cell suppressive capacity. Journal of Experimental Medicine, 2021, 218, .	4.2	5
2368	Single-cell multi-omics sequencing: application trends, COVID-19, data analysis issues and prospects. Briefings in Bioinformatics, 2021, 22, .	3.2	14
2369	Analysis of gene network bifurcation during optic cup morphogenesis in zebrafish. Nature Communications, 2021, 12, 3866.	5.8	14

#	Article	IF	Citations
2370	Regulation of Chromatin Organization in Cell Stemness: The Emerging Role of Long Non-coding RNAs. Stem Cell Reviews and Reports, 2021, 17, 2042-2053.	1.7	9
2372	Single-Cell Mapping of GLP-1 and GIP Receptor Expression in the Dorsal Vagal Complex. Diabetes, 2021, 70, 1945-1955.	0.3	13
2373	A Chinese hamster transcription start site atlas that enables targeted editing of CHO cells. NAR Genomics and Bioinformatics, 2021, 3, lqab061.	1.5	7
2375	Niche stiffening compromises hair follicle stem cell potential during ageing by reducing bivalent promoter accessibility. Nature Cell Biology, 2021, 23, 771-781.	4.6	51
2376	Cortex cis-regulatory switches establish scale colour identity and pattern diversity in Heliconius. ELife, 2021, 10, .	2.8	40
2377	Neonatal thyroxine activation modifies epigenetic programming of the liver. Nature Communications, 2021, 12, 4446.	5.8	11
2378	RoboCOP: jointly computing chromatin occupancy profiles for numerous factors from chromatin accessibility data. Nucleic Acids Research, 2021, 49, 7925-7938.	6.5	3
2380	Chromatin remodelling complexes in cerebral cortex development and neurodevelopmental disorders. Neurochemistry International, 2021, 147, 105055.	1.9	10
2381	The chromatin, topological and regulatory properties of pluripotency-associated poised enhancers are conserved in vivo. Nature Communications, 2021, 12, 4344.	5.8	50
2383	Understanding Arteriosclerosis 2.0: Making Sense of Genetic Variants with scATAC. Circulation Research, 2021, 129, 259-261.	2.0	1
2384	Joint disease-specificity at the regulatory base-pair level. Nature Communications, 2021, 12, 4161.	5.8	18
2385	ANANSE: an enhancer network-based computational approach for predicting key transcription factors in cell fate determination. Nucleic Acids Research, 2021, 49, 7966-7985.	6.5	39
2386	Extensive transcriptional and chromatin changes underlie astrocyte maturation in vivo and in culture. Nature Communications, 2021, 12, 4335.	5.8	60
2388	Transcriptional regulation of N6-methyladenosine orchestrates sex-dimorphic metabolic traits. Nature Metabolism, 2021, 3, 940-953.	5.1	24
2389	Epigenetic scarring of exhausted T cells hinders memory differentiation upon eliminating chronic antigenic stimulation. Nature Immunology, 2021, 22, 1008-1019.	7.0	116
2390	A plate-based single-cell ATAC-seq workflow for fast and robust profiling of chromatin accessibility. Nature Protocols, 2021, 16, 4084-4107.	5.5	40
2391	Integrated Chromatin Accessibility and Transcriptome Landscapes of Doxorubicin-Resistant Breast Cancer Cells. Frontiers in Cell and Developmental Biology, 2021, 9, 708066.	1.8	17
2392	Distinct transcription factor networks control neutrophil-driven inflammation. Nature Immunology, 2021, 22, 1093-1106.	7.0	83

#	Article	IF	Citations
2393	Transcriptional and Epigenetic Landscape of Cardiac Pacemaker Cells: Insights Into Cellular Specialization in the Sinoatrial Node. Frontiers in Physiology, 2021, 12, 712666.	1.3	7
2395	Reactivation of a developmentally silenced embryonic globin gene. Nature Communications, 2021, 12, 4439.	5.8	19
2396	From Reads to Insights: Integrative Pipelines for Biological Interpretation of ATAC-seq Data. Genomics, Proteomics and Bioinformatics, 2021, 19, 519-521.	3.0	4
2397	Application of single cell genomics to focal epilepsies: A call to action. Brain Pathology, 2021, 31, e12958.	2.1	8
2398	Chromatin states shaped by an epigenetic code confer regenerative potential to the mouse liver. Nature Communications, 2021, 12, 4110.	5.8	12
2399	Exploiting Single-Cell Tools in Gene and Cell Therapy. Frontiers in Immunology, 2021, 12, 702636.	2.2	21
2400	Discovering single nucleotide variants and indels from bulk and single-cell ATAC-seq. Nucleic Acids Research, 2021, 49, 7986-7994.	6.5	8
2401	POU4F3 pioneer activity enables ATOH1 to drive diverse mechanoreceptor differentiation through a feed-forward epigenetic mechanism. Proceedings of the National Academy of Sciences of the United States of America, 2021, 118, .	3.3	38
2402	Singleâ€cell imaging of genome organization and dynamics. Molecular Systems Biology, 2021, 17, e9653.	3.2	25
2403	Wholeâ€genome analysis of TET dioxygenase function in regulatory T cells. EMBO Reports, 2021, 22, e52716.	2.0	19
2405	Systematic dissection of transcriptional regulatory networks by genome-scale and single-cell CRISPR screens. Science Advances, 2021, 7, .	4.7	19
2406	Establishment, maintenance, and recall of inflammatory memory. Cell Stem Cell, 2021, 28, 1758-1774.e8.	5.2	98
2407	Multi-omic profiling of primary mouse neutrophils predicts a pattern of sex- and age-related functional regulation. Nature Aging, 2021, 1, 715-733.	5.3	55
2408	A universal framework for detecting cis-regulatory diversity in DNA regions. Genome Research, 2021, 31, 1646-1662.	2.4	3
2409	Method for efficient soluble expression and purification of recombinant hyperactive Tn5 transposase. Protein Expression and Purification, 2021, 183, 105866.	0.6	6
2410	Impaired SNF2L Chromatin Remodeling Prolongs Accessibility at Promoters Enriched for Fos/Jun Binding Sites and Delays Granule Neuron Differentiation. Frontiers in Molecular Neuroscience, 2021, 14, 680280.	1.4	1
2411	Gene Regulatory Network of Human GM-CSF-Secreting T Helper Cells. Journal of Immunology Research, 2021, 2021, 1-24.	0.9	2
2412	High-content single-cell combinatorial indexing. Nature Biotechnology, 2021, 39, 1574-1580.	9.4	39

#	Article	IF	Citations
2413	Uniaxial Cyclic Stretching Promotes Chromatin Accessibility of Gene Loci Associated With Mesenchymal Stem Cells Morphogenesis and Osteogenesis. Frontiers in Cell and Developmental Biology, 2021, 9, 664545.	1.8	9
2414	Genome wide DNA methylation analysis of alveolar capillary dysplasia lung tissue reveals aberrant methylation of genes involved in development including the FOXF1 locus. Clinical Epigenetics, 2021, 13, 148.	1.8	6
2415	Dynamic Transcriptional and Epigenetic Changes Drive Cellular Plasticity in the Liver. Hepatology, 2021, 74, 444-457.	3.6	20
2416	The histone chaperone HIR maintains chromatin states to control nitrogen assimilation and fungal virulence. Cell Reports, 2021, 36, 109406.	2.9	10
2417	High-depth spatial transcriptome analysis by photo-isolation chemistry. Nature Communications, 2021, 12, 4416.	5.8	22
2418	Assay for Transposase-Accessible Chromatin Using Sequencing Analysis Reveals a Widespread Increase in Chromatin Accessibility in Psoriasis. Journal of Investigative Dermatology, 2021, 141, 1745-1753.	0.3	8
2419	Mapping the landscape of chromatin dynamics during naÃ¯ve CD4+â€‰T-cell activation. Scientific Reports, 2021, 11, 14101.	1.6	10
2420	Chromatin Profiling Techniques: Exploring the Chromatin Environment and Its Contributions to Complex Traits. International Journal of Molecular Sciences, 2021, 22, 7612.	1.8	6
2423	BATF regulates progenitor to cytolytic effector CD8+ T cell transition during chronic viral infection. Nature Immunology, 2021, 22, 996-1007.	7.0	78
2424	A comparative integrated multi-omics analysis identifies CA2 as a novel target for chordoma. Neuro-Oncology, 2021, 23, 1709-1722.	0.6	15
2425	Chromatin Landscapes of Human Lung Cells Predict Potentially Functional Chronic Obstructive Pulmonary Disease Genome-Wide Association Study Variants. American Journal of Respiratory Cell and Molecular Biology, 2021, 65, 92-102.	1.4	7
2426	Concepts to Reveal Parvovirusâ€“Nucleus Interactions. Viruses, 2021, 13, 1306.	1.5	6
2427	IL-7R signaling activates widespread VH and DH gene usage to drive antibody diversity in bone marrow B cells. Cell Reports, 2021, 36, 109349.	2.9	6
2428	Epigenetic regulation of reproduction in human and in animal models. Molecular Human Reproduction, 2021, 27, .	1.3	3
2429	Genetic effects on liver chromatin accessibility identify disease regulatory variants. American Journal of Human Genetics, 2021, 108, 1169-1189.	2.6	22
2432	AIAP: A Quality Control and Integrative Analysis Package to Improve ATAC-seq Data Analysis. Genomics, Proteomics and Bioinformatics, 2021, 19, 641-651.	3.0	19
2433	A simple and robust method for simultaneous dual-omics profiling with limited numbers of cells. Cell Reports Methods, 2021, 1, 100041.	1.4	3
2434	Profiling chromatin accessibility in formalin-fixed paraffin-embedded samples. Genome Research, 2022, 32, 150-161.	2.4	16

#	Article	IF	Citations
2435	High-throughput and single-cell T cell receptor sequencing technologies. Nature Methods, 2021, 18, 881-892.	9.0	133
2436	Single-cell and spatial analyses of cancer cells: toward elucidating the molecular mechanisms of clonal evolution and drug resistance acquisition. Inflammation and Regeneration, 2021, 41, 22.	1.5	21
2437	Mesenchymal stromal cells in the bone marrow niche consist of multi-populations with distinct transcriptional and epigenetic properties. Scientific Reports, 2021, 11, 15811.	1.6	11
2438	Metabolic Controls on Epigenetic Reprogramming in Regulatory T Cells. Frontiers in Immunology, 2021, 12, 728783.	2.2	10
2440	Nonâ€redundant functions of H2A.Z.1 and H2A.Z.2 in chromosome segregation and cell cycle progression. EMBO Reports, 2021, 22, e52061.	2.0	23
2442	TFEB-mediated endolysosomal activity controls human hematopoietic stem cell fate. Cell Stem Cell, 2021, 28, 1838-1850.e10.	5.2	69
2443	A Genome Doubling Event Reshapes Rice Morphology and Products by Modulating Chromatin Signatures and Gene Expression Profiling. Rice, 2021, 14, 72.	1.7	6
2445	Transcriptional reprogramming by oxidative stress occurs within a predefined chromatin accessibility landscape. Free Radical Biology and Medicine, 2021, 171, 319-331.	1.3	6
2446	The related coactivator complexes SAGA and ATAC control embryonic stem cell self-renewal through acetyltransferase-independent mechanisms. Cell Reports, 2021, 36, 109598.	2.9	9
2447	Leveraging the Mendelian disorders of the epigenetic machinery to systematically map functional epigenetic variation. ELife, 2021, 10, .	2.8	10
2448	A TALE/HOX code unlocks WNT signalling response towards paraxial mesoderm. Nature Communications, 2021, 12, 5136.	5.8	10
2449	The histone H3.3 chaperone HIRA restrains erythroid-biased differentiation of adult hematopoietic stem cells. Stem Cell Reports, 2021, 16, 2014-2028.	2.3	9
2450	Laser Capture Microdissection of Single Neurons with Morphological Visualization Using Fluorescent Proteins Fused to Transmembrane Proteins. ENeuro, 2021, 8, ENEURO.0275-20.2021.	0.9	1
2451	The non-coding genome in genetic brain disorders: new targets for therapy?. Essays in Biochemistry, 2021, 65, 671-683.	2.1	3
2452	INFIMA leverages multi-omics model organism data to identify effector genes of human GWAS variants. Genome Biology, 2021, 22, 241.	3.8	3
2453	An epigenetic basis of inbreeding depression in maize. Science Advances, 2021, 7, .	4.7	10
2454	Hierarchy of signaling thresholds downstream of the T cell receptor and the Tec kinase ITK. Proceedings of the National Academy of Sciences of the United States of America, 2021, 118, .	3.3	19
2455	Computational identification and experimental characterization of preferred downstream positions in human core promoters. PLoS Computational Biology, 2021, 17, e1009256.	1.5	2

#	Article	IF	Citations
2456	Reactivation of the Hedgehog pathway in esophageal progenitors turns on an embryonic-like program to initiate columnar metaplasia. Cell Stem Cell, 2021, 28, 1411-1427.e7.	5.2	16
2457	ARID1A regulates E-cadherin expression in colorectal cancer cells: a promising candidate therapeutic target. Molecular Biology Reports, 2021, 48, 6749-6756.	1.0	4
2459	Deregulation of HLA-I in cancer and its central importance for immunotherapy. , 2021, 9, e002899.		73
2460	Evidence of pioneer factor activity of an oncogenic fusion transcription factor. IScience, 2021, 24, 102867.	1.9	22
2461	Open chromatin in grapevine marks candidate CREs and with other chromatin features correlates with gene expression. Plant Journal, 2021, 107, 1631-1647.	2.8	17
2462	Deficient H2A.Z deposition is associated with genesis of uterine leiomyoma. Nature, 2021, 596, 398-403.	13.7	53
2464	NF1 regulates mesenchymal glioblastoma plasticity and aggressiveness through the AP-1 transcription factor FOSL1. ELife, 2021, 10, .	2.8	41
2466	LKB1 inactivation modulates chromatin accessibility to drive metastatic progression. Nature Cell Biology, 2021, 23, 915-924.	4.6	26
2467	LineageOT is a unified framework for lineage tracing and trajectory inference. Nature Communications, 2021, 12, 4940.	5.8	29
2468	Dynamic landscape of chromatin accessibility and transcriptomic changes during differentiation of human embryonic stem cells into dopaminergic neurons. Scientific Reports, 2021, 11, 16977.	1.6	11
2469	Mutational bias in spermatogonia impacts the anatomy of regulatory sites in the human genome. Genome Research, 2021, 31, 1994-2007.	2.4	4
2470	Identification of a KLF5-dependent program and drug development for skeletal muscle atrophy. Proceedings of the National Academy of Sciences of the United States of America, 2021, 118, .	3.3	12
2471	DMRT1-mediated reprogramming drives development of cancer resembling human germ cell tumors with features of totipotency. Nature Communications, 2021, 12, 5041.	5.8	17
2472	Dissecting OCT4 defines the role of nucleosome binding in pluripotency. Nature Cell Biology, 2021, 23, 834-845.	4.6	36
2473	Transcriptomic and Epigenetic Profiling of Fibroblasts in Idiopathic Pulmonary Fibrosis. American Journal of Respiratory Cell and Molecular Biology, 2022, 66, 53-63.	1.4	12
2474	Characterization of Chromatin Accessibility and Gene Expression upon Cold Stress Reveals that the RAV1 Transcription Factor Functions in Cold Response inVitis Amurensis. Plant and Cell Physiology, 2021, 62, 1615-1629.	1.5	23
2475	Dissecting dual roles of MyoD during lineage conversion to mature myocytes and myogenic stem cells. Genes and Development, 2021, 35, 1209-1228.	2.7	20
2476	A look into retinal organoids: methods, analytical techniques, and applications. Cellular and Molecular Life Sciences, 2021, 78, 6505-6532.	2.4	36

#	Article	IF	Citations
2477	Chromatin-mediated epigenetic regulation of HSV-1 transcription as a potential target in antiviral therapy. Antiviral Research, 2021, 192, 105103.	1.9	9
2478	Augmenting and directing long-range CRISPR-mediated activation in human cells. Nature Methods, 2021, 18, 1075-1081.	9.0	17
2479	Persistent JunB activation in fibroblasts disrupts stem cell niche interactions enforcing skin aging. Cell Reports, 2021, 36, 109634.	2.9	17
2480	Chromatin accessibility profiling identifies evolutionary conserved loci in activated human satellite cells. Stem Cell Research, 2021, 55, 102496.	0.3	4
2481	Metabolic modeling of single Th17 cells reveals regulators of autoimmunity. Cell, 2021, 184, 4168-4185.e21.	13.5	203
2482	Chromatin accessibility landscapes activated by cell-surface and intracellular immune receptors. Journal of Experimental Botany, 2021, 72, 7927-7941.	2.4	14
2483	Mesomelic dysplasias associated with the HOXD locus are caused by regulatory reallocations. Nature Communications, 2021, 12, 5013.	5.8	14
2484	Acute depletion of CTCF rewires genome-wide chromatin accessibility. Genome Biology, 2021, 22, 244.	3.8	29
2485	Emerging Single-Cell Technological Approaches to Investigate Chromatin Dynamics and Centromere Regulation in Human Health and Disease. International Journal of Molecular Sciences, 2021, 22, 8809.	1.8	7
2486	Glucocorticoid signaling induces transcriptional memory and universally reversible chromatin changes. Life Science Alliance, 2021, 4, e202101080.	1.3	14
2487	The native cistrome and sequence motif families of the maize ear. PLoS Genetics, 2021, 17, e1009689.	1.5	19
2489	Altered function and differentiation of age-associated B cells contribute to the female bias in lupus mice. Nature Communications, 2021, 12, 4813.	5.8	47
2492	Decline in IGF1 in the bone marrow microenvironment initiates hematopoietic stem cell aging. Cell Stem Cell, 2021, 28, 1473-1482.e7.	5.2	87
2493	Activation of Î³-globin gene expression by GATA1 and NF-Y in hereditary persistence of fetal hemoglobin. Nature Genetics, 2021, 53, 1177-1186.	9.4	21
2496	Epitome: predicting epigenetic events in novel cell types with multi-cell deep ensemble learning. Nucleic Acids Research, 2021, 49, e110-e110.	6.5	1
2497	Transient expression of a GABA receptor subunit during early development is critical for inhibitory synapse maturation and function. Current Biology, 2021, 31, 4314-4326.e5.	1.8	5
2498	Tet2 Controls the Responses of Î² cells to Inflammation in Autoimmune Diabetes. Nature Communications, 2021, 12, 5074.	5.8	11
2500	PRC2 Inhibitors Overcome Glucocorticoid Resistance Driven by NSD2 Mutation in Pediatric Acute Lymphoblastic Leukemia. Cancer Discovery, 2022, 12, 186-203.	7.7	17

#	Article	IF	Citations
2503	Addiction-Associated Genetic Variants Implicate Brain Cell Type- and Region-Specific Cis-Regulatory Elements in Addiction Neurobiology. Journal of Neuroscience, 2021, 41, 9008-9030.	1.7	15
2504	Life Cycle Stage-Specific Accessibility of Leishmania donovani Chromatin at Transcription Start Regions. MSystems, 2021, 6, e0062821.	1.7	6
2505	A Multiple Comprehensive Analysis of scATAC-seq Based on Auto-Encoder and Matrix Decomposition. Symmetry, 2021, 13, 1467.	1.1	2
2506	Genome accessibility dynamics in response to phosphate limitation is controlled by the PHR1 family of transcription factors in Arabidopsis. Proceedings of the National Academy of Sciences of the United States of America, 2021, 118, .	3.3	38
2507	Heterogeneity of immune cells in human atherosclerosis revealed by scRNA-Seq. Cardiovascular Research, 2021, 117, 2537-2543.	1.8	39
2508	ATAC-Seq Data for Genome-Wide Profiling of Transcription Factor Binding Sites in the Rice False Smut Fungus Ustilaginoidea virens. Molecular Plant-Microbe Interactions, 2021, 34, MPMI-01-21-0006.	1.4	9
2509	Epigenetic Basis of Psychiatric Disorders: A Narrative Review. CNS and Neurological Disorders - Drug Targets, 2022, 21, 302-315.	0.8	4
2510	The bowfin genome illuminates the developmental evolution of ray-finned fishes. Nature Genetics, 2021, 53, 1373-1384.	9.4	48
2511	Non-Coding Variants in Cancer: Mechanistic Insights and Clinical Potential for Personalized Medicine. Non-coding RNA, 2021, 7, 47.	1.3	6
2512	Identification of New Transcription Factors that Can Promote Pluripotent Reprogramming. Stem Cell Reviews and Reports, 2021, 17, 2223-2234.	1.7	1
2515	Mechanism of Drug Tolerant Persister Cancer Cells: The Landscape and Clinical Implication for Therapy. Journal of Thoracic Oncology, 2021, 16, 1798-1809.	0.5	61
2516	Histone H4 lysine 20 mono-methylation directly facilitates chromatin openness and promotes transcription of housekeeping genes. Nature Communications, 2021, 12, 4800.	5.8	56
2517	Global gene expression and chromatin accessibility of the peripheral nervous system in animal models of persistent pain. Journal of Neuroinflammation, 2021, 18, 185.	3.1	6
2518	Age-dependent instability of mature neuronal fate in induced neurons from Alzheimerâ€™s patients. Cell Stem Cell, 2021, 28, 1533-1548.e6.	5.2	119
2520	Brg1 Supports B Cell Proliferation and Germinal Center Formation Through Enhancer Activation. Frontiers in Immunology, 2021, 12, 705848.	2.2	8
2521	Developmental chromatin programs determine oncogenic competence in melanoma. Science, 2021, 373, eabc1048.	6.0	80
2524	Intratumoral stem-like CCR4+ regulatory T cells orchestrate the immunosuppressive microenvironment in HCC associated with hepatitis B. Journal of Hepatology, 2022, 76, 148-159.	1.8	59
2525	CTCF knockout in zebrafish induces alterations in regulatory landscapes and developmental gene expression. Nature Communications, 2021, 12, 5415.	5.8	27

#	Article	IF	Citations
2526	Genome Maintenance Mechanisms at the Chromatin Level. International Journal of Molecular Sciences, 2021, 22, 10384.	1.8	3
2527	ShinyArchR.UiO: user-friendly,integrative and open-source tool for visualization of single-cell ATAC-seq data using ArchR. Bioinformatics, 2022, 38, 834-836.	1.8	6
2528	Discrete cis-acting element regulates developmentally timed gene-lamina relocation and neural progenitor competence inÂvivo. Developmental Cell, 2021, 56, 2649-2663.e6.	3.1	9
2529	Biomedical Data Commons (BMDC) prioritizes B-lymphocyte non-coding genetic variants in Type 1 Diabetes. PLoS Computational Biology, 2021, 17, e1009382.	1.5	4
2530	Altered regulation of DPF3, a member of the SWI/SNF complexes, underlies the 14q24 renal cancer susceptibility locus. American Journal of Human Genetics, 2021, 108, 1590-1610.	2.6	9
2531	Alveolar macrophages from persons living with HIV show impaired epigenetic response to Mycobacterium tuberculosis. Journal of Clinical Investigation, 2021, 131, .	3.9	19
2532	An inferred functional impact map of genetic variants in rice. Molecular Plant, 2021, 14, 1584-1599.	3.9	48
2533	An L1 retrotransposon insertionâ€“induced deafness mouse model for studying the development and function of the cochlear stria vascularis. Proceedings of the National Academy of Sciences of the United States of America, 2021, 118, e2107933118.	3.3	2
2535	Low-input ATAC&mRNA-seq protocol for simultaneous profiling of chromatin accessibility and gene expression. STAR Protocols, 2021, 2, 100764.	0.5	5
2536	Epithelial memory of inflammation limits tissue damage while promoting pancreatic tumorigenesis. Science, 2021, 373, eabj0486.	6.0	99
2537	Chromatin remodeling due to degradation of citrate carrier impairs osteogenesis of aged mesenchymal stem cells. Nature Aging, 2021, 1, 810-825.	5.3	37
2538	Chromatin-based, in cis and in trans regulatory rewiring underpins distinct oncogenic transcriptomes in multiple myeloma. Nature Communications, 2021, 12, 5450.	5.8	19
2539	Systems Biology of the Vasopressin V2 Receptor: New Tools for Discovery of Molecular Actions of a GPCR. Annual Review of Pharmacology and Toxicology, 2022, 62, 595-616.	4.2	5
2540	The megakaryocytic transcription factor ARID3A suppresses leukemia pathogenesis. Blood, 2022, 139, 651-665.	0.6	20
2542	Chromatin accessibility associates with protein-RNA correlation in human cancer. Nature Communications, 2021, 12, 5732.	5.8	18
2543	FACS-based isolation of fixed mouse neuronal nuclei for ATAC-seq and Hi-C. STAR Protocols, 2021, 2, 100643.	0.5	4
2544	Opportunity to improve livestock traits using 3D genomics. Animal Genetics, 2021, 52, 785-798.	0.6	3
2545	Integration of feeding behavior by the liver circadian clock reveals network dependency of metabolic rhythms. Science Advances, 2021, 7, eabi7828.	4.7	50

#	Article	IF	Citations
2546	Chronic stress primes innate immune responses in mice and humans. Cell Reports, 2021, 36, 109595.	2.9	53
2547	Axon Regeneration: A Subcellular Extension in Multiple Dimensions. Cold Spring Harbor Perspectives in Biology, 2022, 14, a040923.	2.3	9
2548	Systematic evaluation of chromosome conformation capture assays. Nature Methods, 2021, 18, 1046-1055.	9.0	108
2549	Profiling of chromatin accessibility identifies transcription factor binding sites across the genome of Aspergillus species. BMC Biology, 2021, 19, 189.	1.7	10
2550	Multiplatform discovery and regulatory function analysis of structural variations in non-small cell lung carcinoma. Cell Reports, 2021, 36, 109660.	2.9	3
2551	Multi-omic approaches to acute kidney injury and repair. Current Opinion in Biomedical Engineering, 2021, 20, 100344.	1.8	6
2552	Enhancer recruitment of transcription repressors RUNX1 and TLE3 by mis-expressed FOXC1 blocks differentiation in acute myeloid leukemia. Cell Reports, 2021, 36, 109725.	2.9	15
2553	Î²2-Integrin Adhesion Regulates Dendritic Cell Epigenetic and Transcriptional Landscapes to Restrict Dendritic Cell Maturation and Tumor Rejection. Cancer Immunology Research, 2021, 9, 1354-1369.	1.6	10
2556	Brain regionalization by Polycombâ€group proteins and chromatin accessibility. BioEssays, 2021, 43, e2100155.	1.2	2
2557	Museum Genomics. Annual Review of Genetics, 2021, 55, 633-659.	3.2	58
2558	Parallel characterization of cis-regulatory elements for multiple genes using CRISPRpath. Science Advances, 2021, 7, eabi4360.	4.7	16
2559	Disabling de novo DNA methylation in embryonic stem cells allows an illegitimate fate trajectory. Proceedings of the National Academy of Sciences of the United States of America, 2021, 118, .	3.3	14
2561	Hairless regulates heterochromatin maintenance and muscle stem cell function as a histone demethylase antagonist. Proceedings of the National Academy of Sciences of the United States of America, 2021, 118, .	3.3	8
2562	Mechanisms of vascular smooth muscle cell investment and phenotypic diversification in vascular diseases. Biochemical Society Transactions, 2021, 49, 2101-2111.	1.6	25
2563	The NF-ÎºB Transcriptional Footprint Is Essential for SARS-CoV-2 Replication. Journal of Virology, 2021, 95, e0125721.	1.5	69
2564	JUN promotes hypertrophic skin scarring via CD36 in preclinical in vitro and in vivo models. Science Translational Medicine, 2021, 13, eabb3312.	5.8	32
2565	KDM4B promotes acute myeloid leukemia associated with AML1â€ETO by regulating chromatin accessibility. FASEB BioAdvances, 2021, 3, 1020-1033.	1.3	3
2566	Enhancer decommissioning imposes an epigenetic barrier to sensory hair cell regeneration. Developmental Cell, 2021, 56, 2471-2485.e5.	3.1	37

#	Article	IF	Citations
2567	Mutational synergy during leukemia induction remodels chromatin accessibility, histone modifications and three-dimensional DNA topology to alter gene expression. Nature Genetics, 2021, 53, 1443-1455.	9.4	19
2568	Mutations in Noncoding Cis-Regulatory Elements Reveal Cancer Driver Cistromes in Luminal Breast Cancer. Molecular Cancer Research, 2022, 20, 102-113.	1.5	3
2569	State-of-the-art technology for cardiovascular research. Complex Issues of Cardiovascular Diseases, 2021, 10, 103-108.	0.3	1
2572	Comparative genomics provides insights into the aquatic adaptations of mammals. Proceedings of the National Academy of Sciences of the United States of America, 2021, 118, .	3.3	43
2573	Early sample tagging and pooling enables simultaneous SARS-CoV-2 detection and variant sequencing. Science Translational Medicine, 2021, 13, eabj2266.	5.8	9
2575	Overcoming Acquired Epigenetic Resistance to BTK Inhibitors. Blood Cancer Discovery, 2021, 2, 630-647.	2.6	30
2576	A molecular toolkit for superorganisms. Trends in Genetics, 2021, 37, 846-859.	2.9	6
2577	Selection on Accessible Chromatin Regions inCapsella grandiflora. Molecular Biology and Evolution, 2021, 38, 5563-5575.	3.5	6
2578	Panobinostat Effectively Increases Histone Acetylation and Alters Chromatin Accessibility Landscape in Canine Embryonic Fibroblasts but Does Not Enhance Cellular Reprogramming. Frontiers in Veterinary Science, 2021, 8, 716570.	0.9	3
2579	The transcription factor reservoir and chromatin landscape in activated plasmacytoid dendritic cells. BMC Genomic Data, 2021, 22, 37.	0.7	4
2581	Profiling single-cell chromatin accessibility in plants. STAR Protocols, 2021, 2, 100737.	0.5	5
2583	An IRF4â€“MYCâ€“mTORC1 Integrated Pathway Controls Cell Growth and the Proliferative Capacity of Activated B Cells during B Cell Differentiation In Vivo. Journal of Immunology, 2021, 207, 1798-1811.	0.4	16
2584	Epigenetic Regulation of Î² Cell Identity and Dysfunction. Frontiers in Endocrinology, 2021, 12, 725131.	1.5	9
2588	Global molecular features in transcription and chromatin accessibility in human extended pluripotent stem cells. Biochemical and Biophysical Research Communications, 2021, 574, 63-69.	1.0	1
2589	Multi-omic analysis of altered transcriptome and epigenetic signatures in the UV-induced DNA damage response. DNA Repair, 2021, 106, 103172.	1.3	8
2590	Enhancer-associated H3K4 methylation safeguards in vitro germline competence. Nature Communications, 2021, 12, 5771.	5.8	20
2591	Tagmentation-based single-cell genomics. Genome Research, 2021, 31, 1693-1705.	2.4	17
2592	Reprogramming lineage identity through cellâ€“cell fusion. Current Opinion in Genetics and Development, 2021, 70, 15-23.	1.5	9

#	Article	IF	Citations
2593	Tree-Based Co-Clustering Identifies Chromatin Accessibility Patterns Associated With Hematopoietic Lineage Structure. Frontiers in Genetics, 2021, 12, 707117.	1.1	2
2595	Early adaptive chromatin remodeling events precede pathologic phenotypes and are reinforced in the failing heart. Journal of Molecular and Cellular Cardiology, 2021, 160, 73-86.	0.9	17
2596	Differential analysis of chromatin accessibility and gene expression profiles identifies cis-regulatory elements in rat adipose and muscle. Genomics, 2021, 113, 3827-3841.	1.3	11
2597	Pioneer factor Foxa2 enables ligand-dependent activation of type II nuclear receptors FXR and LXRÎ±. Molecular Metabolism, 2021, 53, 101291.	3.0	12
2598	Recent advances in single-cell epigenomics. Current Opinion in Structural Biology, 2021, 71, 116-122.	2.6	14
2599	Enhancing Acsl4 in absence of mTORC2/Rictor drove Î²-cell dedifferentiation via inhibiting FoxO1 and promoting ROS production. Biochimica Et Biophysica Acta - Molecular Basis of Disease, 2021, 1867, 166261.	1.8	4
2600	An optimized ATAC-seq protocol for genome-wide mapping of active regulatory elements in primary mouse cortical neurons. STAR Protocols, 2021, 2, 100854.	0.5	3
2601	Structural insights into the interaction between transcription factors and the nucleosome. Current Opinion in Structural Biology, 2021, 71, 171-179.	2.6	11
2602	Epigenetic programming of the immune responses in cancer. , 2022, , 197-235.		1
2603	Epigenetic heterogeneity in primary bone cancers. , 2022, , 431-445.		0
2604	Single-cell analysis of cis-regulatory elements. Current Opinion in Plant Biology, 2022, 65, 102094.	3.5	21
2606	Gene regulatory networks controlling differentiation, survival, and diversification of hypothalamic Lhx6-expressing GABAergic neurons. Communications Biology, 2021, 4, 95.	2.0	26
2607	Chromatin accessibility profiling methods. Nature Reviews Methods Primers, 2021, 1, .	11.8	95
2608	Photoperiod-responsive changes in chromatin accessibility in phloem companion and epidermis cells of Arabidopsis leaves. Plant Cell, 2021, 33, 475-491.	3.1	23
2609	The Cxxc1 subunit of the Trithorax complex directs epigenetic licensing of CD4+ T cell differentiation. Journal of Experimental Medicine, 2021, 218, .	4.2	10
2610	RORÎ± is a critical checkpoint for T cell and ILC2 commitment in the embryonic thymus. Nature Immunology, 2021, 22, 166-178.	7.0	51
2611	Global histone protein surface accessibility in yeast indicates a uniformly loosely packed genome with canonical nucleosomes. Epigenetics and Chromatin, 2021, 14, 5.	1.8	8
2612	Advances in single-cell multi-omics profiling. RSC Chemical Biology, 2021, 2, 441-449.	2.0	20

#	Article	IF	Citations
2613	Remodeling the chromatin landscape in T lymphocytes by a division of labor among transcription factors. Immunological Reviews, 2021, 300, 167-180.	2.8	7
2614	Zeb1 Promotes Odontoblast Differentiation in a Stage-Dependent Manner. Journal of Dental Research, 2021, 100, 648-657.	2.5	10
2615	Chromatin, nuclear organization and genome stability in mammals. , 2021, , 415-434.		0
2616	DNA methylation-linked chromatin accessibility affects genomic architecture in Arabidopsis. Proceedings of the National Academy of Sciences of the United States of America, 2021, 118, .	3.3	70
2617	Low-Input ATAC&mRNA-Seq: A Simple and Robust Method for Simultaneous Dual-Omics Profiling with Low Cell Number. SSRN Electronic Journal, 0, , .	0.4	0
2618	Simplified Epigenome Profiling Using Antibody-tethered Tagmentation. Bio-protocol, 2021, 11, e4043.	0.2	12
2619	Biological constraints on GWAS SNPs at suggestive significance thresholds reveal additional BMI loci. ELife, 2021, 10, .	2.8	27
2620	Chromatin accessibility dynamics during cell fate reprogramming. EMBO Reports, 2021, 22, e51644.	2.0	20
2623	ATACgraph: Profiling Genome-Wide Chromatin Accessibility From ATAC-seq. Frontiers in Genetics, 2020, 11, 618478.	1.1	8
2625	Formation of a multiâ€layered 3â€dimensional structure of the heterochromatin compartment during early mammalian development. Development Growth and Differentiation, 2021, 63, 5-17.	0.6	4
2626	MECHANISMS IN ENDOCRINOLOGY: Pioneer transcription factors in pituitary development and tumorigenesis. European Journal of Endocrinology, 2021, 184, R1-R15.	1.9	4
2628	Other omics approaches to the study of rare diseases. , 2021, , 229-262.		0
2629	Network for Biomarker Immunoprofiling for Cancer Immunotherapy: Cancer Immune Monitoring and Analysis Centers and Cancer Immunologic Data Commons (CIMAC-CIDC). Clinical Cancer Research, 2021, 27, 5038-5048.	3.2	13
2630	Accessible chromatin regions and their functional interrelations with gene transcription and epigenetic modifications in sorghum genome. Plant Communications, 2021, 2, 100140.	3.6	15
2631	Chromatin Accessibility Regulates Gene Expression and Correlates With Tumor-Infiltrating Immune Cells in Gastric Adenocarcinoma. Frontiers in Oncology, 2020, 10, 609940.	1.3	12
2632	Simultaneous Tagmentation-Based Detection of ChIP/ATAC Signal with Sequencing. Methods in Molecular Biology, 2021, 2351, 337-352.	0.4	1
2634	Alterations in Chromatin Structure and Function in the Microglia. Frontiers in Cell and Developmental Biology, 2020, 8, 626541.	1.8	7
2635	Interrogating the Accessible Chromatin Landscape of Eukaryote Genomes Using ATAC-seq. Methods in Molecular Biology, 2021, 2243, 183-226.	0.4	13

#	Article	IF	Citations
2636	Are dropout imputation methods for scRNA-seq effective for scATAC-seq data?. Briefings in Bioinformatics, 2022, 23, .	3.2	5
2638	Single-Cell DamID to Capture Contacts Between DNA and the Nuclear Lamina in Individual Mammalian Cells. Methods in Molecular Biology, 2021, 2157, 159-172.	0.4	10
2639	Determining Nucleosome Position at Individual Loci After Biotic Stress Using MNase-qPCR. Methods in Molecular Biology, 2016, 1398, 357-372.	0.4	7
2640	Advances in the Characterization of Circulating Tumor Cells in Metastatic Breast Cancer: Single Cell Analyses and Interactions, and Patient-Derived Models for Drug Testing. Advances in Experimental Medicine and Biology, 2020, 1220, 61-80.	0.8	10
2641	Pituitary Development and Organogenesis: Transcription Factors in Development and Disease. Masterclass in Neuroendocrinology, 2020, , 129-177.	0.1	4
2642	Retinoic Acid-Regulated Target Genes During Development: Integrative Genomics Analysis. Sub-Cellular Biochemistry, 2020, 95, 57-85.	1.0	12
2643	Retinoic Acid Signaling and Heart Development. Sub-Cellular Biochemistry, 2020, 95, 119-149.	1.0	8
2644	Linking Enhancer to Epigenetics: New Way to Think About Human Diseases. , 2017, , 1-20.		1
2645	Omics Studies in Hemoglobinopathies. Molecular Diagnosis and Therapy, 2019, 23, 223-234.	1.6	5
2646	Systems Genetics in Human Endothelial Cells Identifies Non-coding Variants Modifying Enhancers, Expression, and Complex Disease Traits. American Journal of Human Genetics, 2020, 106, 748-763.	2.6	40
2647	Genetic variants drive altered epigenetic regulation of endotoxin response in BTBR macrophages. Brain, Behavior, and Immunity, 2020, 89, 20-31.	2.0	4
2648	A High-Resolution Map of Human Enhancer RNA Loci Characterizes Super-enhancer Activities in Cancer. Cancer Cell, 2020, 38, 701-715.e5.	7.7	69
2649	Landscape and Dynamics of the Transcriptional Regulatory Network During Natural Killer Cell Differentiation. Genomics, Proteomics and Bioinformatics, 2020, 18, 501-515.	3.0	16
2650	Developmental Relationships of Four Exhausted CD8+ T Cell Subsets Reveals Underlying Transcriptional and Epigenetic Landscape Control Mechanisms. Immunity, 2020, 52, 825-841.e8.	6.6	497
2651	Epigenetics in formation, function, and failure of the endocrine pancreas. Molecular Metabolism, 2017, 6, 1066-1076.	3.0	32
2652	KAT3-dependent acetylation of cell type-specific genes maintains neuronal identity in the adult mouse brain. Nature Communications, 2020, 11, 2588.	5.8	26
2653	An integrated multi-omics approach identifies the landscape of interferon-Î±-mediated responses of human pancreatic beta cells. Nature Communications, 2020, 11, 2584.	5.8	87
2654	Genetic variant effects on gene expression in human pancreatic islets and their implications for T2D. Nature Communications, 2020, 11, 4912.	5.8	89

#	Article	IF	Citations
2655	MAFG-driven astrocytes promote CNS inflammation. Nature, 2020, 578, 593-599.	13.7	282
2656	Decoding myofibroblast origins in human kidney fibrosis. Nature, 2021, 589, 281-286.	13.7	380
2657	GPSeq reveals the radial organization of chromatin in the cell nucleus. Nature Biotechnology, 2020, 38, 1184-1193.	9.4	49
2658	MANTA2, update of the Mongo database for the analysis of transcription factor binding site alterations. Scientific Data, 2018, 5, 180141.	2.4	11
2659	New perspectives of the cardiac cellular landscape: mapping cellular mediators of cardiac fibrosis using single-cell transcriptomics. Biochemical Society Transactions, 2020, 48, 2483-2493.	1.6	13
2660	Applying gene regulatory network logic to the evolution of social behavior. Proceedings of the National Academy of Sciences of the United States of America, 2017, 114, 5886-5893.	3.3	25
2935	Enhancer Predictions and Genome-Wide Regulatory Circuits. Annual Review of Genomics and Human Genetics, 2020, 21, 37-54.	2.5	18
2936	Single-Cell RNA Sequencing Analysis Reveals a Crucial Role for CTHRC1 (Collagen Triple Helix Repeat) Tj ETQq1 1 0.784314 rgBT /Ove	1.6	132
2937	Super-enhancers maintain renin-expressing cell identity and memory to preserve multi-system homeostasis. Journal of Clinical Investigation, 2018, 128, 4787-4803.	3.9	41
2938	Epigenetic reprogramming of immune cells in injury, repair, and resolution. Journal of Clinical Investigation, 2019, 129, 2994-3005.	3.9	55
2939	Serine-threonine kinase ROCK2 regulates germinal center B cell positioning and cholesterol biosynthesis. Journal of Clinical Investigation, 2020, 130, 3654-3670.	3.9	26
2940	Circadian rhythm influences induction of trained immunity by BCG vaccination. Journal of Clinical Investigation, 2020, 130, 5603-5617.	3.9	95
2941	X chromosome dosage of histone demethylase KDM5C determines sex differences in adiposity. Journal of Clinical Investigation, 2020, 130, 5688-5702.	3.9	62
2942	Probing chromatin landscape reveals roles of endocardial TBX20 in septation. Journal of Clinical Investigation, 2016, 126, 3023-3035.	3.9	30
2943	TRAP-seq identifies cystine/glutamate antiporter as a driver of recovery from liver injury. Journal of Clinical Investigation, 2018, 128, 2297-2309.	3.9	28
2944	Hijacking a key chromatin modulator creates epigenetic vulnerability for MYC-driven cancer. Journal of Clinical Investigation, 2018, 128, 3605-3618.	3.9	26
2945	Targeting nuclear receptor NR4A1â€“dependent adipocyte progenitor quiescence promotes metabolic adaptation to obesity. Journal of Clinical Investigation, 2018, 128, 4898-4911.	3.9	23
2946	Chromatin dynamics during the differentiation of long-term hematopoietic stem cells to multipotent progenitors. Blood Advances, 2017, 1, 887-898.	2.5	17

#	Article	IF	Citations
2947	Model-Based Approach to the Joint Analysis of Single-Cell Data on Chromatin Accessibility and Gene Expression. Statistical Science, 2020, 35, .	1.6	12
2948	StateHub-StatePaintR: rapid and reproducible chromatin state evaluation for custom genome annotation. F1000Research, 0, 7, 214.	0.8	5
2949	StateHub-StatePaintR: rapid and reproducible chromatin state evaluation for custom genome annotation. F1000Research, 0, 7, 214.	0.8	4
2950	Falco: high-speed FastQC emulation for quality control of sequencing data. F1000Research, 2019, 8, 1874.	0.8	159
2951	Fast analysis of scATAC-seq data using a predefined set of genomic regions. F1000Research, 2020, 9, 199.	0.8	11
2952	Genome-wide measurement of spatial expression in patterning mutants of Drosophila melanogaster. F1000Research, 2017, 6, 41.	0.8	27
2953	QuIN: A Web Server for Querying and Visualizing Chromatin Interaction Networks. PLoS Computational Biology, 2016, 12, e1004809.	1.5	10
2954	Integrative QTL analysis of gene expression and chromatin accessibility identifies multi-tissue patterns of genetic regulation. PLoS Genetics, 2020, 16, e1008537.	1.5	35
2955	msCentipede: Modeling Heterogeneity across Genomic Sites and Replicates Improves Accuracy in the Inference of Transcription Factor Binding. PLoS ONE, 2015, 10, e0138030.	1.1	37
2956	Using local chromatin structure to improve CRISPR/Cas9 efficiency in zebrafish. PLoS ONE, 2017, 12, e0182528.	1.1	29
2957	Cell Type-Specific Oxidative Stress Genomic Signatures in the Globus Pallidus of Dopamine-Depleted Mice. Journal of Neuroscience, 2020, 40, 9772-9783.	1.7	14
2958	Distinct ILâ€1Î±â€responsive enhancers promote acute and coordinated changes in chromatin topology in a hierarchical manner. EMBO Journal, 2020, 39, e101533.	3.5	25
2959	<scp>BAZ</scp> 2A safeguards genome architecture of groundâ€state pluripotent stem cells. EMBO Journal, 2020, 39, e105606.	3.5	14
2960	Neuron typeâ€specific increase in lamin B1 contributes to nuclear dysfunction in Huntingtonâ€™s disease. EMBO Molecular Medicine, 2021, 13, e12105.	3.3	28
2961	Identification of genomic enhancers through spatial integration of singleâ€cell transcriptomics and epigenomics. Molecular Systems Biology, 2020, 16, e9438.	3.2	60
2962	Chromatin reprogramming as an adaptation mechanism in advanced prostate cancer. Endocrine-Related Cancer, 2019, 26, R211-R235.	1.6	15
2963	Androgen receptor enhancer usage and the chromatin regulatory landscape in human prostate cancers. Endocrine-Related Cancer, 2019, 26, R267-R285.	1.6	22
2964	Epigenetics explained: a topic â€œprimerâ€•for the epilepsy community by the ILAE Genetics/Epigenetics Task Force. Epileptic Disorders, 2020, 22, 127-141.	0.7	17

#	Article	IF	Citations
2965	Clinical implications of chromatin accessibility in human cancers. Oncotarget, 2020, 11, 1666-1678.	0.8	7
2966	Unlocking the epigenetic code of T cell exhaustion. Translational Cancer Research, 2017, 6, S384-S387.	0.4	12
2967	Epigenetic remodeling in preimplantation embryos: cows are not big mice. Animal Reproduction, 2018, 15, 204-214.	0.4	22
2968	The Comparison of Two Single-cell Sequencing Platforms: BD Rhapsody and 10x Genomics Chromium. Current Genomics, 2020, 21, 602-609.	0.7	49
2969	Single-cell RNA Sequencing in Immunology. Current Genomics, 2020, 21, 564-575.	0.7	14
2970	Low-input Capture-C: A Chromosome Conformation Capture Assay to Analyze Chromatin Architecture in Small Numbers of Cells. Bio-protocol, 2017, 7, .	0.2	15
2971	Collagenase-based Single Cell Isolation of Primary Murine Brain Endothelial Cells Using Flow Cytometry. Bio-protocol, 2018, 8, .	0.2	24
2972	Transcriptional repression by FACT is linked to regulation of chromatin accessibility at the promoter of ES cells. Life Science Alliance, 2018, 1, e201800085.	1.3	30
2973	BZLF1 interacts with chromatin remodelers promoting escape from latent infections with EBV. Life Science Alliance, 2019, 2, e201800108.	1.3	32
2974	Expanding the repertoire of glucocorticoid receptor target genes by engineering genomic response elements. Life Science Alliance, 2019, 2, e201800283.	1.3	13
2975	TAF-ChIP: an ultra-low input approach for genome-wide chromatin immunoprecipitation assay. Life Science Alliance, 2019, 2, e201900318.	1.3	12
2976	Use of the epigenetic toolbox to contextualize common variants associated with schizophrenia risk. Dialogues in Clinical Neuroscience, 2019, 21, 407-416.	1.8	3
2977	The epigenetic landscape of innate immunity. AIMS Molecular Science, 2017, 4, 110-139.	0.3	2
2978	Emerging techniques in single-cell epigenomics and their applications to cancer research. , 2018, 1, .		23
2979	Epigenomic landscapes of retinal rods and cones. ELife, 2016, 5, e11613.	2.8	106
2980	Enhancer regions show high histone H3.3 turnover that changes during differentiation. ELife, 2016, 5, .	2.8	86
2981	Tet2 and Tet3 cooperate with B-lineage transcription factors to regulate DNA modification and chromatin accessibility. ELife, 2016, 5, .	2.8	121
2982	Establishment and maintenance of heritable chromatin structure during early Drosophila embryogenesis. ELife, 2016, 5, .	2.8	139

#	Article	IF	Citations
2983	A dynamic mode of mitotic bookmarking by transcription factors. ELife, 2016, 5, .	2.8	216
2984	Transcriptional networks specifying homeostatic and inflammatory programs of gene expression in human aortic endothelial cells. ELife, 2017, 6, .	2.8	79
2985	Histone gene replacement reveals a post-transcriptional role for H3K36 in maintaining metazoan transcriptome fidelity. ELife, 2017, 6, .	2.8	42
2986	Concentration dependent chromatin states induced by the bicoid morphogen gradient. ELife, 2017, 6, .	2.8	73
2987	Cooperative interactions enable singular olfactory receptor expression in mouse olfactory neurons. ELife, 2017, 6, .	2.8	90
2988	A chemical screen in zebrafish embryonic cells establishes that Akt activation is required for neural crest development. ELife, 2017, 6, .	2.8	37
2989	Epigenetic profiling of growth plate chondrocytes sheds insight into regulatory genetic variation influencing height. ELife, 2017, 6, .	2.8	35
2990	Convergence of topological domain boundaries, insulators, and polytene interbands revealed by high-resolution mapping of chromatin contacts in the early Drosophila melanogaster embryo. ELife, 2017, 6, .	2.8	81
2991	Chromatin accessibility dynamics across C. elegans development and ageing. ELife, 2018, 7, .	2.8	76
2992	Species and cell-type properties of classically defined human and rodent neurons and glia. ELife, 2018, 7, .	2.8	66
2993	Mapping the transcriptional diversity of genetically and anatomically defined cell populations in the mouse brain. ELife, 2019, 8, .	2.8	59
2994	A new experimental platform facilitates assessment of the transcriptional and chromatin landscapes of aging yeast. ELife, 2018, 7, .	2.8	56
2995	Live-cell imaging reveals enhancer-dependent Sox2 transcription in the absence of enhancer proximity. ELife, 2019, 8, .	2.8	220
2996	TRIM28 promotes HIV-1 latency by SUMOylating CDK9 and inhibiting P-TEFb. ELife, 2019, 8, .	2.8	71
2997	Beta-catenin signaling regulates barrier-specific gene expression in circumventricular organ and ocular vasculatures. ELife, 2019, 8, .	2.8	74
2998	Dynamic enhancer partitioning instructs activation of a growth-related gene during exit from naÃ¯ve pluripotency. ELife, 2019, 8, .	2.8	11
2999	Tumor suppressor SMARCB1 suppresses super-enhancers to govern hESC lineage determination. ELife, 2019, 8, .	2.8	30
3000	Evidence for DNA-mediated nuclear compartmentalization distinct from phase separation. ELife, 2019, 8, .	2.8	222

#	Article	IF	Citations
3001	Telomere dysfunction cooperates with epigenetic alterations to impair murine embryonic stem cell fate commitment. ELife, 2020, 9, .	2.8	12
3002	CTCF confers local nucleosome resiliency after DNA replication and during mitosis. ELife, 2019, 8, .	2.8	61
3003	Screening identifies small molecules that enhance the maturation of human pluripotent stem cell-derived myotubes. ELife, 2019, 8, .	2.8	45
3004	Cis-regulatory basis of sister cell type divergence in the vertebrate retina. ELife, 2019, 8, .	2.8	30
3005	Combinatorial chromatin dynamics foster accurate cardiopharyngeal fate choices. ELife, 2019, 8, .	2.8	23
3006	Dynamic regulation of chromatin accessibility by pluripotency transcription factors across the cell cycle. ELife, 2019, 8, .	2.8	61
3007	GLI transcriptional repression regulates tissue-specific enhancer activity in response to Hedgehog signaling. ELife, 2020, 9, .	2.8	29
3008	Herpes simplex viral nucleoprotein creates a competitive transcriptional environment facilitating robust viral transcription and host shut off. ELife, 2019, 8, .	2.8	53
3009	Analysis of zebrafish periderm enhancers facilitates identification of a regulatory variant near human KRT8/18. ELife, 2020, 9, .	2.8	23
3010	Chromatin accessibility dynamics and single cell RNA-Seq reveal new regulators of regeneration in neural progenitors. ELife, 2020, 9, .	2.8	39
3011	Sphingosine 1-phosphate-regulated transcriptomes in heterogenous arterial and lymphatic endothelium of the aorta. ELife, 2020, 9, .	2.8	34
3012	A complex regulatory landscape involved in the development of mammalian external genitals. ELife, 2020, 9, .	2.8	26
3013	Cancer systems immunology. ELife, 2020, 9, .	2.8	14
3014	Zygotic pioneer factor activity of Odd-paired/Zic is necessary for late function of the Drosophila segmentation network. ELife, 2020, 9, .	2.8	36
3015	Spen links RNA-mediated endogenous retrovirus silencing and X chromosome inactivation. ELife, 2020, 9, .	2.8	33
3016	Transposase-assisted tagmentation of RNA/DNA hybrid duplexes. ELife, 2020, 9, .	2.8	40
3017	Hox-dependent coordination of mouse cardiac progenitor cell patterning and differentiation. ELife, 2020, 9, .	2.8	41
3018	Trait-associated noncoding variant regions affect TBX3 regulation and cardiac conduction. ELife, 2020, 9, .	2.8	7

#	Article	IF	Citations
3019	Damage-responsive, maturity-silenced enhancers regulate multiple genes that direct regeneration in Drosophila. ELife, 2020, 9, .	2.8	41
3020	Re-expression of SMARCA4/BRG1 in small cell carcinoma of ovary, hypercalcemic type (SCCOHT) promotes an epithelial-like gene signature through an AP-1-dependent mechanism. ELife, 2020, 9, .	2.8	19
3021	Gene regulation gravitates toward either addition or multiplication when combining the effects of two signals. ELife, 2020, 9, .	2.8	13
3022	A unique chromatin profile defines adaptive genomic regions in a fungal plant pathogen. ELife, 2020, 9, .	2.8	37
3023	Single-cell multiomic profiling of human lungs reveals cell-type-specific and age-dynamic control of SARS-CoV2 host genes. ELife, 2020, 9, .	2.8	129
3024	Individual differences in honey bee behavior enabled by plasticity in brain gene regulatory networks. ELife, 2020, 9, .	2.8	27
3025	Efficient chromatin accessibility mapping in situ by nucleosome-tethered tagmentation. ELife, 2020, 9, .	2.8	78
3026	fluff: exploratory analysis and visualization of high-throughput sequencing data. PeerJ, 2016, 4, e2209.	0.9	58
3027	I-ATAC: interactive pipeline for the management and pre-processing of ATAC-seq samples. PeerJ, 2017, 5, e4040.	0.9	24
3028	ID3 promotes homologous recombination via non-transcriptional and transcriptional mechanisms and its loss confers sensitivity to PARP inhibition. Nucleic Acids Research, 2021, 49, 11666-11689.	6.5	8
3029	DeNOPA: decoding nucleosome positions sensitively with sparse ATAC-seq data. Briefings in Bioinformatics, 2022, 23, .	3.2	4
3030	PRDM1 Drives Human Primary T Cell Hyporesponsiveness by Altering the T Cell Transcriptome and Epigenome. SSRN Electronic Journal, 0, , .	0.4	0
3031	scEnhancer: a single-cell enhancer resource with annotation across hundreds of tissue/cell types in three species. Nucleic Acids Research, 2022, 50, D371-D379.	6.5	16
3032	A set of accessible enhancers enables the initial response of breast cancer cells to physiological progestin concentrations. Nucleic Acids Research, 2021, 49, 12716-12731.	6.5	13
3033	Protein intrinsic disorder on a dynamic nucleosomal landscape. Progress in Molecular Biology and Translational Science, 2021, 183, 295-354.	0.9	1
3035	An atlas of gene regulatory elements in adult mouse cerebrum. Nature, 2021, 598, 129-136.	13.7	95
3037	Copy-scAT: Deconvoluting single-cell chromatin accessibility of genetic subclones in cancer. Science Advances, 2021, 7, eabg6045.	4.7	19
3039	Single-Cell Analysis Using Machine Learning Techniques and Its Application to Medical Research. Biomedicines, 2021, 9, 1513.	1.4	15

#	Article	IF	Citations
3040	Identification and prediction of developmental enhancers in sea urchin embryos. BMC Genomics, 2021, 22, 751.	1.2	9
3042	Segmentation and genome annotation algorithms for identifying chromatin state and other genomic patterns. PLoS Computational Biology, 2021, 17, e1009423.	1.5	21
3043	Escape of hair follicle stem cells causes stem cell exhaustion during aging. Nature Aging, 2021, 1, 889-903.	5.3	31
3044	Morc3 silences endogenous retroviruses by enabling Daxx-mediated histone H3.3 incorporation. Nature Communications, 2021, 12, 5996.	5.8	34
3045	Deep characterization of paired chromatin and transcriptomes in four immune cell types from multiple sclerosis patients. Epigenomics, 2021, 13, 1607-1618.	1.0	4
3046	The expansion of human T-bet ^{high} CD21 ^{low} B cells is T cell dependent. Science Immunology, 2021, 6, eabh0891.	5.6	82
3047	Targeting epigenetically maladapted vascular niche alleviates liver fibrosis in nonalcoholic steatohepatitis. Science Translational Medicine, 2021, 13, eabd1206.	5.8	24
3048	Collective regulation of chromatin modifications predicts replication timing during cell cycle. Cell Reports, 2021, 37, 109799.	2.9	20
3049	Identification of Key eRNAs for Spinal Cord Injury by Integrated Multinomial Bioinformatics Analysis. Frontiers in Cell and Developmental Biology, 2021, 9, 728242.	1.8	5
3050	PI3KÎ´ coordinates transcriptional, chromatin, and metabolic changes to promote effector CD8+ TÂcells at the expense of central memory. Cell Reports, 2021, 37, 109804.	2.9	13
3051	Chromatin Velocity reveals epigenetic dynamics by single-cell profiling of heterochromatin and euchromatin. Nature Biotechnology, 2022, 40, 235-244.	9.4	72
3052	Simultaneous profiling of multiple chromatin proteins in the same cells. Molecular Cell, 2021, 81, 4736-4746.e5.	4.5	62
3053	Single-cell sequencing: the technological revolution behind a new wave of multiomic studies in basic and cancer research. BioTechniques, 2021, 71, 539-542.	0.8	1
3054	Integrated Multiomics Analyses Revealing Different Molecular Profiles Between Early- and Late-Stage Lung Adenocarcinoma. Frontiers in Oncology, 2021, 11, 746943.	1.3	5
3055	Reduction in gene expression noise by targeted increase in accessibility at gene loci. Proceedings of the National Academy of Sciences of the United States of America, 2021, 118, .	3.3	27
3057	Dual detection of chromatin accessibility and DNA methylation using ATAC-Me. Nature Protocols, 2021, 16, 5377-5397.	5.5	10
3058	Comprehensive Combined Proteomics and Genomics Analysis Identifies Prognostic Related Transcription Factors in Breast Cancer and Explores the Role of DMAP1 in Breast Cancer. Journal of Personalized Medicine, 2021, 11, 1068.	1.1	0
3059	Chromatin accessibility and gene expression during adipocyte differentiation identify context-dependent effects at cardiometabolic GWAS loci. PLoS Genetics, 2021, 17, e1009865.	1.5	9

#	Article	IF	Citations
3060	Integrated single-cell transcriptomics and epigenomics reveals strong germinal centerâ€“associated etiology of autoimmune risk loci. Science Immunology, 2021, 6, eabh3768.	5.6	19
3061	Characterization of chromatin accessibility in psoriasis. Frontiers of Medicine, 2021, , 1.	1.5	1
3063	Sites of active gene regulation in the prenatal frontal cortex and their role in neuropsychiatric disorders. American Journal of Medical Genetics Part B: Neuropsychiatric Genetics, 2021, 186, 376-388.	1.1	8
3064	Advanced Genomics-Based Approaches for Defining Allograft Rejection With Single Cell Resolution. Frontiers in Immunology, 2021, 12, 750754.	2.2	5
3065	Short single-stranded DNAs with putative non-canonical structures comprise a new class of plasma cell-free DNA. BMC Biology, 2021, 19, 225.	1.7	19
3066	No Need to Stick Together to Be Connected: Multiple Types of Enhancersâ€™ Networking. Cancers, 2021, 13, 5201.	1.7	2
3069	CoolBox: a flexible toolkit for visual analysis of genomics data. BMC Bioinformatics, 2021, 22, 489.	1.2	19
3070	Changing and stable chromatin accessibility supports transcriptional overhaul during neural stem cell activation and is altered with age. Aging Cell, 2021, 20, e13499.	3.0	13
3071	CHD1 controls H3.3 incorporation in adult brain chromatin to maintain metabolic homeostasis and normal lifespan. Cell Reports, 2021, 37, 109769.	2.9	10
3073	Deficiencies in the DNA Binding Protein ARID3a Alter Chromatin Structures Important for Early Human Erythropoiesis. ImmunoHorizons, 2021, 5, 802-817.	0.8	1
3074	Quality control and evaluation of plant epigenomics data. Plant Cell, 2022, 34, 503-513.	3.1	13
3075	Bioinformatics Analysis Using ATAC-seq and RNA-seq for the Identification of 15 Gene Signatures Associated With the Prediction of Prognosis in Hepatocellular Carcinoma. Frontiers in Oncology, 2021, 11, 726551.	1.3	6
3076	c-FOS drives reversible basal to squamous cell carcinoma transition. Cell Reports, 2021, 37, 109774.	2.9	14
3077	Identification of a Putative Enhancer RNA for EGFR in Hyper-Accessible Regions in Esophageal Squamous Cell Carcinoma Cells by Analysis of Chromatin Accessibility Landscapes. Frontiers in Oncology, 2021, 11, 724687.	1.3	4
3079	Proteome-wide profiling of transcriptional machinery on accessible chromatin with biotinylated transposons. Science Advances, 2021, 7, eabh1022.	4.7	3
3081	Fibroblast pathology in inflammatory diseases. Journal of Clinical Investigation, 2021, 131, .	3.9	65
3082	Targeting the Non-Coding Genome for the Diagnosis of Disorders of Sex Development. Sexual Development, 2021, 15, 392-410.	1.1	9
3083	Current Understanding of Molecular Phase Separation in Chromosomes. International Journal of Molecular Sciences, 2021, 22, 10736.	1.8	13

#	Article	IF	Citations
3085	Epigenomic Measurements in Brain Tissues. , 2015, , 1-41.		0
3089	Epigenomic Measurements in Brain Tissues. , 2016, , 2857-2897.		0
3092	Lymphocyte Identity and Genomic Switches. Epigenetics and Human Health, 2016, , 41-52.	0.2	0
3111	Genome-Wide Approaches to Defining Macrophage Identity and Function. , 0, , 553-570.		0
3155	Chromatyping: Reconstructing Nucleosome Profiles from NOMe Sequencing Data. Lecture Notes in Computer Science, 2018, , 21-36.	1.0	0
3156	Disruption of the TFAP2A Regulatory Domain Causes Banchio-Oculo-Facial Syndrome (BOFS) and Illuminates Pathomechanisms for Other Human Neurocristopathies. SSRN Electronic Journal, 0, , .	0.4	1
3157	Recovering Gene Interactions from Single-Cell Data Using Data Diffusion. SSRN Electronic Journal, 0, , .	0.4	11
3158	Chromatin Accessibility Dynamics During Reprogramming. SSRN Electronic Journal, 0, , .	0.4	0
3159	How Low Can You Go? Calling Robust ATAC-Seq Peaks Through Read Down-Sampling. SSRN Electronic Journal, 0, , .	0.4	0
3222	ATAC-seq on Sorted Adult Mouse Neurons. Bio-protocol, 2019, 9, e3382.	0.2	2
3224	Defining CBX7-Dependent Chromatin Architecture with Rapid Small-Molecule Inhibition. SSRN Electronic Journal, 0, , .	0.4	0
3225	Allele-Specific Gene Regulation by Kdm6a. SSRN Electronic Journal, 0, , .	0.4	0
3228	ModHMM: A Modular Supra-Bayesian Genome Segmentation Method. Lecture Notes in Computer Science, 2019, , 35-50.	1.0	2
3229	Genomic Applications and Insights in Unravelling Cancer Signalling Pathways. , 2019, , 471-511.		0
3230	Multi-Level Chromosome Remodeling Underlying Activation of Human T Cells. SSRN Electronic Journal, 0, , .	0.4	0
3231	Chromatin Epigenomics in Muscle Development and Disease. , 2019, , 31-44.		0
3232	Dysregulation of Cis-Regulatory Elements in Cancer. , 2019, , 173-192.		1
3233	Methods to Detect and Associate Divergence in Cis-Regulatory Elements to Phenotypic Divergence. , 2019, , 113-134.		1

#	Article	IF	Citations
3271	Chromatin Structure Research Methods. Materials and Methods, 0, 9, .	0.0	0
3305	1 Chromatin Structure and Function in Neurospora crassa. , 2020, , 3-24.		1
3331	Developmentally Programmed Tankyrase Activity Upregulates Î²-Catenin and Licenses Progression of Embryonic Genome Activation. Developmental Cell, 2020, 53, 545-560.e7.	3.1	12
3342	G9a/GLP-sensitivity of H3K9me2 Demarcates Two Types of Genomic Compartments. Genomics, Proteomics and Bioinformatics, 2020, 18, 359-370.	3.0	4
3346	Epigenetic Assays in Purified Cardiomyocyte Nuclei. Methods in Molecular Biology, 2021, 2158, 307-321.	0.4	4
3347	Unified Analysis of Multiple ChIP-Seq Datasets. Methods in Molecular Biology, 2021, 2198, 451-465.	0.4	2
3358	Regulation of neuronal commitment in mouse embryonic stem cells by the Reno1/Bahcc1 locus. EMBO Reports, 2020, 21, e51264.	2.0	15
3360	Decoding the Equine Genome: Lessons from ENCODE. Genes, 2021, 12, 1707.	1.0	5
3361	Comprehensive understanding of Tn5 insertion preference improves transcription regulatory element identification. NAR Genomics and Bioinformatics, 2021, 3, lqab094.	1.5	8
3362	Cis-Regulatory Control of Mammalian Sex Determination. Sexual Development, 2021, 15, 317-334.	1.1	6
3364	Inner nuclear protein Matrin-3 coordinates cell differentiation by stabilizing chromatin architecture. Nature Communications, 2021, 12, 6241.	5.8	25
3366	Genomic Marks Associated with Chromatin Compartments in the CTCF, RNAPII Loop and Genomic Windows. International Journal of Molecular Sciences, 2021, 22, 11591.	1.8	1
3367	The immune niche of the liver. Clinical Science, 2021, 135, 2445-2466.	1.8	39
3368	A cis-regulatory element promoting increased transcription at low temperature in cultured ectothermic Drosophila cells. BMC Genomics, 2021, 22, 771.	1.2	3
3369	Single-cell chromatin state analysis with Signac. Nature Methods, 2021, 18, 1333-1341.	9.0	595
3370	An expansion of the non-coding genome and its regulatory potential underlies vertebrate neuronal diversity. Neuron, 2022, 110, 70-85.e6.	3.8	22
3371	Weighted K-Means Clustering with Observation Weight for Single-Cell Epigenomic Data. Emerging Topics in Statistics and Biostatistics, 2020, , 37-64.	0.1	0
3372	HiChew: a Tool for TAD Clustering in Embryogenesis. Lecture Notes in Computer Science, 2020, , 381-388.	1.0	1

#	Article	IF	Citations
3374	Technical advancements in epigenomics and applications in transplantation. Current Opinion in Organ Transplantation, 2021, 26, 23-29.	0.8	5
3376	Single position substitution of hairpin pyrrole-imidazole polyamides imparts distinct DNA-binding profiles across the human genome. PLoS ONE, 2020, 15, e0243905.	1.1	5
3377	Interpretation of Biological Data at a Glance. Journal of Biotechnology and Bioindustry, 2020, 8, 38-47.	0.1	0
3379	Epigenetic Analysis in Ewing Sarcoma. Methods in Molecular Biology, 2021, 2226, 285-302.	0.4	1
3392	Learning Tn5 Sequence Bias from ATAC-seq on Naked Chromatin. Lecture Notes in Computer Science, 2020, , 105-114.	1.0	1
3407	Fast analysis of scATAC-seq data using a predefined set of genomic regions. F1000Research, 2020, 9, 199.	0.8	6
3413	Chromatin accessibility analysis identifies GSTM1 as a prognostic marker in human glioblastoma patients. Clinical Epigenetics, 2021, 13, 201.	1.8	1
3415	Hsa-miR-31 Governs T-Cell Homeostasis in HIV Protection via IFN-Î³-Stat1-T-Bet Axis. Frontiers in Immunology, 2021, 12, 771279.	2.2	3
3416	Chromatin-accessibility estimation from single-cell ATAC-seq data with scOpen. Nature Communications, 2021, 12, 6386.	5.8	57
3417	Inability to switch from ARID1A-BAF to ARID1B-BAF impairs exit from pluripotency and commitment towards neural crest formation in ARID1B-related neurodevelopmental disorders. Nature Communications, 2021, 12, 6469.	5.8	12
3419	The existence of a nonclassical TCA cycle in the nucleus that wires the metabolic-epigenetic circuitry. Signal Transduction and Targeted Therapy, 2021, 6, 375.	7.1	34
3420	Bend family proteins mark chromatin boundaries and synergistically promote early germ cell differentiation. Protein and Cell, 2022, 13, 721-741.	4.8	6
3423	MEF2 is a key regulator of cognitive potential and confers resilience to neurodegeneration. Science Translational Medicine, 2021, 13, eabd7695.	5.8	37
3424	Identification of LZTFL1 as a candidate effector gene at a COVID-19 risk locus. Nature Genetics, 2021, 53, 1606-1615.	9.4	93
3425	Making connections: enhancers in cellular differentiation. Trends in Genetics, 2022, 38, 395-408.	2.9	6
3445	ATAC-Seq for Assaying Chromatin Accessibility Protocol Using Echinoderm Embryos. Methods in Molecular Biology, 2021, 2219, 253-265.	0.4	5
3446	Mapping 5-Hydroxymethylcytosine (5hmC) Modifications in Skeletal Tissues Using High-Throughput Sequencing. Methods in Molecular Biology, 2021, 2221, 101-108.	0.4	1
3461	Myeloid transformation byMLL-ENLdepends strictly on C/EBP. Life Science Alliance, 2021, 4, e202000709.	1.3	5

#	Article	IF	Citations
3462	A saturating mutagenesis CRISPR-Cas9â€“mediated functional genomic screen identifies cis- and trans-regulatory elements of Oct4 in murine ESCs. Journal of Biological Chemistry, 2020, 295, 15797-15809.	1.6	6
3473	Systematic clustering algorithm for chromatin accessibility data and its application to hematopoietic cells. PLoS Computational Biology, 2020, 16, e1008422.	1.5	2
3474	Sexual Dimorphism through the Lens of Genome Manipulation, Forward Genetics, and Spatiotemporal Sequencing. Genome Biology and Evolution, 2021, 13, .	1.1	6
3475	Chromatin features, RNA polymerase II and the comparative expression of lens genes encoding crystallins, transcription factors, and autophagy mediators. Molecular Vision, 2015, 21, 955-73.	1.1	18
3476	From Genotype to Phenotype: A Primer on the Functional Follow-up of Genome-Wide Association Studies in Cardiovascular Disease. Circulation Genomic and Precision Medicine, 2018, 11, .	1.6	5
3479	PRDM1 Drives Human Primary T Cell Hyporesponsiveness by Altering the T Cell Transcriptome and Epigenome. SSRN Electronic Journal, 0, , .	0.4	0
3480	Integration of RNA-Seq and ATAC-Seq Identifies Key Genes and Chromatin Accessibility Changes in Growth Hormone-Secreting Pituitary Adenoma. SSRN Electronic Journal, 0, , .	0.4	0
3481	Epigenetics and precision medicine in allergic diseases. , 2022, , 407-448.		0
3482	Epigenetic regulation in the neurogenic niche of the adult dentate gyrus. Neuroscience Letters, 2022, 766, 136343.	1.0	2
3483	PEPATAC: an optimized pipeline for ATAC-seq data analysis with serial alignments. NAR Genomics and Bioinformatics, 2021, 3, lqab101.	1.5	34
3484	Epigenetics and tissue immunityâ€”Translating environmental cues into functional adaptations*. Immunological Reviews, 2022, 305, 111-136.	2.8	6
3485	TNF-Î±-producing macrophages determine subtype identity and prognosis via AP1 enhancer reprogramming in pancreatic cancer. Nature Cancer, 2021, 2, 1185-1203.	5.7	46
3489	CRISPR screens unveil signal hubs for nutrient licensing of T cell immunity. Nature, 2021, 600, 308-313.	13.7	36
3490	Chromatin-state barriers enforce an irreversible mammalian cell fate decision. Cell Reports, 2021, 37, 109967.	2.9	28
3491	Efficiency of SpCas9 and AsCpf1 (Cas12a) programmable nucleases at genomic safe harbor loci in HEK293 cells. AlÊ¹manah KliniÄ•skoj Mediciny, 2021, 49, 385-395.	0.2	0
3492	Self-guarding of MORC3 enables virulence factor-triggered immunity. Nature, 2021, 600, 138-142.	13.7	27
3493	Transcriptional profile and chromatin accessibility in zebrafish melanocytes and melanoma tumors. G3: Genes, Genomes, Genetics, 2022, 12, .	0.8	3
3494	Sequence logic at enhancers governs a dual mechanism of endodermal organ fate induction by FOXA pioneer factors. Nature Communications, 2021, 12, 6636.	5.8	31

#	Article	IF	Citations
3495	Human and rat skeletal muscle single-nuclei multi-omic integrative analyses nominate causal cell types, regulatory elements, and SNPs for complex traits. Genome Research, 2021, 31, 2258-2275.	2.4	31
3496	Relaxed 3D genome conformation facilitates the pluripotent to totipotent-like state transition in embryonic stem cells. Nucleic Acids Research, 2021, 49, 12167-12177.	6.5	22
3498	COVID-19 genetic risk variants are associated with expression of multiple genes in diverse immune cell types. Nature Communications, 2021, 12, 6760.	5.8	32
3499	Identification of downstream effectors of retinoic acid specifying the zebrafish pancreas by integrative genomics. Scientific Reports, 2021, 11, 22717.	1.6	6
3500	Chromatin Accessibility Predetermines Odontoblast Terminal Differentiation. Frontiers in Cell and Developmental Biology, 2021, 9, 769193.	1.8	3
3501	Integrative analysis reveals mouse strain-dependent responses to acute ozone exposure associated with airway macrophage transcriptional activity. American Journal of Physiology - Lung Cellular and Molecular Physiology, 2022, 322, L33-L49.	1.3	7
3502	Interspecies transcriptomics identify genes that underlie disproportionate foot growth in jerboas. Current Biology, 2022, 32, 289-303.e6.	1.8	13
3504	Genome-wide quantification of transcription factor binding at single-DNA-molecule resolution using methyl-transferase footprinting. Nature Protocols, 2021, 16, 5673-5706.	5.5	6
3505	Targeting the spliceosome through RBM39 degradation results in exceptional responses in high-risk neuroblastoma models. Science Advances, 2021, 7, eabj5405.	4.7	32
3506	Rare Does Not Mean Worthless: How Rare Diseases Have Shaped Neurodevelopment Research in the NGS Era. Biomolecules, 2021, 11, 1713.	1.8	3
3507	Functional genomics data: privacy risk assessment and technological mitigation. Nature Reviews Genetics, 2022, 23, 245-258.	7.7	17
3508	Perspective of the GEMSTONE Consortium on Current and Future Approaches to Functional Validation for Skeletal Genetic Disease Using Cellular, Molecular and Animal-Modeling Techniques. Frontiers in Endocrinology, 2021, 12, 731217.	1.5	12
3509	Single cell multi-omic analysis identifies a Tbx1-dependent multilineage primed population in murine cardiopharyngeal mesoderm. Nature Communications, 2021, 12, 6645.	5.8	31
3510	CHD4 Conceals Aberrant CTCF-Binding Sites at TAD Interiors by Regulating Chromatin Accessibility in Mouse Embryonic Stem Cells. Molecules and Cells, 2021, 44, 805-829.	1.0	7
3511	Fast alignment and preprocessing of chromatin profiles with Chromap. Nature Communications, 2021, 12, 6566.	5.8	39
3512	Stem cells expand potency and alter tissue fitness by accumulating diverse epigenetic memories. Science, 2021, 374, eabh2444.	6.0	56
3514	A single-cell atlas of chromatin accessibility in the human genome. Cell, 2021, 184, 5985-6001.e19.	13.5	194
3515	Histone variant H2A.Z regulates zygotic genome activation. Nature Communications, 2021, 12, 7002.	5.8	24

#	Article	IF	Citations
3516	An NK-like CAR TÂcell transition in CAR TÂcell dysfunction. Cell, 2021, 184, 6081-6100.e26.	13.5	160
3517	SMAD4 target genes are part of a transcriptional network that integrates the response to BMP and SHH signaling during early limb bud patterning. Development (Cambridge), 2021, 148, .	1.2	4
3518	Runx2 Regulates Chromatin Accessibility to Direct Skeletal Cell Programs. SSRN Electronic Journal, 0, , .	0.4	3
3519	SWI/SNF (BAF) complexes: From framework to a functional role in endothelial mechanotransduction. Current Topics in Membranes, 2021, 87, 171-198.	0.5	2
3520	Hypermethylation at the CXCR5 gene locus limits trafficking potential of CD8+ T cells into B-cell follicles during HIV-1 infection. Blood Advances, 2022, 6, 1904-1916.	2.5	6
3521	CTCF Expression and Dynamic Motif Accessibility Modulates Epithelialâ€“Mesenchymal Gene Expression. Cancers, 2022, 14, 209.	1.7	15
3522	Chromatin accessibility and microRNA expression in nephron progenitor cells during kidney development. Genomics, 2022, 114, 278-291.	1.3	4
3523	Distal and proximal cis-regulatory elements sense X chromosome dosage and developmental state at the Xist locus. Molecular Cell, 2022, 82, 190-208.e17.	4.5	23
3524	SUMOylation of linker histone H1 drives chromatin condensation and restriction of embryonic cell fate identity. Molecular Cell, 2022, 82, 106-122.e9.	4.5	19
3525	Maternal gut bacteria drive intestinal inflammation in offspring with neurodevelopmental disorders by altering the chromatin landscape of CD4+ TÂcells. Immunity, 2022, 55, 145-158.e7.	6.6	70
3526	The metabolic stress-activated checkpoint LKB1-MARK3 axis acts as a tumor suppressor in high-grade serous ovarian carcinoma. Communications Biology, 2022, 5, 39.	2.0	11
3527	C/EBPB-dependent adaptation to palmitic acid promotes tumor formation in hormone receptor negative breast cancer. Nature Communications, 2022, 13, 69.	5.8	16
3528	Extendable and explainable deep learning for pan-cancer radiogenomics research. Current Opinion in Chemical Biology, 2022, 66, 102111.	2.8	11
3529	Technologies for profiling the impact of genomic variants on transcription factor binding. Medizinische Genetik, 2021, 33, 147-155.	0.1	1
3530	How to find genomic regions relevant for gene regulation. Medizinische Genetik, 2021, 33, 157-165.	0.1	0
3531	ATAC Sequencing Protocol For Cryopreserved Mammalian Cells. Bio-protocol, 2022, 12, e4294.	0.2	1
3532	Single-cell-resolved dynamics of chromatin architecture delineate cell and regulatory states in zebrafish embryos. Cell Genomics, 2022, 2, 100083.	3.0	8
3533	Prognostic Bone Metastasis-Associated Immune-Related Genes Regulated by Transcription Factors in Mesothelioma. BioMed Research International, 2022, 2022, 1-26.	0.9	1

#	Article	IF	Citations
3535	Alterations in chromatin accessibility during osteoblast and adipocyte differentiation in human mesenchymal stem cells. BMC Medical Genomics, 2022, 15, 17.	0.7	5
3536	Dualâ€layered hydrogels allow complete genome recovery with nucleic acid cytometry. Biotechnology Journal, 2022, 17, e2100483.	1.8	0
3538	Open chromatin interaction maps reveal functional regulatory elements and chromatin architecture variations during wheat evolution. Genome Biology, 2022, 23, 34.	3.8	22
3540	KAS-seq: genome-wide sequencing of single-stranded DNA by N3-kethoxalâ€“assisted labeling. Nature Protocols, 2022, 17, 402-420.	5.5	16
3541	VDR regulates simulated microgravity-induced atrophy in C2C12 myotubes. Scientific Reports, 2022, 12, 1377.	1.6	4
3542	Host T Cell Dedifferentiation Effects Drive HIV-1 Latency Stability. Journal of Virology, 2022, 96, jvi0197421.	1.5	2
3543	Human iPSC-Cardiomyocytes as an Experimental Model to Study Epigenetic Modifiers of Electrophysiology. Cells, 2022, 11, 200.	1.8	12
3544	Fine mapping with epigenetic information and 3D structure. Seminars in Immunopathology, 2022, 44, 115-125.	2.8	8
3545	T Cell Memory in Infection, Cancer, and Autoimmunity. Frontiers in Immunology, 2021, 12, 811968.	2.2	9
3546	Patient-specific MDS-RS iPSCs define the mis-spliced transcript repertoire and chromatin landscape of SF3B1-mutant HSPCs. Blood Advances, 2022, 6, 2992-3005.	2.5	7
3548	Recent advances in single-cell sequencing technologies. Precision Clinical Medicine, 2022, 5, .	1.3	44
3549	Methionine- and Choline-Deficient Diet Identifies an Essential Role for DNA Methylation in Plasmacytoid Dendritic Cell Biology. Journal of Immunology, 2022, 208, 881-897.	0.4	2
3552	Modeling Human Thyroid Development by Fetal Tissueâ€Derived Organoid Culture. Advanced Science, 2022, 9, e2105568.	5.6	14
3553	Scalable in vitro production of defined mouse erythroblasts. PLoS ONE, 2022, 17, e0261950.	1.1	8
3554	Distal regulation, silencers, and a shared combinatorial syntax are hallmarks of animal embryogenesis. Genome Research, 2022, 32, 474-487.	2.4	7
3555	Epigenomic analysis of KLF1 haploinsufficiency in primary human erythroblasts. Scientific Reports, 2022, 12, 336.	1.6	5
3556	SETDB1/NSD-dependent H3K9me3/H3K36me3 dual heterochromatin maintains gene expression profiles by bookmarking poised enhancers. Molecular Cell, 2022, 82, 816-832.e12.	4.5	29
3557	Chromatin topology defines estradiol-primed progesterone receptor and PAX2 binding in endometrial cancer cells. ELife, 2022, 11, .	2.8	10

#	Article	IF	Citations
3558	Distinct gene regulatory signatures of dominance rank and social bond strength in wild baboons. Philosophical Transactions of the Royal Society B: Biological Sciences, 2022, 377, 20200441.	1.8	18
3559	Single-Cell Epigenomics Reveals Mechanisms of Cancer Progression. Annual Review of Cancer Biology, 2022, 6, 167-185.	2.3	9
3560	Functional dissection of inherited non-coding variation influencing multiple myeloma risk. Nature Communications, 2022, 13, 151.	5.8	10
3561	Down-syndrome-induced senescence disrupts the nuclear architecture of neural progenitors. Cell Stem Cell, 2022, 29, 116-130.e7.	5.2	41
3562	PRC1 sustains the integrity of neural fate in the absence of PRC2 function. ELife, 2022, 11, .	2.8	15
3564	Dynamic chromatin state profiling reveals regulatory roles of auxin and cytokinin in shoot regeneration. Developmental Cell, 2022, 57, 526-542.e7.	3.1	39
3566	Integrative epigenomic profiling reveal AP-1 is a key regulator in intrahepatic cholangiocarcinoma. Genomics, 2022, 114, 241-252.	1.3	5
3567	DNA topoisomerase inhibition with the HIF inhibitor acriflavine promotes transcription of lncRNAs in endothelial cells. Molecular Therapy - Nucleic Acids, 2022, 27, 1023-1035.	2.3	7
3568	Single Cell Transcriptomic and Chromatin Profiles Suggest Layer Vb Is the Only Layer With Shared Excitatory Cell Types in the Medial and Lateral Entorhinal Cortex. Frontiers in Neural Circuits, 2021, 15, 806154.	1.4	1
3569	Caenorhabditis elegans transposable elements harbor diverse transcription factor DNA-binding sites. G3: Genes, Genomes, Genetics, 2022, 12, .	0.8	0
3570	Single-Molecule Multikilobase-Scale Profiling of Chromatin Using m6A-SMAC-Seq and m6A-CpG-GpC-SMAC-Seq. Methods in Molecular Biology, 2022, 2458, 269-298.	0.4	1
3571	A deep generative model for multi-view profiling of single-cell RNA-seq and ATAC-seq data. Genome Biology, 2022, 23, 20.	3.8	33
3572	Deconstructing a Syndrome: Genomic Insights Into PCOS Causal Mechanisms and Classification. Endocrine Reviews, 2022, 43, 927-965.	8.9	75
3573	Genome-wide DNA methylation analysis in pediatric acute myeloid leukemia. Blood Advances, 2022, 6, 3207-3219.	2.5	7
3574	ATAC-seq reveals the landscape of open chromatin and cis-regulatory elements in the Phytophthora sojae genome. Molecular Plant-Microbe Interactions, 2022, , .	1.4	5
3575	A multi-omics approach to identify molecular alterations in a mouse model of heart failure. Theranostics, 2022, 12, 1607-1620.	4.6	2
3576	E2F and STAT3 provide transcriptional synergy for histone variant H2AZ activation to sustain glioblastoma chromatin accessibility and tumorigenicity. Cell Death and Differentiation, 2022, 29, 1379-1394.	5.0	9
3577	A single-cell atlas of de novo Î²-cell regeneration reveals the contribution of hybrid Î²/Î´-cells to diabetes recovery in zebrafish. Development (Cambridge), 2022, 149, .	1.2	12

#	Article	IF	Citations
3578	Epigenomic priming of immune genes implicates oligodendroglia in multiple sclerosis susceptibility. Neuron, 2022, 110, 1193-1210.e13.	3.8	36
3579	Reconstruction of dynamic regulatory networks reveals signaling-induced topology changes associated with germ layer specification. Stem Cell Reports, 2022, 17, 427-442.	2.3	7
3581	Characterization of Mammalian Regulatory Complexes at Single-Locus Resolution Using TINC. Methods in Molecular Biology, 2022, 2458, 175-193.	0.4	1
3583	Bioinformatics analysis methods for cell-free DNA. Computers in Biology and Medicine, 2022, 143, 105283.	3.9	3
3584	Kidney cell type-specific changes in the chromatin and transcriptome landscapes following epithelial Hdac1 and Hdac2 knockdown. Physiological Genomics, 2022, 54, 45-57.	1.0	3
3585	NicE-C efficiently reveals open chromatinâ€“associated chromosome interactions at high resolution. Genome Research, 2022, 32, 534-544.	2.4	11
3586	Progesterone Inhibits the Establishment of Activation-Associated Chromatin During TH1 Differentiation. Frontiers in Immunology, 2022, 13, 835625.	2.2	7
3587	Single-Cell Factor Localization on Chromatin using Ultra-Low Input Cleavage Under Targets and Release using Nuclease. Journal of Visualized Experiments, 2022, , .	0.2	0
3589	Assay for transposase-accessible chromatin with high-throughput sequencing reveals radioresistance-related genes in oral squamous cell carcinoma cells. Biochemical and Biophysical Research Communications, 2022, 597, 115-121.	1.0	1
3590	Multi-CUT&Tag to simultaneously profile multiple chromatin factors. STAR Protocols, 2022, 3, 101100.	0.5	3
3591	Bibliometric review of ATAC-Seq and its application in gene expression. Briefings in Bioinformatics, 2022, 23, .	3.2	21
3593	Chemical-induced chromatin remodeling reprograms mouse ESCs to totipotent-like stem cells. Cell Stem Cell, 2022, 29, 400-418.e13.	5.2	68
3594	Wild epigenetics: insights from epigenetic studies on natural populations. Proceedings of the Royal Society B: Biological Sciences, 2022, 289, 20211633.	1.2	18
3595	Epigenetic basis of oncogenic-Kras-mediated epithelial-cellular proliferation and plasticity. Developmental Cell, 2022, 57, 310-328.e9.	3.1	6
3596	BMAL1 drives muscle repair through control of hypoxic NAD⁺ regeneration in satellite cells. Genes and Development, 2022, 36, 149-166.	2.7	13
3597	A distinct role of STING in regulating glucose homeostasis through insulin sensitivity and insulin secretion. Proceedings of the National Academy of Sciences of the United States of America, 2022, 119, .	3.3	26
3598	Pluripotency factors determine gene expression repertoire at zygotic genome activation. Nature Communications, 2022, 13, 788.	5.8	9
3599	Capture-C: a modular and flexible approach for high-resolution chromosome conformation capture. Nature Protocols, 2022, 17, 445-475.	5.5	24

#	Article	IF	Citations
3600	SETD2 loss perturbs the kidney cancer epigenetic landscape to promote metastasis and engenders actionable dependencies on histone chaperone complexes. Nature Cancer, 2022, 3, 188-202.	5.7	26
3601	Analysis of chromatin accessibility in p53 deficient spermatogonial stem cells for high frequency transformation into pluripotent state. Cell Proliferation, 2022, 55, e13195.	2.4	5
3602	RFX transcription factors control a miR-150/PDAP1 axis that restrains the proliferation of human T cells. PLoS Biology, 2022, 20, e3001538.	2.6	4
3605	Two ovarian candidate enhancers, identified by time series enhancer RNA analyses, harbor rare genetic variations identified in ovarian insufficiency. Human Molecular Genetics, 2022, 31, 2223-2235.	1.4	3
3606	Multimodal profiling of the transcriptional regulatory landscape of the developing mouse cortex identifies Neurog2 as a key epigenome remodeler. Nature Neuroscience, 2022, 25, 154-167.	7.1	27
3607	Dual G9A/EZH2 Inhibition Stimulates Antitumor Immune Response in Ovarian High-Grade Serous Carcinoma. Molecular Cancer Therapeutics, 2022, 21, 522-534.	1.9	20
3609	Dynamic Runx1 chromatin boundaries affect gene expression in hematopoietic development. Nature Communications, 2022, 13, 773.	5.8	10
3610	Plant glutamate receptors mediate a bet-hedging strategy between regeneration and defense. Developmental Cell, 2022, 57, 451-465.e6.	3.1	30
3612	Landscape and dynamics of accessible chromatin during pigmentation process in green, white and purple sea cucumber Apostichopus japonicus. Aquaculture Reports, 2022, 23, 101040.	0.7	1
3613	In-silico analysis of the regulatory region of effector protein genes in Verticillium dahliae. Gene Reports, 2022, 27, 101533.	0.4	0
3614	The methyltransferase METTL3 negatively regulates nonalcoholic steatohepatitis (NASH) progression. Nature Communications, 2021, 12, 7213.	5.8	51
3615	Parity-induced changes to mammary epithelial cells control NKT cell expansion and mammary oncogenesis. Cell Reports, 2021, 37, 110099.	2.9	12
3616	Interleukin-10 receptor signaling promotes the maintenance of a PD-1int TCF-1+ CD8+ TÂcell population that sustains anti-tumor immunity. Immunity, 2021, 54, 2825-2841.e10.	6.6	57
3617	Cell-type-specific chromatin occupancy by the pioneer factor Zelda drives key developmental transitions in Drosophila. Nature Communications, 2021, 12, 7153.	5.8	18
3618	Constructing gene regulatory networks using epigenetic data. Npj Systems Biology and Applications, 2021, 7, 45.	1.4	14
3619	Spatial genomics enables multi-modal study of clonal heterogeneity in tissues. Nature, 2022, 601, 85-91.	13.7	117
3620	Targeting SWI/SNF ATPases in enhancer-addicted prostate cancer. Nature, 2022, 601, 434-439.	13.7	110
3621	MNX1-HNF1B Axis Is Indispensable for Intraductal Papillary Mucinous Neoplasm Lineages. Gastroenterology, 2022, 162, 1272-1287.e16.	0.6	16

#	Article	IF	Citations
3622	TCR signal strength defines distinct mechanisms of T cell dysfunction and cancer evasion. Journal of Experimental Medicine, 2022, 219, .	4.2	64
3623	Cis-regulatory sequences in plants: Their importance, discovery, and future challenges. Plant Cell, 2022, 34, 718-741.	3.1	125
3624	Epigenetic regulation of natural killer cell memory*. Immunological Reviews, 2022, 305, 90-110.	2.8	17
3625	Analysis of Enhancers and Transcriptional Networks in Thermogenic Adipocytes. Methods in Molecular Biology, 2022, 2448, 155-175.	0.4	0
3627	Assessing Chromatin Accessibility During WBR in Acoels. Methods in Molecular Biology, 2022, 2450, 549-561.	0.4	2
3629	seqgra: principled selection of neural network architectures for genomics prediction tasks. Bioinformatics, 2022, 38, 2381-2388.	1.8	0
3630	Ð˜ÑÐ»ÐµÐ´Ð¾Ð²Ð°Ð½Ð¸Ñ•Ð¼Ð¾Ð»ÐµÐºÑƒÐ»ÑÑ€Ð½Ð¾Ð¹ Ñ€ÐµÐ³ÑƒÐ»ÑÑ†Ð¸Ð¸ Ñ€Ð¾Ð¶ÐµÐ½Ð¸Ñ†Ñ‹		
3632	A global timing mechanism regulates cell-type-specific wiring programmes. Nature, 2022, 603, 112-118.	13.7	22
3633	Mitochondrial variant enrichment from high-throughput single-cell RNA sequencing resolves clonal populations. Nature Biotechnology, 2022, 40, 1030-1034.	9.4	45
3634	Uncovering the mesendoderm gene regulatory network through multi-omic data integration. Cell Reports, 2022, 38, 110364.	2.9	10
3636	Transcriptional repression of estrogen receptor alpha by YAP reveals the Hippo pathway as therapeutic target for ER+ breast cancer. Nature Communications, 2022, 13, 1061.	5.8	55
3637	Identification of enhancer regulatory elements that direct epicardial gene expression during zebrafish heart regeneration. Development (Cambridge), 2022, 149, .	1.2	14
3639	FACT maintains nucleosomes during transcription and stem cell viability in adult mice. EMBO Reports, 2022, 23, e53684.	2.0	6
3640	E-Protein Inhibition in ILC2 Development Shapes the Function of Mature ILC2s during Allergic Airway Inflammation. Journal of Immunology, 2022, 208, 1007-1020.	0.4	2
3641	Deterministic scRNA-seq captures variation in intestinal crypt and organoid composition. Nature Methods, 2022, 19, 323-330.	9.0	33
3643	HyperChIP: identification of hypervariable signals across ChIP-seq or ATAC-seq samples. Genome Biology, 2022, 23, 62.	3.8	1
3644	In vivo CRISPRâ€Cas9â€mediated DNA chop identifies a cochlear outer hair cellâ€specific enhancer. FASEB Journal, 2022, 36, e22233.	0.2	12
3645	Whole-genome methods to define DNA and histone accessibility and long-range interactions in chromatin. Biochemical Society Transactions, 2022, 50, 199-212.	1.6	2

#	Article	IF	Citations
3646	Integrated Chromatin Accessibility and Transcriptome Landscapes of 5-Fluorouracil-Resistant Colon Cancer Cells. Frontiers in Cell and Developmental Biology, 2022, 10, 838332.	1.8	6
3647	Deciphering the Retinal Epigenome during Development, Disease and Reprogramming: Advancements, Challenges and Perspectives. Cells, 2022, 11, 806.	1.8	3
3649	Diabetes and Its Cardiovascular Complications: Comprehensive Network and Systematic Analyses. Frontiers in Cardiovascular Medicine, 2022, 9, 841928.	1.1	7
3650	The methyltransferase enzymes KMT2D, SETD1B, and ASH1L are key mediators of both metabolic and epigenetic changes during cellular senescence. Molecular Biology of the Cell, 2022, 33, mbcE20080523.	0.9	3
3651	Batf-mediated epigenetic control of effector CD8 ⁺ T cell differentiation. Science Immunology, 2022, 7, eabi4919.	5.6	19
3652	Molecular Manipulations and Intestinal Stem Cell-Derived Organoids in Inflammatory Bowel Disease. Stem Cells, 2022, 40, 447-457.	1.4	6
3653	Transcriptome and chromatin alterations in social fear indicate association of MEG3 with successful extinction of fear. Molecular Psychiatry, 2022, 27, 4064-4076.	4.1	3
3654	AP-2Î± and AP-2Î² cooperatively function in the craniofacial surface ectoderm to regulate chromatin and gene expression dynamics during facial development. ELife, 2022, 11, .	2.8	17
3655	Experimental development of the epigenomic library construction method to elucidate the epigenetic diversity and causal relationship between epigenome and transcriptome at a single-cell level. Genomics and Informatics, 2022, 20, e2.	0.4	0
3656	Nuclear HMGB1 protects from nonalcoholic fatty liver disease through negative regulation of liver X receptor. Science Advances, 2022, 8, eabg9055.	4.7	7
3657	Chromatin accessibility and transcriptome integrative analysis revealed AP-1-mediated genes potentially modulate histopathology features in psoriasis. Clinical Epigenetics, 2022, 14, 38.	1.8	6
3658	Type I interferon transcriptional network regulates expression of coinhibitory receptors in human T cells. Nature Immunology, 2022, 23, 632-642.	7.0	54
3659	Human epigenetic and transcriptional TÂcell differentiation atlas for identifying functional TÂcell-specific enhancers. Immunity, 2022, 55, 557-574.e7.	6.6	47
3660	New Chromatin Run-On Reaction Enables Global Mapping of Active RNA Polymerase Locations in an Enrichment-free Manner. ACS Chemical Biology, 2022, 17, 768-775.	1.6	3
3661	HMGA1 chromatin regulators induce transcriptional networks involved in GATA2 and proliferation during MPN progression. Blood, 2022, 139, 2797-2815.	0.6	20
3662	Revisiting the embryogenesis of lip and palate development. Oral Diseases, 2022, 28, 1306-1326.	1.5	27
3664	Gain of gene regulatory network interconnectivity at the origin of vertebrates. Proceedings of the National Academy of Sciences of the United States of America, 2022, 119, e2114802119.	3.3	9
3665	Resolving patient heterogeneity in critical illness requires multi-scale approaches. EBioMedicine, 2022, 77, 103918.	2.7	1

#	Article	IF	Citations
3666	EBF1 nuclear repositioning instructs chromatin refolding to promote therapy resistance in T leukemic cells. Molecular Cell, 2022, 82, 1003-1020.e15.	4.5	13
3667	GATA4/5/6 family transcription factors are conserved determinants of cardiac versus pharyngeal mesoderm fate. Science Advances, 2022, 8, eabg0834.	4.7	14
3668	The landscape of pioneer factor activity reveals the mechanisms of chromatin reprogramming and genome activation. Molecular Cell, 2022, 82, 986-1002.e9.	4.5	38
3669	ChIP-Atlas 2021 update: a data-mining suite for exploring epigenomic landscapes by fully integrating ChIP-seq, ATAC-seqÂand Bisulfite-seq data. Nucleic Acids Research, 2022, 50, W175-W182.	6.5	135
3670	Base-resolution prediction of transcription factor binding signals by a deep learning framework. PLoS Computational Biology, 2022, 18, e1009941.	1.5	13
3673	CUT&Tag2for1: a modified method for simultaneous profiling of the accessible and silenced regulome in singleÂcells. Genome Biology, 2022, 23, 81.	3.8	30
3674	Epigenetic Activation of Plasmacytoid DCs Drives IFNAR-Dependent Therapeutic Differentiation of AML. Cancer Discovery, 2022, 12, 1560-1579.	7.7	13
3675	DeepCAGE: Incorporating Transcription Factors in Genome-Wide Prediction of Chromatin Accessibility. Genomics, Proteomics and Bioinformatics, 2022, 20, 496-507.	3.0	7
3677	Pioneer factors as master regulators of the epigenome and cell fate. Nature Reviews Molecular Cell Biology, 2022, 23, 449-464.	16.1	88
3678	ATG7-mediated autophagy facilitates embryonic stem cell exit from naive pluripotency and marks commitment to differentiation. Autophagy, 2022, 18, 2946-2968.	4.3	6
3679	Global chromosome rearrangement induced by CRISPR-Cas9 reshapes the genome and transcriptome of human cells. Nucleic Acids Research, 2022, 50, 3456-3474.	6.5	8
3680	CDK7/12/13 inhibition targets an oscillating leukemia stem cell network and synergizes with venetoclax in acute myeloid leukemia. EMBO Molecular Medicine, 2022, 14, e14990.	3.3	14
3682	H3K9 trimethylation in active chromatin restricts the usage of functional CTCF sites in SINE B2 repeats. Genes and Development, 2022, 36, 414-432.	2.7	14
3683	A network of transcription factors governs the dynamics of NODAL/Activin transcriptional responses. Journal of Cell Science, 2022, , .	1.2	6
3684	Osteogenic Commitment of Human Periodontal Ligament Cells Is Predetermined by Methylation, Chromatin Accessibility and Expression of Key Transcription Factors. Cells, 2022, 11, 1126.	1.8	7
3685	SWI/SNF Antagonism of PRC2 Mediates Estrogen-Induced Progesterone Receptor Expression. Cells, 2022, 11, 1000.	1.8	12
3686	Single-cell transcriptomes in the heart: when every epigenome counts. Cardiovascular Research, 2022, , .	1.8	1
3687	Single nucleus multi-omics identifies human cortical cell regulatory genome diversity. Cell Genomics, 2022, 2, 100107.	3.0	58

#	Article	IF	Citations
3689	Cell-specific cis-regulatory elements and mechanisms of non-coding genetic disease in human retina and retinal organoids. Developmental Cell, 2022, 57, 820-836.e6.	3.1	37
3691	Extensive evaluation of ATAC-seq protocols for native or formaldehyde-fixed nuclei. BMC Genomics, 2022, 23, 214.	1.2	7
3693	Vitamin D and Its Target Genes. Nutrients, 2022, 14, 1354.	1.7	52
3694	Mapping the human kidney using single-cell genomics. Nature Reviews Nephrology, 2022, 18, 347-360.	4.1	34
3695	A combinatorial indexing strategy for low-cost epigenomic profiling of plant single cells. Plant Communications, 2022, 3, 100308.	3.6	10
3696	RNA Helicase DHX37 Facilitates Liver Cancer Progression by Cooperating with PLRG1 to Drive Superenhancer-Mediated Transcription of Cyclin D1. Cancer Research, 2022, 82, 1937-1952.	0.4	9
3697	Wt1 transcription factor impairs cardiomyocyte specification and drives a phenotypic switch from myocardium to epicardium. Development (Cambridge), 2022, 149, .	1.2	5
3698	Individual variation in buffalo somatic cell cloning efficiency is related to glycolytic metabolism. Science China Life Sciences, 2022, 65, 2076-2092.	2.3	4
3699	Integrating transcription-factor abundance with chromatin accessibility in human erythroid lineage commitment. Cell Reports Methods, 2022, 2, 100188.	1.4	9
3700	Multimodal Studies in Hepatitis B Virus Associated Hepatocellular Carcinoma. Infectious Diseases & Immunity, 2022, Publish Ahead of Print, .	0.2	0
3701	IL-17 Producing Lymphocytes Cause Dry Eye and Corneal Disease With Aging in RXRÎ± Mutant Mouse. Frontiers in Medicine, 2022, 9, 849990.	1.2	14
3702	HiCAR is a robust and sensitive method to analyze open-chromatin-associated genome organization. Molecular Cell, 2022, 82, 1225-1238.e6.	4.5	26
3703	Prediction of histone post-translational modification patterns based on nascent transcription data. Nature Genetics, 2022, 54, 295-305.	9.4	53
3704	Surveying the Epigenetic Landscape of Tuberculosis in Alveolar Macrophages. Infection and Immunity, 2022, 90, e0052221.	1.0	8
3705	Cell-Type Resolved Insights into the Cis-Regulatory Genome of NAFLD. Cells, 2022, 11, 870.	1.8	1
3706	Time-Course Transcriptional and Chromatin Accessibility Profiling Reveals Genes Associated With Asymmetrical Gonadal Development in Chicken Embryos. Frontiers in Cell and Developmental Biology, 2022, 10, 832132.	1.8	1
3707	Studying of Molecular Regulation of Developmental Processes of Lower Metazoans Exemplified by Cnidaria Using High-Throughput Sequencing. Biochemistry (Moscow), 2022, 87, 269-293.	0.7	0
3708	A robust mechanism for resetting juvenility during each generation in Arabidopsis. Nature Plants, 2022, 8, 257-268.	4.7	17

#	Article	IF	Citations
3709	Exosomal DEK removes chemoradiotherapy resistance by triggering quiescence exit of breast cancer stem cells. Oncogene, 2022, 41, 2624-2637.	2.6	8
3710	Shear stress switches the association of endothelial enhancers from ETV/ETS to KLF transcription factor binding sites. Scientific Reports, 2022, 12, 4795.	1.6	9
3711	Characterization of Accessible Chromatin Regions in Cattle Rumen Epithelial Tissue during Weaning. Genes, 2022, 13, 535.	1.0	4
3712	KLF15 cistromes reveal a hepatocyte pathway governing plasma corticosteroid transport and systemic inflammation. Science Advances, 2022, 8, eabj2917.	4.7	5
3713	HIF activation enhances FcÎ³RIIb expression on mononuclear phagocytes impeding tumor targeting antibody immunotherapy. Journal of Experimental and Clinical Cancer Research, 2022, 41, 131.	3.5	9
3714	The glucocorticoid receptor associates with the cohesin loader NIPBL to promote long-range gene regulation. Science Advances, 2022, 8, eabj8360.	4.7	18
3715	Immune disease variants modulate gene expression in regulatory CD4+ TÂcells. Cell Genomics, 2022, 2, 100117.	3.0	20
3716	Epigenetics in Ecology, Evolution, and Conservation. Frontiers in Ecology and Evolution, 2022, 10, .	1.1	9
3717	PPARdelta activation induces metabolic and contractile maturation of human pluripotent stem cell-derived cardiomyocytes. Cell Stem Cell, 2022, 29, 559-576.e7.	5.2	34
3718	Cytotoxic granzyme Câ€“expressing ILC1s contribute to antitumor immunity and neonatal autoimmunity. Science Immunology, 2022, 7, eabi8642.	5.6	47
3719	Optimization of the Omni-ATAC protocol to chromatin accessibility profiling in snap-frozen rat adipose and muscle tissues. MethodsX, 2022, 9, 101681.	0.7	1
3720	Comparative genomic analyses reveal cis-regulatory divergence after polyploidization in cotton. Crop Journal, 2022, , .	2.3	0
3722	Novel ZNF414 activity characterized by integrative analysis of ChIP-exo, ATAC-seq and RNA-seq data. Biochimica Et Biophysica Acta - Gene Regulatory Mechanisms, 2022, 1865, 194811.	0.9	1
3723	ZNF384 Fusion Oncoproteins Drive Lineage Aberrancy in Acute Leukemia. Blood Cancer Discovery, 2022, 3, 240-263.	2.6	11
3725	Integrative molecular roadmap for direct conversion of fibroblasts into myocytes and myogenic progenitor cells. Science Advances, 2022, 8, eabj4928.	4.7	10
3726	Cell-intrinsic Aryl Hydrocarbon Receptor signalling is required for the resolution of injury-induced colonic stem cells. Nature Communications, 2022, 13, 1827.	5.8	25
3727	Single-cell profiling of transcriptome and histone modifications with EpiDamID. Molecular Cell, 2022, 82, 1956-1970.e14.	4.5	28
3729	SWI/SNF chromatin remodeler complex within the reward pathway is required for behavioral adaptations to stress. Nature Communications, 2022, 13, 1807.	5.8	6

#	Article	IF	Citations
3732	Heads or tails: making the spinal cord. Developmental Biology, 2022, 485, 80-92.	0.9	2
3733	Epigenetic changes in Mycobacterium tuberculosis and its host provide potential targets or biomarkers for drug discovery and clinical diagnosis. Pharmacological Research, 2022, 179, 106195.	3.1	8
3734	Control of Foxp3 induction and maintenance by sequential histone acetylation and DNA demethylation. Cell Reports, 2021, 37, 110124.	2.9	13
3735	Clearing the Haze: How Does Nicotine Affect Hematopoiesis before and after Birth?. Cancers, 2022, 14, 184.	1.7	0
3736	Hierarchical regulation of the resting and activated T cell epigenome by major transcription factor families. Nature Immunology, 2022, 23, 122-134.	7.0	18
3737	Changes in chromatin accessibility landscape and histone H3 core acetylation during valproic acid-induced differentiation of embryonic stem cells. Epigenetics and Chromatin, 2021, 14, 58.	1.8	11
3738	Transcription factor-mediated intestinal metaplasia and the role of a shadow enhancer. Genes and Development, 2022, 36, 38-52.	2.7	11
3739	Profiling of open chromatin in developing pig (Sus scrofa) muscle to identify regulatory regions. G3: Genes, Genomes, Genetics, 2022, 12, .	0.8	13
3741	Epigenetic loss of heterogeneity from low to high grade localized prostate tumours. Nature Communications, 2021, 12, 7292.	5.8	15
3743	Aberrant chromatin landscape following loss of the H3.3 chaperone Daxx in haematopoietic precursors leads to Pu.1-mediated neutrophilia and inflammation. Nature Cell Biology, 2021, 23, 1224-1239.	4.6	10
3744	Accessible Region Conformation Capture (ARC-C) gives high-resolution insights into genome architecture and regulation. Genome Research, 2022, 32, 357-366.	2.4	6
3746	cLoops2: a full-stack comprehensive analytical tool for chromatin interactions. Nucleic Acids Research, 2022, 50, 57-71.	6.5	24
3747	5-Hydroxymethylcytosine-mediated active demethylation is required for mammalian neuronal differentiation and function. ELife, 2021, 10, .	2.8	21
3748	Comparative Enhancer Map of Cattle Muscle Genome Annotated by ATAC-Seq. Frontiers in Veterinary Science, 2021, 8, 782409.	0.9	8
3749	Mapping Chromatin Accessibility in Human NaÃ¯ve Pluripotent Stem Cells Using ATAC-Seq. Methods in Molecular Biology, 2022, 2416, 201-211.	0.4	0
3751	Bhlhe40 function in activated B and TFH cells restrains the GC reaction and prevents lymphomagenesis. Journal of Experimental Medicine, 2022, 219, .	4.2	17
3752	Pangenomics in crop improvementâ€"from coding structural variations to finding regulatory variants with pangenome graphs. Plant Genome, 2022, 15, e20177.	1.6	33
3753	KDM6B promotes activation of the oncogenic CDK4/6-pRB-E2F pathway by maintaining enhancer activity in MYCN-amplified neuroblastoma. Nature Communications, 2021, 12, 7204.	5.8	22

#	Article	IF	Citations
3756	Genome-wide association and functional interrogation identified a variant at 3p26.1 modulating ovarian cancer survival among Chinese women. Cell Discovery, 2021, 7, 121.	3.1	5
3758	Advances in singleâ€cell sequencing and its application to musculoskeletal system research. Cell Proliferation, 2022, 55, e13161.	2.4	3
3759	Parallel Single-Cell Multiomics Analysis of Neonatal Skin Reveals the Transitional Fibroblast States that Restrict Differentiation into Distinct Fates. Journal of Investigative Dermatology, 2022, 142, 1812-1823.e3.	0.3	27
3761	CoRE-ATAC: A deep learning model for the functional classification of regulatory elements from single cell and bulk ATAC-seq data. PLoS Computational Biology, 2021, 17, e1009670.	1.5	7
3762	Retinoic acid signaling drives differentiation toward the absorptive lineage in colorectal cancer. IScience, 2021, 24, 103444.	1.9	10
3763	The Reasonable Effectiveness of Randomness in Scalable and Integrative Gene Regulatory Network Inference and Beyond. Computation, 2021, 9, 146.	1.0	0
3765	One-pot universal NicE-seq: all enzymatic downstream processing of 4% formaldehyde crosslinked cells for chromatin accessibility genomics. Epigenetics and Chromatin, 2021, 14, 53.	1.8	3
3766	Mapping of Nonhomologous End Joining-Mediated Integration Facilitates Genome-Scale Trackable Mutagenesis in Yarrowia lipolytica. ACS Synthetic Biology, 2022, 11, 216-227.	1.9	14
3767	Single-Cell Sequencing and Its Applications in Liver Cancer. Frontiers in Oncology, 2022, 12, 857037.	1.3	11
3768	Sequential enhancer state remodelling defines human germline competence and specification. Nature Cell Biology, 2022, 24, 448-460.	4.6	27
3769	RNA polymerase II pausing factor NELF in CD8+ T cells promotes antitumor immunity. Nature Communications, 2022, 13, 2155.	5.8	7
3770	The Chromatin Accessibility Landscape of Nonalcoholic Fatty Liver Disease Progression. Molecules and Cells, 2022, 45, 343-352.	1.0	5
3771	Interactive single-cell data analysis using Cellar. Nature Communications, 2022, 13, 1998.	5.8	11
3773	Inferring mammalian tissue-specific regulatory conservation by predicting tissue-specific differences in open chromatin. BMC Genomics, 2022, 23, 291.	1.2	8
3774	CD45RA ⁺ CD62L ^{â^'} ILCs in human tissues represent a quiescent local reservoir for the generation of differentiated ILCs. Science Immunology, 2022, 7, eabj8301.	5.6	14
3777	The nuclear receptor ERR cooperates with the cardiogenic factor GATA4 to orchestrate cardiomyocyte maturation. Nature Communications, 2022, 13, 1991.	5.8	20
3778	Cell originâ€“dependent cooperativity of mutant Dnmt3a and Npm1 inÂclonal hematopoiesis and myeloid malignancy. Blood Advances, 2022, 6, 3666-3677.	2.5	8
3779	Emergence of novel cephalopod gene regulation and expression through large-scale genome reorganization. Nature Communications, 2022, 13, 2172.	5.8	21

#	Article	IF	Citations
3780	rDNA array length is a major determinant of replicative lifespan in budding yeast. Proceedings of the National Academy of Sciences of the United States of America, 2022, 119, e2119593119.	3.3	23
3781	Rewiring of 3D Chromatin Topology Orchestrates Transcriptional Reprogramming and the Development of Human Dilated Cardiomyopathy. Circulation, 2022, 145, 1663-1683.	1.6	15
3782	Multidimensional chromatin profiling of zebrafish pancreas to uncover and investigate disease-relevant enhancers. Nature Communications, 2022, 13, 1945.	5.8	5
3783	BRD2 compartmentalizes the accessible genome. Nature Genetics, 2022, 54, 481-491.	9.4	29
3784	The TH1 cell lineage-determining transcription factor T-bet suppresses TH2 gene expression by redistributing GATA3 away from TH2 genes. Nucleic Acids Research, 2022, 50, 4557-4573.	6.5	16
3785	Optimized assay for transposase-accessible chromatin by sequencing (ATAC-seq) library preparation from adult Drosophila melanogaster neurons. Scientific Reports, 2022, 12, 6043.	1.6	5
3786	Identification of the accessible chromatin regions in six tissues in the soybean. Genomics, 2022, 114, 110364.	1.3	7
3851	The mitochondrial pyruvate carrier regulates memory TÂcell differentiation and antitumor function. Cell Metabolism, 2022, 34, 731-746.e9.	7.2	63
3852	Ablation of Proton/Glucose Exporter SLC45A2 Enhances Melanosomal Glycolysis to Inhibit Melanin Biosynthesis and Promote Melanoma Metastasis. Journal of Investigative Dermatology, 2022, 142, 2744-2755.e9.	0.3	5
3853	The nuclear receptor THRB facilitates differentiation of human PSCs into more mature hepatocytes. Cell Stem Cell, 2022, 29, 795-809.e11.	5.2	5
3854	Argonaute proteins regulate a specific network of genes through KLF4 in mouse embryonic stem cells. Stem Cell Reports, 2022, 17, 1070-1080.	2.3	2
3855	Cell-lineage controlled epigenetic regulation in glioblastoma stem cells determines functionally distinct subgroups and predicts patient survival. Nature Communications, 2022, 13, 2236.	5.8	7
3856	Dynamic transcriptional activity and chromatin remodeling of regulatory T cells after varied duration of interleukin-2 receptor signaling. Nature Immunology, 2022, 23, 802-813.	7.0	13
3857	KMT2C deficiency promotes small cell lung cancer metastasis through DNMT3A-mediated epigenetic reprogramming. Nature Cancer, 2022, 3, 753-767.	5.7	41
3858	Screening of ETO2-GLIS2â€“induced Super Enhancers identifies targetable cooperative dependencies in acute megakaryoblastic leukemia. Science Advances, 2022, 8, eabg9455.	4.7	9
3859	DExD/H-box helicase 9 intrinsically controls CD8 ⁺ T cellâ€“mediated antiviral response through noncanonical mechanisms. Science Advances, 2022, 8, eabk2691.	4.7	11
3862	TFAM loss induces nuclear actin assembly upon mDia2 malonylation to promote liver cancer metastasis. EMBO Journal, 2022, 41, e110324.	3.5	24
3863	Intrinsic Differences between the Open Chromatin Regions of Oral and Epidermal Keratinocytes. Chinese journal of dental research: the official journal of the Scientific Section of the Chinese Stomatological Association (CSA), The, 2020, 23, 119-130.	0.1	1

#	Article	IF	Citations
3864	Multi-omics Approaches in Insect-Plant Interactions. , 2022, , 335-368.		2
3865	Exploring Chromatin Accessibility in Mouse Epiblast Stem Cells with ATAC-Seq. Methods in Molecular Biology, 2022, 2490, 93-100.	0.4	0
3866	Deciphering comparative and structural variation that regulates abiotic stress response. , 2022, , 561-586.		0
3867	Epigenetics, Enhancer Function and 3D Chromatin Organization in Reprogramming to Pluripotency. Cells, 2022, 11, 1404.	1.8	4
3868	Comparative methylomics and chromatin accessibility analysis in Osmanthus fragrans uncovers regulation of genic transcription and mechanisms of key floral scent production. Horticulture Research, 2022, 9, .	2.9	10
3871	Succinate dehydrogenase/complex II is critical for metabolic and epigenetic regulation of T cell proliferation and inflammation. Science Immunology, 2022, 7, eabm8161.	5.6	23
3872	Natural and Experimental Rewiring of Gene Regulatory Regions. Annual Review of Genomics and Human Genetics, 2022, 23, .	2.5	1
3873	A high-resolution route map reveals distinct stages of chondrocyte dedifferentiation for cartilage regeneration. Bone Research, 2022, 10, 38.	5.4	13
3874	Exploring epigenetic reprogramming during central nervous system infection. Immunological Reviews, 2022, 311, 112-129.	2.8	7
3875	EWSR1-ATF1 dependent 3D connectivity regulates oncogenic and differentiation programs in Clear Cell Sarcoma. Nature Communications, 2022, 13, 2267.	5.8	18
3876	Regulation of chromatin accessibility by the histone chaperone CAF-1 sustains lineage fidelity. Nature Communications, 2022, 13, 2350.	5.8	8
3877	InÂvivo partial cellular reprogramming enhances liver plasticity and regeneration. Cell Reports, 2022, 39, 110730.	2.9	41
3878	T cell receptor and IL-2 signaling strength control memory CD8+ T cell functional fitness via chromatin remodeling. Nature Communications, 2022, 13, 2240.	5.8	17
3879	Galaxy Dnpatterntools for Computational Analysis of Nucleosome Positioning Sequence Patterns. International Journal of Molecular Sciences, 2022, 23, 4869.	1.8	0
3880	Epigenetic Regulation of Endothelial Cell Lineages During Zebrafish Developmentâ€"New Insights From Technical Advances. Frontiers in Cell and Developmental Biology, 2022, 10, .	1.8	1
3882	Chromatin accessibility profiling by ATAC-seq. Nature Protocols, 2022, 17, 1518-1552.	5.5	105
3883	C/EBPÎ´-induced epigenetic changes control the dynamic gene transcription of S100a8 and S100a9. ELife, 2022, 11, .	2.8	8
3884	Inositol polyphosphate multikinase physically binds to the SWI/SNF complex and modulates BRG1 occupancy in mouse embryonic stem cells. ELife, 2022, 11, .	2.8	5

#	Article	IF	Citations
3886	FOXO Dictates Initiation of B Cell Development and Myeloid Restriction in Common Lymphoid Progenitors. Frontiers in Immunology, 2022, 13, .	2.2	4
3887	FTO mediates LINE1 m ⁶ A demethylation and chromatin regulation in mESCs and mouse development. Science, 2022, 376, 968-973.	6.0	97
3889	Inhibition of pyrimidine biosynthesis targets protein translation in acute myeloid leukemia. EMBO Molecular Medicine, 2022, 14, e15203.	3.3	10
3890	Gene regulatory networks shape developmental plasticity of root cell types under water extremes in rice. Developmental Cell, 2022, 57, 1177-1192.e6.	3.1	27
3891	Wnt11 acts on dermomyotome cells to guide epaxial myotome morphogenesis. ELife, 2022, 11, .	2.8	7
3892	The investigation of sexâ€differential open chromatin in liver, spleen and gonads in Larimichthys crocea through <scp>ATAC</scp> â€seq. Aquaculture Research, 0, , .	0.9	0
3893	Bringing machine learning to research on intellectual and developmental disabilities: taking inspiration from neurological diseases. Journal of Neurodevelopmental Disorders, 2022, 14, 28.	1.5	9
3894	A long non-coding RNA as a direct vitamin D target transcribed from the antisense strand of the human HSD17B2 locus. Bioscience Reports, 2022, 42, .	1.1	2
3895	Enhancer selection dictates gene expression responses in remote organs during tissue regeneration. Nature Cell Biology, 2022, 24, 685-696.	4.6	22
3896	ETV2 functions as a pioneer factor to regulate and reprogram the endothelial lineage. Nature Cell Biology, 2022, 24, 672-684.	4.6	25
3898	Resistance of Sogatella furcifera to triflumezopyrim mediated with the overexpression of CYPSF01 which was regulated by nuclear receptor USP. Ecotoxicology and Environmental Safety, 2022, 238, 113575.	2.9	12
3899	Antagonistic action of a synthetic androgen ligand mediated by chromatin remodeling in a human prostate cancer cell line. Biochemical and Biophysical Research Communications, 2022, 612, 110-118.	1.0	4
3901	Functional Characterization of Genetic Variant Effects on Expression. Annual Review of Biomedical Data Science, 2022, 5, 119-139.	2.8	7
3902	PRDM1 Drives Human Primary T Cell Hyporesponsiveness by Altering the T Cell Transcriptome and Epigenome. Frontiers in Immunology, 2022, 13, 879501.	2.2	4
3903	Epigenetic regulation of innate immune memory in microglia. Journal of Neuroinflammation, 2022, 19, 111.	3.1	30
3904	Mapping Human Reproduction with Single-Cell Genomics. Annual Review of Genomics and Human Genetics, 2022, 23, 523-547.	2.5	5
3905	A conserved YAP/Notch/REST network controls the neuroendocrine cell fate in the lungs. Nature Communications, 2022, 13, 2690.	5.8	19
3906	Machine learning: its challenges and opportunities in plant system biology. Applied Microbiology and Biotechnology, 2022, 106, 3507-3530.	1.7	26

#	Article	IF	Citations
3907	Machine learning sequence prioritization for cell type-specific enhancer design. ELife, 2022, 11, .	2.8	10
3908	The Nuclear DNA Sensor IFI16 Indiscriminately Binds to and Diminishes Accessibility of the HSV-1 Genome to Suppress Infection. MSystems, 2022, 7, e0019822.	1.7	5
3909	Preliminary Interpretations of Epigenetic Profiling of Cord Blood in Preeclampsia. Genes, 2022, 13, 888.	1.0	0
3910	Developments in high-throughput functional epigenomics: CRISPR-single-cell assay for transposase-accessible chromatin using sequencing screens. Epigenomics, 2022, , .	1.0	0
3911	Temporal perturbation of histone deacetylase activity reveals a requirement for HDAC1â€“3 in mesendoderm cell differentiation. Cell Reports, 2022, 39, 110818.	2.9	0
3912	Multiomics Analysis Identifies SOCS1 as Restraining T Cell Activation and Preventing Graftâ€Versusâ€Host Disease. Advanced Science, 2022, 9, e2200978.	5.6	7
3913	Single-nucleus chromatin accessibility profiling highlights regulatory mechanisms of coronary artery disease risk. Nature Genetics, 2022, 54, 804-816.	9.4	51
3914	Histone H3.3 K27M chromatin functions implicate a network of neurodevelopmental factors including ASCL1 and NEUROD1 in DIPG. Epigenetics and Chromatin, 2022, 15, 18.	1.8	9
3915	TFAP2 paralogs facilitate chromatin access for MITF at pigmentation and cell proliferation genes. PLoS Genetics, 2022, 18, e1010207.	1.5	13
3920	Divergent transcriptional regulation of astrocyte reactivity across disorders. Nature, 2022, 606, 557-564.	13.7	69
3922	Extrachromosomal DNA in Cancer. Annual Review of Genomics and Human Genetics, 2022, 23, 29-52.	2.5	16
3923	Oct4 differentially regulates chromatin opening and enhancer transcription in pluripotent stem cells. ELife, 0, 11, .	2.8	15
3925	Comprehensive assessment of differential ChIP-seq tools guides optimal algorithm selection. Genome Biology, 2022, 23, .	3.8	5
3927	Chromosome organization affects genome evolution in Sulfolobus archaea. Nature Microbiology, 2022, 7, 820-830.	5.9	12
3929	Understanding of the various aspects of gene regulatory networks related to crop improvement. Gene, 2022, 833, 146556.	1.0	1
3931	Localization Matters: Epigenetic Regulation of Natural Killer Cells in Different Tissue Microenvironments. Frontiers in Immunology, 0, 13, .	2.2	2
3932	Mapping cis-regulatory elements in human neurons links psychiatric disease heritability and activity-regulated transcriptional programs. Cell Reports, 2022, 39, 110877.	2.9	12
3933	Î³Î´ TÂcells license immature B cells to produce a broad range of polyreactive antibodies. Cell Reports, 2022, 39, 110854.	2.9	4

#	Article	IF	Citations
3936	Harnessing changes in open chromatin determined by ATAC-seq to generate insulin-responsive reporter constructs. BMC Genomics, 2022, 23, .	1.2	11
3937	The Dynamics of Chromatin Accessibility Prompted by Butyrate-Induced Chromatin Modification in Bovine Cells. Ruminants, 2022, 2, 226-243.	0.4	2
3938	Investigating chromatin accessibility during development and differentiation by ATAC-sequencing to guide the identification of cis-regulatory elements. Biochemical Society Transactions, 2022, 50, 1167-1177.	1.6	3
3940	Profiling the quantitative occupancy of myriad transcription factors across conditions by modeling chromatin accessibility data. Genome Research, 2022, 32, 1183-1198.	2.4	1
3941	Epigenetic regulation of T cell exhaustion. Nature Immunology, 2022, 23, 848-860.	7.0	82
3944	Binary outcomes of enhancer activity underlie stable random monoallelic expression. ELife, 0, 11, .	2.8	3
3947	Integration of ATAC-Seq and RNA-Seq identifies the key genes in myocardial ischemia. Genes and Diseases, 2023, 10, 62-64.	1.5	0
3950	Leveraging transcriptome and epigenome landscapes to infer regulatory networks during the onset of sexual maturation. BMC Genomics, 2022, 23, .	1.2	3
3951	Dietary intervention preserves Î² cell function in mice through CTCF-mediated transcriptional reprogramming. Journal of Experimental Medicine, 2022, 219, .	4.2	16
3952	A systems biology approach identifies candidate drugs to reduce mortality in severely ill patients with COVID-19. Science Advances, 2022, 8, .	4.7	14
3953	The SWI/SNF ATPase BRG1 facilitates multiple pro-tumorigenic gene expression programs in SMARCB1-deficient cancer cells. Oncogenesis, 2022, 11, .	2.1	5
3954	Nuclear RIPK1 promotes chromatin remodeling to mediate inflammatory response. Cell Research, 2022, 32, 621-637.	5.7	18
3955	Future directions for precision oncology in prostate cancer. Prostate, 2022, 82, .	1.2	2
3959	Chromatin accessibility analysis from fresh and cryopreserved human ovarian follicles. Molecular Human Reproduction, 2022, 28, .	1.3	2
3962	Recapitulating early human development with 8C-like cells. Cell Reports, 2022, 39, 110994.	2.9	26
3963	Analysis of estrogen-regulated enhancer RNAs identifies a functional motif required for enhancer assembly and gene expression. Cell Reports, 2022, 39, 110944.	2.9	9
3964	Virtual ChIP-seq: predicting transcription factor binding by learning from the transcriptome. Genome Biology, 2022, 23, .	3.8	14
3965	<scp>TDTHub</scp>, a web server tool for the analysis of transcription factor binding sites in plants. Plant Journal, 2022, 111, 1203-1215.	2.8	5

#	Article	IF	Citations
3967	ARID1B, a molecular suppressor of erythropoiesis, is essential for the prevention of Mongeâ€™s disease. Experimental and Molecular Medicine, 2022, 54, 777-787.	3.2	6
3968	Inhibition of a Chromatin and Transcription Modulator, SLTM, Increases HIV-1 Reactivation Identified by a CRISPR Inhibition Screen. Journal of Virology, 2022, 96, .	1.5	7
3969	Comparative parallel multi-omics analysis during the induction of pluripotent and trophectoderm states. Nature Communications, 2022, 13, .	5.8	4
3970	The chromatin remodeller ATRX facilitates diverse nuclear processes, in a stochastic manner, in both heterochromatin and euchromatin. Nature Communications, 2022, 13, .	5.8	20
3971	Advancements in Genomic and Behavioral Neuroscience Analysis for the Study of Normal and Pathological Brain Function. Frontiers in Molecular Neuroscience, 0, 15, .	1.4	0
3973	Phosphorylation-dependent association of human chromatin protein PC4 to linker histone H1 regulates genome organization and transcription. Nucleic Acids Research, 2022, 50, 6116-6136.	6.5	4
3974	Exploitation of epigenetic variation of crop wild relatives for crop improvement and agrobiodiversity preservation. Theoretical and Applied Genetics, 2022, 135, 3987-4003.	1.8	7
3975	Gastric cancer and genomics: review of literature. Journal of Gastroenterology, 2022, 57, 505-516.	2.3	19
3978	YAP1 maintains active chromatin state in head and neck squamous cell carcinomas that promotes tumorigenesis through cooperation with BRD4. Cell Reports, 2022, 39, 110970.	2.9	18
3980	Optimization and validation of CAR transduction into human primary NK cells using CRISPR and AAV. Cell Reports Methods, 2022, 2, 100236.	1.4	19
3981	Advances in Single-Cell Multi-Omics and Application in Cardiovascular Research. Frontiers in Cell and Developmental Biology, 0, 10, .	1.8	5
3982	TCF-1 promotes chromatin interactions across topologically associating domains in T cell progenitors. Nature Immunology, 2022, 23, 1052-1062.	7.0	25
3984	Single-Cell Sequencing on Marine Life: Application and Future Development. Frontiers in Marine Science, 0, 9, .	1.2	1
3985	Foxa2 and Pet1 Direct and Indirect Synergy Drive Serotonergic Neuronal Differentiation. Frontiers in Neuroscience, 0, 16, .	1.4	1
3986	Nucleome programming is required for the foundation of totipotency in mammalian germline development. EMBO Journal, 2022, 41, .	3.5	9
3987	Single-cell transcriptome and accessible chromatin dynamics during endocrine pancreas development. Proceedings of the National Academy of Sciences of the United States of America, 2022, 119, .	3.3	20
3989	Genome-Wide Analysis of Yeast Metabolic Cycle through Metabolic Network Models Reveals Superiority of Integrated ATAC-seq Data over RNA-seq Data. MSystems, 2022, 7, .	1.7	1
3991	Nuclear receptor RORÎ³ inverse agonists/antagonists display tissue- and gene-context selectivity through distinct activities in altering chromatin accessibility and master regulator SREBP2 occupancy. Pharmacological Research, 2022, 182, 106324.	3.1	5

#	Article	IF	Citations
3992	Multifaceted regulation of enhancers in cancer. Biochimica Et Biophysica Acta - Gene Regulatory Mechanisms, 2022, 1865, 194839.	0.9	2
3993	Chromatin accessibility of Meyerozyma guilliermondii under patulin stress. Biological Control, 2022, 172, 104974.	1.4	3
3994	Biological insights into systemic lupus erythematosus through an immune cell-specific transcriptome-wide association study. Annals of the Rheumatic Diseases, 2022, 81, 1273-1280.	0.5	9
3996	Single-cell sequencing: expansion, integration and translation. Briefings in Functional Genomics, 2022, 21, 280-295.	1.3	7
3997	CD8+T cell responsiveness to anti-PD-1 is epigenetically regulated by Suv39h1 in melanomas. Nature Communications, 2022, 13, .	5.8	11
3998	Developmental and evolutionary comparative analysis of a regulatory landscape in mouse and chicken. Development (Cambridge), 2022, 149, .	1.2	3
3999	The era of 3D and spatial genomics. Trends in Genetics, 2022, 38, 1062-1075.	2.9	25
4001	Core transcription programs controlling injury-induced neurodegeneration of retinal ganglion cells. Neuron, 2022, 110, 2607-2624.e8.	3.8	45
4002	ATAC-Seq Optimization for Cancer Epigenetics Research. Journal of Visualized Experiments, 2022, , .	0.2	2
4003	A single-cell map of dynamic chromatin landscapes of immune cells in renal cell carcinoma. Nature Cancer, 2022, 3, 885-898.	5.7	20
4004	Epigenetic Reprogramming Leads to Downregulation of CD4 and Functional Changes in African Green Monkey Memory CD4+ T Cells. Journal of Immunology, 2022, 209, 337-345.	0.4	2
4005	Multi-omic comparisons between CFBE41o- cells stably expressing wild-type CFTR and F508del-mutant CFTR. Journal of Cystic Fibrosis, 2023, 22, 146-155.	0.3	3
4006	Divergent expression of paralogous genes by modification of shared enhancer activity through a promoter-proximal silencer. Current Biology, 2022, 32, 3545-3555.e4.	1.8	12
4007	Multiomic atlas with functional stratification and developmental dynamics of zebrafish cis-regulatory elements. Nature Genetics, 2022, 54, 1037-1050.	9.4	26
4008	The role of toll-like receptors (TLRs) in pan-cancer. Annals of Medicine, 2022, 54, 1918-1937.	1.5	4
4009	Sox8 remodels the cranial ectoderm to generate the ear. Proceedings of the National Academy of Sciences of the United States of America, 2022, 119, .	3.3	7
4010	Cell cycle arrest explains the observed bulk 3D genomic alterations in response to long-term heat shock in K562 cells. Genome Research, 0, , .	2.4	0
4011	Epigenetic Memories in Hematopoietic Stem and Progenitor Cells. Cells, 2022, 11, 2187.	1.8	3

#	Article	IF	Citations
4014	Identification of enhancers responsible for the coordinated expression of myosin heavy chain isoforms in skeletal muscle. BMC Genomics, 2022, 23, .	1.2	6
4015	Genome-wide identification of functional enhancers and their potential roles in pig breeding. Journal of Animal Science and Biotechnology, 2022, 13, .	2.1	3
4016	Gene-Regulatory Network Study of Rheumatoid Arthritis in Single-Cell Chromatin Landscapes of Peripheral Blood Mononuclear Cells. Modern Rheumatology, 0, , .	0.9	1
4017	Cis-regulatory chromatin loops analysis identifies GRHL3 as a master regulator of surface epithelium commitment. Science Advances, 2022, 8, .	4.7	3
4018	CRISPR screening uncovers a central requirement for HHEX in pancreatic lineage commitment and plasticity restriction. Nature Cell Biology, 2022, 24, 1064-1076.	4.6	15
4019	Heme as a differentiation-regulatory transcriptional cofactor. International Journal of Hematology, 2022, 116, 174-181.	0.7	3
4020	Inhibition of Cancer Cell Migration and Glycolysis by Terahertz Wave Modulation via Altered Chromatin Accessibility. Research, 2022, 2022, .	2.8	8
4021	Characterizing cis-regulatory elements using single-cell epigenomics. Nature Reviews Genetics, 2023, 24, 21-43.	7.7	72
4022	Applications of singleâ€cell multiâ€omics sequencing in deep understanding of brain diseases. Clinical and Translational Discovery, 2022, 2, .	0.2	0
4023	RPA1 controls chromatin architecture and maintains lipid metabolic homeostasis. Cell Reports, 2022, 40, 111071.	2.9	6
4024	Dissecting the treatment-naive ecosystem of human melanoma brain metastasis. Cell, 2022, 185, 2591-2608.e30.	13.5	62
4025	Targeting KDM4 for treating PAX3-FOXO1â€“driven alveolar rhabdomyosarcoma. Science Translational Medicine, 2022, 14, .	5.8	16
4028	Benchmarking of ATAC Sequencing Data From BGIâ€™s Low-Cost DNBSEQ-G400 Instrument for Identification of Open and Occupied Chromatin Regions. Frontiers in Molecular Biosciences, 0, 9, .	1.6	2
4029	Exploring the significance of <scp>PAK1</scp> through chromosome conformation signatures in ibrutinibâ€resistant chronic lymphocytic leukaemia. Molecular Oncology, 2022, 16, 2920-2935.	2.1	3
4031	Plant synthetic epigenomic engineering for crop improvement. Science China Life Sciences, 2022, 65, 2191-2204.	2.3	9
4032	TGFÎ² reprograms TNF stimulation of macrophages towards a non-canonical pathway driving inflammatory osteoclastogenesis. Nature Communications, 2022, 13, .	5.8	21
4033	Inactivation of Sirt6 ameliorates muscular dystrophy in mdx mice by releasing suppression of utrophin expression. Nature Communications, 2022, 13, .	5.8	6
4034	Techniques for Profiling the Cellular Immune Response and Their Implications for Interventional Oncology. Cancers, 2022, 14, 3628.	1.7	4

#	Article	IF	Citations
4035	Large-scale manipulation of promoter DNA methylation reveals context-specific transcriptional responses and stability. Genome Biology, 2022, 23, .	3.8	25
4036	The Landscape of Liver Chromatin Accessibility and Conserved Non-coding Elements in Larimichthys crocea, Nibea albiflora, and Lateolabrax maculatus. Marine Biotechnology, 0, , .	1.1	0
4038	Integration of ATAC-seq and RNA-seq identifies active G-protein coupled receptors functioning in molting process in muscle of Eriocheir sinensis. Frontiers in Marine Science, 0, 9, .	1.2	3
4039	Sex-biased and parental allele-specific gene regulation by KDM6A. Biology of Sex Differences, 2022, 13, .	1.8	10
4041	Molecular Regulation of Skeletal Muscle Stem Cells. , 2022, , .		0
4044	SOX9 reprograms endothelial cells by altering the chromatin landscape. Nucleic Acids Research, 2022, 50, 8547-8565.	6.5	12
4045	Joint analysis of scATAC-seq datasets using epiConv. BMC Bioinformatics, 2022, 23, .	1.2	1
4047	Lineage-specific rearrangement of chromatin loops and epigenomic features during adipocytes and osteoblasts commitment. Cell Death and Differentiation, 2022, 29, 2503-2518.	5.0	9
4048	Tracing the Origin of Cell-Free DNA Molecules through Tissue-Specific Epigenetic Signatures. Diagnostics, 2022, 12, 1834.	1.3	14
4049	Tumor-intrinsic PRC2 inactivation drives a context-dependent immune-desert microenvironment and is sensitized by immunogenic viruses. Journal of Clinical Investigation, 2022, 132, .	3.9	8
4050	Neuro-immune interactions at single-cell resolution in neurodevelopmental, infectious, and neurodegenerative diseases. Animal Cells and Systems, 2022, 26, 137-147.	0.8	5
4051	ATAC-STARR-seq reveals transcription factorâ€“bound activators and silencers within chromatin-accessible regions of the human genome. Genome Research, 2022, 32, 1529-1541.	2.4	14
4052	The HDAC7â€“TET2 epigenetic axis is essential during early B lymphocyte development. Nucleic Acids Research, 2022, 50, 8471-8490.	6.5	4
4053	Loss of Monoallelic Expression of IGF2 in the Adult Liver Via Alternative Promoter Usage and Chromatin Reorganization. Frontiers in Genetics, 0, 13, .	1.1	4
4054	Human T-bet governs the generation of a distinct subset of CD11c ^{high} CD21 ^{low} B cells. Science Immunology, 2022, 7, .	5.6	33
4057	Genomeâ€wide survey of open chromatin regions in two swallowtail butterflies Papilio machaon Âand P. bianor. Archives of Insect Biochemistry and Physiology, 0, , .	0.6	0
4058	Etv2 regulates enhancer chromatin status to initiate Shh expression in the limb bud. Nature Communications, 2022, 13, .	5.8	7
4059	â€œStripeâ€•transcription factors provide accessibility to co-binding partners in mammalian genomes. Molecular Cell, 2022, 82, 3398-3411.e11.	4.5	20

#	Article	IF	Citations
4060	Chromatin accessibility landscape and active transcription factors in primary human invasive lobular and ductal breast carcinomas. Breast Cancer Research, 2022, 24, .	2.2	1
4062	Chromatin Dynamics in Digestive System Cancer: Commander and Regulator. Frontiers in Oncology, 0, 12, .	1.3	1
4063	TET enzymes regulate skeletal development through increasing chromatin accessibility of RUNX2 target genes. Nature Communications, 2022, 13, .	5.8	12
4064	The developmental impacts of natural selection on human pelvic morphology. Science Advances, 2022, 8, .	4.7	9
4067	Temporally divergent regulatory mechanisms govern neuronal diversification and maturation in the mouse and marmoset neocortex. Nature Neuroscience, 2022, 25, 1049-1058.	7.1	16
4068	Multi-omics analysis of naÃ¯ve B cells of patients harboring the C104R mutation in TACI. Frontiers in Immunology, 0, 13, .	2.2	2
4070	NetTIME: a Multitask and Base-pair Resolution Framework for Improved Transcription Factor Binding Site Prediction. Bioinformatics, 0, , .	1.8	1
4071	Adrenergic receptor signaling induced by Klf15, a regulator of regeneration enhancer, promotes kidney reconstruction. Proceedings of the National Academy of Sciences of the United States of America, 2022, 119, .	3.3	7
4072	Elucidation of insecticide resistance mechanisms using NGS and future prospects. Japanese Journal of Pesticide Science, 2022, 47, 93-98.	0.0	0
4074	Lactate is an epigenetic metabolite that drives survival in model systems of glioblastoma. Molecular Cell, 2022, 82, 3061-3076.e6.	4.5	29
4077	A SOX2-engineered epigenetic silencer factor represses the glioblastoma genetic program and restrains tumor development. Science Advances, 2022, 8, .	4.7	6
4078	TET proteins regulate T cell and iNKT cell lineage specification in a TET2 catalytic dependent manner. Frontiers in Immunology, 0, 13, .	2.2	6
4079	BindVAE: Dirichlet variational autoencoders for de novo motif discovery from accessible chromatin. Genome Biology, 2022, 23, .	3.8	4
4081	Comparative functional genomics identifies unique molecular features of EPSCs. Life Science Alliance, 2022, 5, e202201608.	1.3	3
4082	Î²BÎ¶ controls IL-17-triggered gene expression program in intestinal epithelial cells that restricts colonization of SFB and prevents Th17-associated pathologies. Mucosal Immunology, 2022, 15, 1321-1337.	2.7	2
4083	EHMT2 methyltransferase governs cell identity in the lung and is required for KRAS G12D tumor development and propagation. ELife, 0, 11, .	2.8	1
4084	Global chromatin accessibility profiling analysis reveals a chronic activation state in aged muscle stem cells. IScience, 2022, 25, 104954.	1.9	13
4085	KLF4 recruits SWI/SNF to increase chromatin accessibility and reprogram the endothelial enhancer landscape under laminar shear stress. Nature Communications, 2022, 13, .	5.8	21

#	Article	IF	Citations
4086	Phase separation in epigenetics and cancer stem cells. Frontiers in Oncology, 0, 12, .	1.3	3
4088	FFPEâ€ATAC: A Highly Sensitive Method for Profiling Chromatin Accessibility in Formalinâ€Fixed Paraffinâ€Embedded Samples. Current Protocols, 2022, 2, .	1.3	4
4089	Transcriptional regulation of the thymus master regulator Foxn1. Science Immunology, 2022, 7, .	5.6	6
4090	PI3K signaling specifies proximal-distal fate by driving a developmental gene regulatory network in SOX9+ mouse lung progenitors. ELife, 0, 11, .	2.8	8
4091	Global changes in chromatin accessibility and transcription in growth hormone-secreting pituitary adenoma. Endocrine, 2022, 78, 329-342.	1.1	1
4092	Three distinctAtoh1enhancers cooperate for sound receptor hair cell development. Proceedings of the National Academy of Sciences of the United States of America, 2022, 119, .	3.3	14
4093	Multiomic Analysis of Neurons with Divergent Projection Patterns Identifies Novel Regulators of Axon Pathfinding. Advanced Science, 2022, 9, .	5.6	8
4094	The transcription factor Cdx2 regulates inflammasome activity through expression of the NLRP3 suppressor TRIM31 to maintain intestinal homeostasis. Journal of Biological Chemistry, 2022, 298, 102386.	1.6	5
4096	Comparative chromatin accessibility upon BDNF stimulation delineates neuronal regulatory elements. Molecular Systems Biology, 2022, 18, .	3.2	7
4097	KLF5 governs sphingolipid metabolism and barrier function of the skin. Genes and Development, 2022, 36, 822-842.	2.7	5
4098	Transcriptomics, regulatory syntax, and enhancer identification in mesoderm-induced ESCs at single-cell resolution. Cell Reports, 2022, 40, 111219.	2.9	8
4099	Spatial profiling of chromatin accessibility in mouse and human tissues. Nature, 2022, 609, 375-383.	13.7	119
4100	Single-nucleus chromatin accessibility profiling highlights distinct astrocyte signatures in progressive supranuclear palsy and corticobasal degeneration. Acta Neuropathologica, 2022, 144, 615-635.	3.9	4
4101	Targeting histone methylation to reprogram the transcriptional state that drives survival of drug-tolerant myeloid leukemia persisters. IScience, 2022, 25, 105013.	1.9	6
4102	Identification of putative enhancer-like elements predicts regulatory networks active in planarian adult stem cells. ELife, 0, 11, .	2.8	9
4104	Deficiency of WTAP in hepatocytes induces lipoatrophy and non-alcoholic steatohepatitis (NASH). Nature Communications, 2022, 13, .	5.8	13
4106	Radiation target: Moving from theory to practice. , 2022, 1, 100024.		0
4107	Epigenomics of rats' liver and its cross-species functional annotation reveals key regulatory genes underlying short term heat-stress response. Genomics, 2022, 114, 110449.	1.3	4

#	Article	IF	Citations
4108	Polyvinyl alcohol/gelatin hydrogels regulate cell adhesion and chromatin accessibility. International Journal of Biological Macromolecules, 2022, 219, 672-684.	3.6	6
4109	Inhibition of Arid1a increases stem/progenitor cell-like properties of liver cancer. Cancer Letters, 2022, 546, 215869.	3.2	4
4110	mTORC1 is required for epigenetic silencing during Î²-cell functional maturation. Molecular Metabolism, 2022, 64, 101559.	3.0	7
4113	Early anteroposterior regionalisation of human neural crest is shaped by a pro-mesodermal factor. ELife, 0, 11, .	2.8	6
4116	A butterfly pan-genome reveals that a large amount of structural variation underlies the evolution of chromatin accessibility. Genome Research, 2022, 32, 1862-1875.	2.4	10
4117	Distinct Cell Adhesion Signature Defines Glioblastoma Myeloid-Derived Suppressor Cell Subsets. Cancer Research, 2022, 82, 4274-4287.	0.4	11
4119	Plant Epigenomics. , 2023, , 263-286.		3
4120	Genomic Insights into Non-steroidal Nuclear Receptors in Prostate and Breast Cancer. Advances in Experimental Medicine and Biology, 2022, , 227-239.	0.8	2
4121	Regeneration and Developmental Enhancers are Differentially Compatible with Minimal Promoters. SSRN Electronic Journal, 0, , .	0.4	0
4122	Useful methods to study epigenetic marks: DNA methylation, histone modifications, chromatin structure, and noncoding RNAs. , 2022, , 283-310.		1
4123	Decoding mechanism of action and sensitivity to drug candidates from integrated transcriptome and chromatin state. ELife, 0, 11, .	2.8	3
4124	Integrated Analysis of Transcriptome, microRNAs, and Chromatin Accessibility Revealed Potential Early B-Cell Factor1-Regulated Transcriptional Networks during the Early Development of Fetal Brown Adipose Tissues in Rabbits. Cells, 2022, 11, 2675.	1.8	1
4125	WhichTF is functionally important in your open chromatin data?. PLoS Computational Biology, 2022, 18, e1010378.	1.5	33
4126	Rapid in vivo multiplexed editing (RIME) of the adult mouse liver. Hepatology, 2023, 78, 486-502.	3.6	5
4128	The Landscape of Accessible Chromatin during Yak Adipocyte Differentiation. International Journal of Molecular Sciences, 2022, 23, 9960.	1.8	4
4129	Changes in chromatin accessibility are not concordant with transcriptional changes for singleâ€factor perturbations. Molecular Systems Biology, 2022, 18, .	3.2	22
4130	Function and mechanism of histone Î²-hydroxybutyrylation in health and disease. Frontiers in Immunology, 0, 13, .	2.2	19
4132	Librarian: A quality control tool to analyse sequencing library compositions. F1000Research, 0, 11, 1122.	0.8	2

#	Article	IF	Citations
4133	Runx2 regulates chromatin accessibility to direct the osteoblast program at neonatal stages. Cell Reports, 2022, 40, 111315.	2.9	12
4135	Integrating ATAC-seq and RNA-seq Reveals the Dynamics of Chromatin Accessibility and Gene Expression in Apple Response to Drought. International Journal of Molecular Sciences, 2022, 23, 11191.	1.8	12
4140	A Unique Glimpse into the Crosstalk Between Different Epigenetic Mechanisms in Porcine Embryonic Development. Biology of Reproduction, 0, , .	1.2	0
4143	Lamin A/C impairments cause mitochondrial dysfunction by attenuating PGC1Î± and the NAMPT-NAD+ pathway. Nucleic Acids Research, 2022, 50, 9948-9965.	6.5	13
4144	Integrated metabolic, transcriptomic and chromatin accessibility analyses provide novel insights into the competition for anthocyanins and flavonols biosynthesis during fruit ripening in red apple. Frontiers in Plant Science, 0, 13, .	1.7	7
4145	Highly sensitive single-cell chromatin accessibility assay and transcriptome coassay with METATAC. Proceedings of the National Academy of Sciences of the United States of America, 2022, 119, .	3.3	5
4146	Dynamics of transcriptome and chromatin accessibility revealed sequential regulation of potential transcription factors during the brown adipose tissue whitening in rabbits. Frontiers in Cell and Developmental Biology, 0, 10, .	1.8	3
4147	Nonparametric single-cell multiomic characterization of trio relationships between transcription factors, target genes, and cis-regulatory regions. Cell Systems, 2022, 13, 737-751.e4.	2.9	16
4148	Applying genetic technologies to combat infectious diseases in aquaculture. Reviews in Aquaculture, 2023, 15, 491-535.	4.6	11
4149	Multiscale 3D genome organization underlies ILC2 ontogenesis and allergic airway inflammation. Nature Immunology, 2023, 24, 42-54.	7.0	10
4150	Massively parallel genomic perturbations with multi-target CRISPR interrogates Cas9 activity and DNA repair at endogenous sites. Nature Cell Biology, 2022, 24, 1433-1444.	4.6	14
4151	Multiplexed functional genomic assays to decipher the noncoding genome. Human Molecular Genetics, 2022, 31, R84-R96.	1.4	4
4152	Identification of risk loci for primary aldosteronism in genome-wide association studies. Nature Communications, 2022, 13, .	5.8	17
4153	InÂvivo G-CSF treatment activates the GR-SOCS1 axis to suppress IFN-Î³ secretion by natural killer cells. Cell Reports, 2022, 40, 111342.	2.9	3
4154	Unified rhombic lip origins of group 3 and group 4 medulloblastoma. Nature, 2022, 609, 1012-1020.	13.7	44
4155	In situ tools for chromatin structural epigenomics. Protein Science, 2022, 31, .	3.1	5
4156	Aging is associated with increased chromatin accessibility and reduced polymerase pausing in liver. Molecular Systems Biology, 2022, 18, .	3.2	13
4157	Human anti-smallpox long-lived memory B cells are defined by dynamic interactions in the splenic niche and long-lasting germinal center imprinting. Immunity, 2022, 55, 1872-1890.e9.	6.6	17

#	Article	IF	Citations
4160	Unraveling the epigenomic and transcriptomic interplay during alcohol-induced anxiolysis. Molecular Psychiatry, 2022, 27, 4624-4632.	4.1	10
4163	Time-resolved single-cell RNA-seq using metabolic RNA labelling. Nature Reviews Methods Primers, 2022, 2, .	11.8	21
4164	Intrinsic bias estimation for improved analysis of bulk and single-cell chromatin accessibility profiles using SELMA. Nature Communications, 2022, 13, .	5.8	2
4165	C/EBPÎ² regulates lipid metabolism and Pparg isoform 2 expression in alveolar macrophages. Science Immunology, 2022, 7, .	5.6	5
4167	Promoting validation and cross-phylogenetic integration in model organism research. DMM Disease Models and Mechanisms, 2022, 15, .	1.2	8
4168	CTCF and cohesin promote focal detachment of DNA from the nuclear lamina. Genome Biology, 2022, 23, .	3.8	11
4171	The histone modification reader ZCWPW1 promotes double-strand break repair by regulating cross-talk of histone modifications and chromatin accessibility at meiotic hotspots. Genome Biology, 2022, 23, .	3.8	6
4172	Fundamental and practical approaches for single-cell ATAC-seq analysis. ABIOTECH, 2022, 3, 212-223.	1.8	2
4173	Imaging Chromatin Accessibility by Assay of Transposase-Accessible Chromatin with Visualization. Methods in Molecular Biology, 2023, , 93-101.	0.4	1
4174	ATAC-Seq Analysis of Accessible Chromatin: From Experimental Steps to Data Analysis. Methods in Molecular Biology, 2023, , 65-81.	0.4	1
4175	Interpretation of the role of germline and somatic non-coding mutations in cancer: expression and chromatin conformation informed analysis. Clinical Epigenetics, 2022, 14, .	1.8	3
4176	PD-1 combination therapy with IL-2 modifies CD8+ T cell exhaustion program. Nature, 2022, 610, 173-181.	13.7	96
4178	Profiling Cell Type-Specific Gene Regulatory Regions in Human Cortical Organoids. Neuromethods, 2023, , 17-41.	0.2	2
4179	The chromatin accessibility landscape of pistils and anthers in rice. Plant Physiology, 2022, 190, 2797-2811.	2.3	1
4180	scATACpipe: A nextflow pipeline for comprehensive and reproducible analyses of single cell ATAC-seq data. Frontiers in Cell and Developmental Biology, 0, 10, .	1.8	1
4183	EBF1 primes B-lymphoid enhancers and limits the myeloid bias in murine multipotent progenitors. Journal of Experimental Medicine, 2022, 219, .	4.2	8
4184	Genomic insights into host and parasite interactions during intracellular infection by Toxoplasma gondii. PLoS ONE, 2022, 17, e0275226.	1.1	2
4185	Acquired semi-squamatization during chemotherapy suggests differentiation as a therapeutic strategy for bladder cancer. Cancer Cell, 2022, 40, 1044-1059.e8.	7.7	18

#	Article	IF	Citations
4186	Integration of multi-omics data reveals cis-regulatory variants that are associated with phenotypic differentiation of eastern from western pigs. Genetics Selection Evolution, 2022, 54, .	1.2	9
4187	Human-gained heart enhancers are associated with species-specific cardiac attributes. , 2022, 1, 830-843.		1
4188	Hedgehog signaling activates a mammalian heterochronic gene regulatory network controlling differentiation timing across lineages. Developmental Cell, 2022, 57, 2181-2203.e9.	3.1	5
4189	Single-Cell Chromatin Accessibility Data Combined with GWAS Improves Detection of Relevant Cell Types in 59 Complex Phenotypes. International Journal of Molecular Sciences, 2022, 23, 11456.	1.8	1
4191	Short telomeres impede germ cell specification by upregulating MAPK and TGFÎ² signaling. Science China Life Sciences, 2023, 66, 324-339.	2.3	2
4193	LncRNA SNHG1 regulates neuroblastoma cell fate via interactions with HDAC1/2. Cell Death and Disease, 2022, 13, .	2.7	4
4194	BACH2 restricts NK cell maturation and function, limiting immunity to cancer metastasis. Journal of Experimental Medicine, 2022, 219, .	4.2	8
4195	A costâ€effective tsCUT&Tag method for profiling transcription factor binding landscape. Journal of Integrative Plant Biology, 2022, 64, 2033-2038.	4.1	11
4196	p300/CBP sustains Polycomb silencing by non-enzymatic functions. Molecular Cell, 2022, 82, 3580-3597.e9.	4.5	9
4197	The expanding vistas of spatial transcriptomics. Nature Biotechnology, 2023, 41, 773-782.	9.4	84
4198	Diff-ATAC-STARR-Seq: A Method for Genome-Wide Functional Screening of Enhancer Activity <i>in Vivo</i>. Biological and Pharmaceutical Bulletin, 2022, 45, 1590-1595.	0.6	0
4199	Accurate prediction of functional states of cis-regulatory modules reveals common epigenetic rules in humans and mice. BMC Biology, 2022, 20, .	1.7	5
4200	Mechanoceutical forces squeeze the epigenetic changes. Matter, 2022, 5, 3097-3099.	5.0	1
4201	Integration of ATAC-seq and RNA-seq analysis identifies key genes affecting intramuscular fat content in pigs. Frontiers in Nutrition, 0, 9, .	1.6	8
4203	Insights into the sperm chromatin and implications for male infertility from a protein perspective. WIREs Mechanisms of Disease, 2023, 15, .	1.5	9
4204	Endothelial cell cycle state determines propensity for arterial-venous fate. Nature Communications, 2022, 13, .	5.8	22
4207	Decoding the spatial chromatin organization and dynamic epigenetic landscapes of macrophage cells during differentiation and immune activation. Nature Communications, 2022, 13, .	5.8	14
4208	Young transposable elements rewired gene regulatory networks in human and chimpanzee hippocampal intermediate progenitors. Development (Cambridge), 2022, 149, .	1.2	8

#	Article	IF	Citations
4210	Genome organization in cardiomyocytes expressing mutated A-type lamins. Frontiers in Cell and Developmental Biology, 0, 10, .	1.8	1
4211	BATF epigenetically and transcriptionally controls the activation program of regulatory T cells in human tumors. Science Immunology, 2022, 7, .	5.6	23
4212	Regeneration and developmental enhancers are differentially compatible with minimal promoters. Developmental Biology, 2022, 492, 47-58.	0.9	1
4213	Epigenomic Measurements in Brain Tissues. , 2022, , 3221-3261.		0
4214	Revolution in Genetics. , 2022, , 3153-3200.		0
4215	Approaches to benchmark and characterize in vitro human model systems. Development (Cambridge), 2022, 149, .	1.2	5
4216	The rearing environment persistently modulates mouse phenotypes from the molecular to the behavioural level. PLoS Biology, 2022, 20, e3001837.	2.6	11
4218	Trained immunity â€" basic concepts and contributions to immunopathology. Nature Reviews Nephrology, 2023, 19, 23-37.	4.1	57
4219	Consecutive BNT162b2 mRNA vaccination induces short-term epigenetic memory in innate immune cells. JCI Insight, 2022, 7, .	2.3	15
4220	Rescue of deficits by Brwd1 copy number restoration in the Ts65Dn mouse model of Down syndrome. Nature Communications, 2022, 13, .	5.8	7
4221	Phenotypic selection during laboratory evolution of yeast populations leads to a genome-wide sustainable chromatin compaction shift. Frontiers in Microbiology, 0, 13, .	1.5	0
4222	Hypoxia promotes osteogenesis by facilitating <scp>acetylâ€CoA</scp>â€mediated mitochondrialâ€"nuclear communication. EMBO Journal, 2022, 41, .	3.5	6
4223	Deep cis-regulatory homology of the butterfly wing pattern ground plan. Science, 2022, 378, 304-308.	6.0	23
4224	P300 promotes tumor recurrence by regulating radiation-induced conversion of glioma stem cells to vascular-like cells. Nature Communications, 2022, 13, .	5.8	5
4225	Transcriptomic and chromatin accessibility dynamics of porcine alveolar macrophages in exposure to fumonisin B1. Frontiers in Cell and Developmental Biology, 0, 10, .	1.8	0
4226	Ancient homomorphy of molluscan sex chromosomes sustained by reversible sex-biased genes and sex determiner translocation. Nature Ecology and Evolution, 2022, 6, 1891-1906.	3.4	23
4227	Transcription factor RORÎ± enforces stability of the Th17 cell effector program by binding to a Rorc cis-regulatory element. Immunity, 2022, 55, 2027-2043.e9.	6.6	15
4230	Genome-Wide Identification of Open Chromatin in Plants Using MH-Seq. Methods in Molecular Biology, 2023, , 29-43.	0.4	2

#	Article	IF	Citations
4232	Topological gelation of reconnecting polymers. Proceedings of the National Academy of Sciences of the United States of America, 2022, 119, .	3.3	5
4233	The Defects of Epigenetic Reprogramming in Dox-Dependent Porcine-iPSCs. International Journal of Molecular Sciences, 2022, 23, 11941.	1.8	1
4235	Chromatin Accessibility and Transcriptional Differences in Human Stem Cell-Derived Early-Stage Retinal Organoids. Cells, 2022, 11, 3412.	1.8	3
4236	A single transcription factor facilitates an insect host combating Bacillus thuringiensis infection while maintaining fitness. Nature Communications, 2022, 13, .	5.8	15
4237	scNanoATAC-seq: a long-read single-cell ATAC sequencing method to detect chromatin accessibility and genetic variants simultaneously within an individual cell. Cell Research, 2023, 33, 83-86.	5.7	12
4238	A map of cis-regulatory modules and constituent transcription factor binding sites in 80% of the mouse genome. BMC Genomics, 2022, 23, .	1.2	3
4240	Alleleâ€specific expression and chromatin accessibility contribute to heterosis in tea plants (Camellia sinensis). Plant Journal, 2022, 112, 1194-1211.	2.8	17
4242	Diverse environmental perturbations reveal the evolution and context-dependency of genetic effects on gene expression levels. Genome Research, 0, , .	2.4	6
4243	Epigenetics of neural differentiation: Spotlight on enhancers. Frontiers in Cell and Developmental Biology, 0, 10, .	1.8	5
4244	G9a Modulates Lipid Metabolism in CD4 T Cells to Regulate Intestinal Inflammation. Gastroenterology, 2023, 164, 256-271.e10.	0.6	6
4245	Systems-biology analysis of rheumatoid arthritis fibroblast-like synoviocytes implicates cell line-specific transcription factor function. Nature Communications, 2022, 13, .	5.8	12
4246	Time-restricted feeding mitigates obesity through adipocyte thermogenesis. Science, 2022, 378, 276-284.	6.0	53
4247	Navigation and Use of Custom Tracks within the Axolotl Genome Browser. Methods in Molecular Biology, 2023, , 273-289.	0.4	0
4248	PlantCADB: A Comprehensive Plant Chromatin Accessibility Database. Genomics, Proteomics and Bioinformatics, 2023, 21, 311-323.	3.0	3
4249	The co-evolution of the genome and epigenome in colorectal cancer. Nature, 2022, 611, 733-743.	13.7	39
4251	Multiomics analysis reveals that hepatocyte nuclear factor 1Î² regulates axon guidance genes in the developing mouse kidney. Scientific Reports, 2022, 12, .	1.6	2
4252	Adolescent cocaine differentially impacts psychomotor sensitization and epigenetic profiles in adult male rats with divergent affective phenotypes. Frontiers in Psychiatry, 0, 13, .	1.3	3
4254	Progress Towards Germline Transformation of Ticks. , 2022, , 375-394.		0

#	Article	IF	Citations
4255	Temporal analysis suggests a reciprocal relationship between 3D chromatin structure and transcription. Cell Reports, 2022, 41, 111567.	2.9	19
4256	IReNA: Integrated regulatory network analysis of single-cell transcriptomes and chromatin accessibility profiles. IScience, 2022, 25, 105359.	1.9	10
4257	HIF1Î±-AS1 is a DNA:DNA:RNA triplex-forming lncRNA interacting with the HUSH complex. Nature Communications, 2022, 13, .	5.8	13
4258	BRD9-containing non-canonical BAF complex maintains somatic cell transcriptome and acts as a barrier to human reprogramming. Stem Cell Reports, 2022, 17, 2629-2642.	2.3	6
4259	Normalization benchmark of ATAC-seq datasets shows the importance of accounting for GC-content effects. Cell Reports Methods, 2022, 2, 100321.	1.4	6
4260	Chronic cAMP activation induces adipocyte browning through discordant biphasic remodeling of transcriptome and chromatin accessibility. Molecular Metabolism, 2022, 66, 101619.	3.0	3
4261	Current and Emerging Technologies for the Analysis of the Genome-Wide and Locus-Specific DNA Methylation Patterns. Advances in Experimental Medicine and Biology, 2022, , 395-469.	0.8	2
4262	<scp>RNA</scp>â€seq and <scp>ATAC</scp>â€seq analysis of <scp>CD163</scp>⁺ macrophageâ€induced progestinâ€insensitive endometrial cancer cells. Cancer Medicine, 2023, 12, 5964-5978.	1.3	2
4263	Single-cell transcriptome analysis reveals cellular heterogeneity in mouse intra- and extra articular ligaments. Communications Biology, 2022, 5, .	2.0	4
4264	Hi-TrAC reveals division of labor of transcription factors in organizing chromatin loops. Nature Communications, 2022, 13, .	5.8	16
4265	Vector genome loss and epigenetic modifications mediate decline in transgene expression of AAV5 vectors produced in mammalian and insect cells. Molecular Therapy, 2022, 30, 3570-3586.	3.7	12
4266	Activation of HIV-1 proviruses increases downstream chromatin accessibility. IScience, 2022, 25, 105490.	1.9	5
4267	Spatial and Temporal Organization of Chromatin at Small and Large Scales. Annual Review of Condensed Matter Physics, 2023, 14, 193-210.	5.2	2
4268	Inflammatory Cytokines That Enhance Antigen Responsiveness of NaÃ¯ve CD8+ T Lymphocytes Modulate Chromatin Accessibility of Genes Impacted by Antigen Stimulation. International Journal of Molecular Sciences, 2022, 23, 14122.	1.8	1
4269	Histone chaperone ASF1 mediates H3.3-H4 deposition in Arabidopsis. Nature Communications, 2022, 13, .	5.8	8
4270	Sequencing Illumina libraries at high accuracy on the ONT MinION using R2C2. Genome Research, 2022, 32, 2092-2106.	2.4	6
4272	ADRA1Aâ€“Gî±q signalling potentiates adipocyte thermogenesis through CKB and TNAP. Nature Metabolism, 2022, 4, 1459-1473.	5.1	13
4273	On-microscope staging of live cells reveals changes in the dynamics of transcriptional bursting during differentiation. Nature Communications, 2022, 13, .	5.8	3

#	Article	IF	Citations
4274	Chromatin accessibility-based characterisation of brain gene regulatory networks in three distinct honey bee polyphenisms. Nucleic Acids Research, 2022, 50, 11550-11562.	6.5	4
4276	Gene expression changes during the evolution of the tetrapod limb. Biologia Futura, 0, , .	0.6	1
4277	Temporal change in chromatin accessibility predicts regulators of nodulation in Medicago truncatula. BMC Biology, 2022, 20, .	1.7	2
4278	Tissue dissociation for single-cell and single-nuclei RNA sequencing for low amounts of input material. Frontiers in Zoology, 2022, 19, .	0.9	7
4279	Mapping open chromatin by ATAC-seq in bread wheat. Frontiers in Plant Science, 0, 13, .	1.7	4
4280	Endocrine resistance and breast cancer plasticity are controlled by CoREST. Nature Structural and Molecular Biology, 2022, 29, 1122-1135.	3.6	11
4281	A chronicle review of new techniques that facilitate the understanding and development of optimal individualized therapeutic strategies for chordoma. Frontiers in Oncology, 0, 12, .	1.3	2
4282	Chromosome-level genome assembly of the Muscovy duck provides insight into fatty liver susceptibility. Genomics, 2022, 114, 110518.	1.3	2
4283	Whole-genome sequencing of chronic lymphocytic leukemia identifies subgroups with distinct biological and clinical features. Nature Genetics, 2022, 54, 1675-1689.	9.4	21
4285	FRET-FISH probes chromatin compaction at individual genomic loci in single cells. Nature Communications, 2022, 13, .	5.8	4
4286	Transcription factor antagonism regulates heterogeneity in embryonic stem cell states. Molecular Cell, 2022, 82, 4410-4427.e12.	4.5	5
4289	DNA replication initiation shapes the mutational landscape and expression of the human genome. Science Advances, 2022, 8, .	4.7	4
4290	Exhaustion and over-activation of immune cells in COVID-19: Challenges and therapeutic opportunities. Clinical Immunology, 2022, 245, 109177.	1.4	12
4292	Novel biological insights revealed from the investigation of multiscale genome architecture. Computational and Structural Biotechnology Journal, 2023, 21, 312-325.	1.9	2
4293	Microfluidics-based single cell analysis: from transcriptomics to spatiotemporal multi-omics. TrAC - Trends in Analytical Chemistry, 2023, 158, 116868.	5.8	6
4294	Systems toxicology to advance human and environmental hazard assessment: A roadmap for advanced materials. Nano Today, 2023, 48, 101735.	6.2	4
4295	Low-affinity SPL binding sites contribute to subgenome expression divergence in allohexaploid wheat. Science China Life Sciences, 2023, 66, 819-834.	2.3	10
4299	Screening and Regulation Mechanism of Key Transcription Factors of Penicillium expansum Infecting Postharvest Pears by ATAC-Seq Analysis. Foods, 2022, 11, 3855.	1.9	2

#	Article	IF	Citations
4301	Dissecting Locus-Specific Chromatin Interactions by CRISPR CAPTURE. Methods in Molecular Biology, 2023, , 69-97.	0.4	1
4302	High-content CRISPR screening in tumor immunology. Frontiers in Immunology, 0, 13, .	2.2	3
4303	Fishing for Developmental Regulatory Regions: Zebrafish Tissue-Specific ATAC-seq. Methods in Molecular Biology, 2023, , 271-282.	0.4	0
4304	Integration of 3D genome topology and local chromatin features uncovers enhancers underlying craniofacial-specific cartilage defects. Science Advances, 2022, 8, .	4.7	4
4305	In Situ Hybridization as a Method to Examine Gene Regulatory Activity In Vivo. Methods in Molecular Biology, 2023, , 241-254.	0.4	0
4306	Collagen type I-mediated mechanotransduction controls epithelial cell fate conversion during intestinal inflammation. Inflammation and Regeneration, 2022, 42, .	1.5	6
4308	Ras drives malignancy through stem cell crosstalk with the microenvironment. Nature, 2022, 612, 555-563.	13.7	17
4309	Chromatin accessibility: methods, mechanisms, and biological insights. Nucleus, 2022, 13, 238-278.	0.6	16
4310	Activation of Wnt/Î²-catenin signaling by Zeb1 in endothelial progenitors induces vascular quiescence entry. Cell Reports, 2022, 41, 111694.	2.9	2
4312	AMPK induces degradation of the transcriptional repressor PROX1 impairing branched amino acid metabolism and tumourigenesis. Nature Communications, 2022, 13, .	5.8	6
4313	Integrated chromatin accessibility and DNA methylation analysis to reveal the critical epigenetic modification and regulatory mechanism in gonadal differentiation of the sequentially hermaphroditic fish, Monopterus albus. Biology of Sex Differences, 2022, 13, .	1.8	2
4315	Simultaneous profiling of histone modifications and DNA methylation via nanopore sequencing. Nature Communications, 2022, 13, .	5.8	6
4317	Profound phenotypic and epigenetic heterogeneity of the HIV-1-infected CD4+ T cell reservoir. Nature Immunology, 2023, 24, 359-370.	7.0	23
4318	Dynamic chromatin accessibility deploys heterotypic cis/trans-acting factors driving stomatal cell-fate commitment. Nature Plants, 2022, 8, 1453-1466.	4.7	12
4319	AtMCM10 promotes DNA replicationâ€coupled nucleosome assembly in Arabidopsis. Journal of Integrative Plant Biology, 2023, 65, 203-222.	4.1	3
4320	Î”Np63/p73 drive metastatic colonization by controlling a regenerative epithelial stem cell program in quasi-mesenchymal cancer stem cells. Developmental Cell, 2022, 57, 2714-2730.e8.	3.1	10
4321	Massively Parallel CRISPRâ€Based Genetic Perturbation Screening at Singleâ€Cell Resolution. Advanced Science, 2023, 10, .	5.6	6
4322	Chromatin modules and their implication in genomic organization and gene regulation. Trends in Genetics, 2023, 39, 140-153.	2.9	9

#	Article	IF	Citations
4323	Learning single-cell chromatin accessibility profiles using meta-analytic marker genes. Briefings in Bioinformatics, 2023, 24, .	3.2	1
4325	A secondâ€generation capture panel for costâ€effective sequencing of genome regulatory regions in wheat and relatives. Plant Genome, 2023, 16, .	1.6	1
4326	Microglial pattern recognition via IL-33 promotes synaptic refinement in developing corticothalamic circuits in mice. Journal of Experimental Medicine, 2023, 220, .	4.2	12
4327	Recruitment of CTCF to an Fto enhancer is responsible for transgenerational inheritance of BPA-induced obesity. Proceedings of the National Academy of Sciences of the United States of America, 2022, 119, .	3.3	17
4328	Viewing AML through a New Lens: Technological Advances in the Study of Epigenetic Regulation. Cancers, 2022, 14, 5989.	1.7	0
4329	Age-dependent Lamin changes induce cardiac dysfunction via dysregulation of cardiac transcriptional programs. Nature Aging, 2023, 3, 17-33.	5.3	6
4330	CRAG: de novo characterization of cell-free DNA fragmentation hotspots in plasma whole-genome sequencing. Genome Medicine, 2022, 14, .	3.6	6
4331	Chromatin accessibility illuminates single-cell regulatory dynamics of rice root tips. BMC Biology, 2022, 20, .	1.7	11
4332	Analysis of Chromatin Openness in Testicle Tissue of Yak and Cattle-Yak. International Journal of Molecular Sciences, 2022, 23, 15810.	1.8	4
4335	Multivalent state transitions shape the intratumoral composition of small cell lung carcinoma. Science Advances, 2022, 8, .	4.7	4
4337	ATACâ€seq exposes differences in chromatin accessibility leading to distinct leaf shapes in mulberry. Plant Direct, 2022, 6, .	0.8	1
4338	Strategies for activity analysis of single nucleotide polymorphisms associated with human diseases. Clinical Genetics, 2023, 103, 392-400.	1.0	3
4339	Integrated bioinformatics analysis of the transcription factor-mediated gene regulatory networks in the formation of spermatogonial stem cells. Frontiers in Physiology, 0, 13, .	1.3	2
4340	ERK1/2 signalling dynamics promote neural differentiation by regulating chromatin accessibility andÂthe polycomb repressive complex. PLoS Biology, 2022, 20, e3000221.	2.6	9
4341	Computational Integration of HSV-1 Multi-omics Data. Methods in Molecular Biology, 2023, , 31-48.	0.4	1
4342	Epigenetic priming of immune/inflammatory pathways activation and abnormal activity of cell cycle pathway in a perinatal model of white matter injury. Cell Death and Disease, 2022, 13, .	2.7	2
4343	KMT2D deficiency drives lung squamous cell carcinoma and hypersensitivity to RTK-RAS inhibition. Cancer Cell, 2023, 41, 88-105.e8.	7.7	12
4345	Increased post-mitotic senescence in aged human neurons is a pathological feature of Alzheimerâ€™s disease. Cell Stem Cell, 2022, 29, 1637-1652.e6.	5.2	42

#	Article	IF	Citations
4347	Rational Protein Design Yields a CD20 CAR with Superior Antitumor Efficacy Compared with CD19 CAR. Cancer Immunology Research, 2023, 11, 150-163.	1.6	5
4348	EKLF/Klf1 regulates erythroid transcription by its pioneering activity and selective control of RNA Pol II pause-release. Cell Reports, 2022, 41, 111830.	2.9	6
4350	Dysregulation of PRMT5 in chronic lymphocytic leukemia promotes progression with high risk of Richterâ€™s transformation. Nature Communications, 2023, 14, .	5.8	10
4351	Solid-phase capture and profiling of open chromatin by spatial ATAC. Nature Biotechnology, 2023, 41, 1085-1088.	9.4	14
4352	ATAC-seq and RNA-seq analysis unravel the mechanism of sex differentiation and infertility in sex reversal chicken. Epigenetics and Chromatin, 2023, 16, .	1.8	2
4353	A chromosome-scale epigenetic map of theHydragenome reveals conserved regulators of cell state. Genome Research, 2023, 33, 283-298.	2.4	19
4356	Microtubule Assists Actomyosin to Regulate Cell Nuclear Mechanics and Chromatin Accessibility. Research, 2023, 6, .	2.8	14
4357	ChIATAC is an efficient strategy for multi-omics mapping of 3D epigenomes from low-cell inputs. Nature Communications, 2023, 14, .	5.8	4
4358	Past history of obesity triggers persistent epigenetic changes in innate immunity and exacerbates neuroinflammation. Science, 2023, 379, 45-62.	6.0	39
4359	Machine learning dissection of human accelerated regions in primate neurodevelopment. Neuron, 2023, 111, 857-873.e8.	3.8	27
4360	Artificial intelligence-based multi-omics analysis fuels cancer precision medicine. Seminars in Cancer Biology, 2023, 88, 187-200.	4.3	36
4361	A stem cell epigenome is associated with primary nonresponse to CD19 CAR T cells in pediatric acute lymphoblastic leukemia. Blood Advances, 2023, 7, 4218-4232.	2.5	5
4362	Profiling Chromatin Accessibility Responses in Goat Bronchial Epithelial Cells Infected with Pasteurella multocida. International Journal of Molecular Sciences, 2023, 24, 1312.	1.8	1
4363	Osteocyte Egln1/Phd2 links oxygen sensing and biomineralization via FGF23. Bone Research, 2023, 11, .	5.4	6
4365	The Recurrent-Specific Regulation Network of Prognostic Stemness-Related Signatures in Low-Grade Glioma. Disease Markers, 2023, 2023, 1-29.	0.6	0
4367	Practical application of massively parallel reporter assay in biotechnology and medicine. Journal of Clinical Practice, 2023, 13, 74-87.	0.2	0
4369	TLE3 and TLE4-coordinated colonic macrophage-CD4+ T cell crosstalk maintains intestinal immune homeostasis. Mucosal Immunology, 2023, 16, 50-60.	2.7	1
4370	Human SMARCA5 is continuously required to maintain nucleosome spacing. Molecular Cell, 2023, 83, 507-522.e6.	4.5	11

#	Article	IF	Citations
4371	Advances in sequencing technologies for amyotrophic lateral sclerosis research. Molecular Neurodegeneration, 2023, 18, .	4.4	4
4372	Hydrozoan sperm-specific SPKK motif-containing histone H2B variants stabilise chromatin with limited compaction. Development (Cambridge), 2023, 150, .	1.2	0
4373	DNA methylation analysis explores the molecular basis of plasma cell-free DNA fragmentation. Nature Communications, 2023, 14, .	5.8	16
4374	Decoding the Auxin Matrix: Auxin Biology Through the Eye of the Computer. Annual Review of Plant Biology, 2023, 74, 387-413.	8.6	3
4375	Profiling the Epigenetic Landscape of the Tumor Microenvironment Using Chromatin Immunoprecipitation Sequencing. Methods in Molecular Biology, 2023, , 313-348.	0.4	0
4376	ZFP462 safeguards neural lineage specification by targeting G9A/GLP-mediated heterochromatin to silence enhancers. Nature Cell Biology, 2023, 25, 42-55.	4.6	6
4377	ONECUT2 regulates RANKL-dependent enterocyte and microfold cell differentiation in the small intestine; a multi-omics study. Nucleic Acids Research, 2023, 51, 1277-1296.	6.5	2
4379	Characterizing crosstalk in epigenetic signaling to understand disease physiology. Biochemical Journal, 2023, 480, 57-85.	1.7	4
4380	The rates of adult neurogenesis and oligodendrogenesis are linked to cell cycle regulation through p27-dependent gene repression of SOX2. Cellular and Molecular Life Sciences, 2023, 80, .	2.4	0
4381	Single-cell RNA-seq integrated with multi-omics reveals SERPINE2 as a target for metastasis in advanced renal cell carcinoma. Cell Death and Disease, 2023, 14, .	2.7	8
4382	Reporter gene assays and chromatin-level assays define substantially non-overlapping sets of enhancer sequences. BMC Genomics, 2023, 24, .	1.2	4
4383	Integrated single-cell profiling dissects cell-state-specific enhancer landscapes of human tumor-infiltrating CD8+ TÂcells. Molecular Cell, 2023, 83, 622-636.e10.	4.5	7
4384	Applications of deep learning in understanding gene regulation. Cell Reports Methods, 2023, 3, 100384.	1.4	13
4386	Wnt/Î²-catenin signalling is required for pole-specific chromatin remodeling during planarian regeneration. Nature Communications, 2023, 14, .	5.8	9
4387	Sample Preparation and Integrative Data Analysis of a Droplet-based Single-Cell ATAC-sequencing Using Murine Thymic Epithelial Cells. Bio-protocol, 2023, 13, .	0.2	0
4388	DNA dioxygenases Tet2/3 regulate gene promoter accessibility and chromatin topology in lineage-specific loci to control epithelial differentiation. Science Advances, 2023, 9, .	4.7	3
4390	scAVENGERS: a genotype-based deconvolution of individuals in multiplexed single-cell ATAC-seq data without reference genotypes. NAR Genomics and Bioinformatics, 2022, 4, .	1.5	3
4392	Quality assessment and refinement of chromatin accessibility data using a sequence-based predictive model. Proceedings of the National Academy of Sciences of the United States of America, 2022, 119, .	3.3	4

#	Article	IF	Citations
4393	scIAC: clustering scATAC-seq data based on Studentâ€™s t-distribution similarity imputation and denoising autoencoder. , 2022, , .		2
4395	A chromosome-scale genome assembly of Dasypyrum villosum provides insights into its application as a broad-spectrum disease resistance resource for wheat improvement. Molecular Plant, 2023, 16, 432-451.	3.9	9
4396	The autism risk factor CHD8 is a chromatin activator in human neurons and functionally dependent on the ERK-MAPK pathway effector ELK1. Scientific Reports, 2022, 12, .	1.6	3
4397	A heterogeneous graph cross-omics attention model for single-cell representation learning. , 2022, , .		0
4398	Epigenetic regulation of cis-regulatory elements and transcription factors during development. , 2023, , 71-113.		1
4399	Genomeâ€wide association studies demonstrate the genes associated with perimysial thickness in ducks. Animal Genetics, 2023, 54, 363-374.	0.6	3
4400	ZBTB18 restricts chromatin accessibility and prevents transcriptional adaptations that drive metastasis. Science Advances, 2023, 9, .	4.7	3
4401	Epigenetic and transcriptional regulations prime cell fate before division during human pluripotent stem cell differentiation. Nature Communications, 2023, 14, .	5.8	8
4402	Computational approaches to understand transcription regulation in development. Biochemical Society Transactions, 0, , .	1.6	3
4406	Epigenetic remodeling of the immune landscape in cancer: therapeutic hurdles and opportunities. Journal of Biomedical Science, 2023, 30, .	2.6	7
4411	HSFA1a modulates plant heat stress responses and alters the 3D chromatin organization of enhancer-promoter interactions. Nature Communications, 2023, 14, .	5.8	18
4412	Multi-modular structure of the gene regulatory network for specification and commitment of murine T cells. Frontiers in Immunology, 0, 14, .	2.2	5
4413	Into the multi-omics era: Progress of T cells profiling in the context of solid organ transplantation. Frontiers in Immunology, 0, 14, .	2.2	2
4414	Enhancers for Selective Targeting. Neuromethods, 2023, , 169-184.	0.2	0
4415	ATAC-DEA: A Web-Based ATAC-Seq Data Differential Peak and Annotation Analysis Application. Journal of Computational Biology, 0, , .	0.8	0
4416	Integration of chromatin accessibility and gene expression reveals new regulators of cold hardening to enhance freezing tolerance inPrunus mume. Journal of Experimental Botany, 2023, 74, 2173-2187.	2.4	4
4417	Epiblast-like stem cells established by Wnt/Î²-catenin signaling manifest distinct features of formative pluripotency and germline competence. Cell Reports, 2023, 42, 112021.	2.9	2
4418	Transcriptomic Definition of Neuron Types. Neuromethods, 2023, , 153-167.	0.2	0

#	Article	IF	Citations
4419	maxATAC: Genome-scale transcription-factor binding prediction from ATAC-seq with deep neural networks. PLoS Computational Biology, 2023, 19, e1010863.	1.5	6
4421	Single cell cortical bone transcriptomics define novel osteolineage gene sets altered in chronic kidney disease. Frontiers in Endocrinology, 0, 14, .	1.5	9
4423	Key transcription factors influence the epigenetic landscape to regulate retinal cell differentiation. Nucleic Acids Research, 2023, 51, 2151-2176.	6.5	4
4424	Epigenetic and transcriptional activation of the secretory kinase FAM20C as an oncogene in glioma. Journal of Genetics and Genomics, 2023, 50, 422-433.	1.7	2
4426	Epigenetics in cardiovascular health and disease. Progress in Molecular Biology and Translational Science, 2023, , 105-134.	0.9	2
4428	Transcription factor TFII-I fine tunes innate properties of B lymphocytes. Frontiers in Immunology, 0, 14, .	2.2	1
4429	Single-Molecule Mapping of Chromatin Accessibility Using NOMe-seq/dSMF. Methods in Molecular Biology, 2023, , 101-119.	0.4	1
4430	Epigenomic Profiling of Dorsal Root Ganglia upon Regenerative and Non-regenerative Axonal Injury. Methods in Molecular Biology, 2023, , 101-144.	0.4	0
4431	Advances in AAV technology for delivering genetically encoded cargo to the nonhuman primate nervous system. Current Research in Neurobiology, 2023, 4, 100086.	1.1	10
4432	Analysis of Chromatin Interaction and Accessibility by Trac-Looping. Methods in Molecular Biology, 2023, , 85-97.	0.4	0
4433	Itaconate ameliorates autoimmunity by modulating T cell imbalance via metabolic and epigenetic reprogramming. Nature Communications, 2023, 14, .	5.8	26
4434	Characterization of De Novo Promoter Variants in Autism Spectrum Disorder with Massively Parallel Reporter Assays. International Journal of Molecular Sciences, 2023, 24, 3509.	1.8	3
4435	Nuclear and cytoplasmic <scp>lncRNAs</scp> in root tips of the model legume <scp>Medicago truncatula</scp> under control and submergence. IUBMB Life, 2023, 75, 580-594.	1.5	0
4437	Pyruvate dehydrogenase fuels a critical citrate pool that is essential for Th17 cell effector functions. Cell Reports, 2023, 42, 112153.	2.9	7
4438	Transcriptional and Chromatin Accessibility Profiling of Neural Stem Cells Differentiating into Astrocytes Reveal Dynamic Signatures Affected under Inflammatory Conditions. Cells, 2023, 12, 948.	1.8	0
4440	Progress in the study of parvovirus entry pathway. Virology Journal, 2023, 20, .	1.4	2
4442	The Neurovasculome: Key Roles in Brain Health and Cognitive Impairment: A Scientific Statement From the American Heart Association/American Stroke Association. Stroke, 2023, 54, .	1.0	28
4443	OBERON3 and SUPPRESSOR OF MAX2 1-LIKE proteins form a regulatory module driving phloem development. Nature Communications, 2023, 14, .	5.8	4

#	Article	IF	Citations
4444	Evaluation of MYBL1 as the master regulator for pachytene spermatocyte genes dysregulated in interspecific hybrid dzo. Journal of Dairy Science, 2023, , .	1.4	0
4445	Neutral Models of De Novo Gene Emergence Suggest that Gene Evolution has a Preferred Trajectory. Molecular Biology and Evolution, 2023, 40, .	3.5	7
4447	ETV4 mediates dosage-dependent prostate tumor initiation and cooperates with p53 loss to generate prostate cancer. Science Advances, 2023, 9, .	4.7	2
4448	Regulation and Immunotherapeutic Targeting of the Epigenome in Exhausted CD8 T Cell Responses. Journal of Immunology, 2023, 210, 869-879.	0.4	2
4449	Systems biology approaches to unravel lymphocyte subsets and function. Current Opinion in Immunology, 2023, 82, 102323.	2.4	0
4450	Integrated genome-wide chromatin accessibility and expression profile identify key transcription factors involved in bud endodormancy break in tea plants. Scientia Horticulturae, 2023, 317, 112022.	1.7	3
4453	Protocol for Bulk-ATAC sequencing in head and neck squamous cell carcinoma. STAR Protocols, 2023, 4, 102233.	0.5	0
4454	Advances in Epigenetics and Integration of Omics in Lupus. European Medical Journal Rheumatology, 0, , 90-97.	0.0	0
4455	Interphase chromosomes of the Aedes aegypti mosquito are liquid crystalline and can sense mechanical cues. Nature Communications, 2023, 14, .	5.8	6
4456	Deciphering the multi-scale, quantitative cis-regulatory code. Molecular Cell, 2023, 83, 373-392.	4.5	65
4458	Recycling of parental histones preserves the epigenetic landscape during embryonic development. Science Advances, 2023, 9, .	4.7	4
4459	Chromatin profile-based identification of a novel ER-positive breast cancer subgroup with reduced ER-responsive element accessibility. British Journal of Cancer, 2023, 128, 1208-1222.	2.9	2
4460	Threeâ€dimensional chromatin reâ€organization during muscle stem cell aging. Aging Cell, 2023, 22, .	3.0	5
4461	Integrated analysis of ATAC-seq and RNA-seq reveals the transcriptional regulation network in SLE. International Immunopharmacology, 2023, 116, 109803.	1.7	1
4462	Centromere repositioning and shifts in wheat evolution. Plant Communications, 2023, 4, 100556.	3.6	16
4463	Emerging RUNX2-Mediated Gene Regulatory Mechanisms Consisting of Multi-Layered Regulatory Networks in Skeletal Development. International Journal of Molecular Sciences, 2023, 24, 2979.	1.8	5
4466	The Foundational Data Initiative for Parkinson Disease: Enabling efficient translation from genetic maps to mechanism. Cell Genomics, 2023, 3, 100261.	3.0	12
4467	Chromatin immunoprecipitation with mouse adipocytes using hypotonic buffer to enrich nuclear fraction before fixation. STAR Protocols, 2023, 4, 102093.	0.5	1

#	Article	IF	Citations
4468	Mycobacterium tuberculosisinfection triggers epigenetic changes that are enriched in a type I IFN signature. MicroLife, 2023, 4, .	1.0	2
4469	Factors and Methods for the Detection of Gene Expression Regulation. Biomolecules, 2023, 13, 304.	1.8	0
4470	TET2 guards against unchecked BATF3-induced CAR T cell expansion. Nature, 2023, 615, 315-322.	13.7	32
4472	Deletion of histone demethylase Lsd1 (Kdm1a) during retinal development leads to defects in retinal function and structure. Frontiers in Cellular Neuroscience, 0, 17, .	1.8	0
4473	Chromatin accessibility landscapes revealed the subgenome-divergent regulation networks during wheat grain development. ABIOTECH, 2023, 4, 8-19.	1.8	5
4474	Histone remodeling reflects conserved mechanismsÂof bovine and human preimplantationÂdevelopment. EMBO Reports, 2023, 24, .	2.0	7
4475	Leveraging massively parallel reporter assays for evolutionary questions. Genome Biology, 2023, 24, .	3.8	10
4476	Atlas-scale single-cell chromatin accessibility using nanowell-based combinatorial indexing. Genome Research, 2023, 33, 208-217.	2.4	1
4478	A NPAS4â€“NuA4 complex couples synaptic activity to DNA repair. Nature, 2023, 614, 732-741.	13.7	36
4480	Integrative ATAC-seq and RNA-seq analyses of IPEC-J2 cells reveals porcine transcription and chromatin accessibility changes associated with Escherichia coli F18ac inhibited by Lactobacillus reuteri. Frontiers in Microbiology, 0, 14, .	1.5	1
4482	DddA homolog search and engineering expand sequence compatibility of mitochondrial base editing. Nature Communications, 2023, 14, .	5.8	25
4483	Mini-review: Gene regulatory network benefits from three-dimensional chromatin conformation and structural biology. Computational and Structural Biotechnology Journal, 2023, 21, 1728-1737.	1.9	2
4484	Nsun2 coupling with RoRÎ³t shapes the fate of Th17 cells and promotes colitis. Nature Communications, 2023, 14, .	5.8	3
4485	Dek219 encodes the DICER-LIKE1 protein that affects chromatin accessibility and kernel development in maize. Journal of Integrative Agriculture, 2023, 22, 2961-2980.	1.7	2
4486	BRG1 HSA domain interactions with BCL7 proteins are critical for remodeling and gene expression. Life Science Alliance, 2023, 6, e202201770.	1.3	2
4488	Deciphering transcription factors and their corresponding regulatory elements during inhibitory interneuron differentiation using deep neural networks. Frontiers in Cell and Developmental Biology, 0, 11, .	1.8	0
4489	Unraveling the Impact of Intratumoral Heterogeneity on EGFR Tyrosine Kinase Inhibitor Resistance in EGFR-Mutated NSCLC. International Journal of Molecular Sciences, 2023, 24, 4126.	1.8	3
4490	Phosphorylation of ATF2 promotes odontoblastic differentiation via intrinsic HAT activity. Journal of Genetics and Genomics, 2023, , .	1.7	0

#	Article	IF	Citations
4491	A dataset of definitive endoderm and hepatocyte differentiations from human induced pluripotent stem cells. Scientific Data, 2023, 10, .	2.4	0
4492	SETD2 regulates chromatin accessibility and transcription to suppress lung tumorigenesis. JCI Insight, 2023, 8, .	2.3	3
4494	Single-cell RNA sequencing in orthopedic research. Bone Research, 2023, 11, .	5.4	6
4497	Multifaceted role for p53 in pancreatic cancer suppression. Proceedings of the National Academy of Sciences of the United States of America, 2023, 120, .	3.3	6
4498	A neurodevelopmental epigenetic programme mediated by SMARCD3â€“DAB1â€“Reelin signalling is hijacked to promote medulloblastoma metastasis. Nature Cell Biology, 2023, 25, 493-507.	4.6	10
4499	ATAC-See: A Tn5 Transposase-Mediated Assay for Detection of Chromatin Accessibility with Imaging. Methods in Molecular Biology, 2023, , 285-291.	0.4	0
4500	Deep Learning on Chromatin Accessibility. Methods in Molecular Biology, 2023, , 325-333.	0.4	0
4501	Simultaneous Single-Cell Profiling of the Transcriptome and Accessible Chromatin Using SHARE-seq. Methods in Molecular Biology, 2023, , 187-230.	0.4	0
4502	Concomitant Sequencing of Accessible Chromatin and Mitochondrial Genomes in Single Cells Using mtscATAC-Seq. Methods in Molecular Biology, 2023, , 269-282.	0.4	0
4503	Measuring Inaccessible Chromatin Genome-Wide Using Protect-seq. Methods in Molecular Biology, 2023, , 53-61.	0.4	0
4504	Single-cell multiome sequencing clarifies enteric glial diversity and identifies an intraganglionic population poised for neurogenesis. Cell Reports, 2023, 42, 112194.	2.9	12
4505	Profiling Chromatin Accessibility on Replicated DNA with repli-ATAC-Seq. Methods in Molecular Biology, 2023, , 71-84.	0.4	1
4506	Universal NicE-Seq: A Simple and Quick Method for Accessible Chromatin Detection in Fixed Cells. Methods in Molecular Biology, 2023, , 39-52.	0.4	0
4507	NicE-viewSeq: An Integrative Visualization and Genomics Method to Detect Accessible Chromatin in Fixed Cells. Methods in Molecular Biology, 2023, , 293-302.	0.4	0
4508	ATAC-seq Data Processing. Methods in Molecular Biology, 2023, , 305-323.	0.4	1
4509	Single-Cell Joint Profiling of Open Chromatin and Transcriptome by Paired-Seq. Methods in Molecular Biology, 2023, , 155-185.	0.4	0
4510	Dynamics and regulation of mitotic chromatin accessibility bookmarking at single-cell resolution. Science Advances, 2023, 9, .	4.7	4
4511	Determination of the Chromatin Openness in Bacterial Genomes. Methods in Molecular Biology, 2023, , 63-69.	0.4	0

#	Article	IF	Citations
4512	Genome-Wide Mapping of Active Regulatory Elements Using ATAC-seq. Methods in Molecular Biology, 2023, , 3-19.	0.4	1
4513	Key Stages of Flax Bast Fiber Development Through the Prism of Transcriptomics. Compendium of Plant Genomes, 2023, , 149-198.	0.3	1
4514	Characterization of chromatin accessibility patterns in different mouse cell types using machine learning methods at single-cell resolution. Frontiers in Genetics, 0, 14, .	1.1	2
4515	Expression of Human Endogenous Retrovirus Group K (HERV-K) HML-2 Correlates with Immune Activation of Macrophages and Type I Interferon Response. Microbiology Spectrum, 2023, 11, .	1.2	6
4516	Single-Cell Molecular Barcoding to Decode Multimodal Information Defining Cell States. Molecules and Cells, 2023, 46, 74-85.	1.0	3
4517	Using QTL to Identify Genes and Pathways Underlying the Regulation and Production of Milk Components in Cattle. Animals, 2023, 13, 911.	1.0	1
4518	Epigenetic Regulations in Mammalian Cells: Roles and Profiling Techniques. Molecules and Cells, 2023, 46, 86-98.	1.0	5
4519	hPSC-derived sacral neural crest enables rescue in a severe model of Hirschsprungâ€™s disease. Cell Stem Cell, 2023, 30, 264-282.e9.	5.2	15
4520	A gene regulatory network for neural induction. ELife, 0, 12, .	2.8	9
4521	Oncogenic YAP mediates changes in chromatin accessibility and activity that drive cell cycle gene expression and cell migration. Nucleic Acids Research, 2023, 51, 4266-4283.	6.5	4
4523	Genotype-phenotype mapping of a patient-derived lung cancer organoid biobank identifies NKX2-1-defined Wnt dependency in lung adenocarcinoma. Cell Reports, 2023, 42, 112212.	2.9	12
4524	Chromatin Remodeling via Retinoic Acid Action during Murine Spermatogonial Development. Life, 2023, 13, 690.	1.1	0
4525	RGT: a toolbox for the integrative analysis of high throughput regulatory genomics data. BMC Bioinformatics, 2023, 24, .	1.2	3
4527	<scp>DNA</scp> demethylation fineâ€tunes <scp>IL</scp>â€2 production during thymic regulatory T cell differentiation. EMBO Reports, 2023, 24, .	2.0	2
4531	Pharmacological disruption of mSWI/SNF complex activity restricts SARS-CoV-2 infection. Nature Genetics, 2023, 55, 471-483.	9.4	14
4532	Complex Analysis of Single-Cell RNA Sequencing Data. Biochemistry (Moscow), 2023, 88, 231-252.	0.7	4
4535	Are extraordinary nucleosome structures more ordinary than we thought?. Chromosoma, 2023, 132, 139-152.	1.0	2
4536	Heparanase Modulates Chromatin Accessibility. Cells, 2023, 12, 891.	1.8	1

#	Article	IF	Citations
4537	Integrated ATAC-Seq and RNA-Seq Data Analysis to Reveal OsbZIP14 Function in Rice in Response to Heat Stress. International Journal of Molecular Sciences, 2023, 24, 5619.	1.8	5
4538	Approaches for Modes of Action Study of Long Non-Coding RNAs: From Single Verification to Genome-Wide Determination. International Journal of Molecular Sciences, 2023, 24, 5562.	1.8	1
4541	Lineage-specific differences and regulatory networks governing human chondrocyte development. ELife, 0, 12, .	2.8	7
4544	Chromatin profiling identifies transcriptional readthrough as a conserved mechanism for piRNA biogenesis in mosquitoes. Cell Reports, 2023, 42, 112257.	2.9	2
4545	One genome, multiple phenotypes: decoding the evolution and mechanisms of environmentally induced developmental plasticity in insects. Biochemical Society Transactions, 2023, 51, 675-689.	1.6	5
4547	TXNIP loss expands Myc-dependent transcriptional programs by increasing Myc genomic binding. PLoS Biology, 2023, 21, e3001778.	2.6	3
4548	Omics-based approaches to guide the design of biomaterials. Materials Today, 2023, 64, 98-120.	8.3	5
4549	Pioneer factor ASCL1 cooperates with the mSWI/SNF complex at distal regulatory elements to regulate human neural differentiation. Genes and Development, 2023, 37, 218-242.	2.7	13
4550	Dynamics of Chromatin Accessibility During Hematopoietic Stem Cell Differentiation Into Progressively Lineage-Committed Progeny. Stem Cells, 2023, 41, 520-539.	1.4	1
4551	Stepwise activities of mSWI/SNF family chromatin remodeling complexes direct T cell activation and exhaustion. Molecular Cell, 2023, 83, 1216-1236.e12.	4.5	13
4552	Integrative epigenetic analysis reveals AP-1 promotes activation of tumor-infiltrating regulatory T cells in HCC. Cellular and Molecular Life Sciences, 2023, 80, .	2.4	0
4553	Chromatin Accessibility and Transcriptional Landscape during Inhibition of Salmonella enterica by Lactobacillus reuteri in IPEC-J2 Cells. Cells, 2023, 12, 968.	1.8	2
4554	Genomic Analysis of Foxp3 Function in Regulatory T Cells. Journal of Immunology, 2023, 210, 880-887.	0.4	3
4555	Mena regulates nesprin-2 to control actinâ€“nuclear lamina associations, trans-nuclear membrane signalling and gene expression. Nature Communications, 2023, 14, .	5.8	8
4556	Loss of H3K9 trimethylation alters chromosome compaction and transcription factor retention during mitosis. Nature Structural and Molecular Biology, 2023, 30, 489-501.	3.6	2
4557	Snapshot: a package for clustering and visualizing epigenetic history during cell differentiation. BMC Bioinformatics, 2023, 24, .	1.2	3
4558	SEACells infers transcriptional and epigenomic cellular states from single-cell genomics data. Nature Biotechnology, 2023, 41, 1746-1757.	9.4	30
4559	Dose rate dependent reduction in chromatin accessibility at transcriptional start sites long time after exposure to gamma radiation. Epigenetics, 2023, 18, .	1.3	1

#	Article	IF	Citations
4560	Integrative epigenome profiling of 47XXY provides insights into whole genomic DNA hypermethylation and active chromatin accessibility. Frontiers in Molecular Biosciences, 0, 10, .	1.6	0
4561	Toward a comprehensive catalog of regulatory elements. Human Genetics, 2023, 142, 1091-1111.	1.8	4
4562	A-MYB and BRDT-dependent RNA Polymerase II pause release orchestrates transcriptional regulation in mammalian meiosis. Nature Communications, 2023, 14, .	5.8	8
4564	High level of novelty under the hood of convergent evolution. Science, 2023, 379, 1043-1049.	6.0	17
4565	Chemical modulation of Schistosoma mansoni lysine specific demethylase 1 (SmLSD1) induces wide-scale biological and epigenomic changes. Wellcome Open Research, 0, 8, 146.	0.9	1
4566	Assay for Transposase-Accessible Chromatin Using Sequencing of Freshly Isolated Muscle Stem Cells. Methods in Molecular Biology, 2023, , 397-412.	0.4	0
4567	Nuclei on the Rise: When Nuclei-Based Methods Meet Next-Generation Sequencing. Cells, 2023, 12, 1051.	1.8	1
4569	Distinct transcriptomic and epigenomic modalities underpin human memory T cell subsets and their activation potential. Communications Biology, 2023, 6, .	2.0	3
4571	TRACEâ€seq: Rapid, Lowâ€Input, Oneâ€Tube RNAâ€seq Library Construction Based on Tagmentation of RNA/DNA Hybrids. Current Protocols, 2023, 3, .	1.3	1
4572	Spurious intragenic transcription is a feature of mammalian cellular senescence and tissue aging. Nature Aging, 2023, 3, 402-417.	5.3	9
4573	Parallel recovery of chromatin accessibility and gene expression dynamics from frozen human regulatory T cells. Scientific Reports, 2023, 13, .	1.6	5
4575	C/EBPÎ± Confers Dependence to Fatty Acid Anabolic Pathways and Vulnerability to Lipid Oxidative Stressâ€“Induced Ferroptosis inFLT3-Mutant Leukemia. Cancer Discovery, 2023, 13, 1720-1747.	7.7	19
4576	NeuronMotif: Deciphering cis-regulatory codes by layer-wise demixing of deep neural networks. Proceedings of the National Academy of Sciences of the United States of America, 2023, 120, .	3.3	1
4577	Dual functions of TET1 in germ layer lineage bifurcation distinguished by genomic context and dependence on 5-methylcytosine oxidation. Nucleic Acids Research, 2023, 51, 5469-5498.	6.5	1
4578	Graded BMP signaling within intestinal crypt architecture directs self-organization of the Wnt-secreting stem cell niche. Cell Stem Cell, 2023, 30, 433-449.e8.	5.2	15
4579	Escape from oncogene-induced senescence is controlled by POU2F2 and memorized by chromatin scars. Cell Genomics, 2023, 3, 100293.	3.0	6
4580	Analysis of the P.Âlividus sea urchin genome highlights contrasting trends of genomic and regulatory evolution in deuterostomes. Cell Genomics, 2023, 3, 100295.	3.0	11
4583	Genome-wide chromatin accessibility and gene expression profiling during flatfish metamorphosis. Scientific Data, 2023, 10, .	2.4	1

#	Article	IF	Citations
4584	FOXK1 regulates Wnt signalling to promote cardiogenesis. Cardiovascular Research, 2023, 119, 1728-1739.	1.8	8
4585	DisP-seq reveals the genome-wide functional organization of DNA-associated disordered proteins. Nature Biotechnology, 2024, 42, 52-64.	9.4	4
4586	Aberrant cell state plasticity mediated by developmental reprogramming precedes colorectal cancer initiation. Science Advances, 2023, 9, .	4.7	11
4587	Toward cis-regulation in soybean: a 3D genome scope. Molecular Breeding, 2023, 43, .	1.0	1
4588	A multi-omics atlas of the human retina at single-cell resolution. Cell Genomics, 2023, 3, 100298.	3.0	10
4589	Reprogramming of human peripheral blood mononuclear cells into induced mesenchymal stromal cells using non-integrating vectors. Communications Biology, 2023, 6, .	2.0	1
4591	Dynamic chromatin architectures provide insights into the genetics of cattle myogenesis. Journal of Animal Science and Biotechnology, 2023, 14, .	2.1	1
4593	Chromatin accessibility differences between alpha, beta, and delta cells identifies common and cell type-specific enhancers. BMC Genomics, 2023, 24, .	1.2	3
4594	Optimized protocol for assay for transposase-accessible chromatin by sequencing (ATAC-seq) from Drosophila melanogaster brain tissue. STAR Protocols, 2023, 4, 102153.	0.5	1
4595	Quantitative Imaging Analysis of NF-Î²B for Mathematical Modeling Applications. Methods in Molecular Biology, 2023, , 253-266.	0.4	0
4598	Direct correction of haemoglobin E Î²-thalassaemia using base editors. Nature Communications, 2023, 14, .	5.8	6
4600	Experimental Validation and Prediction of Super-Enhancers: Advances and Challenges. Cells, 2023, 12, 1191.	1.8	1
4601	Multiomics Analysis Reveals Novel Genetic Determinants for Lens Differentiation, Structure, and Transparency. Biomolecules, 2023, 13, 693.	1.8	3
4602	Single-cell technologies for multimodal omics measurements. Frontiers in Systems Biology, 0, 3, .	0.5	0
4603	<scp>BORIS</scp> / <scp>CTCFL</scp> â€mediated chromatin accessibility alterations promote a proâ€invasive transcriptional signature in melanoma cells. Pigment Cell and Melanoma Research, 0, , .	1.5	0
4604	BMP4 triggers regulatory circuits specifying the cardiac mesoderm lineage. Development (Cambridge), 2023, 150, .	1.2	3
4605	The Principles and Applications of High-Throughput Sequencing Technologies. Development & Reproduction, 2023, 27, 9-24.	0.1	0
4624	Challenges for single-cell epigenetic analysis. , 2023, , 553-576.		0

#	Article	IF	Citations
4639	Profiling the Epigenetic Landscape of the Spermatogonial Stem Cellâ€”Part 1: Epigenomics Assays. Methods in Molecular Biology, 2023, , 71-108.	0.4	0
4647	The technological landscape and applications of single-cell multi-omics. Nature Reviews Molecular Cell Biology, 2023, 24, 695-713.	16.1	73
4684	The omics era: a nexus of untapped potential for Mendelian chromatinopathies. Human Genetics, 0, , .	1.8	5
4704	Analyzing the Genome-Wide Distribution of Histone Marks by CUT&Tag in Drosophila Embryos. Methods in Molecular Biology, 2023, , 1-17.	0.4	0
4716	Gene regulatory network inference in the era of single-cell multi-omics. Nature Reviews Genetics, 2023, 24, 739-754.	7.7	40
4807	Linking environmental risk factors with epigenetic mechanisms in Parkinsonâ€™s disease. Npj Parkinson's Disease, 2023, 9, .	2.5	6
4811	Combined Analysis of mRNA Expression and Open Chromatin in Microglia. Methods in Molecular Biology, 2024, , 543-571.	0.4	1
4893	Precision clinical genomics and single subject studies of multi-omics data. , 2024, , 41-56.		0
4901	Molecular Techniques in the Diagnosis and Monitoring of Acute and Chronic Leukaemias. , 2023, , 23-45.		0
4907	CUT&RUN and CUT&Tag: Low-input methods for genome-wide mapping of chromatin proteins. , 2024, , 371-385.		0
4912	Gene regulatory network reconstruction: harnessing the power of single-cell multi-omic data. Npj Systems Biology and Applications, 2023, 9, .	1.4	2
4940	Bioinformatics of epigenetic data generated from next-generation sequencing. , 2024, , 37-82.		0
4967	Vitamin D, chromatin, and epigenetics. , 2024, , 229-239.		0
4968	Analysis of Xylem Cells by Nucleus-Based Transcriptomics and Chromatin Profiling. Methods in Molecular Biology, 2024, , 67-78.	0.4	0
4993	Multimodal Methods for Knowledge Discovery from Bulk and Single-Cell Multi-Omics Data. , 2024, , 39-74.		0
5071	Cancer epigenetics: from laboratory studies and clinical trials to precision medicine. Cell Death Discovery, 2024, 10, .	2.0	0
5073	Sensors of Intracellular Nucleic Acids Activating STING-Dependent Production of Interferons in Immunocompetent Cells. Biochemistry (Moscow) Supplement Series A: Membrane and Cell Biology, 2023, 17, S1-S19.	0.3	0
5075	Best practices for the ATAC-seq assay and its data analysis. , 2024, , 285-318.		0

#	Article	IF	Citations
5094	Single-Nucleus ATAC-seq for Mapping Chromatin Accessibility in Individual Cells of Murine Hearts. Methods in Molecular Biology, 2024, , 245-257.	0.4	0
5123	Genomic Innovations for Improving Crops: The CRISPR Way. , 2023, , 273-286.		0
5128	Transcriptional Regulation of Early B-Cell Development. , 2024, , 141-159.		0
5150	Translational bioinformatics approach to combat cardiovascular disease and cancers. Advances in Protein Chemistry and Structural Biology, 2024, , 221-261.	1.0	1
5152	Chromatin organization of muscle stem cell. Current Topics in Developmental Biology, 2024, , 375-406.	1.0	0
5185	The cardiac conduction system: History, development, and disease. Current Topics in Developmental Biology, 2024, , 157-200.	1.0	0
5207	Dissecting the Immune SystemÂthroughÂGene Regulation. Advances in Experimental Medicine and Biology, 2024, , 219-235.	0.8	0