deepTools2: a next generation web server for deep-sequ

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Citation Report

#	Article	IF	Citations
3	RYBP stimulates PRC1 to shape chromatin-based communication between Polycomb repressive complexes. ELife, 2016, 5, .	2.8	111
4	O-Linked N-Acetylglucosamine (O-GlcNAc) Expression Levels Epigenetically Regulate Colon Cancer Tumorigenesis by Affecting the Cancer Stem Cell Compartment via Modulating Expression of Transcriptional Factor MYBL1. Journal of Biological Chemistry, 2017, 292, 4123-4137.	1.6	50
5	The evolutionary capacitor HSP90 buffers the regulatory effects of mammalian endogenous retroviruses. Nature Structural and Molecular Biology, 2017, 24, 234-242.	3.6	65
6	Inhibition of Inflammatory Gene Transcription by IL-10 Is Associated with Rapid Suppression of Lipopolysaccharide-Induced Enhancer Activation. Journal of Immunology, 2017, 198, 2906-2915.	0.4	30
7	The 7SK snRNP associates with the little elongation complex to promote snRNA gene expression. EMBO Journal, 2017, 36, 934-948.	3.5	35
8	Maintenance of macrophage transcriptional programs and intestinal homeostasis by epigenetic reader SP140. Science Immunology, 2017, 2, .	5.6	54
9	Integration of Shh and Fgf signaling in controlling <i>Hox</i> gene expression in cultured limb cells. Proceedings of the National Academy of Sciences of the United States of America, 2017, 114, 3139-3144.	3.3	21
10	A tiling-deletion-based genetic screen for cis-regulatory element identification in mammalian cells. Nature Methods, 2017, 14, 629-635.	9.0	217
11	GSuite HyperBrowser: integrative analysis of dataset collections across the genome and epigenome. GigaScience, 2017, 6, 1-12.	3.3	22
12	Regulation of DNA demethylation by the XPC DNA repair complex in somatic and pluripotent stem cells. Genes and Development, 2017, 31, 830-844.	2.7	21
13	Divergent Requirements for EZH1 in Heart Development Versus Regeneration. Circulation Research, 2017, 121, 106-112.	2.0	60
14	CHD1 regulates cell fate determination by activation of differentiation-induced genes. Nucleic Acids Research, 2017, 45, 7722-7735.	6.5	28
15	Impact of cytosine methylation on DNA binding specificities of human transcription factors. Science, 2017, 356, .	6.0	912
16	Piwi interacts with chromatin at nuclear pores and promiscuously binds nuclear transcripts in Drosophila ovarian somatic cells. Nucleic Acids Research, 2017, 45, 7666-7680.	6.5	32
17	Genome-Wide Profiling of Histone Modifications and Histone Variants in Arabidopsis thaliana and Marchantia polymorpha. Methods in Molecular Biology, 2017, 1610, 93-106.	0.4	9
18	Piwi Is Required during Drosophila Embryogenesis to License Dual-Strand piRNA Clusters for Transposon Repression in Adult Ovaries. Molecular Cell, 2017, 66, 411-419.e4.	4.5	69
19	Nucleus-Translocated ACSS2 Promotes Gene Transcription for Lysosomal Biogenesis and Autophagy. Molecular Cell, 2017, 66, 684-697.e9.	4.5	227
20	Chromatin Architecture Emerges during Zygotic Genome Activation Independent of Transcription. Cell, 2017, 169, 216-228.e19.	13.5	411

#	Article	IF	Citations
21	DHX9 suppresses RNA processing defects originating from the Alu invasion of the human genome. Nature, 2017, 544, 115-119.	13.7	415
22	CRISPRi-based genome-scale identification of functional long noncoding RNA loci in human cells. Science, 2017, 355, .	6.0	566
23	A mutually exclusive stemâ€“loop arrangement in roX2 RNA is essential for X-chromosome regulation in <i>Drosophila</i>. Genes and Development, 2017, 31, 1973-1987.	2.7	24
24	Mutant p53 shapes the enhancer landscape of cancer cells in response to chronic immune signaling. Nature Communications, 2017, 8, 754.	5.8	71
25	Relevance of iPSC-derived human PGC-like cells at the surface of embryoid bodies to prechemotaxis migrating PGCs. Proceedings of the National Academy of Sciences of the United States of America, 2017, 114, E9913-E9922.	3.3	41
26	ZNF281 enhances cardiac reprogramming by modulating cardiac and inflammatory gene expression. Genes and Development, 2017, 31, 1770-1783.	2.7	87
27	UTX-guided neural crest function underlies craniofacial features of Kabuki syndrome. Proceedings of the National Academy of Sciences of the United States of America, 2017, 114, E9046-E9055.	3.3	67
28	Genome-wide open chromatin regions and their effects on the regulation of silk protein genes in Bombyx mori. Scientific Reports, 2017, 7, 12919.	1.6	13
29	Thiol-linked alkylation of RNA to assess expression dynamics. Nature Methods, 2017, 14, 1198-1204.	9.0	411
30	Cytosolic acetyl-CoA promotes histone acetylation predominantly at H3K27 in Arabidopsis. Nature Plants, 2017, 3, 814-824.	4.7	85
31	A hyperdynamic H3.3 nucleosome marks promoter regions in pluripotent embryonic stem cells. Nucleic Acids Research, 2017, 45, 12181-12194.	6.5	28
32	Identification of the direct regulon of NtcA during early acclimation to nitrogen starvation in the cyanobacterium Synechocystis sp. PCC 6803. Nucleic Acids Research, 2017, 45, 11800-11820.	6.5	82
33	An architecture for genomics analysis in a clinical setting using Galaxy and Docker. GigaScience, 2017, 6, 1-9.	3.3	10
34	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
35	NEAT1 scaffolds RNA-binding proteins and the Microprocessor to globally enhance pri-miRNA processing. Nature Structural and Molecular Biology, 2017, 24, 816-824.	3.6	165
36	PAF1 regulation of promoter-proximal pause release via enhancer activation. Science, 2017, 357, 1294-1298.	6.0	95
37	The requirement of Mettl3-promoted <i>MyoD</i> mRNA maintenance in proliferative myoblasts for skeletal muscle differentiation. Open Biology, 2017, 7, 170119.	1.5	71
38	Yeast silencing factor Sir4 and a subset of nucleoporins form a complex distinct from nuclear pore complexes. Journal of Cell Biology, 2017, 216, 3145-3159.	2.3	40

#	ARTICLE	IF	CITATIONS
39	Histone Acetylation, Not Stoichiometry, Regulates Linker Histone Binding in Saccharomyces cerevisiae. Genetics, 2017, 207, 347-355.	1.2	9
40	An NF-Î°B Transcription-Factor-Dependent Lineage-Specific Transcriptional Program Promotes Regulatory T Cell Identity and Function. Immunity, 2017, 47, 450-465.e5.	6.6	161
41	Maternal H3K27me3 controls DNA methylation-independent imprinting. Nature, 2017, 547, 419-424.	13.7	349
42	Robust Identification of Developmentally Active Endothelial Enhancers in Zebrafish Using FANS-Assisted ATAC-Seq. Cell Reports, 2017, 20, 709-720.	2.9	62
43	Breast Cancer Suppression by Progesterone Receptors Is Mediated by Their Modulation of Estrogen Receptors and RNA Polymerase III. Cancer Research, 2017, 77, 4934-4946.	0.4	51
44	3D Chromatin Structures of Mature Gametes and Structural Reprogramming during Mammalian Embryogenesis. Cell, 2017, 170, 367-381.e20.	13.5	415
45	ETV4 and AP1 Transcription Factors Form Multivalent Interactions with three Sites on the MED25 Activator-Interacting Domain. Journal of Molecular Biology, 2017, 429, 2975-2995.	2.0	34
46	Histone Methyltransferase G9a Is Required for Cardiomyocyte Homeostasis and Hypertrophy. Circulation, 2017, 136, 1233-1246.	1.6	78
47	CCCTC-Binding Factor Translates Interleukin 2- and Î±-Ketoglutarate-Sensitive Metabolic Changes in TÂCells into Context-Dependent Gene Programs. Immunity, 2017, 47, 251-267.e7.	6.6	84
48	A sequence-specific core promoter-binding transcription factor recruits TRF2 to coordinately transcribe ribosomal protein genes. Nucleic Acids Research, 2017, 45, 10481-10491.	6.5	38
49	DNA replicationâ€“coupled histone modification maintains Polycomb gene silencing in plants. Science, 2017, 357, 1146-1149.	6.0	144
50	H3K14ac is linked to methylation of H3K9 by the triple Tudor domain of SETDB1. Nature Communications, 2017, 8, 2057.	5.8	72
51	Aberrant Activation of a Gastrointestinal Transcriptional Circuit in Prostate Cancer Mediates Castration Resistance. Cancer Cell, 2017, 32, 792-806.e7.	7.7	61
52	Cohesin facilitates zygotic genome activation in zebrafish. Development (Cambridge), 2018, 145, .	1.2	47
53	Arid1a Has Context-Dependent Oncogenic and Tumor Suppressor Functions in Liver Cancer. Cancer Cell, 2017, 32, 574-589.e6.	7.7	172
54	Convergent origination of a <i>Drosophila</i>-like dosage compensation mechanism in a reptile lineage. Genome Research, 2017, 27, 1974-1987.	2.4	81
55	Effects of a parental exposure to diuron on Pacific oyster spat methylome. Environmental Epigenetics, 2017, 3, dvx004.	0.9	56
56	Dosage compensation and sex-specific epigenetic landscape of the X chromosome in the pea aphid. Epigenetics and Chromatin, 2017, 10, 30.	1.8	34

#	Article	IF	Citations
57	Transcription factor-dependent â€˜anti-repressiveâ€™ mammalian enhancers exclude H3K27me3 from extended genomic domains. Genes and Development, 2017, 31, 2391-2404.	2.7	34
58	Characterization of the Polycomb-Group Mark H3K27me3 in Unicellular Algae. Frontiers in Plant Science, 2017, 8, 607.	1.7	38
59	Catalog of Differentially Expressed Long Non-Coding RNA following Activation of Human and Mouse Innate Immune Response. Frontiers in Immunology, 2017, 8, 1038.	2.2	66
60	Topological organization and dynamic regulation of human tRNA genes during macrophage differentiation. Genome Biology, 2017, 18, 180.	3.8	27
61	Optimized reduced representation bisulfite sequencing reveals tissue-specific mCHH islands in maize. Epigenetics and Chromatin, 2017, 10, 42.	1.8	19
62	Co-regulation of transcription by BRG1 and BRM, two mutually exclusive SWI/SNF ATPase subunits. Epigenetics and Chromatin, 2017, 10, 62.	1.8	37
63	CTCF and cohesin regulate chromatin loop stability with distinct dynamics. ELife, 2017, 6, .	2.8	476
64	Genome-wide mapping of endogenous G-quadruplex DNA structures by chromatin immunoprecipitation and high-throughput sequencing. Nature Protocols, 2018, 13, 551-564.	5.5	214
65	Computational Analysis of RNAâ€“Protein Interactions via Deep Sequencing. Methods in Molecular Biology, 2018, 1751, 171-182.	0.4	3
66	Chromatin Accessibility Landscape in Human Early Embryos and Its Association with Evolution. Cell, 2018, 173, 248-259.e15.	13.5	159
67	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
68	PRDM9 Methyltransferase Activity Is Essential for Meiotic DNA Double-Strand Break Formation at Its Binding Sites. Molecular Cell, 2018, 69, 853-865.e6.	4.5	110
69	Identification of Two Distinct Classes of the Human INO80 Complex Genome-Wide. G3: Genes, Genomes, Genetics, 2018, 8, 1095-1102.	0.8	21
70	Regeneration of the lung alveolus by an evolutionarily conserved epithelial progenitor. Nature, 2018, 555, 251-255.	13.7	537
71	The Transcriptionally Permissive Chromatin State of Embryonic Stem Cells Is Acutely Tuned to Translational Output. Cell Stem Cell, 2018, 22, 369-383.e8.	5.2	75
72	An Integrated Platform for Genome-wide Mapping of Chromatin States Using High-throughput ChIP-sequencing in Tumor Tissues. Journal of Visualized Experiments, 2018, , .	0.2	24
73	TCL1A, a Novel Transcription Factor and a Coregulator of Nuclear Factor ÎºB p65: Single Nucleotide Polymorphism and Estrogen Dependence. Journal of Pharmacology and Experimental Therapeutics, 2018, 365, 700-710.	1.3	9
74	The long nonâ€coding <scp>RNA</scp> <i>Paupar</i> promotes <scp>KAP</scp> 1â€dependent chromatin changes and regulatesÂolfactory bulb neurogenesis. EMBO Journal, 2018, 37, .	3.5	45

#	Article	IF	Citations
75	A Family of Vertebrate-Specific Polycombs Encoded by the LCOR/LCORL Genes Balance PRC2 Subtype Activities. Molecular Cell, 2018, 70, 408-421.e8.	4.5	121
76	Reciprocal Signaling between Glioblastoma Stem Cells and Differentiated Tumor Cells Promotes Malignant Progression. Cell Stem Cell, 2018, 22, 514-528.e5.	5.2	185
77	SLAM-seq defines direct gene-regulatory functions of the BRD4-MYC axis. Science, 2018, 360, 800-805.	6.0	284
78	A comprehensive map coupling histone modifications with gene regulation in adult dopaminergic and serotonergic neurons. Nature Communications, 2018, 9, 1226.	5.8	35
79	Warming Induces Significant Reprogramming of Beige, but Not Brown, Adipocyte Cellular Identity. Cell Metabolism, 2018, 27, 1121-1137.e5.	7.2	168
80	PLAG1 and USF2 Co-regulate Expression of Musashi-2 in Human Hematopoietic Stem and Progenitor Cells. Stem Cell Reports, 2018, 10, 1384-1397.	2.3	23
81	Functional crosstalk between histone H2B ubiquitylation and H2A modifications and variants. Nature Communications, 2018, 9, 1394.	5.8	59
82	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
83	Single-cell full-length total RNA sequencing uncovers dynamics of recursive splicing and enhancer RNAs. Nature Communications, 2018, 9, 619.	5.8	192
84	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
85	Regulation of the positive transcriptional effect of PLZF through a non-canonical EZH2 activity. Nucleic Acids Research, 2018, 46, 3339-3350.	6.5	26
86	Xrn2 accelerates termination by RNA polymerase II, which is underpinned by CPSF73 activity. Genes and Development, 2018, 32, 127-139.	2.7	107
87	Dynamic EBF1 occupancy directs sequential epigenetic and transcriptional events in B-cell programming. Genes and Development, 2018, 32, 96-111.	2.7	76
88	Identification of piRNA Binding Sites Reveals the Argonaute Regulatory Landscape of the C.Âelegans Germline. Cell, 2018, 172, 937-951.e18.	13.5	189
89	Isolation and Cultivation of Neural Progenitors Followed by Chromatin-Immunoprecipitation of Histone 3 Lysine 79 Dimethylation Mark. Journal of Visualized Experiments, 2018, , .	0.2	1
90	BRD4 interacts with NIPBL and BRD4 is mutated in a Cornelia de Langeâ€"like syndrome. Nature Genetics, 2018, 50, 329-332.	9.4	96
91	High-resolution TADs reveal DNA sequences underlying genome organization in flies. Nature Communications, 2018, 9, 189.	5.8	652
92	Loss of ASXL1 in the bone marrow niche dysregulates hematopoietic stem and progenitor cell fates. Cell Discovery, 2018, 4, 4.	3.1	28

#	ARTICLE	IF	CITATIONS
93	Mitochondrial translation requires folate-dependent tRNA methylation. Nature, 2018, 554, 128-132.	13.7	213
94	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
95	A molecular roadmap for the emergence of early-embryonic-like cells in culture. Nature Genetics, 2018, 50, 106-119.	9.4	144
96	Molecular Mechanisms for CFIm-Mediated Regulation of mRNA Alternative Polyadenylation. Molecular Cell, 2018, 69, 62-74.e4.	4.5	160
97	Genome-Wide Analysis of the Arabidopsis Replication Timing Program. Plant Physiology, 2018, 176, 2166-2185.	2.3	36
98	Robust Sub-nanomolar Library Preparation for High Throughput Next Generation Sequencing. BMC Genomics, 2018, 19, 326.	1.2	16
99	A Specific PfEMP1 Is Expressed in P.Âfalciparum Sporozoites and Plays a Role in Hepatocyte Infection. Cell Reports, 2018, 22, 2951-2963.	2.9	99
100	Atrx inactivation drives disease-defining phenotypes in glioma cells of origin through global epigenomic remodeling. Nature Communications, 2018, 9, 1057.	5.8	66
101	Direct Promoter Repression by BCL11A Controls the Fetal to Adult Hemoglobin Switch. Cell, 2018, 173, 430-442.e17.	13.5	328
102	The H3K36me2 Methyltransferase Nsd1 Demarcates PRC2-Mediated H3K27me2 and H3K27me3 Domains in Embryonic Stem Cells. Molecular Cell, 2018, 70, 371-379.e5.	4.5	137
103	uvCLAP is a fast and non-radioactive method to identify in vivo targets of RNA-binding proteins. Nature Communications, 2018, 9, 1142.	5.8	22
104	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
105	Mapping transcription factor occupancy using minimal numbers of cells in vitro and in vivo. Genome Research, 2018, 28, 592-605.	2.4	46
106	Root Development. Methods in Molecular Biology, 2018, , .	0.4	3
107	Chromatin Immunoprecipitation Sequencing (ChIP-Seq) for Transcription Factors and Chromatin Factors in Arabidopsis thaliana Roots: From Material Collection to Data Analysis. Methods in Molecular Biology, 2018, 1761, 231-248.	0.4	11
108	Sensitive and robust assessment of ChIP-seq read distribution using a strand-shift profile. Bioinformatics, 2018, 34, 2356-2363.	1.8	21
109	Zc3h13/Flacc is required for adenosine methylation by bridging the mRNA-binding factor Rbm15/Spenito to the m⁶A machinery component Wtap/Fl(2)d. Genes and Development, 2018, 32, 415-429.	2.7	416
110	Intranuclear and higherâ€order chromatin organization of the major histone gene cluster in breast cancer. Journal of Cellular Physiology, 2018, 233, 1278-1290.	2.0	40

#	Article	IF	Citations
111	Chromatinâ€remodeling factor OsINO80 is involved in regulation of gibberellin biosynthesis and is crucial for rice plant growth and development. Journal of Integrative Plant Biology, 2018, 60, 144-159.	4.1	30
112	FOXF1 Defines the Core-Regulatory Circuitry in Gastrointestinal Stromal Tumor. Cancer Discovery, 2018, 8, 234-251.	7.7	49
113	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
114	Nudt21 Controls Cell Fate by Connecting Alternative Polyadenylation to Chromatin Signaling. Cell, 2018, 172, 106-120.e21.	13.5	123
115	Î²â€Actinâ€dependent global chromatin organization and gene expression programs control cellular identity. FASEB Journal, 2018, 32, 1296-1314.	0.2	50
116	RELACS nuclei barcoding enables high-throughput ChIP-seq. Communications Biology, 2018, 1, 214.	2.0	30
117	PI3K: A master regulator of brain metastasisâ€promoting macrophages/microglia. Glia, 2018, 66, 2438-2455.	2.5	59
118	Effect of CFIm25 knockout on RNA polymerase II transcription. BMC Research Notes, 2018, 11, 894.	0.6	9
119	Profiling RNA Polymerase II Phosphorylation Genome-Wide in Fission Yeast. Methods in Enzymology, 2018, 612, 489-504.	0.4	2
120	<i>Leishmania</i> Genome Dynamics during Environmental Adaptation Reveal Strain-Specific Differences in Gene Copy Number Variation, Karyotype Instability, and Telomeric Amplification. MBio, 2018, 9, .	1.8	82
121	Mechanism of FACT removal from transcribed genes by anticancer drugs curaxins. Science Advances, 2018, 4, eaav2131.	4.7	47
122	JARID2 Functions as a Tumor Suppressor in Myeloid Neoplasms by Repressing Self-Renewal in Hematopoietic Progenitor Cells. Cancer Cell, 2018, 34, 741-756.e8.	7.7	44
123	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
124	ONECUT2 is a targetable master regulator of lethal prostate cancer that suppresses the androgen axis. Nature Medicine, 2018, 24, 1887-1898.	15.2	113
125	Similarities and differences in the regulation of HoxD genes during chick and mouse limb development. PLoS Biology, 2018, 16, e3000004.	2.6	28
126	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
127	The Heterochromatin Landscape in Migrating Cells and the Importance of H3K27me3 for Associated Transcriptome Alterations. Cells, 2018, 7, 205.	1.8	26
128	Chromatin Immunoprecipitation of Murine Brown Adipose Tissue. Journal of Visualized Experiments, 2018, , .	0.2	1

#	Article	IF	Citations
129	HDAC stimulates gene expression through BRD4 availability in response to IFN and in interferonopathies. Journal of Experimental Medicine, 2018, 215, 3194-3212.	4.2	39
130	Pergola: Boosting Visualization and Analysis of Longitudinal Data by Unlocking Genomic Analysis Tools. IScience, 2018, 9, 244-257.	1.9	5
131	Genomic landscape of oxidative DNA damage and repair reveals regioselective protection from mutagenesis. Genome Biology, 2018, 19, 215.	3.8	84
132	Mitochondrial Membrane Potential Regulates Nuclear Gene Expression in Macrophages Exposed to Prostaglandin E2. Immunity, 2018, 49, 1021-1033.e6.	6.6	75
133	The Transcription Factor Ets1 Suppresses T Follicular Helper Type 2 Cell Differentiation to Halt the Onset of Systemic Lupus Erythematosus. Immunity, 2018, 49, 1034-1048.e8.	6.6	97
134	Casein Kinase II Phosphorylation of Spt6 Enforces Transcriptional Fidelity by Maintaining Spn1-Spt6 Interaction. Cell Reports, 2018, 25, 3476-3489.e5.	2.9	20
135	BRCA2 controls DNA:RNA hybrid level at DSBs by mediating RNase H2 recruitment. Nature Communications, 2018, 9, 5376.	5.8	176
136	HoxA9 transforms murine myeloid cells by a feedback loop driving expression of key oncogenes and cell cycle control genes. Blood Advances, 2018, 2, 3137-3148.	2.5	31
137	Automated in situ chromatin profiling efficiently resolves cell types and gene regulatory programs. Epigenetics and Chromatin, 2018, 11, 74.	1.8	53
138	Single-molecule imaging correlates decreasing nuclear volume with increasing TF-chromatin associations during zebrafish development. Nature Communications, 2018, 9, 5218.	5.8	45
139	SOG1 activator and MYB3R repressors regulate a complex DNA damage network in <i>Arabidopsis</i>. Proceedings of the National Academy of Sciences of the United States of America, 2018, 115, E12453-E12462.	3.3	115
140	A DNA methylation reader complex that enhances gene transcription. Science, 2018, 362, 1182-1186.	6.0	181
141	Molecular Programming of Perivascular Stem Cell Precursors. Stem Cells, 2018, 36, 1890-1904.	1.4	25
142	Transcription Promotes the Interaction of the FAcilitates Chromatin Transactions (FACT) Complex with Nucleosomes in<i>Saccharomyces cerevisiae</i>. Genetics, 2018, 210, 869-881.	1.2	45
143	Downregulation of ERG and FLI1 expression in endothelial cells triggers endothelial-to-mesenchymal transition. PLoS Genetics, 2018, 14, e1007826.	1.5	54
144	High-throughput sequencing of sorted expression libraries reveals inhibitors of bacterial cell division. BMC Genomics, 2018, 19, 781.	1.2	6
145	From Pioneer to Repressor: Bimodal foxd3 Activity Dynamically Remodels Neural Crest Regulatory Landscape InÂVivo. Developmental Cell, 2018, 47, 608-628.e6.	3.1	92
146	Lymphocyte-Specific Chromatin Accessibility Pre-determines Glucocorticoid Resistance in Acute Lymphoblastic Leukemia. Cancer Cell, 2018, 34, 906-921.e8.	7.7	51

#	Article	IF	Citations
147	Transcription-associated histone pruning demarcates macroH2A chromatin domains. Nature Structural and Molecular Biology, 2018, 25, 958-970.	3.6	36
148	DNA Methylation by Restriction Modification Systems Affects the Global Transcriptome Profile in Borrelia burgdorferi. Journal of Bacteriology, 2018, 200, .	1.0	30
149	The synthetic histone-binding regulator protein PcTF activates interferon genes in breast cancer cells. BMC Systems Biology, 2018, 12, 83.	3.0	10
150	Transcriptional and epigenomic landscapes of CNS and non-CNS vascular endothelial cells. ELife, 2018, 7, .	2.8	180
151	Disruption of the RNA exosome reveals the hidden face of the malaria parasite transcriptome. RNA Biology, 2018, 15, 1206-1214.	1.5	16
152	Essential Nucleoid Associated Protein mIHF (Rv1388) Controls Virulence and Housekeeping Genes in Mycobacterium tuberculosis. Scientific Reports, 2018, 8, 14214.	1.6	19
153	A comprehensive analysis of 195 DNA methylomes reveals shared and cell-specific features of partially methylated domains. Genome Biology, 2018, 19, 150.	3.8	71
154	DNA G-quadruplex structures mold the DNA methylome. Nature Structural and Molecular Biology, 2018, 25, 951-957.	3.6	185
155	TET2 Deficiency Causes Germinal Center Hyperplasia, Impairs Plasma Cell Differentiation, and Promotes B-cell Lymphomagenesis. Cancer Discovery, 2018, 8, 1632-1653.	7.7	120
156	Histone deacetylase (HDAC) 1 and 2 complexes regulate both histone acetylation and crotonylation in vivo. Scientific Reports, 2018, 8, 14690.	1.6	84
157	Elongation/Termination Factor Exchange Mediated by PP1 Phosphatase Orchestrates Transcription Termination. Cell Reports, 2018, 25, 259-269.e5.	2.9	58
158	Genome-wide Identification of Structure-Forming Repeats as Principal Sites of Fork Collapse upon ATR Inhibition. Molecular Cell, 2018, 72, 222-238.e11.	4.5	55
159	DNA damage sensitivity of SWI/SNF-deficient cells depends on TFIIH subunit p62/GTF2H1. Nature Communications, 2018, 9, 4067.	5.8	25
160	Mapping of histone-binding sites in histone replacement-completed spermatozoa. Nature Communications, 2018, 9, 3885.	5.8	53
161	Accurate annotation of accessible chromatin in mouse and human primordial germ cells. Cell Research, 2018, 28, 1077-1089.	5.7	17
162	The H3K9 methyltransferase SETDB1 maintains female identity in Drosophila germ cells. Nature Communications, 2018, 9, 4155.	5.8	45
163	Enhancer, transcriptional, and cell fate plasticity precedes intestinal determination during endoderm development. Genes and Development, 2018, 32, 1430-1442.	2.7	34
164	DAF-16/FOXO and HLH-30/TFEB function as combinatorial transcription factors to promote stress resistance and longevity. Nature Communications, 2018, 9, 4400.	5.8	113

#	Article	IF	Citations
165	Global transcriptional activity dynamics reveal functional enhancer RNAs. Genome Research, 2018, 28, 1799-1811.	2.4	34
166	Electrostatic repulsion causes anticooperative DNA binding between tumor suppressor ETS transcription factors and JUNâ€"FOS at composite DNA sites. Journal of Biological Chemistry, 2018, 293, 18624-18635.	1.6	13
167	Unliganded Progesterone Receptor Governs Estrogen Receptor Gene Expression by Regulating DNA Methylation in Breast Cancer Cells. Cancers, 2018, 10, 371.	1.7	15
168	Nervous System Regionalization Entails Axial Allocation before Neural Differentiation. Cell, 2018, 175, 1105-1118.e17.	13.5	128
169	TRPS1 Is a Lineage-Specific Transcriptional Dependency in Breast Cancer. Cell Reports, 2018, 25, 1255-1267.e5.	2.9	46
170	The DNA binding landscape of the maize AUXIN RESPONSE FACTOR family. Nature Communications, 2018, 9, 4526.	5.8	146
171	N-methyladenine DNA Modification in Glioblastoma. Cell, 2018, 175, 1228-1243.e20.	13.5	236
172	Multiple modes of PRC2 inhibition elicit global chromatin alterations in H3K27M pediatric glioma. Science Advances, 2018, 4, eaau5935.	4.7	126
173	p73 Is Required for Ovarian Follicle Development and Regulates a Gene Network Involved in Cell-to-Cell Adhesion. IScience, 2018, 8, 236-249.	1.9	17
174	Variant PRC1 competes with retinoic acid-related signals to repress <i>Meis2</i> in distal forelimb bud. Development (Cambridge), 2018, 145, .	1.2	15
175	Dot1 promotes H2B ubiquitination by a methyltransferase-independent mechanism. Nucleic Acids Research, 2018, 46, 11251-11261.	6.5	24
176	Transcription Factors Drive Tet2-Mediated Enhancer Demethylation to Reprogram Cell Fate. Cell Stem Cell, 2018, 23, 727-741.e9.	5.2	156
177	Facultative dosage compensation of developmental genes on autosomes in Drosophila and mouse embryonic stem cells. Nature Communications, 2018, 9, 3626.	5.8	21
178	The Challenges of Genome-Wide Studies in a Unicellular Eukaryote With Two Nuclear Genomes. Methods in Enzymology, 2018, 612, 101-126.	0.4	3
179	Internal RNAs overlapping coding sequences can drive the production of alternative proteins in archaea. RNA Biology, 2018, 15, 1-14.	1.5	14
180	Pseudomonas aeruginosa partitioning protein ParB acts as a nucleoid-associated protein binding to multiple copies of a parS-related motif. Nucleic Acids Research, 2018, 46, 4592-4606.	6.5	27
181	Disease-Associated Short Tandem Repeats Co-localize with Chromatin Domain Boundaries. Cell, 2018, 175, 224-238.e15.	13.5	169
182	A Nuclear Export Block Triggers the Decay of Newly Synthesized Polyadenylated RNA. Cell Reports, 2018, 24, 2457-2467.e7.	2.9	34

#	ARTICLE	IF	CITATIONS
183	Study of mitotic chromatin supports a model of bookmarking by histone modifications and reveals nucleosome deposition patterns. Genome Research, 2018, 28, 1455-1466.	2.4	35
184	ASXL1 impairs osteoclast formation by epigenetic regulation of NFATc1. Blood Advances, 2018, 2, 2467-2477.	2.5	21
185	The Epigenetic State of PRDM16-Regulated Enhancers in Radial Glia Controls Cortical Neuron Position. Neuron, 2018, 98, 945-962.e8.	3.8	54
186	Cyclin-dependent kinase 1 (CDK1) and CDK2 have opposing roles in regulating interactions of splicing factor 3B1 with chromatin. Journal of Biological Chemistry, 2018, 293, 10220-10234.	1.6	15
187	The Galaxy platform for accessible, reproducible and collaborative biomedical analyses: 2018 update. Nucleic Acids Research, 2018, 46, W537-W544.	6.5	3,003
188	Activity-dependent neuroprotective protein recruits HP1 and CHD4 to control lineage-specifying genes. Nature, 2018, 557, 739-743.	13.7	169
189	The GWIPSâ€•viz Browser. Current Protocols in Bioinformatics, 2018, 62, e50.	25.8	4
190	The Polycomb-Dependent Epigenome Controls Î² Cell Dysfunction, Dedifferentiation, and Diabetes. Cell Metabolism, 2018, 27, 1294-1308.e7.	7.2	109
191	The Chromatin Remodelers PKL and PIE1 Act in an Epigenetic Pathway That Determines H3K27me3 Homeostasis in Arabidopsis. Plant Cell, 2018, 30, 1337-1352.	3.1	97
192	Revised roles of ISL1 in a hES cell-based model of human heart chamber specification. ELife, 2018, 7, .	2.8	38
193	Chromatin-associated RNA sequencing (ChAR-seq) maps genome-wide RNA-to-DNA contacts. ELife, 2018, 7, .	2.8	121
194	EZH2-Mediated Primary Cilium Deconstruction Drives Metastatic Melanoma Formation. Cancer Cell, 2018, 34, 69-84.e14.	7.7	123
195	The Nucleosome Remodeling and Deacetylation Complex Modulates Chromatin Structure at Sites of Active Transcription to Fine-Tune Gene Expression. Molecular Cell, 2018, 71, 56-72.e4.	4.5	132
196	A stable mode of bookmarking by TBP recruits RNA polymerase II to mitotic chromosomes. ELife, 2018, 7, .	2.8	92
197	MCM2â€“7-dependent cohesin loading during S phase promotes sister-chromatid cohesion. ELife, 2018, 7, .	2.8	57
198	Systemic Loss and Gain of Chromatin Architecture throughout Zebrafish Development. Cell Reports, 2018, 24, 1-10.e4.	2.9	124
199	The Transcription Factor ETV1 Induces Atrial Remodeling and Arrhythmia. Circulation Research, 2018, 123, 550-563.	2.0	40
200	Galaxy HiCExplorer: a web server for reproducible Hi-C data analysis, quality control and visualization. Nucleic Acids Research, 2018, 46, W11-W16.	6.5	168

#	ARTICLE	IF	CITATIONS
201	Persistent accumulation of unrepaired DNA damage in rat cortical neurons: nuclear organization and ChIP-seq analysis of damaged DNA. Acta Neuropathologica Communications, 2018, 6, 68.	2.4	16
202	A Single-Cell Atlas of InÂVivo Mammalian Chromatin Accessibility. Cell, 2018, 174, 1309-1324.e18.	13.5	620
203	FACT Sets a Barrier for Cell Fate Reprogramming in Caenorhabditis elegans and Human Cells. Developmental Cell, 2018, 46, 611-626.e12.	3.1	89
204	Chikungunya virus evolution following a large 3â€²UTR deletion results in host-specific molecular changes in protein-coding regions. Virus Evolution, 2018, 4, vey012.	2.2	24
205	Polycomb-mediated gene silencing by the BAHâ€"EMF1 complex in plants. Nature Genetics, 2018, 50, 1254-1261.	9.4	79
206	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
207	SWI/SNF regulates half of its targets without the need of ATP-driven nucleosome remodeling by Brahma. BMC Genomics, 2018, 19, 367.	1.2	20
208	Canonical PRC2 function is essential for mammary gland development and affects chromatin compaction in mammary organoids. PLoS Biology, 2018, 16, e2004986.	2.6	10
209	KDM5 histone demethylases repress immune response via suppression of STING. PLoS Biology, 2018, 16, e2006134.	2.6	106
210	ATAC2GRN: optimized ATAC-seq and DNase1-seq pipelines for rapid and accurate genome regulatory network inference. BMC Genomics, 2018, 19, 563.	1.2	19
211	Dynamic bimodal changes in CpG and non-CpG methylation genome-wide upon CGGBP1 loss-of-function. BMC Research Notes, 2018, 11, 419.	0.6	15
212	Decoding the chromatin proteome of a single genomic locus by DNA sequencing. PLoS Biology, 2018, 16, e2005542.	2.6	14
213	H3K4me2 and WDR5 enriched chromatin interacting long non-coding RNAs maintain transcriptionally competent chromatin at divergent transcriptional units. Nucleic Acids Research, 2018, 46, 9384-9400.	6.5	28
214	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
215	Characterization of the accessible genome in the human malaria parasite Plasmodium falciparum. Nucleic Acids Research, 2018, 46, 9414-9431.	6.5	50
216	Episomal HBV persistence within transcribed host nuclear chromatin compartments involves HBx. Epigenetics and Chromatin, 2018, 11, 34.	1.8	23
217	Adaptation of an amplicon-based human cancer next-generation sequencing panel assay for murine tumors. Analytical Biochemistry, 2018, 551, 26-28.	1.1	0
218	Genome-wide analysis reveals a role for TDG in estrogen receptor-mediated enhancer RNA transcription and 3-dimensional reorganization. Epigenetics and Chromatin, 2018, 11, 5.	1.8	19

#	Article	IF	Citations
219	Individual retrotransposon integrants are differentially controlled by KZFP/KAP1-dependent histone methylation, DNA methylation and TET-mediated hydroxymethylation in naÃ¯ve embryonic stem cells. Epigenetics and Chromatin, 2018, 11, 7.	1.8	39
220	Locus-specific control of the de novo DNA methylation pathway in Arabidopsis by the CLASSY family. Nature Genetics, 2018, 50, 865-873.	9.4	103
221	Emerin modulates spatial organization of chromosome territories in cells on softer matrices. Nucleic Acids Research, 2018, 46, 5561-5586.	6.5	24
222	Patterns of chromatin accessibility along the anterior-posterior axis in the early Drosophila embryo. PLoS Genetics, 2018, 14, e1007367.	1.5	38
224	Identifying Genomic Sites of ADP-Ribosylation Mediated by Specific Nuclear PARP Enzymes Using Click-ChIP. Methods in Molecular Biology, 2018, 1813, 371-387.	0.4	1
225	Epigenetic analyses of planarian stem cells demonstrate conservation of bivalent histone modifications in animal stem cells. Genome Research, 2018, 28, 1543-1554.	2.4	32
226	Rice nucleosome patterns undergo remodeling coincident with stress-induced gene expression. BMC Genomics, 2018, 19, 97.	1.2	12
227	Cooperative Enhancer Activation by TLX1 and STAT5 Drives Development of NUP214-ABL1/TLX1-Positive T Cell Acute Lymphoblastic Leukemia. Cancer Cell, 2018, 34, 271-285.e7.	7.7	48
228	The transcriptional landscape of polyploid wheat. Science, 2018, 361, .	6.0	768
229	MCM2 promotes symmetric inheritance of modified histones during DNA replication. Science, 2018, 361, 1389-1392.	6.0	207
230	Ascorbate Suppresses VEGF Expression in Retinal Pigment Epithelial Cells. , 2018, 59, 3608.		21
231	Distinct roles of cohesin-SA1 and cohesin-SA2 in 3D chromosome organization. Nature Structural and Molecular Biology, 2018, 25, 496-504.	3.6	128
232	SWI/SNF interacts with cleavage and polyadenylation factors and facilitates pre-mRNA 3â€² end processing. Nucleic Acids Research, 2018, 46, 8557-8573.	6.5	10
233	NF90/ILF3 is a transcription factor that promotes proliferation over differentiation by hierarchical regulation in K562 erythroleukemia cells. PLoS ONE, 2018, 13, e0193126.	1.1	21
234	Mutations in the SWI/SNF complex induce a targetable dependence on oxidative phosphorylation in lung cancer. Nature Medicine, 2018, 24, 1047-1057.	15.2	175
235	A Cdk9â€“PP1 switch regulates the elongationâ€“termination transition of RNA polymerase II. Nature, 2018, 558, 460-464.	13.7	105
236	Casein kinase 2 mediated phosphorylation of Spt6 modulates histone dynamics and regulates spurious transcription. Nucleic Acids Research, 2018, 46, 7612-7630.	6.5	22
237	Unique patterns of trimethylation of histone H3 lysine 4 are prone to changes during aging in Caenorhabditis elegans somatic cells. PLoS Genetics, 2018, 14, e1007466.	1.5	33

#	Article	IF	Citations
238	Epigenetic Optical Mapping of 5-Hydroxymethylcytosine in Nanochannel Arrays. ACS Nano, 2018, 12, 7148-7158.	7.3	46
239	The epiGenomic Efficient Correlator (epiGeEC) tool allows fast comparison of user datasets with thousands of public epigenomic datasets. Bioinformatics, 2019, 35, 674-676.	1.8	5
240	Oxidative DNA damage is associated more with genome accessibility than spatial positioning in the nucleus. Journal of Biomolecular Structure and Dynamics, 2019, 37, 1857-1862.	2.0	2
241	Trichloroethylene exposure alters dimethylated histone three lysine four in protein kinase A signaling pathway chromatin of rat spermâ€. Biology of Reproduction, 2019, 101, 875-877.	1.2	3
242	Methyl-CpG-binding domain 9 (MBD9) is required for H2A.Z incorporation into chromatin at a subset of H2A.Z-enriched regions in the Arabidopsis genome. PLoS Genetics, 2019, 15, e1008326.	1.5	34
243	Linker histones are fine-scale chromatin architects modulating developmental decisions in Arabidopsis. Genome Biology, 2019, 20, 157.	3.8	67
244	Increase in DNA Damage by MYCN Knockdown Through Regulating Nucleosome Organization and Chromatin State in Neuroblastoma. Frontiers in Genetics, 2019, 10, 684.	1.1	4
245	A general approach for detecting expressed mutations in AML cells using single cell RNA-sequencing. Nature Communications, 2019, 10, 3660.	5.8	147
246	HNF4 factors control chromatin accessibility and are redundantly required for maturation of the fetal intestine. Development (Cambridge), 2019, 146, .	1.2	22
247	NET-prism enables RNA polymerase-dedicated transcriptional interrogation at nucleotide resolution. RNA Biology, 2019, 16, 1156-1165.	1.5	5
248	Pluripotency reprogramming by competent and incompetent POU factors uncovers temporal dependency for Oct4 and Sox2. Nature Communications, 2019, 10, 3477.	5.8	60
249	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
250	Biased gene retention during diploidization in Brassica linked to three-dimensional genome organization. Nature Plants, 2019, 5, 822-832.	4.7	52
251	Transcriptome-wide dynamics of extensive m6A mRNA methylation during Plasmodium falciparum blood-stage development. Nature Microbiology, 2019, 4, 2246-2259.	5.9	66
252	The Histone Deacetylase SIRT6 Restrains Transcription Elongation via Promoter-Proximal Pausing. Molecular Cell, 2019, 75, 683-699.e7.	4.5	50
253	Ketone Body Signaling Mediates Intestinal Stem Cell Homeostasis and Adaptation to Diet. Cell, 2019, 178, 1115-1131.e15.	13.5	231
254	Genomic Resolution of DLX-Orchestrated Transcriptional Circuits Driving Development of Forebrain GABAergic Neurons. Cell Reports, 2019, 28, 2048-2063.e8.	2.9	68
255	The Eleanor ncRNAs activate the topological domain of the ESR1 locus to balance against apoptosis. Nature Communications, 2019, 10, 3778.	5.8	28

#	ARTICLE	IF	CITATIONS
256	Functional interplay between Mediator and RNA polymerase II in Rad2/XPG loading to the chromatin. Nucleic Acids Research, 2019, 47, 8988-9004.	6.5	17
257	Tasks, Techniques, and Tools for Genomic Data Visualization. Computer Graphics Forum, 2019, 38, 781-805.	1.8	61
258	Activation of neuronal genes via LINE-1 elements upon global DNA demethylation in human neural progenitors. Nature Communications, 2019, 10, 3182.	5.8	76
259	Chromatin Profiles of Chromosomally Integrated Human Herpesvirus-6A. Frontiers in Microbiology, 2019, 10, 1408.	1.5	22
260	Monoallelic expression and epigenetic inheritance sustained by a Trypanosoma brucei variant surface glycoprotein exclusion complex. Nature Communications, 2019, 10, 3023.	5.8	73
261	Retention of paternal DNA methylome in the developing zebrafish germline. Nature Communications, 2019, 10, 3054.	5.8	99
262	Pioneer and repressive functions of p63 during zebrafish embryonic ectoderm specification. Nature Communications, 2019, 10, 3049.	5.8	39
263	Genome-wide mapping and profiling of Î³H2AX binding hotspots in response to different replication stress inducers. BMC Genomics, 2019, 20, 579.	1.2	20
264	Three-Dimensional Genomic Structure and Cohesin Occupancy Correlate with Transcriptional Activity during Spermatogenesis. Cell Reports, 2019, 28, 352-367.e9.	2.9	112
265	Toxin-mediated ribosome stalling reprograms the Mycobacterium tuberculosis proteome. Nature Communications, 2019, 10, 3035.	5.8	22
266	Elevated H3K27ac in aged skeletal muscle leads to increase in extracellular matrix and fibrogenic conversion of muscle satellite cells. Aging Cell, 2019, 18, e12996.	3.0	35
267	Crosstalk between chromatin structure, cohesin activity and transcription. Epigenetics and Chromatin, 2019, 12, 47.	1.8	17
268	Chromatin Profiling of the Repetitive and Nonrepetitive Genomes of the Human Fungal Pathogen Candida albicans. MBio, 2019, 10, .	1.8	19
269	Stabilizing heterochromatin by DGCR8 alleviates senescence and osteoarthritis. Nature Communications, 2019, 10, 3329.	5.8	82
270	Functional dissection of the Sox9â€"Kcnj2 locus identifies nonessential and instructive roles of TAD architecture. Nature Genetics, 2019, 51, 1263-1271.	9.4	223
271	Novel cell adhesion/migration pathways are predictive markers of HDAC inhibitor resistance in cutaneous T cell lymphoma. EBioMedicine, 2019, 46, 170-183.	2.7	26
272	MAPCap allows high-resolution detection and differential expression analysis of transcription start sites. Nature Communications, 2019, 10, 3219.	5.8	16
273	Spatial chromatin architecture alteration by structural variations in human genomes at the population scale. Genome Biology, 2019, 20, 148.	3.8	36

#	ARTICLE	IF	CITATIONS
274	Chemotherapeutic Drugs Inhibiting Topoisomerase 1 Activity Impede Cytokine-Induced and NF-ÎºB p65-Regulated Gene Expression. Cancers, 2019, 11, 883.	1.7	11
275	A Genomeâ€Wide Association Study of Nonâ€Photochemical Quenching in response to local seasonal climates in <i>Arabidopsis thaliana</i>. Plant Direct, 2019, 3, e00138.	0.8	25
276	Epigenetic Compensation Promotes Liver Regeneration. Developmental Cell, 2019, 50, 43-56.e6.	3.1	49
277	CPF Recruitment to Non-canonical Transcription Termination Sites Triggers Heterochromatin Assembly and Gene Silencing. Cell Reports, 2019, 28, 267-281.e5.	2.9	33
278	TOX is a critical regulator of tumour-specific T cell differentiation. Nature, 2019, 571, 270-274.	13.7	697
279	Defining Genetic Variation in Widely Used Congenic and Backcrossed Mouse Models Reveals Varied Regulation of Genes Important for Immune Responses. Immunity, 2019, 51, 155-168.e5.	6.6	29
280	Pioneer Factor-Nucleosome Binding Events during Differentiation Are Motif Encoded. Molecular Cell, 2019, 75, 562-575.e5.	4.5	98
281	Identification of the m6Am Methyltransferase PCIF1 Reveals the Location and Functions of m6Am in the Transcriptome. Molecular Cell, 2019, 75, 631-643.e8.	4.5	183
282	H3K4me2 functions as a repressive epigenetic mark in plants. Epigenetics and Chromatin, 2019, 12, 40.	1.8	51
283	The transcription factor OsSUF4 interacts with SDG725 in promoting H3K36me3 establishment. Nature Communications, 2019, 10, 2999.	5.8	29
284	Re-programing Chromatin with a Bifunctional LSD1/HDAC Inhibitor Induces Therapeutic Differentiation in DIPG. Cancer Cell, 2019, 36, 528-544.e10.	7.7	128
285	Recapitulation and Reversal of Schizophrenia-Related Phenotypes in Setd1a-Deficient Mice. Neuron, 2019, 104, 471-487.e12.	3.8	79
286	Reconstruction of the Global Neural Crest Gene Regulatory Network InÂVivo. Developmental Cell, 2019, 51, 255-276.e7.	3.1	108
287	The Lineage Determining Factor GRHL2 Collaborates with FOXA1 to Establish a Targetable Pathway in Endocrine Therapy-Resistant Breast Cancer. Cell Reports, 2019, 29, 889-903.e10.	2.9	40
288	Activation of Oncogenic Super-Enhancers Is Coupled with DNA Repair by RAD51. Cell Reports, 2019, 29, 560-572.e4.	2.9	39
289	PARP1 Co-Regulates EP300â€“BRG1-Dependent Transcription of Genes Involved in Breast Cancer Cell Proliferation and DNA Repair. Cancers, 2019, 11, 1539.	1.7	26
290	The RNA-Binding Protein A1CF Regulates Hepatic Fructose and Glycerol Metabolism via Alternative RNA Splicing. Cell Reports, 2019, 29, 283-300.e8.	2.9	35
291	Hi-C guided assemblies reveal conserved regulatory topologies on X and autosomes despite extensive genome shuffling. Genes and Development, 2019, 33, 1591-1612.	2.7	43

#	Article	IF	Citations
292	Analysing the rice young panicle transcriptome reveals the gene regulatory network controlled by TRIANGULAR HULL1. Rice, 2019, 12, 6.	1.7	9
293	A reference map of murine cardiac transcription factor chromatin occupancy identifies dynamic and conserved enhancers. Nature Communications, 2019, 10, 4907.	5.8	100
294	rDNA Clusters Make Contact with Genes that Are Involved in Differentiation and Cancer and Change Contacts after Heat Shock Treatment. Cells, 2019, 8, 1393.	1.8	13
295	Histone acetylation orchestrates wound-induced transcriptional activation and cellular reprogramming in Arabidopsis. Communications Biology, 2019, 2, 404.	2.0	65
296	Recognition of Histone Crotonylation by Taf14 Links Metabolic State to Gene Expression. Molecular Cell, 2019, 76, 909-921.e3.	4.5	83
297	Thermal Manipulation During Embryogenesis Impacts H3K4me3 and H3K27me3 Histone Marks in Chicken Hypothalamus. Frontiers in Genetics, 2019, 10, 1207.	1.1	39
298	Early Diverging Fungus Mucor circinelloides Lacks Centromeric Histone CENP-A and Displays a Mosaic of Point and Regional Centromeres. Current Biology, 2019, 29, 3791-3802.e6.	1.8	77
299	Disease modeling of a mutation in Î±â€actinin 2 guides clinical therapy in hypertrophic cardiomyopathy. EMBO Molecular Medicine, 2019, 11, e11115.	3.3	88
300	Mapping Native R-Loops Genome-wide Using a Targeted Nuclease Approach. Cell Reports, 2019, 29, 1369-1380.e5.	2.9	64
301	The Leukemogenic TCF3-HLF Complex Rewires Enhancers Driving Cellular Identity and Self-Renewal Conferring EP300 Vulnerability. Cancer Cell, 2019, 36, 630-644.e9.	7.7	35
302	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
303	R-Loops Promote Antisense Transcription across the Mammalian Genome. Molecular Cell, 2019, 76, 600-616.e6.	4.5	112
304	Methylation changes in the peripheral blood of filipinos with type 2 diabetes suggest spurious transcription initiation at TXNIP. Human Molecular Genetics, 2019, 28, 4208-4218.	1.4	12
305	Heat-Shock Protein 90 Controls the Expression of Cell-Cycle Genes by Stabilizing Metazoan-Specific Host-Cell Factor HCFC1. Cell Reports, 2019, 29, 1645-1659.e9.	2.9	22
306	Genome-wide Analyses of Chromatin State in Human Mast Cells Reveal Molecular Drivers and Mediators of Allergic and Inflammatory Diseases. Immunity, 2019, 51, 949-965.e6.	6.6	37
307	The quorum sensing transcription factor AphA directly regulates natural competence in Vibrio cholerae. PLoS Genetics, 2019, 15, e1008362.	1.5	25
308	The Ovulatory Signal Precipitates LRH-1 Transcriptional Switching Mediated by Differential Chromatin Accessibility. Cell Reports, 2019, 28, 2443-2454.e4.	2.9	19
309	Endothelial TGF-Î² signalling drives vascular inflammation and atherosclerosis. Nature Metabolism, 2019, 1, 912-926.	5.1	172

#	Article	IF	Citations
310	Changes in chromatin accessibility ensure robust cell cycle exit in terminally differentiated cells. PLoS Biology, 2019, 17, e3000378.	2.6	41
311	Comparative analysis demonstrates cell type-specific conservation of SOX9 targets between mouse and chicken. Scientific Reports, 2019, 9, 12560.	1.6	22
312	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
313	Germ Granules Coordinate RNA-Based Epigenetic Inheritance Pathways. Developmental Cell, 2019, 50, 704-715.e4.	3.1	62
314	CoBATCH for High-Throughput Single-Cell Epigenomic Profiling. Molecular Cell, 2019, 76, 206-216.e7.	4.5	147
315	Comprehensive analysis of long noncoding RNA (lncRNA)-chromatin interactions reveals lncRNA functions dependent on binding diverse regulatory elements. Journal of Biological Chemistry, 2019, 294, 15613-15622.	1.6	32
316	Eukaryotic Adaptation to Years-Long Starvation Resembles that of Bacteria. IScience, 2019, 19, 545-558.	1.9	11
317	Profiling chromatin states using single-cell itChIP-seq. Nature Cell Biology, 2019, 21, 1164-1172.	4.6	109
318	Immediate and deferred epigenomic signatures of in vivo neuronal activation in mouse hippocampus. Nature Neuroscience, 2019, 22, 1718-1730.	7.1	114
319	High-quality Schistosoma haematobium genome achieved by single-molecule and long-range sequencing. GigaScience, 2019, 8, .	3.3	41
320	Distinct Classes of Chromatin Loops Revealed by Deletion of an RNA-Binding Region in CTCF. Molecular Cell, 2019, 76, 395-411.e13.	4.5	172
321	PRC2.1 and PRC2.2 Synergize to Coordinate H3K27 Trimethylation. Molecular Cell, 2019, 76, 437-452.e6.	4.5	137
322	SETD5 Regulates Chromatin Methylation State and Preserves Global Transcriptional Fidelity during Brain Development and Neuronal Wiring. Neuron, 2019, 104, 271-289.e13.	3.8	75
323	A high-resolution 3D epigenomic map reveals insights into the creation of the prostate cancer transcriptome. Nature Communications, 2019, 10, 4154.	5.8	87
324	A Complex of U1 snRNP with Cleavage and Polyadenylation Factors Controls Telescripting, Regulating mRNA Transcription in Human Cells. Molecular Cell, 2019, 76, 590-599.e4.	4.5	72
325	RNA Interactions Are Essential for CTCF-Mediated Genome Organization. Molecular Cell, 2019, 76, 412-422.e5.	4.5	183
326	Evolutionary flexibility in flooding response circuitry in angiosperms. Science, 2019, 365, 1291-1295.	6.0	101
327	Effect of CFIm68 knockdown on RNA polymerase II transcription. BMC Research Notes, 2019, 12, 554.	0.6	2

#	ARTICLE	IF	CITATIONS
328	Mitochondrial Reprogramming Underlies Resistance to BCL-2 Inhibition in Lymphoid Malignancies. Cancer Cell, 2019, 36, 369-384.e13.	7.7	224
329	BAP1 regulates epigenetic switch from pluripotency to differentiation in developmental lineages giving rise to BAP1-mutant cancers. Science Advances, 2019, 5, eaax1738.	4.7	57
330	Physical and Functional Compartmentalization of Archaeal Chromosomes. Cell, 2019, 179, 165-179.e18.	13.5	62
331	Perturbed myoepithelial cell differentiation in BRCA mutation carriers and in ductal carcinoma in situ. Nature Communications, 2019, 10, 4182.	5.8	37
332	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
333	Taggerâ€"A Swiss army knife for multiomics to dissect cell typeâ€"specific mechanisms of gene expression in mice. PLoS Biology, 2019, 17, e3000374.	2.6	12
334	A Pandas complex adapted for piRNA-guided transcriptional silencing and heterochromatin formation. Nature Cell Biology, 2019, 21, 1261-1272.	4.6	49
335	Distinct transcriptional roles for Histone H3-K56 acetylation during the cell cycle in Yeast. Nature Communications, 2019, 10, 4372.	5.8	40
336	X Chromosome Domain Architecture Regulates Caenorhabditis elegans Lifespan but Not Dosage Compensation. Developmental Cell, 2019, 51, 192-207.e6.	3.1	39
337	New High-Throughput Screening Identifies Compounds That Reduce Viability Specifically in Liver Cancer Cells That Express High Levels of SALL4 by Inhibiting Oxidative Phosphorylation. Gastroenterology, 2019, 157, 1615-1629.e17.	0.6	42
338	Circadian rhythmâ€"dependent and circadian rhythmâ€"independent impacts of the molecular clock on type 3 innate lymphoid cells. Science Immunology, 2019, 4, .	5.6	65
339	LEDGF and HDGF2 relieve the nucleosome-induced barrier to transcription in differentiated cells. Science Advances, 2019, 5, eaay3068.	4.7	61
340	Discovery and Characterization of a Cellular Potent Positive Allosteric Modulator of the Polycomb Repressive Complex 1 Chromodomain, CBX7. Cell Chemical Biology, 2019, 26, 1365-1379.e22.	2.5	38
341	Transcription-dependent targeting of Hda1C to hyperactive genes mediates H4-specific deacetylation in yeast. Nature Communications, 2019, 10, 4270.	5.8	14
342	Chromatin-Based Classification of Genetically Heterogeneous AMLs into Two Distinct Subtypes with Diverse Stemness Phenotypes. Cell Reports, 2019, 26, 1059-1069.e6.	2.9	33
343	C1 CAGE detects transcription start sites and enhancer activity at single-cell resolution. Nature Communications, 2019, 10, 360.	5.8	102
344	An integrated chromatin accessibility and transcriptome landscape of human pre-implantation embryos. Nature Communications, 2019, 10, 364.	5.8	82
345	Widespread interâ€individual gene expression variability in <i>Arabidopsis thaliana</i>. Molecular Systems Biology, 2019, 15, e8591.	3.2	55

#	ARTICLE	IF	CITATIONS
346	The Lupus Susceptibility Locus Sgp3 Encodes the Suppressor of Endogenous Retrovirus Expression SNERV. Immunity, 2019, 50, 334-347.e9.	6.6	61
347	Comparative Epigenomics Reveals that RNA Polymerase II Pausing and Chromatin Domain Organization Control Nematode piRNA Biogenesis. Developmental Cell, 2019, 48, 793-810.e6.	3.1	37
348	Promoter-proximal pausing mediated by the exon junction complex regulates splicing. Nature Communications, 2019, 10, 521.	5.8	28
349	TRF2 positively regulates SULF2 expression increasing VEGF-A release and activity in tumor microenvironment. Nucleic Acids Research, 2019, 47, 3365-3382.	6.5	34
350	Historical Meiotic Crossover Hotspots Fueled Patterns of Evolutionary Divergence in Rice. Plant Cell, 2019, 31, 645-662.	3.1	41
351	Sex-specific histone modifications in mouse fetal and neonatal germ cells. Epigenomics, 2019, 11, 543-561.	1.0	15
352	The ReproGenomics Viewer: a multi-omics and cross-species resource compatible with single-cell studies for the reproductive science community. Bioinformatics, 2019, 35, 3133-3139.	1.8	49
353	A dynamic and integrated epigenetic program at distal regions orchestrates transcriptional responses to VEGFA. Genome Research, 2019, 29, 193-207.	2.4	13
354	Meiocyte-Specific and AtSPO11-1â€“Dependent Small RNAs and Their Association with Meiotic Gene Expression and Recombination. Plant Cell, 2019, 31, 444-464.	3.1	37
355	The Histone H3K4 Demethylase JMJ16 Represses Leaf Senescence in Arabidopsis. Plant Cell, 2019, 31, 430-443.	3.1	89
356	Nascent-protein ubiquitination is required for heat shockâ€“induced gene downregulation in human cells. Nature Structural and Molecular Biology, 2019, 26, 137-146.	3.6	42
357	Arabidopsis S2Lb links AtCOMPASS-like and SDG2 activity in H3K4me3 independently from histone H2B monoubiquitination. Genome Biology, 2019, 20, 100.	3.8	56
358	Control of p53-dependent transcription and enhancer activity by the p53 family member p63. Journal of Biological Chemistry, 2019, 294, 10720-10736.	1.6	27
359	RNA polymerase II-independent recruitment of SPT6L at transcription start sites in Arabidopsis. Nucleic Acids Research, 2019, 47, 6714-6725.	6.5	24
360	PP4â€dependent HDAC3 dephosphorylation discriminates between axonal regeneration and regenerative failure. EMBO Journal, 2019, 38, e101032.	3.5	32
361	MTHFD1 interaction with BRD4 links folate metabolism to transcriptional regulation. Nature Genetics, 2019, 51, 990-998.	9.4	61
362	Global Quantitative Mapping of Enhancers in Rice by STARR-seq. Genomics, Proteomics and Bioinformatics, 2019, 17, 140-153.	3.0	43
363	The alarmin S100A9 hampers osteoclast differentiation from human circulating precursors by reducing the expression of RANK. FASEB Journal, 2019, 33, 10104-10115.	0.2	9

#	ARTICLE	IF	CITATIONS
364	Genetic and Epigenetic Fine Mapping of Complex Trait Associated Loci in the Human Liver. American Journal of Human Genetics, 2019, 105, 89-107.	2.6	35
365	Specific Contributions of Cohesin-SA1 and Cohesin-SA2 to TADs and Polycomb Domains in Embryonic Stem Cells. Cell Reports, 2019, 27, 3500-3510.e4.	2.9	60
366	EZH2 upregulates the PI3K/AKT pathway through IGF1R and MYC in clinically aggressive chronic lymphocytic leukaemia. Epigenetics, 2019, 14, 1125-1140.	1.3	24
367	GR and LSD1/KDM1A-Targeted Gene Activation Requires Selective H3K4me2 Demethylation at Enhancers. Cell Reports, 2019, 27, 3522-3532.e3.	2.9	23
368	SIRT7 mediates L1 elements transcriptional repression and their association with the nuclear lamina. Nucleic Acids Research, 2019, 47, 7870-7885.	6.5	55
369	Open chromatin dynamics in prosensory cells of the embryonic mouse cochlea. Scientific Reports, 2019, 9, 9060.	1.6	14
370	SpinachBase: a central portal for spinach genomics. Database: the Journal of Biological Databases and Curation, 2019, 2019, .	1.4	30
371	DNMT3B shapes the mCA landscape and regulates mCG for promoter bivalency in human embryonic stem cells. Nucleic Acids Research, 2019, 47, 7460-7475.	6.5	14
372	ARID1A facilitates KRAS signaling-regulatedÂenhancer activity in an AP1-dependent manner in colorectal cancer cells. Clinical Epigenetics, 2019, 11, 92.	1.8	36
373	Two Separation-of-Function Isoforms of Human TPP1 Dictate Telomerase Regulation in Somatic and Germ Cells. Cell Reports, 2019, 27, 3511-3521.e7.	2.9	20
374	Specific basic patchâ€dependent multimerization of Saccharomyces cerevisiae ORC on singleâ€stranded DNA promotes ATP hydrolysis. Genes To Cells, 2019, 24, 608-618.	0.5	1
375	Distinct structural classes of activating FOXA1 alterations in advanced prostate cancer. Nature, 2019, 571, 413-418.	13.7	192
376	Phosphorylation of TET2 by AMPK is indispensable in myogenic differentiation. Epigenetics and Chromatin, 2019, 12, 32.	1.8	24
377	Codon usage optimization in pluripotent embryonic stem cells. Genome Biology, 2019, 20, 119.	3.8	43
378	Disruption of Broad Epigenetic Domains in PDAC Cells by HAT Inhibitors. Epigenomes, 2019, 3, 11.	0.8	12
379	Comprehensive Integration of Single-Cell Data. Cell, 2019, 177, 1888-1902.e21.	13.5	9,755
380	Hybrid Assembly of the Genome of the Entomopathogenic Nematode <i>Steinernema carpocapsae</i> Identifies the X-Chromosome. G3: Genes, Genomes, Genetics, 2019, 9, 2687-2697.	0.8	18
381	Preformed chromatin topology assists transcriptional robustness of <i>Shh</i> during limb development. Proceedings of the National Academy of Sciences of the United States of America, 2019, 116, 12390-12399.	3.3	131

#	Article	IF	Citations
382	SAGA DUBm-mediated surveillance regulates prompt export of stress-inducible transcripts for proteostasis. Nature Communications, 2019, 10, 2458.	5.8	11
383	methyl-ATAC-seq measures DNA methylation at accessible chromatin. Genome Research, 2019, 29, 969-977.	2.4	32
384	Yeast Sirtuin Family Members Maintain Transcription Homeostasis to Ensure Genome Stability. Cell Reports, 2019, 27, 2978-2989.e5.	2.9	22
385	Spatial Chromosome Folding and Active Transcription Drive DNA Fragility and Formation of Oncogenic MLL Translocations. Molecular Cell, 2019, 75, 267-283.e12.	4.5	104
386	Chromatin interaction maps reveal genetic regulation for quantitative traits in maize. Nature Communications, 2019, 10, 2632.	5.8	93
387	Genome-wide RNA pol II initiation and pausing in neural progenitors of the rat. BMC Genomics, 2019, 20, 477.	1.2	8
388	Loss of PRC1 activity in different stem cell compartments activates a common transcriptional program with cell typeâ€“dependent outcomes. Science Advances, 2019, 5, eaav1594.	4.7	20
389	Hand2 Selectively Reorganizes Chromatin Accessibility to Induce Pacemaker-like Transcriptional Reprogramming. Cell Reports, 2019, 27, 2354-2369.e7.	2.9	23
390	Zfp281 Shapes the Transcriptome of Trophoblast Stem Cells and Is Essential for Placental Development. Cell Reports, 2019, 27, 1742-1754.e6.	2.9	34
391	Evidence of developmental escape from transcriptional gene silencing in <i><scp>MESSI</scp></i> retrotransposons. New Phytologist, 2019, 223, 950-964.	3.5	6
392	Cardiac Reprogramming Factors Synergistically Activate Genome-wide Cardiogenic Stage-Specific Enhancers. Cell Stem Cell, 2019, 25, 69-86.e5.	5.2	72
393	Trimitomics: An efficient pipeline for mitochondrial assembly from transcriptomic reads in nonmodel species. Molecular Ecology Resources, 2019, 19, 1230-1239.	2.2	13
394	4q-D4Z4 chromatin architecture regulates the transcription of muscle atrophic genes in facioscapulohumeral muscular dystrophy. Genome Research, 2019, 29, 883-895.	2.4	18
395	<i>Klf4</i> Promotes Dentinogenesis and Odontoblastic Differentiation via Modulation of TGF-Î² Signaling Pathway and Interaction With Histone Acetylation. Journal of Bone and Mineral Research, 2019, 34, 1502-1516.	3.1	44
396	Identification of genes under dynamic post-transcriptional regulation from time-series epigenomic data. Epigenomics, 2019, 11, 619-638.	1.0	2
397	Acetate Promotes T Cell Effector Function during Glucose Restriction. Cell Reports, 2019, 27, 2063-2074.e5.	2.9	205
398	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
399	Aging Human Hematopoietic Stem Cells Manifest Profound Epigenetic Reprogramming of Enhancers That May Predispose to Leukemia. Cancer Discovery, 2019, 9, 1080-1101.	7.7	119

#	Article	IF	Citations
400	Histone H3 lysine 4 methyltransferase is required for facultative heterochromatin at specific loci. BMC Genomics, 2019, 20, 350.	1.2	10
401	Contrasting Roles of Transcription Factors Spineless and EcR in the Highly Dynamic Chromatin Landscape of Butterfly Wing Metamorphosis. Cell Reports, 2019, 27, 1027-1038.e3.	2.9	32
402	The telomeric Cdc13â€"Stn1â€"Ten1 complex regulates RNA polymerase II transcription. Nucleic Acids Research, 2019, 47, 6250-6268.	6.5	8
403	Destabilization of chromosome structure by histone H3 lysine 27 methylation. PLoS Genetics, 2019, 15, e1008093.	1.5	75
404	P-TEFb Regulates Transcriptional Activation in Non-coding RNA Genes. Frontiers in Genetics, 2019, 10, 342.	1.1	12
405	PAD2-Mediated Citrullination Contributes to Efficient Oligodendrocyte Differentiation and Myelination. Cell Reports, 2019, 27, 1090-1102.e10.	2.9	59
406	Long intergenic non-coding RNAs regulate human lung fibroblast function: Implications for idiopathic pulmonary fibrosis. Scientific Reports, 2019, 9, 6020.	1.6	25
407	Mouse ANKRD31 Regulates Spatiotemporal Patterning of Meiotic Recombination Initiation and Ensures Recombination between X and Y Sex Chromosomes. Molecular Cell, 2019, 74, 1069-1085.e11.	4.5	74
408	TAF5L and TAF6L Maintain Self-Renewal of Embryonic Stem Cells via the MYC Regulatory Network. Molecular Cell, 2019, 74, 1148-1163.e7.	4.5	36
409	Genomeâ€wide occupancy of histone H3K27 methyltransferases <scp>CURLY LEAF</scp> and <scp>SWINGER</scp> in <i>Arabidopsis</i> seedlings. Plant Direct, 2019, 3, e00100.	0.8	70
410	Specific chromatin changes mark lateral organ founder cells in the Arabidopsis inflorescence meristem. Journal of Experimental Botany, 2019, 70, 3867-3879.	2.4	17
411	DNA methylation repels targeting of Arabidopsis REF6. Nature Communications, 2019, 10, 2063.	5.8	53
412	Crosstalk between RNA Pol II C-Terminal Domain Acetylation and Phosphorylation via RPRD Proteins. Molecular Cell, 2019, 74, 1164-1174.e4.	4.5	22
413	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
414	The Primary Antisense Transcriptome of Halobacterium salinarum NRC-1. Genes, 2019, 10, 280.	1.0	11
415	Complementary Activity of ETV5, RBPJ, and TCF3 Drives Formative Transition from Naive Pluripotency. Cell Stem Cell, 2019, 24, 785-801.e7.	5.2	85
416	Direct Induction of the Three Pre-implantation Blastocyst Cell Types from Fibroblasts. Cell Stem Cell, 2019, 24, 983-994.e7.	5.2	47
417	TET enzymes augment activation-induced deaminase (AID) expression via 5-hydroxymethylcytosine modifications at the <i>Aicda</i> superenhancer. Science Immunology, 2019, 4, .	5.6	65

#	Article	IF	Citations
418	Functional Landscape of PCGF Proteins Reveals Both RING1A/B-Dependent-and RING1A/B-Independent-Specific Activities. Molecular Cell, 2019, 74, 1037-1052.e7.	4.5	128
419	H3K27me3 Depletion during Differentiation Promotes Myogenic Transcription in Porcine Satellite Cells. Genes, 2019, 10, 231.	1.0	13
420	Drosophila p53 directs nonapoptotic programs in postmitotic tissue. Molecular Biology of the Cell, 2019, 30, 1339-1351.	0.9	14
421	Deletion of Cdkn1b in ACI rats leads to increased proliferation and pregnancy-associated changes in the mammary gland due to perturbed systemic endocrine environment. PLoS Genetics, 2019, 15, e1008002.	1.5	11
422	Helicase/SUMO-targeted ubiquitin ligase Uls1 interacts with the Holliday junction resolvase Yen1. PLoS ONE, 2019, 14, e0214102.	1.1	6
423	Inactivating Mutation in <i>IRF8</i> Promotes Osteoclast Transcriptional Programs and Increases Susceptibility to Tooth Root Resorption. Journal of Bone and Mineral Research, 2019, 34, 1155-1168.	3.1	22
424	Human Pluripotent Stem Cell-Derived Multipotent Vascular Progenitors of the Mesothelium Lineage Have Utility in Tissue Engineering and Repair. Cell Reports, 2019, 26, 2566-2579.e10.	2.9	28
425	Cell cycleâ€" and genomic distanceâ€"dependent dynamics of a discrete chromosomal region. Journal of Cell Biology, 2019, 218, 1467-1477.	2.3	40
426	Antagonistic Actions of FPA and IBM2 Regulate Transcript Processing from Genes Containing Heterochromatin. Plant Physiology, 2019, 180, 392-403.	2.3	24
427	Extensive Recovery of Embryonic Enhancer and Gene Memory Stored in Hypomethylated Enhancer DNA. Molecular Cell, 2019, 74, 542-554.e5.	4.5	65
428	FactorNet: A deep learning framework for predicting cell type specific transcription factor binding from nucleotide-resolution sequential data. Methods, 2019, 166, 40-47.	1.9	137
429	H3K27M induces defective chromatin spread of PRC2-mediated repressive H3K27me2/me3 and is essential for glioma tumorigenesis. Nature Communications, 2019, 10, 1262.	5.8	215
430	Differential role for phosphorylation in alternative polyadenylation function versus nuclear import of SR-like protein CPSF6. Nucleic Acids Research, 2019, 47, 4663-4683.	6.5	35
431	MYC Recruits SPT5 to RNA Polymerase II to Promote Processive Transcription Elongation. Molecular Cell, 2019, 74, 674-687.e11.	4.5	89
432	Unbiased subgenome evolution following a recent whole-genome duplication in pear (Pyrus) Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50 182	2.9	54
433	Inflammatory macrophage dependence on NAD+ salvage is a consequence of reactive oxygen speciesâ€"mediated DNA damage. Nature Immunology, 2019, 20, 420-432.	7.0	169
434	Hypoxia induces rapid changes to histone methylation and reprograms chromatin. Science, 2019, 363, 1222-1226.	6.0	266
435	Identification of a primitive intestinal transcription factor network shared between esophageal adenocarcinoma and its precancerous precursor state. Genome Research, 2019, 29, 723-736.	2.4	50

#	Article	IF	Citations
436	CEH-60/PBX and UNC-62/MEIS Coordinate a Metabolic Switch that Supports Reproduction in C.Âelegans. Developmental Cell, 2019, 49, 235-250.e7.	3.1	32
437	Dissecting the role of H3K27 acetylation and methylation in PRC2 mediated control of cellular identity. Nature Communications, 2019, 10, 1679.	5.8	148
438	Research in Computational Molecular Biology. Lecture Notes in Computer Science, 2019, , .	1.0	0
439	PLZF limits enhancer activity during hematopoietic progenitor aging. Nucleic Acids Research, 2019, 47, 4509-4520.	6.5	15
440	PAN-INTACT enables direct isolation of lineage-specific nuclei from fibrous tissues. PLoS ONE, 2019, 14, e0214677.	1.1	8
441	A reinforcing HNF4â€“SMAD4 feed-forward module stabilizes enterocyte identity. Nature Genetics, 2019, 51, 777-785.	9.4	110
442	Promoter-Intrinsic and Local Chromatin Features Determine Gene Repression in LADs. Cell, 2019, 177, 852-864.e14.	13.5	108
443	Autophagy Regulation of Metabolism Is Required for CD8+ T Cell Anti-tumor Immunity. Cell Reports, 2019, 27, 502-513.e5.	2.9	134
444	The anti-cancer drugs curaxins target spatial genome organization. Nature Communications, 2019, 10, 1441.	5.8	44
445	<i>Hoxa13</i> regulates expression of common <i>Hox</i> target genes involved in cartilage development to coordinate the expansion of the autopodal anlage. Development Growth and Differentiation, 2019, 61, 228-251.	0.6	13
446	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
447	Genome-Wide Discovery of DEAD-Box RNA Helicase Targets Reveals RNA Structural Remodeling in Transcription Termination. Genetics, 2019, 212, 153-174.	1.2	19
448	Kdm6b regulates context-dependent hematopoietic stem cell self-renewal and leukemogenesis. Leukemia, 2019, 33, 2506-2521.	3.3	49
449	A genome-wide analysis of carbon catabolite repression in Schizosaccharomyces pombe. BMC Genomics, 2019, 20, 251.	1.2	20
450	Insulin Receptor Associates with Promoters Genome-wide and Regulates Gene Expression. Cell, 2019, 177, 722-736.e22.	13.5	101
451	The genomic distribution of histone H3K4me2 in spermatogonia is highly conserved in spermâ€. Biology of Reproduction, 2019, 100, 1661-1672.	1.2	15
452	A versatile mouse model of epitope-tagged histone H3.3 to study epigenome dynamics. Journal of Biological Chemistry, 2019, 294, 1904-1914.	1.6	10
453	A conserved dimer interface connects ERH and YTH family proteins to promote gene silencing. Nature Communications, 2019, 10, 251.	5.8	36

#	Article	IF	Citations
454	Integrated epigenomic analysis stratifies chromatin remodellers into distinct functional groups. Epigenetics and Chromatin, 2019, 12, 12.	1.8	23
455	Maternal and zygotic gene regulatory effects of endogenous RNAi pathways. PLoS Genetics, 2019, 15, e1007784.	1.5	19
456	Low-input chromatin profiling in Arabidopsis endosperm using CUT&RUN. Plant Reproduction, 2019, 32, 63-75.	1.3	46
457	DNA Hypermethylation Encroachment at CpG Island Borders in Cancer Is Predisposed by H3K4 Monomethylation Patterns. Cancer Cell, 2019, 35, 297-314.e8.	7.7	62
458	Ipa1 Is an RNA Polymerase II Elongation Factor that Facilitates Termination by Maintaining Levels of the Poly(A) Site Endonuclease Ysh1. Cell Reports, 2019, 26, 1919-1933.e5.	2.9	8
459	Genomic Reorganization of Lamin-Associated Domains in Cardiac Myocytes Is Associated With Differential Gene Expression and DNA Methylation in Human Dilated Cardiomyopathy. Circulation Research, 2019, 124, 1198-1213.	2.0	72
460	Cell-autonomous and redundant roles of Hey1 and HeyL in muscle stem cells: HeyL requires Hes1 to bind diverse DNA sites. Development (Cambridge), 2019, 146, .	1.2	34
461	EMT is associated with an epigenetic signature of ECM remodeling genes. Cell Death and Disease, 2019, 10, 205.	2.7	99
462	NFIA is a gliogenic switch enabling rapid derivation of functional human astrocytes from pluripotent stem cells. Nature Biotechnology, 2019, 37, 267-275.	9.4	150
463	Extensive epigenomic integration of the glucocorticoid response in primary human monocytes and in vitro derived macrophages. Scientific Reports, 2019, 9, 2772.	1.6	27
464	Attenuated chromatin compartmentalization in meiosis and its maturation in sperm development. Nature Structural and Molecular Biology, 2019, 26, 175-184.	3.6	92
465	Trabectedin Inhibits EWS-FLI1 and Evicts SWI/SNF from Chromatin in a Schedule-dependent Manner. Clinical Cancer Research, 2019, 25, 3417-3429.	3.2	32
466	Coupling of PARP1-mediated chromatin structural changes to transcriptional RNA polymerase II elongation and cotranscriptional splicing. Epigenetics and Chromatin, 2019, 12, 15.	1.8	39
467	Chromatin changes in Anopheles gambiae induced by Plasmodium falciparum infection. Epigenetics and Chromatin, 2019, 12, 5.	1.8	32
468	YAP Partially Reprograms Chromatin Accessibility to Directly Induce Adult Cardiogenesis InÂVivo. Developmental Cell, 2019, 48, 765-779.e7.	3.1	171
469	MCF-7 as a Model for Functional Analysis of Breast Cancer Risk Variants. Cancer Epidemiology Biomarkers and Prevention, 2019, 28, 1735-1745.	1.1	7
470	Genome-wide analysis of the H3K27me3 epigenome and transcriptome in Brassica rapa. GigaScience, 2019, 8, .	3.3	27
471	Maintenance of spatial gene expression by Polycomb-mediated repression after formation of a vertebrate body plan. Development (Cambridge), 2019, 146, .	1.2	13

#	ARTICLE	IF	CITATIONS
472	The Paf1 Complex Broadly Impacts the Transcriptome of <i>Saccharomyces cerevisiae</i>. Genetics, 2019, 212, 711-728.	1.2	10
473	Recurrent SMARCB1 Mutations Reveal a Nucleosome Acidic Patch Interaction Site That Potentiates mSWI/SNF Complex Chromatin Remodeling. Cell, 2019, 179, 1342-1356.e23.	13.5	72
474	A Read/Write Mechanism Connects p300 Bromodomain Function to H2A.Z Acetylation. IScience, 2019, 21, 773-788.	1.9	16
475	RSAT variation-tools: An accessible and flexible framework to predict the impact of regulatory variants on transcription factor binding. Computational and Structural Biotechnology Journal, 2019, 17, 1415-1428.	1.9	9
476	Dichotomy of Dosage Compensation along the Neo Z Chromosome of the Monarch Butterfly. Current Biology, 2019, 29, 4071-4077.e3.	1.8	66
477	A Novel Approach to Identify Enhancer lincRNAs by Integrating Genome, Epigenome, and Regulatome. Frontiers in Bioengineering and Biotechnology, 2019, 7, 427.	2.0	4
478	Regional Gene Repression by DNA Double-Strand Breaks in G₁ Phase Cells. Molecular and Cellular Biology, 2019, 39, .	1.1	15
479	Functional Enhancers Shape Extrachromosomal Oncogene Amplifications. Cell, 2019, 179, 1330-1341.e13.	13.5	206
480	An RNA-Binding Protein Secreted by a Bacterial Pathogen Modulates RIG-I Signaling. Cell Host and Microbe, 2019, 26, 823-835.e11.	5.1	55
481	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
482	Transcriptomic profiling of porcine pluripotency identifies species-specific reprogramming requirements for culturing iPSCs. Stem Cell Research, 2019, 41, 101645.	0.3	8
483	Global chromatin conformation differences in the Drosophila dosage compensated chromosome X. Nature Communications, 2019, 10, 5355.	5.8	28
484	MLL1 Inhibition and Vitamin D Signaling Cooperate to Facilitate the Expanded Pluripotency State. Cell Reports, 2019, 29, 2659-2671.e6.	2.9	8
485	EpiMethylTag: simultaneous detection of ATAC-seq or ChIP-seq signals with DNA methylation. Genome Biology, 2019, 20, 248.	3.8	27
486	Dynamics of activating and repressive histone modifications in <i>Drosophila</i> neural stem cell lineages and brain tumors. Development (Cambridge), 2019, 146, .	1.2	7
487	Comprehensive epigenome characterization reveals diverse transcriptional regulation across human vascular endothelial cells. Epigenetics and Chromatin, 2019, 12, 77.	1.8	34
488	The acute myeloid leukemia associated AML1-ETO fusion protein alters the transcriptome and cellular progression in a single-oncogene expressing in vitro induced pluripotent stem cell based granulocyte differentiation model. PLoS ONE, 2019, 14, e0226435.	1.1	15
489	miR824/AGAMOUS-LIKE16 Module Integrates Recurring Environmental Heat Stress Changes to Fine-Tune Poststress Development. Frontiers in Plant Science, 2019, 10, 1454.	1.7	27

#	Article	IF	Citations
490	A primate-specific retroviral enhancer wires the XACT lncRNA into the core pluripotency network in humans. Nature Communications, 2019, 10, 5652.	5.8	21
491	NSD2 overexpression drives clustered chromatin and transcriptional changes in a subset of insulated domains. Nature Communications, 2019, 10, 4843.	5.8	57
492	ASCL1 is a MYCN- and LMO1-dependent member of the adrenergic neuroblastoma core regulatory circuitry. Nature Communications, 2019, 10, 5622.	5.8	56
493	Gastrointestinal transcription factors drive lineage-specific developmental programs in organ specification and cancer. Science Advances, 2019, 5, eaax8898.	4.7	26
494	Key role for CTCF in establishing chromatin structure in human embryos. Nature, 2019, 576, 306-310.	13.7	131
495	ONECUT2 overexpression promotes RAS-driven lung adenocarcinoma progression. Scientific Reports, 2019, 9, 20021.	1.6	26
496	Identification and epigenetic analysis of divergent long non-coding RNAs in multilineage differentiation of human Neural Progenitor Cells. RNA Biology, 2019, 16, 13-24.	1.5	16
497	Condensin-Dependent Chromatin Compaction Represses Transcription Globally during Quiescence. Molecular Cell, 2019, 73, 533-546.e4.	4.5	83
498	Nucleosome Positioning by an Evolutionarily Conserved Chromatin Remodeler Prevents Aberrant DNA Methylation in <i>Neurospora</i>. Genetics, 2019, 211, 563-578.	1.2	13
499	MRG-1/MRG15 Is a Barrier for Germ Cell to Neuron Reprogramming in <i>Caenorhabditis elegans</i>. Genetics, 2019, 211, 121-139.	1.2	38
500	Loss of Estrogen-Related Receptor Alpha Facilitates Angiogenesis in Endothelial Cells. Molecular and Cellular Biology, 2019, 39, .	1.1	16
501	Detection of splice isoforms and rare intermediates using multiplexed primer extension sequencing. Nature Methods, 2019, 16, 55-58.	9.0	15
502	EP300-HDAC1-SWI/SNF functional unit defines transcription of some DNA repair enzymes during differentiation of human macrophages. Biochimica Et Biophysica Acta - Gene Regulatory Mechanisms, 2019, 1862, 198-208.	0.9	21
503	A neuronal enhancer network upstream of MEF2C is compromised in patients with Rett-like characteristics. Human Molecular Genetics, 2019, 28, 818-827.	1.4	14
504	Plant HP1 protein ADCP1 links multivalent H3K9 methylation readout to heterochromatin formation. Cell Research, 2019, 29, 54-66.	5.7	83
505	<scp>TCF</scp> / <scp>LEF</scp> dependent and independent transcriptional regulation of Wnt/Î²â€catenin target genes. EMBO Journal, 2019, 38, .	3.5	142
506	Arginine Citrullination at the C-Terminal Domain Controls RNA Polymerase II Transcription. Molecular Cell, 2019, 73, 84-96.e7.	4.5	50
507	Novel Bioinformatics Methods for Toxicoepigenetics. , 2019, , 265-288.		11

#	Article	IF	Citations
508	GADD45A binds R-loops and recruits TET1 to CpG island promoters. Nature Genetics, 2019, 51, 217-223.	9.4	173
509	Pathological priming causes developmental gene network heterochronicity in autistic subject-derived neurons. Nature Neuroscience, 2019, 22, 243-255.	7.1	209
510	LHX2- and LDB1-mediated trans interactions regulate olfactory receptor choice. Nature, 2019, 565, 448-453.	13.7	215
511	Characterization of inv(3) cell line OCI-AML-20 with stroma-dependent CD34 expression. Experimental Hematology, 2019, 69, 27-36.	0.2	5
512	Human SETMAR is a DNA sequence-specific histone-methylase with a broad effect on the transcriptome. Nucleic Acids Research, 2019, 47, 122-133.	6.5	23
513	DOT1L promotes progenitor proliferation and primes neuronal layer identity in the developing cerebral cortex. Nucleic Acids Research, 2019, 47, 168-183.	6.5	49
514	The transcription factor c-Maf is essential for the commitment of IL-17-producing Î³Î´ T cells. Nature Immunology, 2019, 20, 73-85.	7.0	98
515	Directed Nucleosome Sliding during the Formation of the Simian Virus 40 Particle Exposes DNA Sequences Required for Early Transcription. Journal of Virology, 2019, 93, .	1.5	7
516	Maelstrom Represses Canonical Polymerase II Transcription within Bi-directional piRNA Clusters in Drosophila melanogaster. Molecular Cell, 2019, 73, 291-303.e6.	4.5	33
517	SWI/SNF remains localized to chromatin in the presence of SCHLAP1. Nature Genetics, 2019, 51, 26-29.	9.4	28
518	Nuclear Transcriptomes of the Seven Neuronal Cell Types That Constitute the<i>Drosophila</i>Mushroom Bodies. G3: Genes, Genomes, Genetics, 2019, 9, 81-94.	0.8	46
519	Integrated Genomic and Proteomic Analyses Reveal Novel Mechanisms of the Methyltransferase SETD2 in Renal Cell Carcinoma Development. Molecular and Cellular Proteomics, 2019, 18, 437-447.	2.5	22
520	Differential Methylation of H3K79 Reveals DOT1L Target Genes and Function in the Cerebellum In Vivo. Molecular Neurobiology, 2019, 56, 4273-4287.	1.9	19
521	DNase-seq to Study Chromatin Accessibility in Early <i>Xenopus tropicalis</i> Embryos. Cold Spring Harbor Protocols, 2019, 2019, pdb.prot098335.	0.2	4
522	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
523	Analysis of Mammalian Native Elongating Transcript sequencing (mNET-seq) high-throughput data. Methods, 2020, 178, 89-95.	1.9	11
524	Meltos: multi-sample tumor phylogeny reconstruction for structural variants. Bioinformatics, 2020, 36, 1082-1090.	1.8	9
525	Global changes in chromatin accessibility and transcription following <i>ATRX</i> inactivation in human cancer cells. FEBS Letters, 2020, 594, 67-78.	1.3	15

#	ARTICLE	IF	CITATIONS
526	Epigenetic signatures of stress adaptation and flowering regulation in response to extended drought and recovery in <scp><i>Zea mays</i></scp>. Plant, Cell and Environment, 2020, 43, 55-75.	2.8	51
527	DNA Methylation and Histone H1 Jointly Repress Transposable Elements and Aberrant Intragenic Transcripts. Molecular Cell, 2020, 77, 310-323.e7.	4.5	99
528	Data of epigenomic profiling of histone marks and CTCF binding sites in bovine rumen epithelial primary cells before and after butyrate treatment. Data in Brief, 2020, 28, 104983.	0.5	3
529	Clustered CTCF binding is an evolutionary mechanism to maintain topologically associating domains. Genome Biology, 2020, 21, 5.	3.8	89
530	Mitochondrial Integrity Regulated by Lipid Metabolism Is a Cell-Intrinsic Checkpoint for Treg Suppressive Function. Cell Metabolism, 2020, 31, 422-437.e5.	7.2	215
531	Histone H2AK119 Mono-Ubiquitination Is Essential for Polycomb-Mediated Transcriptional Repression. Molecular Cell, 2020, 77, 840-856.e5.	4.5	234
532	Heterodimerization of TFAP2 pioneer factors drives epigenomic remodeling during neural crest specification. Genome Research, 2020, 30, 35-48.	2.4	78
533	The torpedo effect in<i>Bacillus subtilis</i>:<scp>RN</scp>ase J1 resolves stalled transcription complexes. EMBO Journal, 2020, 39, e102500.	3.5	27
534	<i>FLOWERING LOCUS T</i> Improves Cucumber Adaptation to Higher Latitudes. Plant Physiology, 2020, 182, 908-918.	2.3	30
535	Saliva as a comparable-quality source of DNA for Whole Exome Sequencing on Ion platforms. Genomics, 2020, 112, 1437-1443.	1.3	4
536	SETDB1-Mediated Cell Fate Transition between 2C-Like and Pluripotent States. Cell Reports, 2020, 30, 25-36.e6.	2.9	64
537	BPTF regulates growth of adult and pediatric high-grade glioma through the MYC pathway. Oncogene, 2020, 39, 2305-2327.	2.6	31
538	Protein arginine methyltransferase 5 represses tumor suppressor miRNAs that down-regulate CYCLIN D1 and c-MYC expression in aggressive B-cell lymphoma. Journal of Biological Chemistry, 2020, 295, 1165-1180.	1.6	21
539	FLASH: ultra-fast protocol to identify RNAâ€"protein interactions in cells. Nucleic Acids Research, 2020, 48, e15-e15.	6.5	21
540	Set1/COMPASS repels heterochromatin invasion at euchromatic sites by disrupting Suv39/Clr4 activity and nucleosome stability. Genes and Development, 2020, 34, 99-117.	2.7	26
541	Histone Lysine Methylation Dynamics Control<i>EGFR</i>DNA Copy-Number Amplification. Cancer Discovery, 2020, 10, 306-325.	7.7	31
542	Protect-seq: genome-wide profiling of nuclease inaccessible domains reveals physical properties of chromatin. Nucleic Acids Research, 2020, 48, e16-e16.	6.5	10
543	HBO1 is required for the maintenance of leukaemia stem cells. Nature, 2020, 577, 266-270.	13.7	105

#	ARTICLE	IF	CITATIONS
544	Discovery of a new predominant cytosine DNA modification that is linked to gene expression in malaria parasites. Nucleic Acids Research, 2020, 48, 184-199.	6.5	24
545	HNF4 Regulates Fatty Acid Oxidation and Is Required for Renewal of Intestinal Stem Cells in Mice. Gastroenterology, 2020, 158, 985-999.e9.	0.6	115
546	Mapping Exosomeâ€"Substrate Interactions In Vivo by UV Cross-Linking. Methods in Molecular Biology, 2020, 2062, 105-126.	0.4	0
547	MeCP2 Represses the Rate of Transcriptional Initiation of Highly Methylated Long Genes. Molecular Cell, 2020, 77, 294-309.e9.	4.5	72
548	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
549	Functionally Annotating Regulatory Elements in the Equine Genome Using Histone Mark ChIP-Seq. Genes, 2020, 11, 3.	1.0	34
550	EBF1 and Pax5 safeguard leukemic transformation by limiting IL-7 signaling, Myc expression, and folate metabolism. Genes and Development, 2020, 34, 1503-1519.	2.7	15
551	Epstein-Barr Virus Episome Physically Interacts with Active Regions of the Host Genome in Lymphoblastoid Cells. Journal of Virology, 2020, 94, .	1.5	26
552	German-Wide Interlaboratory Study Compares Consistency, Accuracy and Reproducibility of Whole-Genome Short Read Sequencing. Frontiers in Microbiology, 2020, 11, 573972.	1.5	12
553	CTCF orchestrates long-range cohesin-driven V(D)J recombinational scanning. Nature, 2020, 586, 305-310.	13.7	82
554	DOT1L-mediated murine neuronal differentiation associates with H3K79me2 accumulation and preserves SOX2-enhancer accessibility. Nature Communications, 2020, 11, 5200.	5.8	29
555	Regulation of single-cell genome organization into TADs and chromatin nanodomains. Nature Genetics, 2020, 52, 1151-1157.	9.4	127
556	DOT1L-controlled cell-fate determination and transcription elongation are independent of H3K79 methylation. Proceedings of the National Academy of Sciences of the United States of America, 2020, 117, 27365-27373.	3.3	43
557	NFIA differentially controls adipogenic and myogenic gene program through distinct pathways to ensure brown and beige adipocyte differentiation. PLoS Genetics, 2020, 16, e1009044.	1.5	20
558	BRD4 Prevents R-Loop Formation and Transcription-Replication Conflicts by Ensuring Efficient Transcription Elongation. Cell Reports, 2020, 32, 108166.	2.9	46
559	Binding of the Treslin-MTBP Complex to Specific Regions of the Human Genome Promotes the Initiation of DNA Replication. Cell Reports, 2020, 32, 108178.	2.9	16
560	Multivalent Proteins Rapidly and Reversibly Phase-Separate upon Osmotic Cell Volume Change. Molecular Cell, 2020, 79, 978-990.e5.	4.5	86
561	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

#	Article	IF	Citations
562	STAT3â€“BDNFâ€“TrkB signalling promotes alveolar epithelial regeneration after lung injury. Nature Cell Biology, 2020, 22, 1197-1210.	4.6	71
563	ELAV and FNE Determine Neuronal Transcript Signatures through EXon-Activated Rescue. Molecular Cell, 2020, 80, 156-163.e6.	4.5	29
564	Adipocytes fail to maintain cellular identity during obesity due to reduced PPARÎ³ activity and elevated TGFÎ²-SMAD signaling. Molecular Metabolism, 2020, 42, 101086.	3.0	16
565	Universal NicE-seq for high-resolution accessible chromatin profiling for formaldehyde-fixed and FFPE tissues. Clinical Epigenetics, 2020, 12, 143.	1.8	12
566	TET1 Interacts Directly with NANOG via Independent Domains Containing Hydrophobic and Aromatic Residues. Journal of Molecular Biology, 2020, 432, 6075-6091.	2.0	3
567	Sperm histone H3 lysine 4 trimethylation is altered in a genetic mouse model of transgenerational epigenetic inheritance. Nucleic Acids Research, 2020, 48, 11380-11393.	6.5	65
568	Down-regulation of Beclin1 promotes direct cardiac reprogramming. Science Translational Medicine, 2020, 12, .	5.8	41
569	Chromatin Landscape Underpinning Human Dendritic Cell Heterogeneity. Cell Reports, 2020, 32, 108180.	2.9	18
570	Enhancer Reprogramming Confers Dependence on Glycolysis and IGF Signaling in KMT2D Mutant Melanoma. Cell Reports, 2020, 33, 108293.	2.9	39
571	Epigenetic therapy induces transcription of inverted SINEs and ADAR1 dependency. Nature, 2020, 588, 169-173.	13.7	149
572	Efficient and accurate determination of genome-wide DNA methylation patterns in Arabidopsis thaliana with enzymatic methyl sequencing. Epigenetics and Chromatin, 2020, 13, 42.	1.8	60
573	A Hyper-IgM Syndrome Mutation in Activation-Induced Cytidine Deaminase Disrupts G-Quadruplex Binding and Genome-wide Chromatin Localization. Immunity, 2020, 53, 952-970.e11.	6.6	21
574	An optogenetic switch for the Set2 methyltransferase provides evidence for transcription-dependent and -independent dynamics of H3K36 methylation. Genome Research, 2020, 30, 1605-1617.	2.4	10
575	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
576	H3 K27M and EZHIP Impede H3K27-Methylation Spreading by Inhibiting Allosterically Stimulated PRC2. Molecular Cell, 2020, 80, 726-735.e7.	4.5	83
577	Degradation of Non-coding RNAs Promotes Recycling of Termination Factors at Sites of Transcription. Cell Reports, 2020, 32, 107942.	2.9	19
578	TERMINAL FLOWER 1-FD complex target genes and competition with FLOWERING LOCUS T. Nature Communications, 2020, 11, 5118.	5.8	100
579	Detection of genomic G-quadruplexes in living cells using a small artificial protein. Nucleic Acids Research, 2020, 48, 11706-11720.	6.5	100

#	ARTICLE	IF	CITATIONS
580	ATAC-Seq Reveals an <i>Isl1</i> Enhancer That Regulates Sinoatrial Node Development and Function. Circulation Research, 2020, 127, 1502-1518.	2.0	35
581	INO80C Remodeler Maintains Genomic Stability by Preventing Promiscuous Transcription at Replication Origins. Cell Reports, 2020, 32, 108106.	2.9	9
582	Prostate cancer reactivates developmental epigenomic programs during metastatic progression. Nature Genetics, 2020, 52, 790-799.	9.4	174
583	Reorganized 3D Genome Structures Support Transcriptional Regulation in Mouse Spermatogenesis. IScience, 2020, 23, 101034.	1.9	36
584	Histone H3.3 phosphorylation amplifies stimulation-induced transcription. Nature, 2020, 583, 852-857.	13.7	88
585	Epigenetic hallmarks of age-related macular degeneration are recapitulated in a photosensitive mouse model. Human Molecular Genetics, 2020, 29, 2611-2624.	1.4	10
586	Persistence of a regeneration-associated, transitional alveolar epithelial cell state in pulmonary fibrosis. Nature Cell Biology, 2020, 22, 934-946.	4.6	296
587	Battle of the Sex Chromosomes: Competition between X and Y Chromosome-Encoded Proteins for Partner Interaction and Chromatin Occupancy Drives Multicopy Gene Expression and Evolution in Muroid Rodents. Molecular Biology and Evolution, 2020, 37, 3453-3468.	3.5	25
588	ChIA-PIPE: A fully automated pipeline for comprehensive ChIA-PET data analysis and visualization. Science Advances, 2020, 6, eaay2078.	4.7	22
589	A non-canonical RNAi pathway controls virulence and genome stability in Mucorales. PLoS Genetics, 2020, 16, e1008611.	1.5	21
590	Nucleolar RNA polymerase II drives ribosome biogenesis. Nature, 2020, 585, 298-302.	13.7	135
591	ASXL3 bridges BRD4 to BAP1 complex and governs enhancer activity in small cell lung cancer. Genome Medicine, 2020, 12, 63.	3.6	34
592	Antagonism between splicing and microprocessor complex dictates the serum-induced processing of lnc-MIRHG for efficient cell cycle reentry. Rna, 2020, 26, 1603-1620.	1.6	12
593	The chromatin remodeling enzyme Chd4 regulates genome architecture in the mouse brain. Nature Communications, 2020, 11, 3419.	5.8	33
594	Comparative sequencing data analysis of Ion Torrent and MinION sequencing platforms using a clinical diagnostic haematology panel. International Journal of Laboratory Hematology, 2020, 42, 833-841.	0.7	6
595	Normal Patterns of Histone H3K27 Methylation Require the Histone Variant H2A.Z in Neurospora crassa. Genetics, 2020, 216, 51-66.	1.2	14
596	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
597	WGVD: an integrated web-database for wheat genome variation and selective signatures. Database: the Journal of Biological Databases and Curation, 2020, 2020, .	1.4	7

#	ARTICLE	IF	CITATIONS
598	Galaxy CLIP-Explorer: a web server for CLIP-Seq data analysis. GigaScience, 2020, 9, .	3.3	8
599	H3K27M in Gliomas Causes a One-Step Decrease in H3K27 Methylation and Reduced Spreading within the Constraints of H3K36 Methylation. Cell Reports, 2020, 33, 108390.	2.9	50
600	Requisite Chromatin Remodeling for Myeloid and Erythroid Lineage Differentiation from Erythromyeloid Progenitors. Cell Reports, 2020, 33, 108395.	2.9	6
601	Dinucleosome specificity and allosteric switch of the ISW1a ATP-dependent chromatin remodeler in transcription regulation. Nature Communications, 2020, 11, 5913.	5.8	15
602	An Integrated Epigenomic and Transcriptomic Map of Mouse and Human Î±Î² T Cell Development. Immunity, 2020, 53, 1182-1201.e8.	6.6	49
603	Unique Immune Cell Coactivators Specify Locus Control Region Function and Cell Stage. Molecular Cell, 2020, 80, 845-861.e10.	4.5	21
604	HP1Î³ regulates H3K36 methylation and pluripotency in embryonic stem cells. Nucleic Acids Research, 2020, 48, 12660-12674.	6.5	9
605	Dynamic changes in chromatin accessibility, altered adipogenic gene expression, and total versus de novo fatty acid synthesis in subcutaneous adipose stem cells of normal-weight polycystic ovary syndrome (PCOS) women during adipogenesis: evidence of cellular programming. Clinical Epigenetics, 2020, 12, 181.	1.8	17
606	Characterization of Organoid Cultures to Study the Effects of Pregnancy Hormones on the Epigenome and Transcriptional Output of Mammary Epithelial Cells. Journal of Mammary Gland Biology and Neoplasia, 2020, 25, 351-366.	1.0	13
607	Direct RNA sequencing reveals m6A modifications on adenovirus RNA are necessary for efficient splicing. Nature Communications, 2020, 11, 6016.	5.8	111
608	A map of cis-regulatory elements and 3D genome structures in zebrafish. Nature, 2020, 588, 337-343.	13.7	80
609	Hâ€NSâ€like proteins inPseudomonas aeruginosacoordinately silence intragenic transcription. Molecular Microbiology, 2020, 115, 1138-1151.	1.2	14
610	KLF3 Mediates Epidermal Differentiation through the Epigenomic Writer CBP. IScience, 2020, 23, 101320.	1.9	15
611	Transcription-dependent cohesin repositioning rewires chromatin loops in cellular senescence. Nature Communications, 2020, 11, 6049.	5.8	42
612	IRF-1 expressed in the inner cell mass of the porcine early blastocyst enhances the pluripotency of induced pluripotent stem cells. Stem Cell Research and Therapy, 2020, 11, 505.	2.4	9
613	I-KCKT allows dissection-free RNA profiling of adult Drosophila intestinal progenitor cells. Development (Cambridge), 2020, 148, .	1.2	9
614	Recent evolution of a TET-controlled and DPPA3/STELLA-driven pathway of passive DNA demethylation in mammals. Nature Communications, 2020, 11, 5972.	5.8	38
615	Single-Nucleotide RNA Maps for the Two Major Nosocomial Pathogens Enterococcus faecalis and Enterococcus faecium. Frontiers in Cellular and Infection Microbiology, 2020, 10, 600325.	1.8	16

#	Article	IF	Citations
616	An optimised chromatin immunoprecipitation (ChIP) method for starchy leaves of Nicotiana benthamiana to study histone modifications of an allotetraploid plant. Molecular Biology Reports, 2020, 47, 9499-9509.	1.0	4
617	OsChz1 acts as a histone chaperone in modulating chromatin organization and genome function in rice. Nature Communications, 2020, 11, 5717.	5.8	9
618	Lysine demethylase 7a regulates murine anterior-posterior development by modulating the transcription of Hox gene cluster. Communications Biology, 2020, 3, 725.	2.0	7
619	Dedifferentiation and neuronal repression define familial Alzheimerâ€™s disease. Science Advances, 2020, 6, .	4.7	44
620	Coupling of H3K27me3 recognition with transcriptional repression through the BAH-PHD-CPL2 complex in Arabidopsis. Nature Communications, 2020, 11, 6212.	5.8	38
621	A small UTX stabilization domain of Trr is conserved within mammalian MLL3-4/COMPASS and is sufficient to rescue loss of viability in null animals. Genes and Development, 2020, 34, 1493-1502.	2.7	14
622	Rapid and Scalable Profiling of Nascent RNA with fastGRO. Cell Reports, 2020, 33, 108373.	2.9	20
623	Loss of histone H3.3 results in DNA replication defects and altered origin dynamics in <i>C. elegans</i>. Genome Research, 2020, 30, 1740-1751.	2.4	11
624	Persistent epigenetic reprogramming of sweet taste by diet. Science Advances, 2020, 6, .	4.7	31
625	A human cell atlas of fetal chromatin accessibility. Science, 2020, 370, .	6.0	265
626	Enhancer hijacking determines extrachromosomal circular MYCN amplicon architecture in neuroblastoma. Nature Communications, 2020, 11, 5823.	5.8	104
627	Development of specialized sensory neurons engages a nuclear receptor required for functional plasticity. Genes and Development, 2020, 34, 1666-1679.	2.7	3
628	Inter-Strain Epigenomic Profiling Reveals a Candidate IAP Master Copy in C3H Mice. Viruses, 2020, 12, 783.	1.5	9
629	HDA6-dependent histone deacetylation regulates mRNA polyadenylation in <i>Arabidopsis</i>. Genome Research, 2020, 30, 1407-1417.	2.4	21
630	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
631	N6-Methyladenosine co-transcriptionally directs the demethylation of histone H3K9me2. Nature Genetics, 2020, 52, 870-877.	9.4	157
632	FXR Isoforms Control Different Metabolic Functions in Liver Cells via Binding to Specific DNA Motifs. Gastroenterology, 2020, 159, 1853-1865.e10.	0.6	47
633	LncRNAs are regulated by chromatin states and affect the skeletal muscle cell differentiation. Cell Proliferation, 2020, 53, e12879.	2.4	12

#	Article	IF	Citations
634	Self-Reporting Transposons Enable SimultaneousÂReadout of Gene Expression and TranscriptionÂFactor Binding in Single Cells. Cell, 2020, 182, 992-1008.e21.	13.5	54
635	Predicting gene regulatory regions with a convolutional neural network for processing double-strand genome sequence information. PLoS ONE, 2020, 15, e0235748.	1.1	9
636	The Meningioma Enhancer Landscape Delineates Novel Subgroups and Drives Druggable Dependencies. Cancer Discovery, 2020, 10, 1722-1741.	7.7	30
637	Differential contribution of p300 and CBP to regulatory element acetylation in mESCs. BMC Molecular and Cell Biology, 2020, 21, 55.	1.0	44
638	A chromosomeâ€level genome assembly provides new insights into paternal genome elimination in the cotton mealybug <i>Phenacoccus solenopsis</i>. Molecular Ecology Resources, 2020, 20, 1733-1747.	2.2	12
639	The Human Integrator Complex Facilitates Transcriptional Elongation by Endonucleolytic Cleavage of Nascent Transcripts. Cell Reports, 2020, 32, 107917.	2.9	68
640	Occupancy maps of 208 chromatin-associated proteins in one human cell type. Nature, 2020, 583, 720-728.	13.7	90
641	Spatiotemporal DNA methylome dynamics of the developing mouse fetus. Nature, 2020, 583, 752-759.	13.7	84
642	Control of Early B Cell Development by the RNA N6-Methyladenosine Methylation. Cell Reports, 2020, 31, 107819.	2.9	77
643	ARID1A loss in neuroblastoma promotes the adrenergic-to-mesenchymal transition by regulating enhancer-mediated gene expression. Science Advances, 2020, 6, eaaz3440.	4.7	47
644	Human fetal microglia acquire homeostatic immune-sensing properties early in development. Science, 2020, 369, 530-537.	6.0	104
645	Memory Sequencing Reveals Heritable Single-Cell Gene Expression Programs Associated with Distinct Cellular Behaviors. Cell, 2020, 182, 947-959.e17.	13.5	132
646	CDYL2 Epigenetically Regulates MIR124 to Control NF-Î°B/STAT3-Dependent Breast Cancer Cell Plasticity. IScience, 2020, 23, 101141.	1.9	22
647	<i>Oryza sativa</i> RNA-Dependent RNA Polymerase 6 Contributes to Double-Strand Break Formation in Meiosis. Plant Cell, 2020, 32, 3273-3289.	3.1	20
648	Cross-species analysis of enhancer logic using deep learning. Genome Research, 2020, 30, 1815-1834.	2.4	65
649	Inflammatory Signals Induce AT2 Cell-Derived Damage-Associated Transient Progenitors that Mediate Alveolar Regeneration. Cell Stem Cell, 2020, 27, 366-382.e7.	5.2	303
650	BRAHMA-interacting proteins BRIP1 and BRIP2 are core subunits of Arabidopsis SWI/SNF complexes. Nature Plants, 2020, 6, 996-1007.	4.7	33
651	Epigenetic Targeting of Mcl-1 Is Synthetically Lethal with Bcl-xL/Bcl-2 Inhibition in Model Systems of Glioblastoma. Cancers, 2020, 12, 2137.	1.7	18

#	Article	IF	Citations
652	Host Transcriptional Response to Persistent Infection with a Live-Attenuated Porcine Reproductive and Respiratory Syndrome Virus Strain. Viruses, 2020, 12, 817.	1.5	6
653	AutoRELACS: automated generation and analysis of ultra-parallel ChIP-seq. Scientific Reports, 2020, 10, 12400.	1.6	1
654	The RNA exosome shapes the expression of key protein-coding genes. Nucleic Acids Research, 2020, 48, 8509-8528.	6.5	12
655	Ybx1 fine-tunes PRC2 activities to control embryonic brain development. Nature Communications, 2020, 11, 4060.	5.8	29
656	Developmental changes in the accessible chromatin, transcriptome and Ascl1-binding correlate with the loss in MÃ¼ller Glial regenerative potential. Scientific Reports, 2020, 10, 13615.	1.6	21
657	CUT&RUN detects distinct DNA footprints of RNA polymerase II near the transcription start sites. Chromosome Research, 2020, 28, 381-393.	1.0	7
658	Chromatin-Level Differences Elucidate Potential Determinants of Contrasting Levels of Cold Sensitivity in Maize Lines. Plant Molecular Biology Reporter, 2021, 39, 335-350.	1.0	7
659	Perivascular mesenchymal cells control adipose-tissue macrophage accrual in obesity. Nature Metabolism, 2020, 2, 1332-1349.	5.1	53
660	BAHCC1 binds H3K27me3 via a conserved BAH module to mediate gene silencing and oncogenesis. Nature Genetics, 2020, 52, 1384-1396.	9.4	57
661	Activation of Clustered IFNÎ³ Target Genes Drives Cohesin-Controlled Transcriptional Memory. Molecular Cell, 2020, 80, 396-409.e6.	4.5	32
662	Integrated multi-omics reveal epigenomic disturbance of assisted reproductive technologies in human offspring. EBioMedicine, 2020, 61, 103076.	2.7	41
663	MIR2111-5 locus and shoot-accumulated mature miR2111 systemically enhance nodulation depending on HAR1 in Lotus japonicus. Nature Communications, 2020, 11, 5192.	5.8	31
664	The landscape of RNA Pol II binding reveals a stepwise transition during ZGA. Nature, 2020, 587, 139-144.	13.7	71
665	Incomplete removal of ribosomal RNA can affect chromatin RNA-seq data analysis. Transcription, 2020, 11, 230-235.	1.7	7
666	Î²-actin contributes to open chromatin for activation of the adipogenic pioneer factor CEBPA during transcriptional reprograming. Molecular Biology of the Cell, 2020, 31, 2511-2521.	0.9	16
667	Somatic mutations in colorectal cancer are associated with the epigenetic modifications. Journal of Cellular and Molecular Medicine, 2020, 24, 11828-11836.	1.6	5
668	Overlapping but Distinct Sequences Play Roles in the Insulator and Promoter Activities of the <i>Drosophila</i> BEAF-Dependent scsâ€™ Insulator. Genetics, 2020, 215, 1003-1012.	1.2	4
669	Systematic screening of CTCF binding partners identifies that BHLHE40 regulates CTCF genome-wide distribution and long-range chromatin interactions. Nucleic Acids Research, 2020, 48, 9606-9620.	6.5	30

#	Article	IF	Citations
670	Multiplexed and Ultralow-Input ChIP-seq Enabled by Tagmentation-Based Indexing and Facile Microfluidics. Analytical Chemistry, 2020, 92, 13661-13666.	3.2	3
671	NCBP3 positively impacts mRNA biogenesis. Nucleic Acids Research, 2020, 48, 10413-10427.	6.5	27
672	GATAâ€1â€dependent histone H3K27 acetylation mediates erythroid cellâ€specific chromatin interaction between CTCF sites. FASEB Journal, 2020, 34, 14736-14749.	0.2	8
673	An epigenetic mechanism underlying chromosome 17p deletion-driven tumorigenesis. Cancer Discovery, 2020, 11, CD-20-0336.	7.7	15
674	H3.3 G34W Promotes Growth and Impedes Differentiation of Osteoblast-Like Mesenchymal Progenitors in Giant Cell Tumor of Bone. Cancer Discovery, 2020, 10, 1968-1987.	7.7	40
675	Sterol regulatory element-binding protein Sre1 regulates carotenogenesis in the red yeast Xanthophyllomyces dendrorhous. Journal of Lipid Research, 2020, 61, 1658-1674.	2.0	9
676	FOXA1 Mutations Reveal Distinct Chromatin Profiles and Influence Therapeutic Response in Breast Cancer. Cancer Cell, 2020, 38, 534-550.e9.	7.7	67
677	Chromatin regulates expression of small RNAs to help maintain transposon methylome homeostasis in Arabidopsis. Genome Biology, 2020, 21, 251.	3.8	61
678	LSD1 prevents aberrant heterochromatin formation in Neurospora crassa. Nucleic Acids Research, 2020, 48, 10199-10210.	6.5	4
679	High-resolution analysis of Merkel Cell Polyomavirus in Merkel Cell Carcinoma reveals distinct integration patterns and suggests NHEJ and MMBIR as underlying mechanisms. PLoS Pathogens, 2020, 16, e1008562.	2.1	24
680	ATAC-seq footprinting unravels kinetics of transcription factor binding during zygotic genome activation. Nature Communications, 2020, 11, 4267.	5.8	318
681	Distinct Cdk9-phosphatase switches act at the beginning and end of elongation by RNA polymerase II. Nature Communications, 2020, 11, 4338.	5.8	37
682	Improved Reference Genome Uncovers Novel Sex-Linked Regions in the Guppy (Poecilia reticulata). Genome Biology and Evolution, 2020, 12, 1789-1805.	1.1	36
683	Seasonal plasticity and diel stability of H3K27me3 in natural fluctuating environments. Nature Plants, 2020, 6, 1091-1097.	4.7	21
684	Epimutations driven by small RNAs arise frequently but most have limited duration in Caenorhabditis elegans. Nature Ecology and Evolution, 2020, 4, 1539-1548.	3.4	33
685	Alteration of genome folding via contact domain boundary insertion. Nature Genetics, 2020, 52, 1076-1087.	9.4	35
686	Chromatin binding of FOXA1 is promoted by LSD1-mediated demethylation in prostate cancer. Nature Genetics, 2020, 52, 1011-1017.	9.4	78
687	Histone deacetylase HDA-1 modulates mitochondrial stress response and longevity. Nature Communications, 2020, 11, 4639.	5.8	63

#	ARTICLE	IF	CITATIONS
688	Discovering functional sequences with RELICS, an analysis method for CRISPR screens. PLoS Computational Biology, 2020, 16, e1008194.	1.5	7
689	Epigenetic silencing of clustered tRNA genes in Arabidopsis. Nucleic Acids Research, 2020, 48, 10297-10312.	6.5	12
690	lncRNA DIGIT and BRD3 protein form phase-separated condensates to regulate endoderm differentiation. Nature Cell Biology, 2020, 22, 1211-1222.	4.6	100
691	Exploring the virulence gene interactome with<scp>CRISPR</scp>/<scp>dC</scp>as9 in the human malaria parasite. Molecular Systems Biology, 2020, 16, e9569.	3.2	32
692	Epigenetic gene silencing by heterochromatin primes fungal resistance. Nature, 2020, 585, 453-458.	13.7	68
693	Efficient low-cost chromatin profiling with CUT&Tag. Nature Protocols, 2020, 15, 3264-3283.	5.5	181
694	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
695	Repetitive Elements Contribute to the Diversity and Evolution of Centromeres in the Fungal Genus <i>Verticillium</i>. MBio, 2020, 11, .	1.8	26
696	LSD1 represses a neonatal/reparative gene program in adult intestinal epithelium. Science Advances, 2020, 6, .	4.7	18
697	Biology and Physics of Heterochromatin-Like Domains/Complexes. Cells, 2020, 9, 1881.	1.8	8
698	Decapping enzyme 1A breaks X-chromosome symmetry by controlling Tsix elongation and RNA turnover. Nature Cell Biology, 2020, 22, 1116-1129.	4.6	19
699	<i>MYCN</i> drives chemoresistance in small cell lung cancer while USP7 inhibition can restore chemosensitivity. Genes and Development, 2020, 34, 1210-1226.	2.7	46
700	STAT3 and GR Cooperate to Drive Gene Expression and Growth of Basal-Like Triple-Negative Breast Cancer. Cancer Research, 2020, 80, 4355-4370.	0.4	17
701	DNA polymerase stalling at structured DNA constrains the expansion of short tandem repeats. Genome Biology, 2020, 21, 209.	3.8	40
702	Exhausted CD4+ T Cells during Malaria Exhibit Reduced mTORc1 Activity Correlated with Loss of T-bet Expression. Journal of Immunology, 2020, 205, 1608-1619.	0.4	10
703	S-adenosyl- <scp>l</scp> -homocysteine hydrolase links methionine metabolism to the circadian clock and chromatin remodeling. Science Advances, 2020, 6, .	4.7	49
704	The Regulatory Role of Histone Modification on Gene Expression in the Early Stage of Myocardial Infarction. Frontiers in Cardiovascular Medicine, 2020, 7, 594325.	1.1	6
705	FAN-C: a feature-rich framework for the analysis and visualisation of chromosome conformation capture data. Genome Biology, 2020, 21, 303.	3.8	100

#	Article	IF	Citations
706	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
707	Fine-mapping and cell-specific enrichment at corneal resistance factor loci prioritize candidate causal regulatory variants. Communications Biology, 2020, 3, 762.	2.0	6
708	Glioblastoma epigenome profiling identifies SOX10 as a master regulator of molecular tumour subtype. Nature Communications, 2020, 11, 6434.	5.8	48
709	Creation of bladder assembloids mimicking tissue regeneration and cancer. Nature, 2020, 588, 664-669.	13.7	133
710	Predicting transcription factor binding in single cells through deep learning. Science Advances, 2020, 6, .	4.7	41
711	Human T-bet Governs Innate and Innate-like Adaptive IFN-Î³ Immunity against Mycobacteria. Cell, 2020, 183, 1826-1847.e31.	13.5	83
712	Epigenomic Reprogramming toward Mesenchymal-Epithelial Transition in Ovarian-Cancer-Associated Mesenchymal Stem Cells Drives Metastasis. Cell Reports, 2020, 33, 108473.	2.9	34
713	Extensive nuclear gyration and pervasive non-genic transcription during primordial germ cell development in zebrafish. Development (Cambridge), 2021, 148, .	1.2	4
714	Dynamics of Whole-Genome Contacts of Nucleoli in Drosophila Cells Suggests a Role for rDNA Genes in Global Epigenetic Regulation. Cells, 2020, 9, 2587.	1.8	6
715	Impact of AHR Ligand TCDD on Human Embryonic Stem Cells and Early Differentiation. International Journal of Molecular Sciences, 2020, 21, 9052.	1.8	4
716	Transcriptome and translatome changes in germinated pollen under heat stress uncover roles of transporter genes involved in pollen tube growth. Plant, Cell and Environment, 2021, 44, 2167-2184.	2.8	25
717	Î²-catenin drives distinct transcriptional networks in proliferative and non-proliferative cardiomyocytes. Development (Cambridge), 2020, 147, .	1.2	24
718	Genotypic and Phenotypic Changes in Candida albicans as a Result of Cold Plasma Treatment. International Journal of Molecular Sciences, 2020, 21, 8100.	1.8	8
719	Evolution from adherent to suspension: systems biology of HEK293 cell line development. Scientific Reports, 2020, 10, 18996.	1.6	49
720	Data Sanitization to Reduce Private Information Leakage from Functional Genomics. Cell, 2020, 183, 905-917.e16.	13.5	28
721	Lineage-Resolved Enhancer and Promoter Usage during a Time Course of Embryogenesis. Developmental Cell, 2020, 55, 648-664.e9.	3.1	47
722	Genomic architecture of a genetically assimilated seasonal color pattern. Science, 2020, 370, 721-725.	6.0	48
723	G9a Promotes Breast Cancer Recurrence through Repression of a Pro-inflammatory Program. Cell Reports, 2020, 33, 108341.	2.9	19

#	ARTICLE	IF	CITATIONS
724	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
725	A Prion-like Domain in Transcription Factor EBF1 Promotes Phase Separation and Enables B Cell Programming of Progenitor Chromatin. Immunity, 2020, 53, 1151-1167.e6.	6.6	47
726	meCLICK-Seq, a Substrate-Hijacking and RNA Degradation Strategy for the Study of RNA Methylation. ACS Central Science, 2020, 6, 2196-2208.	5.3	31
727	Xrn1 influence on gene transcription results from the combination of general effects on elongating RNA pol II and gene-specific chromatin configuration. RNA Biology, 2021, 18, 1310-1323.	1.5	12
728	Interplay of pericentromeric genome organization and chromatin landscape regulates the expression of Drosophila melanogaster heterochromatic genes. Epigenetics and Chromatin, 2020, 13, 41.	1.8	14
729	A histone H3.3K36M mutation in mice causes an imbalance of histone modifications and defects in chondrocyte differentiation. Epigenetics, 2021, 16, 1123-1134.	1.3	8
730	Barrier-to-Autointegration Factor 1 Protects against a Basal cGAS-STING Response. MBio, 2020, 11, .	1.8	33
731	Coactivation of NF-Î°B and Notch signaling is sufficient to induce B-cell transformation and enables B-myeloid conversion. Blood, 2020, 135, 108-120.	0.6	14
732	Selection following Gene Duplication Shapes Recent Genome Evolution in the Pea Aphid Acyrthosiphon pisum. Molecular Biology and Evolution, 2020, 37, 2601-2615.	3.5	12
733	Prenet: Predictive network from ATAC-SEQ data. Journal of Bioinformatics and Computational Biology, 2020, 18, 2040003.	0.3	2
734	<i>EZH2</i>-Deficient T-cell Acute Lymphoblastic Leukemia Is Sensitized to CHK1 Inhibition through Enhanced Replication Stress. Cancer Discovery, 2020, 10, 998-1017.	7.7	29
735	FMRP Control of Ribosome Translocation Promotes Chromatin Modifications and Alternative Splicing of Neuronal Genes Linked to Autism. Cell Reports, 2020, 30, 4459-4472.e6.	2.9	63
736	A single-cell transcriptomic landscape of primate arterial aging. Nature Communications, 2020, 11, 2202.	5.8	95
737	The proteasome activator PA200 regulates expression of genes involved in cell survival upon selective mitochondrial inhibition in neuroblastoma cells. Journal of Cellular and Molecular Medicine, 2020, 24, 6716-6730.	1.6	7
738	Conserved protein Pir2ARS2 mediates gene repression through cryptic introns in lncRNAs. Nature Communications, 2020, 11, 2412.	5.8	15
739	Integrative genome-wide analysis reveals the role of WIP proteins in inhibition of growth and development. Communications Biology, 2020, 3, 239.	2.0	16
740	Fine Chromatin-Driven Mechanism of Transcription Interference by Antisense Noncoding Transcription. Cell Reports, 2020, 31, 107612.	2.9	25
741	ZKSCAN3 counteracts cellular senescence by stabilizing heterochromatin. Nucleic Acids Research, 2020, 48, 6001-6018.	6.5	54

#	ARTICLE	IF	CITATIONS
742	Temporal expression of MOF acetyltransferase primes transcription factor networks for erythroid fate. Science Advances, 2020, 6, eaaz4815.	4.7	17
743	Histone deacetylase 1 and 2 drive differentiation and fusion of progenitor cells in human placental trophoblasts. Cell Death and Disease, 2020, 11, 311.	2.7	30
744	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
745	BMP4 resets mouse epiblast stem cells to naive pluripotency through ZBTB7A/B-mediated chromatin remodelling. Nature Cell Biology, 2020, 22, 651-662.	4.6	34
746	Uncoupling histone H3K4 trimethylation from developmental gene expression via an equilibrium of COMPASS, Polycomb and DNA methylation. Nature Genetics, 2020, 52, 615-625.	9.4	76
747	The transcription factor GLI1 cooperates with the chromatin remodeler SMARCA2 to regulate chromatin accessibility at distal DNA regulatory elements. Journal of Biological Chemistry, 2020, 295, 8725-8735.	1.6	7
748	Control of tissue morphogenesis by the HOX gene <i>Ultrabithorax</i>. Development (Cambridge), 2020, 147, .	1.2	21
749	Evolutionary conserved NSL complex/BRD4 axis controls transcription activation via histone acetylation. Nature Communications, 2020, 11, 2243.	5.8	21
750	Evolutionarily ancient BAHâ€“PHD protein mediates Polycomb silencing. Proceedings of the National Academy of Sciences of the United States of America, 2020, 117, 11614-11623.	3.3	30
751	Defining the relative and combined contribution of CTCF and CTCFL to genomic regulation. Genome Biology, 2020, 21, 108.	3.8	37
752	A Unified Model for the Function of YTHDF Proteins in Regulating m6A-Modified mRNA. Cell, 2020, 181, 1582-1595.e18.	13.5	448
753	High-Resolution InÂVivo Identification of miRNA Targets by Halo-Enhanced Ago2 Pull-Down. Molecular Cell, 2020, 79, 167-179.e11.	4.5	36
754	PIWI-interacting RNAs are differentially expressed during cardiac differentiation of human pluripotent stem cells. PLoS ONE, 2020, 15, e0232715.	1.1	12
755	Unblending of Transcriptional Condensates in Human Repeat Expansion Disease. Cell, 2020, 181, 1062-1079.e30.	13.5	115
756	A DMP-triggered in vivo maternal haploid induction system in the dicotyledonous Arabidopsis. Nature Plants, 2020, 6, 466-472.	4.7	78
757	The NSD2 p.E1099K Mutation Is Enriched at Relapse and Confers Drug Resistance in a Cell Contextâ€“Dependent Manner in Pediatric Acute Lymphoblastic Leukemia. Molecular Cancer Research, 2020, 18, 1153-1165.	1.5	20
758	Microbiota-Induced Type I Interferons Instruct a Poised Basal State of Dendritic Cells. Cell, 2020, 181, 1080-1096.e19.	13.5	139
759	Transcriptional down-regulation of metabolic genes by Gdown1 ablation induces quiescent cell re-entry into the cell cycle. Genes and Development, 2020, 34, 767-784.	2.7	5

#	ARTICLE	IF	CITATIONS
760	Expression of RUNX1-ETO Rapidly Alters the Chromatin Landscape and Growth of Early Human Myeloid Precursor Cells. Cell Reports, 2020, 31, 107691.	2.9	20
761	Clinical use of NGS data from the targeted gene panel for mitochondrial diseases screening. Computer Methods and Programs in Biomedicine, 2020, 194, 105529.	2.6	1
762	Combined inhibition of JAK/STAT pathway and lysine-specific demethylase 1 as a therapeutic strategy in CSF3R/CEBPA mutant acute myeloid leukemia. Proceedings of the National Academy of Sciences of the United States of America, 2020, 117, 13670-13679.	3.3	24
763	TATA box-binding protein-related factor 3 drives the mesendoderm specification of human embryonic stem cells by globally interacting with the TATA box of key mesendodermal genes. Stem Cell Research and Therapy, 2020, 11, 196.	2.4	3
764	UAP56/DDX39B is a major cotranscriptional RNAâ€"DNA helicase that unwinds harmful R loops genome-wide. Genes and Development, 2020, 34, 898-912.	2.7	83
765	The essential genome of Ralstonia solanacearum. Microbiological Research, 2020, 238, 126500.	2.5	13
766	Genome-Wide Characterization of DNase I-Hypersensitive Sites and Cold Response Regulatory Landscapes in Grasses. Plant Cell, 2020, 32, 2457-2473.	3.1	29
767	The <i>Gossypium longicalyx</i> Genome as a Resource for Cotton Breeding and Evolution. G3: Genes, Genomes, Genetics, 2020, 10, 1457-1467.	0.8	32
768	A novel sensitive detection method for DNA methylation in circulating free DNA of pancreatic cancer. PLoS ONE, 2020, 15, e0233782.	1.1	21
769	Single-cell ATAC sequencing analysis: From data preprocessing to hypothesis generation. Computational and Structural Biotechnology Journal, 2020, 18, 1429-1439.	1.9	91
770	Alternative splicing regulation by the androgen receptor in prostate cancer cells. Journal of Steroid Biochemistry and Molecular Biology, 2020, 202, 105710.	1.2	8
771	The Number of Transcription Factors at an Enhancer Determines Switch-like Gene Expression. Cell Reports, 2020, 31, 107724.	2.9	25
772	The Transcription Co-Repressors MTG8 and MTG16 Regulate Exit of Intestinal Stem Cells From Their Niche and Differentiation Into Enterocyte vs Secretory Lineages. Gastroenterology, 2020, 159, 1328-1341.e3.	0.6	24
773	The Chromatin Regulator ZMYM2 Restricts Human Pluripotent Stem Cell Growth and Is Essential for Teratoma Formation. Stem Cell Reports, 2020, 15, 1275-1286.	2.3	13
774	Analysis of Genome Architecture during SCNT Reveals a Role of Cohesin in Impeding Minor ZGA. Molecular Cell, 2020, 79, 234-250.e9.	4.5	39
775	DNA double-strand breaks induce H2Ax phosphorylation domains in a contact-dependent manner. Nature Communications, 2020, 11, 3158.	5.8	97
776	Active transcription and Orc1 drive chromatin association of the AAA+ ATPase Pch2 during meiotic G2/prophase. PLoS Genetics, 2020, 16, e1008905.	1.5	7
777	CSI NGS Portal: An Online Platform for Automated NGS Data Analysis and Sharing. International Journal of Molecular Sciences, 2020, 21, 3828.	1.8	19

#	ARTICLE	IF	CITATIONS
778	Intergenerationally Maintained Histone H4 Lysine 16 Acetylation Is Instructive for Future Gene Activation. Cell, 2020, 182, 127-144.e23.	13.5	57
779	Removal of H2Aub1 by ubiquitin-specific proteases 12 and 13 is required for stable Polycomb-mediated gene repression in Arabidopsis. Genome Biology, 2020, 21, 144.	3.8	34
780	A Human Pluripotent Stem Cell-based Platform to Study SARS-CoV-2 Tropism and Model Virus Infection in Human Cells and Organoids. Cell Stem Cell, 2020, 27, 125-136.e7.	5.2	543
781	Hippo-YAP signaling controls lineage differentiation of mouse embryonic stem cells through modulating the formation of super-enhancers. Nucleic Acids Research, 2020, 48, 7182-7196.	6.5	41
782	Dynamic chromatin accessibility profiling reveals changes in host genome organization in response to baculovirus infection. PLoS Pathogens, 2020, 16, e1008633.	2.1	12
783	Epigenetic competition reveals density-dependent regulation and target site plasticity of phosphorothioate epigenetics in bacteria. Proceedings of the National Academy of Sciences of the United States of America, 2020, 117, 14322-14330.	3.3	25
784	Low-Phosphate Chromatin Dynamics Predict a Cell Wall Remodeling Network in Rice Shoots. Plant Physiology, 2020, 182, 1494-1509.	2.3	14
785	Actin-related protein Arp4 regulates euchromatic gene expression and development through H2A.Z deposition in blood-stage Plasmodium falciparum. Parasites and Vectors, 2020, 13, 314.	1.0	8
786	Dissecting myogenin-mediated retinoid X receptor signaling in myogenic differentiation. Communications Biology, 2020, 3, 315.	2.0	5
787	An NMF-based approach to discover overlooked differentially expressed gene regions from single-cell RNA-seq data. NAR Genomics and Bioinformatics, 2020, 2, lqz020.	1.5	5
788	Proximity-dependent biotin labelling reveals CP190 as an EcR/Usp molecular partner. Scientific Reports, 2020, 10, 4793.	1.6	18
789	RNAi pathways repress reprogramming of C. elegans germ cells during heat stress. Nucleic Acids Research, 2020, 48, 4256-4273.	6.5	32
790	ATF7-Dependent Epigenetic Changes Are Required for the Intergenerational Effect of a Paternal Low-Protein Diet. Molecular Cell, 2020, 78, 445-458.e6.	4.5	52
791	A critical role of PRDM14 in human primordial germ cell fate revealed by inducible degrons. Nature Communications, 2020, 11, 1282.	5.8	71
792	NELF Regulates a Promoter-Proximal Step Distinct from RNA Pol II Pause-Release. Molecular Cell, 2020, 78, 261-274.e5.	4.5	110
793	The GATA Transcription Factor Gaf1 Represses tRNAs, Inhibits Growth, and Extends Chronological Lifespan Downstream of Fission Yeast TORC1. Cell Reports, 2020, 30, 3240-3249.e4.	2.9	33
794	Enhancer occlusion transcripts regulate the activity of human enhancer domains via transcriptional interference: a computational perspective. Nucleic Acids Research, 2020, 48, 3435-3454.	6.5	5
795	Locally acting transcription factors regulate p53-dependent cis-regulatory element activity. Nucleic Acids Research, 2020, 48, 4195-4213.	6.5	16

#	ARTICLE	IF	CITATIONS
796	Multiplexed capture of spatial configuration and temporal dynamics of locus-specific 3D chromatin by biotinylated dCas9. Genome Biology, 2020, 21, 59.	3.8	27
797	pyBedGraph: a python package for fast operations on 1D genomic signal tracks. Bioinformatics, 2020, 36, 3234-3235.	1.8	1
798	Chromosome organization by a conserved condensin-ParB system in the actinobacterium Corynebacterium glutamicum. Nature Communications, 2020, 11, 1485.	5.8	64
799	AT-Hook Transcription Factors Restrict Petiole Growth by Antagonizing PIFs. Current Biology, 2020, 30, 1454-1466.e6.	1.8	39
800	Three-dimensional chromatin landscapes in T cell acute lymphoblastic leukemia. Nature Genetics, 2020, 52, 388-400.	9.4	118
801	Precise and Cost-Effective Nanopore Sequencing for Post-GWAS Fine-Mapping and Causal Variant Identification. IScience, 2020, 23, 100971.	1.9	7
802	RNA helicase DDX21 mediates nucleotide stress responses in neural crest and melanoma cells. Nature Cell Biology, 2020, 22, 372-379.	4.6	37
803	HNF1A recruits KDM6A to activate differentiated acinar cell programs that suppress pancreatic cancer. EMBO Journal, 2020, 39, e102808.	3.5	44
804	C/EBPÎ²-Dependent Epigenetic Memory Induces Trained Immunity in Hematopoietic Stem Cells. Cell Stem Cell, 2020, 26, 657-674.e8.	5.2	180
805	The transcriptional regulator MEIS2 sets up the ground state for palatal osteogenesis in mice. Journal of Biological Chemistry, 2020, 295, 5449-5460.	1.6	15
806	Neurofibromin Is an Estrogen Receptor-Î± Transcriptional Co-repressor in Breast Cancer. Cancer Cell, 2020, 37, 387-402.e7.	7.7	59
807	Lysine 4 of histone H3.3 is required for embryonic stem cell differentiation, histone enrichment at regulatory regions and transcription accuracy. Nature Genetics, 2020, 52, 273-282.	9.4	37
808	BRD4 Is Necessary for Differentiation Downstream of Epidermal Lineage-Determining Transcription Factors. Journal of Investigative Dermatology, 2020, 140, 2077-2081.e5.	0.3	9
809	Transient genome-wide interactions of the master transcription factor NLP7 initiate a rapid nitrogen-response cascade. Nature Communications, 2020, 11, 1157.	5.8	99
810	Heterochromatin establishment during early mammalian development is regulated by pericentromeric RNA and characterized by non-repressive H3K9me3. Nature Cell Biology, 2020, 22, 767-778.	4.6	71
811	Chd4 choreographs self-antigen expression for central immune tolerance. Nature Immunology, 2020, 21, 892-901.	7.0	42
812	The Configuration of RPA, RAD51, and DMC1 Binding in Meiosis Reveals the Nature of Critical Recombination Intermediates. Molecular Cell, 2020, 79, 689-701.e10.	4.5	87
813	METTL3 and N6-Methyladenosine Promote Homologous Recombination-Mediated Repair of DSBs by Modulating DNA-RNA Hybrid Accumulation. Molecular Cell, 2020, 79, 425-442.e7.	4.5	182

#	ARTICLE	IF	CITATIONS
814	Histone Acetyltransferase MOF Blocks Acquisition of Quiescence in Ground-State ESCs through Activating Fatty Acid Oxidation. Cell Stem Cell, 2020, 27, 441-458.e10.	5.2	37
815	Genome-wide analyses of chromatin interactions after the loss of Pol I, Pol II, and Pol III. Genome Biology, 2020, 21, 158.	3.8	89
816	Conditional knockout of RAD51-related genes in Leishmania major reveals a critical role for homologous recombination during genome replication. PLoS Genetics, 2020, 16, e1008828.	1.5	21
817	Genome-wide R-loop Landscapes during Cell Differentiation and Reprogramming. Cell Reports, 2020, 32, 107870.	2.9	51
818	Integrator restrains paraspeckles assembly by promoting isoform switching of the lncRNA <i>NEAT1</i>. Science Advances, 2020, 6, eaaz9072.	4.7	33
819	Nascent Transcript Folding Plays a Major Role in Determining RNA Polymerase Elongation Rates. Molecular Cell, 2020, 79, 488-503.e11.	4.5	52
820	FiTAc-seq: fixed-tissue ChIP-seq for H3K27ac profiling and super-enhancer analysis of FFPE tissues. Nature Protocols, 2020, 15, 2503-2518.	5.5	20
821	PuHox52â€mediated hierarchical multilayered gene regulatory network promotes adventitious root formation in <i>Populus ussuriensis</i>. New Phytologist, 2020, 228, 1369-1385.	3.5	33
822	Coordinated regulation of cellular identityâ€“associated H3K4me3 breadth by the COMPASS family. Science Advances, 2020, 6, eaaz4764.	4.7	37
823	Long-Read cDNA Sequencing Enables a â€œGene-Likeâ€• Transcript Annotation of Transposable Elements. Plant Cell, 2020, 32, 2687-2698.	3.1	48
824	The RNA quality control pathway nonsense-mediated mRNA decay targets cellular and viral RNAs to restrict KSHV. Nature Communications, 2020, 11, 3345.	5.8	25
825	A Light-Inducible Strain for Genome-Wide Histone Turnover Profiling in <i>Neurospora crassa</i>. Genetics, 2020, 215, 569-578.	1.2	6
826	Cell type- and stage-specific expression of Otx2 is regulated by multiple transcription factors and<i>cis</i>-regulatory modules in the retina. Development (Cambridge), 2020, 147, .	1.2	23
827	Acetate supplementation restores chromatin accessibility and promotes tumor cell differentiation under hypoxia. Cell Death and Disease, 2020, 11, 102.	2.7	39
828	Characterizing chromatin landscape from aggregate and single-cell genomic assays using flexible duration modeling. Nature Communications, 2020, 11, 747.	5.8	11
829	BRG1 Activates Proliferation and Transcription of Cell Cycle-Dependent Genes in Breast Cancer Cells. Cancers, 2020, 12, 349.	1.7	21
830	Dense Transposon Integration Reveals Essential Cleavage and Polyadenylation Factors Promote Heterochromatin Formation. Cell Reports, 2020, 30, 2686-2698.e8.	2.9	23
831	Dissecting the Regulatory Strategies of NF-Î°B RelA Target Genes in the Inflammatory Response Reveals Differential Transactivation Logics. Cell Reports, 2020, 30, 2758-2775.e6.	2.9	35

#	ARTICLE	IF	CITATIONS
832	A lncRNA-SWI/SNF complex crosstalk controls transcriptional activation at specific promoter regions. Nature Communications, 2020, 11, 936.	5.8	69
833	In situ dissection of domain boundaries affect genome topology and gene transcription in Drosophila. Nature Communications, 2020, 11, 894.	5.8	31
834	Ascl2-Dependent Cell Dedifferentiation Drives Regeneration of Ablated Intestinal Stem Cells. Cell Stem Cell, 2020, 26, 377-390.e6.	5.2	152
835	Distinct Mesenchymal Cell Populations Generate the Essential Intestinal BMP Signaling Gradient. Cell Stem Cell, 2020, 26, 391-402.e5.	5.2	211
836	The R-Loop Atlas of Arabidopsis Development and Responses to Environmental Stimuli. Plant Cell, 2020, 32, 888-903.	3.1	61
837	Human THO maintains the stability of repetitive DNA. Genes To Cells, 2020, 25, 334-342.	0.5	3
838	Altered chromatin landscape and enhancer engagement underlie transcriptional dysregulation in MED12 mutant uterine leiomyomas. Nature Communications, 2020, 11, 1019.	5.8	34
839	Regenerating zebrafish fin epigenome is characterized by stable lineage-specific DNA methylation and dynamic chromatin accessibility. Genome Biology, 2020, 21, 52.	3.8	44
840	Shared PPARÎ±/Î³ Target Genes Regulate Brown Adipocyte Thermogenic Function. Cell Reports, 2020, 30, 3079-3091.e5.	2.9	26
841	GsmPlot: a web server to visualize epigenome data in NCBI. BMC Bioinformatics, 2020, 21, 55.	1.2	2
842	ChIP-seq and RNA-seq for complex and low-abundance tree buds reveal chromatin and expression co-dynamics during sweet cherry bud dormancy. Tree Genetics and Genomes, 2020, 16, 1.	0.6	20
843	Triclosan induces zebrafish neurotoxicity by abnormal expression of miR-219 targeting oligodendrocyte differentiation of central nervous system. Archives of Toxicology, 2020, 94, 857-871.	1.9	18
844	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
845	Treatment-Induced Tumor Dormancy through YAP-Mediated Transcriptional Reprogramming of the Apoptotic Pathway. Cancer Cell, 2020, 37, 104-122.e12.	7.7	267
846	Engineering of Effector Domains for Targeted DNA Methylation with Reduced Off-Target Effects. International Journal of Molecular Sciences, 2020, 21, 502.	1.8	34
847	p53 Integrates Temporal WDR5 Inputs during Neuroectoderm and Mesoderm Differentiation of Mouse Embryonic Stem Cells. Cell Reports, 2020, 30, 465-480.e6.	2.9	17
848	Zika Virus Targets Glioblastoma Stem Cells through a SOX2-Integrin Î±vÎ²5 Axis. Cell Stem Cell, 2020, 26, 187-204.e10.	5.2	126
849	12-h clock regulation of genetic information flow by XBP1s. PLoS Biology, 2020, 18, e3000580.	2.6	46

#	ARTICLE	IF	CITATIONS
850	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
851	Rules and Exceptions: The Role of Chromosomal ParB in DNA Segregation and Other Cellular Processes. Microorganisms, 2020, 8, 105.	1.6	32
852	A transcriptome-wide antitermination mechanism sustaining identity of embryonic stem cells. Nature Communications, 2020, 11, 361.	5.8	20
853	ModHMM: A Modular Supra-Bayesian Genome Segmentation Method. Journal of Computational Biology, 2020, 27, 442-457.	0.8	6
854	Triangular correlation (TrC) between cancer aggressiveness, cell uptake capability, and cell deformability. Science Advances, 2020, 6, eaax2861.	4.7	24
855	Characterization of Insect Immune Systems from Genomic Data. Springer Protocols, 2020, , 3-34.	0.1	4
856	Inference of Bacterial Pathogen Instantaneous Population Growth Dynamics. Molecular Plant-Microbe Interactions, 2020, 33, 402-411.	1.4	5
857	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
858	Chromatin Organization in Early Land Plants Reveals an Ancestral Association between H3K27me3, Transposons, and Constitutive Heterochromatin. Current Biology, 2020, 30, 573-588.e7.	1.8	160
859	Widespread activation of developmental gene expression characterized by PRC1-dependent chromatin looping. Science Advances, 2020, 6, eaax4001.	4.7	72
860	DAF-16/FOXO requires Protein Phosphatase 4 to initiate transcription of stress resistance and longevity promoting genes. Nature Communications, 2020, 11, 138.	5.8	30
861	Snake Recombination Landscapes Are Concentrated in Functional Regions despite PRDM9. Molecular Biology and Evolution, 2020, 37, 1272-1294.	3.5	45
862	Localized Inhibition of Protein Phosphatase 1 by NUAK1 Promotes Spliceosome Activity and Reveals a MYC-Sensitive Feedback Control of Transcription. Molecular Cell, 2020, 77, 1322-1339.e11.	4.5	34
863	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
864	A native chromatin immunoprecipitation (ChIP) protocol for studying histone modifications in strawberry fruits. Plant Methods, 2020, 16, 10.	1.9	9
865	Replicational Dilution of H3K27me3 in Mammalian Cells and the Role of Poised Promoters. Molecular Cell, 2020, 78, 141-151.e5.	4.5	52
866	Antibody-free enzyme-assisted chemical approach for detection of N6-methyladenosine. Nature Chemical Biology, 2020, 16, 896-903.	3.9	125
867	Structural and functional insights into CWC27/CWC22 heterodimer linking the exon junction complex to spliceosomes. Nucleic Acids Research, 2020, 48, 5670-5683.	6.5	20

#	Article	IF	Citations
868	Wheat chromatin architecture is organized in genome territories and transcription factories. Genome Biology, 2020, 21, 104.	3.8	99
869	Combining signal and sequence to detect RNA polymerase initiation in ATAC-seq data. PLoS ONE, 2020, 15, e0232332.	1.1	1
870	Loss of CHD1 Promotes Heterogeneous Mechanisms of Resistance to AR-Targeted Therapy via Chromatin Dysregulation. Cancer Cell, 2020, 37, 584-598.e11.	7.7	96
871	KMT2D Deficiency Impairs Super-Enhancers to Confer a Glycolytic Vulnerability in Lung Cancer. Cancer Cell, 2020, 37, 599-617.e7.	7.7	137
872	Metabolic Reprogramming Promotes Neural Crest Migration via Yap/Tead Signaling. Developmental Cell, 2020, 53, 199-211.e6.	3.1	102
873	Division of Labor between PCNA Loaders in DNA Replication and Sister Chromatid Cohesion Establishment. Molecular Cell, 2020, 78, 725-738.e4.	4.5	45
874	Chromatin Hyperacetylation Impacts Chromosome Folding by Forming a Nuclear Subcompartment. Molecular Cell, 2020, 78, 112-126.e12.	4.5	62
875	Smooth Muscle Cell Reprogramming in Aortic Aneurysms. Cell Stem Cell, 2020, 26, 542-557.e11.	5.2	114
876	Spt5-mediated enhancer transcription directly couples enhancer activation with physical promoter interaction. Nature Genetics, 2020, 52, 505-515.	9.4	62
877	Systematic alteration of ATAC-seq for profiling open chromatin in cryopreserved nuclei preparations from livestock tissues. Scientific Reports, 2020, 10, 5230.	1.6	26
878	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
879	On the relations of phase separation and Hi-C maps to epigenetics. Royal Society Open Science, 2020, 7, 191976.	1.1	18
880	Developmental regulation of cell type-specific transcription by novel promoter-proximal sequence elements. Genes and Development, 2020, 34, 663-677.	2.7	23
881	Redundant and specific roles of cohesin STAG subunits in chromatin looping and transcriptional control. Genome Research, 2020, 30, 515-527.	2.4	54
882	Arabidopsis DNA Replication Initiates in Intergenic, AT-Rich Open Chromatin. Plant Physiology, 2020, 183, 206-220.	2.3	9
883	No evidence for DNA <i>N</i> ⁶ -methyladenine in mammals. Science Advances, 2020, 6, eaay3335.	4.7	102
884	JunB Controls Intestinal Effector Programs in Regulatory T Cells. Frontiers in Immunology, 2020, 11, 444.	2.2	9
885	Characterization of RNP Networks of PUM1 and PUM2 Post-Transcriptional Regulators in TCam-2 Cells, a Human Male Germ Cell Model. Cells, 2020, 9, 984.	1.8	3

#	Article	IF	Citations
886	Darolutamide antagonizes androgen signaling by blocking enhancer and superâ€enhancer activation. Molecular Oncology, 2020, 14, 2022-2039.	2.1	28
887	Inhibition of the epigenetic suppressor EZH2 primes osteogenic differentiation mediated by BMP2. Journal of Biological Chemistry, 2020, 295, 7877-7893.	1.6	51
888	Hotspots of Aberrant Enhancer Activity in Fibrolamellar Carcinoma Reveal Candidate Oncogenic Pathways and Therapeutic Vulnerabilities. Cell Reports, 2020, 31, 107509.	2.9	28
889	Absolute Quantification of Transcription Factors Reveals Principles of Gene Regulation in Erythropoiesis. Molecular Cell, 2020, 78, 960-974.e11.	4.5	83
890	Targeting the scaffolding role of LSD1 (KDM1A) poises acute myeloid leukemia cells for retinoic acidâ€"induced differentiation. Science Advances, 2020, 6, eaax2746.	4.7	56
891	Functions of <i>Gtf2i</i> and <i>Gtf2ird1</i> in the developing brain: transcription, DNA binding and long-term behavioral consequences. Human Molecular Genetics, 2020, 29, 1498-1519.	1.4	18
892	Identification of a PRC2 Accessory Subunit Required for Subtelomeric H3K27 Methylation in <i>Neurospora crassa</i>. Molecular and Cellular Biology, 2020, 40, .	1.1	12
893	A WIZ/Cohesin/CTCF Complex Anchors DNA Loops to Define Gene Expression and Cell Identity. Cell Reports, 2020, 31, 107503.	2.9	26
894	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
895	Gene-Specific Control of tRNA Expression by RNA Polymerase II. Molecular Cell, 2020, 78, 765-778.e7.	4.5	48
896	Region-Specific Transcriptional Control of Astrocyte Function Oversees Local Circuit Activities. Neuron, 2020, 106, 992-1008.e9.	3.8	92
897	Epigenomic profiling of neuroblastoma cell lines. Scientific Data, 2020, 7, 116.	2.4	32
898	An epigenetic map of malaria parasite development from host to vector. Scientific Reports, 2020, 10, 6354.	1.6	26
899	Release of promoterâ€"proximal paused Pol II in response to histone deacetylase inhibition. Nucleic Acids Research, 2020, 48, 4877-4890.	6.5	32
900	Conservation and Divergence in the Meiocyte sRNAomes of Arabidopsis, Soybean, and Cucumber. Plant Physiology, 2020, 182, 301-317.	2.3	13
901	Polycomb regulation is coupled to cell cycle transition in pluripotent stem cells. Science Advances, 2020, 6, eaay4768.	4.7	36
902	Performance and Accuracy of Four Open-Source Tools for <i>In Silico</i> Serotyping of <i>Salmonella</i> spp. Based on Whole-Genome Short-Read Sequencing Data. Applied and Environmental Microbiology, 2020, 86, .	1.4	40
903	An RB-Condensin II Complex Mediates Long-Range Chromosome Interactions and Influences Expression at Divergently Paired Genes. Molecular and Cellular Biology, 2020, 40, .	1.1	8

#	ARTICLE	IF	CITATIONS
904	scATAC-pro: a comprehensive workbench for single-cell chromatin accessibility sequencing data. Genome Biology, 2020, 21, 94.	3.8	28
905	The barley stripe mosaic virus expression system reveals the wheat C2H2 zinc finger protein TaZFP1B as a key regulator of drought tolerance. BMC Plant Biology, 2020, 20, 144.	1.6	26
906	Adaptation to Industrial Stressors Through Genomic and Transcriptional Plasticity in a Bioethanol Producing Fission Yeast Isolate. G3: Genes, Genomes, Genetics, 2020, 10, 1375-1391.	0.8	1
907	Chromatin architecture reorganization in murine somatic cell nuclear transfer embryos. Nature Communications, 2020, 11, 1813.	5.8	43
908	RUNX1-EVI1 disrupts lineage determination and the cell cycle by interfering with RUNX1 and EVI1 driven gene regulatory networks. Haematologica, 2021, 106, 1569-1580.	1.7	8
909	Methods for ChIP-seq analysis: A practical workflow and advanced applications. Methods, 2021, 187, 44-53.	1.9	114
910	Chromatin-associated SUMOylation controls the transcriptional switch between plant development and heat stress responses. Plant Communications, 2021, 2, 100091.	3.6	14
911	Transcriptomic and Epigenetic Preservation of Genetic Sex Identity in Estrogen-feminized Male Chicken Embryonic Gonads. Endocrinology, 2021, 162, .	1.4	17
912	Reprogramming of the histone H3.3 landscape in the early mouse embryo. Nature Structural and Molecular Biology, 2021, 28, 38-49.	3.6	45
913	Isolating live cell clones from barcoded populations using CRISPRa-inducible reporters. Nature Biotechnology, 2021, 39, 174-178.	9.4	63
914	Identification and characterization of the long noncoding RNA Dreg1 as a novel regulator of Gata3. Immunology and Cell Biology, 2021, 99, 323-332.	1.0	9
915	Genome-wide CRISPR Screens Reveal Host Factors Critical for SARS-CoV-2 Infection. Cell, 2021, 184, 76-91.e13.	13.5	418
916	Non-canonical Targets of HIF1a Impair Oligodendrocyte Progenitor Cell Function. Cell Stem Cell, 2021, 28, 257-272.e11.	5.2	25
917	Estrogen Receptor Alpha Mutations in Breast Cancer Cells Cause Gene Expression Changes through Constant Activity and Secondary Effects. Cancer Research, 2021, 81, 539-551.	0.4	35
918	Epigenetic Alterations in Keratinocyte Carcinoma. Journal of Investigative Dermatology, 2021, 141, 1207-1218.	0.3	9
919	Capture of Mouse and Human Stem Cells with Features of Formative Pluripotency. Cell Stem Cell, 2021, 28, 453-471.e8.	5.2	151
920	The transcriptional repressors VAL1 and VAL2 recruit PRC2 for genome-wide Polycomb silencing in <i>Arabidopsis</i>. Nucleic Acids Research, 2021, 49, 98-113.	6.5	50
921	Meiotic Cells Counteract Programmed Retrotransposon Activation via RNA-Binding Translational Repressor Assemblies. Developmental Cell, 2021, 56, 22-35.e7.	3.1	8

#	Article	IF	Citations
922	A Role for the Mre11-Rad50-Xrs2 Complex in Gene Expression and Chromosome Organization. Molecular Cell, 2021, 81, 183-197.e6.	4.5	15
923	Stromal SOX2 Upregulation Promotes Tumorigenesis through the Generation of a SFRP1/2-Expressing Cancer-Associated Fibroblast Population. Developmental Cell, 2021, 56, 95-110.e10.	3.1	50
924	Decitabine Induces Gene Derepression on Monosomic Chromosomes: <i>In Vitro</i> and <i>In Vivo</i> Effects in Adverse-Risk Cytogenetics AML. Cancer Research, 2021, 81, 834-846.	0.4	18
925	Formation of the CenH3-Deficient Holocentromere in Lepidoptera Avoids Active Chromatin. Current Biology, 2021, 31, 173-181.e7.	1.8	36
926	RNA nucleation by MSL2 induces selective X chromosome compartmentalization. Nature, 2021, 589, 137-142.	13.7	34
927	Control of adipogenic commitment by a STAT3-VSTM2A axis. American Journal of Physiology - Endocrinology and Metabolism, 2021, 320, E259-E269.	1.8	8
928	The nuclear factor CECR2 promotes somatic cell reprogramming by reorganizing the chromatin structure. Journal of Biological Chemistry, 2021, 296, 100022.	1.6	2
929	Super enhancers define regulatory subtypes and cell identity in neuroblastoma. Nature Cancer, 2021, 2, 114-128.	5.7	73
930	Genome-wide investigation of the dynamic changes of epigenome modifications after global DNA methylation editing. Nucleic Acids Research, 2021, 49, 158-176.	6.5	20
931	Epigenomic differences in the human and chimpanzee genomes are associated with structural variation. Genome Research, 2021, 31, 279-290.	2.4	7
932	The CBP/p300 histone acetyltransferases function as plantâ€specific MEDIATOR subunits in <i>Arabidopsis</i>. Journal of Integrative Plant Biology, 2021, 63, 755-771.	4.1	29
933	BRD9 Is a Critical Regulator of Androgen Receptor Signaling and Prostate Cancer Progression. Cancer Research, 2021, 81, 820-833.	0.4	43
934	WAPL maintains a cohesin loading cycle to preserve cell-type-specific distal gene regulation. Nature Genetics, 2021, 53, 100-109.	9.4	101
935	A Synthetic Approach to Reconstruct the Evolutionary and Functional Innovations of the Plant Histone Variant H2A.W. Current Biology, 2021, 31, 182-191.e5.	1.8	20
936	FBXO44 promotes DNA replication-coupled repetitive element silencing in cancer cells. Cell, 2021, 184, 352-369.e23.	13.5	50
937	New insights into homoeologous copy number variations in the hexaploid wheat genome. Plant Genome, 2021, 14, e20069.	1.6	16
938	Competition between PRC2.1 and 2.2 subcomplexes regulates PRC2 chromatin occupancy in human stem cells. Molecular Cell, 2021, 81, 488-501.e9.	4.5	38
939	A long non-coding RNA specifically expressed in early embryos programs the metabolic balance in adult mice. Biochimica Et Biophysica Acta - Molecular Basis of Disease, 2021, 1867, 165988.	1.8	3

#	ARTICLE	IF	CITATIONS
940	Identification of the mutation signature of the cancer genome caused by irradiation. Radiotherapy and Oncology, 2021, 155, 10-16.	0.3	6
941	Histone H3K27 dimethylation landscapes contribute to genome stability and genetic recombination during wheat polyploidization. Plant Journal, 2021, 105, 678-690.	2.8	24
942	Deconstructing Stepwise Fate Conversion of Human Fibroblasts to Neurons by MicroRNAs. Cell Stem Cell, 2021, 28, 127-140.e9.	5.2	39
943	Comparing a new method for mapping nucleosomes in simian virus 40 chromatin to standard procedures. Epigenetics, 2021, 16, 587-596.	1.3	2
944	Epigenetic regulation of the lineage specificity of primary human dermal lymphatic and blood vascular endothelial cells. Angiogenesis, 2021, 24, 67-82.	3.7	20
945	Chromatin profiling reveals relocalization of lysine-specific demethylase 1 by an oncogenic fusion protein. Epigenetics, 2021, 16, 405-424.	1.3	18
946	Integrated chromatin and transcriptomic profiling of patient-derived colon cancer organoids identifies personalized drug targets to overcome oxaliplatin resistance. Genes and Diseases, 2021, 8, 203-214.	1.5	10
947	Nucleosome landscape reflects phenotypic differences in Trypanosoma cruzi life forms. PLoS Pathogens, 2021, 17, e1009272.	2.1	13
948	AtxA-Controlled Small RNAs of Bacillus anthracis Virulence Plasmid pXO1 Regulate Gene Expression in trans. Frontiers in Microbiology, 2020, 11, 610036.	1.5	8
949	Differential Impact of Fluid Shear Stress and YAP/TAZ on BMP/TGFâ€Î² Induced Osteogenic Target Genes. Advanced Biology, 2021, 5, 2000051.	1.4	10
953	Intestinal differentiation involves cleavage of histone H3 N-terminal tails by multiple proteases. Nucleic Acids Research, 2021, 49, 791-804.	6.5	21
954	Acute perturbation strategies in interrogating RNA polymerase II elongation factor function in gene expression. Genes and Development, 2021, 35, 273-285.	2.7	25
955	H3.1K27me1 maintains transcriptional silencing and genome stability by preventing GCN5-mediated histone acetylation. Plant Cell, 2021, 33, 961-979.	3.1	22
956	Comprehensive RNP profiling in cells identifies U1 snRNP complexes with cleavage and polyadenylation factors active in telescripting. Methods in Enzymology, 2021, 655, 325-347.	0.4	3
957	Multiple Modes of Regulation Control Dynamic Transcription Patterns During the Mitosis-G1 Transition. SSRN Electronic Journal, 0, , .	0.4	0
958	Natural variation in plant telomere length is associated with flowering time. Plant Cell, 2021, 33, 1118-1134.	3.1	29
959	Hexavalent chromium promotes differential binding of CTCF to its cognate sites in Euchromatin. Epigenetics, 2021, 16, 1-16.	1.3	3
960	LEAFY is a pioneer transcription factor and licenses cell reprogramming to floral fate. Nature Communications, 2021, 12, 626.	5.8	68

#	Article	IF	Citations
961	Genome-Wide Histone Modifications and CTCF Enrichment Predict Gene Expression in Sheep Macrophages. Frontiers in Genetics, 2020, 11, 612031.	1.1	9
962	Genome-wide CRISPR-Cas9 screen identified KLF11 as a druggable suppressor for sarcoma cancer stem cells. Science Advances, 2021, 7, .	4.7	21
963	METTL3 regulates heterochromatin in mouse embryonic stem cells. Nature, 2021, 591, 317-321.	13.7	187
964	BACH1 recruits NANOG and histone H3 lysine 4 methyltransferase MLL/SET1 complexes to regulate enhancerâ€"promoter activity and maintains pluripotency. Nucleic Acids Research, 2021, 49, 1972-1986.	6.5	24
965	The Arabidopsis active demethylase ROS1 cis-regulates defence genes by erasing DNA methylation at promoter-regulatory regions. ELife, 2021, 10, .	2.8	62
968	CRISPR/Cas9 Genome Editing of the Human Topoisomerase II<i>Î±</i>Intron 19 5â€² Splice Site Circumvents Etoposide Resistance in Human Leukemia K562 Cells. Molecular Pharmacology, 2021, 99, 226-241.	1.0	9
969	Three-dimensional interactions between enhancers and promoters during intestinal differentiation depend upon HNF4. Cell Reports, 2021, 34, 108679.	2.9	15
970	ZNF143 mediates CTCF-bound promoterâ€"enhancer loops required for murine hematopoietic stem and progenitor cell function. Nature Communications, 2021, 12, 43.	5.8	45
971	Regulatory roles of Escherichia coli 5' UTR and ORF-internal RNAs detected by 3' end mapping. ELife, 2021, 10, .	2.8	60
972	m6A RNA methylation regulates the fate of endogenous retroviruses. Nature, 2021, 591, 312-316.	13.7	156
973	TgAP2IX-5 is a key transcriptional regulator of the asexual cell cycle division in Toxoplasma gondii. Nature Communications, 2021, 12, 116.	5.8	24
974	SetDB1 and Su(var)3-9 play non-overlapping roles in somatic cell chromosomes of <i>Drosophila melanogaster</i>. Journal of Cell Science, 2021, 134, .	1.2	6
975	The T-box transcription factor Eomesodermin governs haemogenic competence of yolk sac mesodermal progenitors. Nature Cell Biology, 2021, 23, 61-74.	4.6	10
976	Decreases in different Dnmt3b activities drive distinct development of hematologic malignancies in mice. Journal of Biological Chemistry, 2021, 296, 100285.	1.6	6
978	A regulatory sub-circuit downstream of Wnt signaling controls developmental transitions in neural crest formation. PLoS Genetics, 2021, 17, e1009296.	1.5	12
979	High-resolution targeted 3C interrogation of cis-regulatory element organization at genome-wide scale. Nature Communications, 2021, 12, 531.	5.8	32
980	RNA inhibits dMi-2/CHD4 Chromatin Binding and Nucleosome Remodelling. SSRN Electronic Journal, 0, , .	0.4	0
982	Foxc1 establishes enhancer accessibility for craniofacial cartilage differentiation. ELife, 2021, 10, .	2.8	24

#	ARTICLE	IF	CITATIONS
984	Subtraction-free and bisulfite-free specific sequencing of 5-methylcytosine and its oxidized derivatives at base resolution. Nature Communications, 2021, 12, 618.	5.8	45
985	S100A8/S100A9 cytokine acts as a transcriptional coactivator during breast cellular transformation. Science Advances, 2021, 7, .	4.7	29
987	High-Resolution Mapping of Transcription Initiation in the Asexual Stages of Toxoplasma gondii. Frontiers in Cellular and Infection Microbiology, 2020, 10, 617998.	1.8	11
988	Spatial integration of transcription and splicing in a dedicated compartment sustains monogenic antigen expression in African trypanosomes. Nature Microbiology, 2021, 6, 289-300.	5.9	50
989	Transcriptome-wide high-throughput mapping of proteinâ€“RNA occupancy profiles using POP-seq. Scientific Reports, 2021, 11, 1175.	1.6	6
990	The androgen receptor is a tumor suppressor in estrogen receptorâ€“positive breast cancer. Nature Medicine, 2021, 27, 310-320.	15.2	122
991	Computational Epigenetics in Rice Research. , 2021, , 113-140.		0
992	Increased ACTL6A Occupancy within mSWI/SNF Chromatin Remodelers Drives Human Squamous Cell Carcinoma. SSRN Electronic Journal, 0, , .	0.4	0
993	Reduced RNA turnover as a driver of cellular senescence. Life Science Alliance, 2021, 4, e202000809.	1.3	12
994	Monitoring genome-wide replication fork directionality by Okazaki fragment sequencing in mammalian cells. Nature Protocols, 2021, 16, 1193-1218.	5.5	5
995	The Centromere Histone Is Conserved and Associated with Tandem Repeats Sharing a Conserved 19-bp Box in the Holocentromere of <i>Meloidogyne</i> Nematodes. Molecular Biology and Evolution, 2021, 38, 1943-1965.	3.5	16
1000	The negative elongation factor NELF promotes induced transcriptional response of Drosophila ecdysone-dependent genes. Scientific Reports, 2021, 11, 172.	1.6	15
1001	A High-Throughput Chromatin Immunoprecipitation Sequencing Approach to Study the Role of MYC on the Epigenetic Landscape. Methods in Molecular Biology, 2021, 2318, 187-208.	0.4	0
1002	Genome-Wide Profiling of Proteinâ€“DNA Interactions with Chromatin Endogenous Cleavage and High-Throughput Sequencing (ChEC-Seq). Methods in Molecular Biology, 2021, 2351, 289-303.	0.4	2
1003	The regulatory genome of the malaria vector <i>Anopheles gambiae</i>: integrating chromatin accessibility and gene expression. NAR Genomics and Bioinformatics, 2021, 3, lqaa113.	1.5	12
1004	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
1005	H2AK121ub in Arabidopsis associates with a less accessible chromatin state at transcriptional regulation hotspots. Nature Communications, 2021, 12, 315.	5.8	35
1006	Histone modifications during the life cycle of the brown alga Ectocarpus. Genome Biology, 2021, 22, 12.	3.8	29

#	ARTICLE	IF	CITATIONS
1007	The circadian cryptochrome, CRY1, is a pro-tumorigenic factor that rhythmically modulates DNA repair. Nature Communications, 2021, 12, 401.	5.8	60
1009	Proximity-dependent Mapping of the Androgen Receptor Identifies Kruppel-like Factor 4 as a Functional Partner. Molecular and Cellular Proteomics, 2021, 20, 100064.	2.5	11
1010	Splicing-associated chromatin signatures: a combinatorial and position-dependent role for histone marks in splicing definition. Nature Communications, 2021, 12, 682.	5.8	43
1011	Tool recommender system in Galaxy using deep learning. GigaScience, 2021, 10, .	3.3	9
1013	Characterization of SALL2 Gene Isoforms and Targets Across Cell Types Reveals Highly Conserved Networks. Frontiers in Genetics, 2021, 12, 613808.	1.1	5
1015	Sulfur sequestration promotes multicellularity during nutrient limitation. Nature, 2021, 591, 471-476.	13.7	24
1016	Big Data: The good, the bad and the ugly. International Journal of Cancer, 2021, 148, 2870-2871.	2.3	2
1017	Decoding the protein composition of whole nucleosomes with Nuc-MS. Nature Methods, 2021, 18, 303-308.	9.0	31
1018	Bisulfite-free epigenomics and genomics of single cells through methylation-sensitive restriction. Communications Biology, 2021, 4, 153.	2.0	17
1019	A nuclease- and bisulfite-based strategy captures strand-specific R-loops genome-wide. ELife, 2021, 10, .	2.8	25
1020	The glucocorticoid receptor recruits the COMPASS complex to regulate inflammatory transcription at macrophage enhancers. Cell Reports, 2021, 34, 108742.	2.9	27
1021	Distinct mechanisms for TMPRSS2 expression explain organ-specific inhibition of SARS-CoV-2 infection by enzalutamide. Nature Communications, 2021, 12, 866.	5.8	73
1022	BRCA2 promotes DNAâ€RNA hybrid resolution by DDX5 helicase at DNA breaks to facilitate their repairâ€¡. EMBO Journal, 2021, 40, e106018.	3.5	63
1023	LINE retrotransposons characterize mammalian tissue-specific and evolutionarily dynamic regulatory regions. Genome Biology, 2021, 22, 62.	3.8	38
1024	Potential Mechanism of Immune Evasion Associated with the Master Regulator ASCL2 in Microsatellite Stability in Colorectal Cancer. Journal of Immunology Research, 2021, 2021, 1-12.	0.9	9
1025	BRG1 knockdown inhibits proliferation through multiple cellular pathways in prostate cancer. Clinical Epigenetics, 2021, 13, 37.	1.8	14
1026	Comprehensive benchmarking of software for mapping whole genome bisulfite data: from read alignment to DNA methylation analysis. Briefings in Bioinformatics, 2021, 22, .	3.2	14
1028	Bacterial ClpP Protease Is a Potential Target for Methyl Gallate. Frontiers in Microbiology, 2020, 11, 598692.	1.5	7

#	Article	IF	Citations
1029	ZNF416 is a pivotal transcriptional regulator of fibroblast mechanoactivation. Journal of Cell Biology, 2021, 220, .	2.3	23
1030	A geneâ€“environment-induced epigenetic program initiates tumorigenesis. Nature, 2021, 590, 642-648.	13.7	133
1031	Ubiquitylation of MYC couples transcription elongation with double-strand break repair at active promoters. Molecular Cell, 2021, 81, 830-844.e13.	4.5	28
1032	A novel canine reference genome resolves genomic architecture and uncovers transcript complexity. Communications Biology, 2021, 4, 185.	2.0	59
1033	Positioning of nucleosomes containing Î³-H2AX precedes active DNA demethylation and transcription initiation. Nature Communications, 2021, 12, 1072.	5.8	30
1034	The innate sensor ZBP1-IRF3 axis regulates cell proliferation in multiple myeloma. Haematologica, 2022, 107, 721-732.	1.7	17
1035	Alternative lengthening of telomeres in childhood neuroblastoma from genome to proteome. Nature Communications, 2021, 12, 1269.	5.8	46
1036	Multi-scale architecture of archaeal chromosomes. Molecular Cell, 2021, 81, 473-487.e6.	4.5	24
1037	Definition of a small core transcriptional circuit regulated by AML1-ETO. Molecular Cell, 2021, 81, 530-545.e5.	4.5	45
1038	Euryarchaeal genomes are folded into SMC-dependent loops and domains, but lack transcription-mediated compartmentalization. Molecular Cell, 2021, 81, 459-472.e10.	4.5	42
1039	ZMYND11-MBTD1 induces leukemogenesis through hijacking NuA4/TIP60 acetyltransferase complex and a PWWP-mediated chromatin association mechanism. Nature Communications, 2021, 12, 1045.	5.8	27
1040	Differentiated glioblastoma cells accelerate tumor progression by shaping the tumor microenvironment via CCN1-mediated macrophage infiltration. Acta Neuropathologica Communications, 2021, 9, 29.	2.4	27
1043	Developmental hourglass and heterochronic shifts in fin and limb development. ELife, 2021, 10, .	2.8	10
1045	Non-coding deletions identify Maenli lncRNA as a limb-specific En1 regulator. Nature, 2021, 592, 93-98.	13.7	53
1046	Pancreatic progenitor epigenome maps prioritize type 2 diabetes risk genes with roles in development. ELife, 2021, 10, .	2.8	15
1047	Recurrent evolution of vertebrate transcription factors by transposase capture. Science, 2021, 371, .	6.0	102
1048	Acute BAF perturbation causes immediate changes in chromatin accessibility. Nature Genetics, 2021, 53, 269-278.	9.4	103
1049	Cross-species examination of X-chromosome inactivation highlights domains of escape from silencing. Epigenetics and Chromatin, 2021, 14, 12.	1.8	23

#	ARTICLE	IF	CITATIONS
1050	Divergence in alternative polyadenylation contributes to gene regulatory differences between humans and chimpanzees. ELife, 2021, 10, .	2.8	11
1051	ESR1 ChIP-Seq Identifies Distinct Ligand-Free ESR1 Genomic Binding Sites in Human Hepatocytes and Liver Tissue. International Journal of Molecular Sciences, 2021, 22, 1461.	1.8	8
1052	Disruption of a Hedgehog-Foxf1-Rspo2 signaling axis leads to tracheomalacia and a loss of Sox9+ tracheal chondrocytes. DMM Disease Models and Mechanisms, 2021, 14, .	1.2	16
1054	The PfAP2â€G2 transcription factor is a critical regulator of gametocyte maturation. Molecular Microbiology, 2021, 115, 1005-1024.	1.2	36
1055	BRCA1 and RNAi factors promote repair mediated by small RNAs and PALB2â€"RAD52. Nature, 2021, 591, 665-670.	13.7	30
1056	Intronic enhancer region governs transcript-specific Bdnf expression in rodent neurons. ELife, 2021, 10, .	2.8	22
1057	Acetyltransferase Enok regulates transposon silencing and piRNA cluster transcription. PLoS Genetics, 2021, 17, e1009349.	1.5	5
1058	Hyperosmotic stress alters the RNA polymerase II interactome and induces readthrough transcription despite widespread transcriptional repression. Molecular Cell, 2021, 81, 502-513.e4.	4.5	61
1059	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
1062	TCP transcription factors suppress cotyledon trichomes by impeding a cell differentiation-regulating complex. Plant Physiology, 2021, 186, 434-451.	2.3	20
1063	Chromatin dysregulation associated with NSD1 mutation in head and neck squamous cell carcinoma. Cell Reports, 2021, 34, 108769.	2.9	42
1067	<i>Caenorhabditis elegans</i> establishes germline versus soma by balancing inherited histone methylation. Development (Cambridge), 2021, 148, .	1.2	13
1068	Fruitless decommissions regulatory elements to implement cell-type-specific neuronal masculinization. PLoS Genetics, 2021, 17, e1009338.	1.5	18
1069	The RNAi Mechanism Regulates a New Exonuclease Gene Involved in the Virulence of Mucorales. International Journal of Molecular Sciences, 2021, 22, 2282.	1.8	9
1070	SNPC-1.3 is a sex-specific transcription factor that drives male piRNA expression in C. elegans. ELife, 2021, 10, .	2.8	7
1071	Topologically associating domains and their role in the evolution of genome structure and function in<i>Drosophila</i>. Genome Research, 2021, 31, 397-410.	2.4	36
1072	A first exon termination checkpoint preferentially suppresses extragenic transcription. Nature Structural and Molecular Biology, 2021, 28, 337-346.	3.6	30
1073	Tumor methionine metabolism drives T-cell exhaustion in hepatocellular carcinoma. Nature Communications, 2021, 12, 1455.	5.8	96

#	Article	IF	Citations
1076	A hotspot mutation in transcription factor IKZF3 drives B cell neoplasia via transcriptional dysregulation. Cancer Cell, 2021, 39, 380-393.e8.	7.7	27
1077	Epigenetic effects induced by the ectopic expression of Pax7 in 3T3-L1. Journal of Biochemistry, 2021, 170, 107-117.	0.9	1
1078	The corepressors GPS2 and SMRT control enhancer and silencer remodeling via eRNA transcription during inflammatory activation of macrophages. Molecular Cell, 2021, 81, 953-968.e9.	4.5	27
1079	Post-transcriptional regulation of antiviral gene expression by N6-methyladenosine. Cell Reports, 2021, 34, 108798.	2.9	46
1080	Co-transcriptional splicing regulates 3â€² end cleavage during mammalian erythropoiesis. Molecular Cell, 2021, 81, 998-1012.e7.	4.5	102
1081	MAP3K2-regulated intestinal stromal cells define a distinct stem cell niche. Nature, 2021, 592, 606-610.	13.7	53
1082	Time-resolved single-cell analysis of Brca1 associated mammary tumourigenesis reveals aberrant differentiation of luminal progenitors. Nature Communications, 2021, 12, 1502.	5.8	34
1085	â€œAdopt-a-Tissueâ€• Initiative Advances Efforts to Identify Tissue-Specific Histone Marks in the Mare. Frontiers in Genetics, 2021, 12, 649959.	1.1	8
1087	Transcriptome and DNA Methylation Profiles of Mouse Fetus and Placenta Generated by Round Spermatid Injection. Frontiers in Cell and Developmental Biology, 2021, 9, 632183.	1.8	4
1090	GAF is essential for zygotic genome activation and chromatin accessibility in the early Drosophila embryo. ELife, 2021, 10, .	2.8	75
1091	<i>ZNF91</i> deletion in human embryonic stem cells leads to ectopic activation of SVA retrotransposons and up-regulation of KRAB zinc finger gene clusters. Genome Research, 2021, 31, 551-563.	2.4	22
1093	A neural m6A/Ythdf pathway is required for learning and memory in Drosophila. Nature Communications, 2021, 12, 1458.	5.8	54
1094	Transcription initiation mapping in 31 bovine tissues reveals complex promoter activity, pervasive transcription, and tissue-specific promoter usage. Genome Research, 2021, 31, 732-744.	2.4	11
1095	Generic injuries are sufficient to induce ectopic Wnt organizers in Hydra. ELife, 2021, 10, .	2.8	24
1096	Histone H3 lysine 4 trimethylation in sperm is transmitted to the embryo and associated with diet-induced phenotypes in the offspring. Developmental Cell, 2021, 56, 671-686.e6.	3.1	70
1097	The RNA m6A reader YTHDC1 silences retrotransposons and guards ES cell identity. Nature, 2021, 591, 322-326.	13.7	187
1099	ARID2 deficiency promotes tumor progression and is associated with higher sensitivity to chemotherapy in lung cancer. Oncogene, 2021, 40, 2923-2935.	2.6	22
1100	MACF1 promotes osteoblast differentiation by sequestering repressors in cytoplasm. Cell Death and Differentiation, 2021, 28, 2160-2178.	5.0	9

#	Article	IF	Citations
1101	Integrated genomic analysis reveals regulatory pathways and dynamic landscapes of the tRNA transcriptome. Scientific Reports, 2021, 11, 5226.	1.6	2
1104	Kinome-Wide RNAi Screen Uncovers Role of Ballchen in Maintenance of Gene Activation by Trithorax Group in Drosophila. Frontiers in Cell and Developmental Biology, 2021, 9, 637873.	1.8	3
1105	Molecular mechanism of cytokinin-activated cell division in <i>Arabidopsis</i>. Science, 2021, 371, 1350-1355.	6.0	79
1106	Super-Enhancer-Associated Transcription Factors Maintain Transcriptional Regulation in Mature Podocytes. Journal of the American Society of Nephrology: JASN, 2021, 32, 1323-1337.	3.0	4
1107	KDM5 inhibition offers a novel therapeutic strategy for the treatment of <i>KMT2D</i> mutant lymphomas. Blood, 2021, 138, 370-381.	0.6	33
1108	Systematic characterization of mutations altering protein degradation in human cancers. Molecular Cell, 2021, 81, 1292-1308.e11.	4.5	36
1109	Transcription factor competition at the Î³-globin promoters controls hemoglobin switching. Nature Genetics, 2021, 53, 511-520.	9.4	43
1110	Anaerobic endosymbiont generates energy for ciliate host by denitrification. Nature, 2021, 591, 445-450.	13.7	53
1111	Integrative network analysis reveals USP7 haploinsufficiency inhibits E-protein activity in pediatric T-lineage acute lymphoblastic leukemia (T-ALL). Scientific Reports, 2021, 11, 5154.	1.6	10
1112	The deubiquitinase Usp9x regulates PRC2-mediated chromatin reprogramming during mouse development. Nature Communications, 2021, 12, 1865.	5.8	11
1116	Atoh7-independent specification of retinal ganglion cell identity. Science Advances, 2021, 7, .	4.7	41
1117	Human ORC/MCM density is low in active genes and correlates with replication time but does not delimit initiation zones. ELife, 2021, 10, .	2.8	23
1119	Fine-tuning the performance of ddRAD-seq in the peach genome. Scientific Reports, 2021, 11, 6298.	1.6	7
1122	Profile of Small RNAs, vDNA Forms and Viral Integrations in Late Chikungunya Virus Infection of Aedes albopictus Mosquitoes. Viruses, 2021, 13, 553.	1.5	13
1124	N6-methyladenosine modification of MALAT1 promotes metastasis via reshaping nuclear speckles. Developmental Cell, 2021, 56, 702-715.e8.	3.1	71
1125	Stress-induced nuclear condensation of NELF drives transcriptional downregulation. Molecular Cell, 2021, 81, 1013-1026.e11.	4.5	83
1126	Neuronal enhancers are hotspots for DNA single-strand break repair. Nature, 2021, 593, 440-444.	13.7	126
1127	SIRT3 consolidates heterochromatin and counteracts senescence. Nucleic Acids Research, 2021, 49, 4203-4219.	6.5	74

#	Article	IF	Citations
1128	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
1130	A cohesin cancer mutation reveals a role for the hinge domain in genome organization and gene expression. PLoS Genetics, 2021, 17, e1009435.	1.5	16
1131	Activation of endogenous retroviruses during brain development causes an inflammatory response. EMBO Journal, 2021, 40, e106423.	3.5	38
1132	Identifying transposable element expression dynamics and heterogeneity during development at the single-cell level with a processing pipeline scTE. Nature Communications, 2021, 12, 1456.	5.8	74
1133	A streamlined solution for processing, elucidating and quality control of cyclobutane pyrimidine dimer sequencing data. Nature Protocols, 2021, 16, 2190-2212.	5.5	3
1134	LASCA: loop and significant contact annotation pipeline. Scientific Reports, 2021, 11, 6361.	1.6	4
1137	Hybrid genome de novo assembly with methylome analysis of the anaerobic thermophilic subsurface bacterium Thermanaerosceptrum fracticalcis strain DRI-13T. BMC Genomics, 2021, 22, 209.	1.2	3
1139	Correcting signal biases and detecting regulatory elements in STARR-seq data. Genome Research, 2021, 31, 877-889.	2.4	11
1140	Altered chromatin architecture and gene expression during polyploidization and domestication of soybean. Plant Cell, 2021, 33, 1430-1446.	3.1	55
1141	Age-related changes in polycomb gene regulation disrupt lineage fidelity in intestinal stem cells. ELife, 2021, 10, .	2.8	20
1142	Megadepth: efficient coverage quantification for BigWigs and BAMs. Bioinformatics, 2021, 37, 3014-3016.	1.8	18
1143	Deletion of the mitochondria-shaping protein Opa1 during early thymocyte maturation impacts mature memory T cell metabolism. Cell Death and Differentiation, 2021, 28, 2194-2206.	5.0	18
1144	Epigenetic and transcriptional analysis reveals a core transcriptional program conserved in clonal prostate cancer metastases. Molecular Oncology, 2021, 15, 1942-1955.	2.1	10
1145	Germline inherited small RNAs facilitate the clearance of untranslated maternal mRNAs in C. elegans embryos. Nature Communications, 2021, 12, 1441.	5.8	29
1146	HOXBLINC long non-coding RNA activation promotes leukemogenesis in NPM1-mutant acute myeloid leukemia. Nature Communications, 2021, 12, 1956.	5.8	28
1147	Maize decrease in DNA methylation 1 targets RNA-directed DNA methylation on active chromatin. Plant Cell, 2021, 33, 2183-2196.	3.1	11
1149	Accessible chromatin reveals regulatory mechanisms underlying cell fate decisions during early embryogenesis. Scientific Reports, 2021, 11, 7896.	1.6	3
1150	Mapping Astrocyte Transcriptional Signatures in Response to Neuroactive Compounds. International Journal of Molecular Sciences, 2021, 22, 3975.	1.8	12

#	ARTICLE	IF	CITATIONS
1152	Single cell regulatory landscape of the mouse kidney highlights cellular differentiation programs and disease targets. Nature Communications, 2021, 12, 2277.	5.8	122
1153	Genome-wide proximity between RNA polymerase and DNA topoisomerase I supports transcription in Streptococcus pneumoniae. PLoS Genetics, 2021, 17, e1009542.	1.5	11
1155	The Usefulness of Cell-Based and Liquid-Based Urine Tests in Clarifying the Diagnosis and Monitoring the Course of Urothelial Carcinoma. Identification of Novel, Potentially Actionable, RB1 and ERBB2 Somatic Mutations. Journal of Personalized Medicine, 2021, 11, 362.	1.1	0
1156	The chromatin remodeler DDM1 prevents transposon mobility through deposition of histone variant H2A.W. Nature Cell Biology, 2021, 23, 391-400.	4.6	73
1157	Negative elongation factor regulates muscle progenitor expansion for efficient myofiber repair and stem cell pool repopulation. Developmental Cell, 2021, 56, 1014-1029.e7.	3.1	18
1159	SARS-CoV-2 drives JAK1/2-dependent local complement hyperactivation. Science Immunology, 2021, 6, .	5.6	144
1160	Epigenomic landscape of human colorectal cancer unveils an aberrant core of pan-cancer enhancers orchestrated by YAP/TAZ. Nature Communications, 2021, 12, 2340.	5.8	43
1161	Suppression of liquidâ€"liquid phase separation by 1,6-hexanediol partially compromises the 3D genome organization in living cells. Nucleic Acids Research, 2021, 49, 10524-10541.	6.5	68
1163	Type 1 conventional dendritic cell fate and function are controlled by DC-SCRIPT. Science Immunology, 2021, 6, .	5.6	19
1164	Comparative genomics of the coconut crab and other decapod crustaceans: exploring the molecular basis of terrestrial adaptation. BMC Genomics, 2021, 22, 313.	1.2	11
1165	UTX promotes CD8+ TÂcell-mediated antiviral defenses but reduces TÂcell durability. Cell Reports, 2021, 35, 108966.	2.9	9
1166	QSER1 protects DNA methylation valleys from de novo methylation. Science, 2021, 372, .	6.0	69
1167	The MarR-Type Regulator PA3458 Is Involved in Osmoadaptation Control in Pseudomonas aeruginosa. International Journal of Molecular Sciences, 2021, 22, 3982.	1.8	12
1168	Integrated requirement of nonâ€specific and sequenceâ€specific DNA binding in Mycâ€driven transcription. EMBO Journal, 2021, 40, e105464.	3.5	24
1169	Antisense RNAs during early vertebrate development are divided in groups with distinct features. Genome Research, 2021, 31, 995-1010.	2.4	7
1170	Targeted degradation of the enhancer lysine acetyltransferases CBP and p300. Cell Chemical Biology, 2021, 28, 503-514.e12.	2.5	80
1171	Identification and characterization of centromeric sequences in <i>Xenopus laevis</i>. Genome Research, 2021, 31, 958-967.	2.4	12
1172	A conserved BAH module within mammalian BAHD1 connects H3K27me3 to Polycomb gene silencing. Nucleic Acids Research, 2021, 49, 4441-4455.	6.5	15

#	ARTICLE	IF	CITATIONS
1173	DNA hypomethylating agents increase activation and cytolytic activity of CD8+ TÂcells. Molecular Cell, 2021, 81, 1469-1483.e8.	4.5	52
1174	ELAV/Hu RNA binding proteins determine multiple programs of neural alternative splicing. PLoS Genetics, 2021, 17, e1009439.	1.5	32
1175	Conserved pleiotropy of an ancient plant homeobox gene uncovered by cis-regulatory dissection. Cell, 2021, 184, 1724-1739.e16.	13.5	103
1176	Cotranscriptional and Posttranscriptional Features of the Transcriptome in Soybean Shoot Apex and Leaf. Frontiers in Plant Science, 2021, 12, 649634.	1.7	6
1178	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
1180	Epigenetic modulation of immune synaptic-cytoskeletal networks potentiates Î³Î´ T cell-mediated cytotoxicity in lung cancer. Nature Communications, 2021, 12, 2163.	5.8	16
1181	A unique histone 3 lysine 14 chromatin signature underlies tissue-specific gene regulation. Molecular Cell, 2021, 81, 1766-1780.e10.	4.5	17
1182	Different DNA-binding specificities of NLP and NIN transcription factors underlie nitrate-induced control of root nodulation. Plant Cell, 2021, 33, 2340-2359.	3.1	52
1185	Chromatin occupancy and target genes of the haematopoietic master transcription factor MYB. Scientific Reports, 2021, 11, 9008.	1.6	12
1186	Genome-Wide Chromatin Analysis of FFPE Tissues Using a Dual-Arm Robot with Clinical Potential. Cancers, 2021, 13, 2126.	1.7	7
1188	Single-cell CUT&Tag profiles histone modifications and transcription factors in complex tissues. Nature Biotechnology, 2021, 39, 825-835.	9.4	221
1189	Silencing of LINE-1 retrotransposons is a selective dependency of myeloid leukemia. Nature Genetics, 2021, 53, 672-682.	9.4	47
1190	Histone crotonylation promotes mesoendodermal commitment of human embryonic stem cells. Cell Stem Cell, 2021, 28, 748-763.e7.	5.2	59
1192	Data from crosslinking and analysis of cDNAs (CRAC) of Nab3 in yeast cells expressing a circular ncRNA decoy. Data in Brief, 2021, 35, 106951.	0.5	1
1193	A functional LSD1 coregulator screen reveals a novel transcriptional regulatory cascade connecting R-loop homeostasis with epigenetic regulation. Nucleic Acids Research, 2021, 49, 4350-4370.	6.5	13
1194	Differential Transcriptomes and Methylomes of Trophoblast Stem Cells From Naturally-Fertilized and Somatic Cell Nuclear-Transferred Embryos. Frontiers in Cell and Developmental Biology, 2021, 9, 664178.	1.8	0
1196	Modeling transcriptional regulation of model species with deep learning. Genome Research, 2021, 31, 1097-1105.	2.4	5
1197	Channel nuclear pore complex subunits are required for transposon silencing in Drosophila. ELife, 2021, 10, .	2.8	14

#	Article	IF	Citations
1198	Inositol treatment inhibits medulloblastoma through suppression of epigenetic-driven metabolic adaptation. Nature Communications, 2021, 12, 2148.	5.8	20
1199	The ZMYND8-regulated mevalonate pathway endows YAP-high intestinal cancer with metabolic vulnerability. Molecular Cell, 2021, 81, 2736-2751.e8.	4.5	20
1201	Identification of X-chromosomal genes that drive sex differences in embryonic stem cells through a hierarchical CRISPR screening approach. Genome Biology, 2021, 22, 110.	3.8	28
1202	Genome-wide programmable transcriptional memory by CRISPR-based epigenome editing. Cell, 2021, 184, 2503-2519.e17.	13.5	312
1203	RNA-induced liquid phase separation of SARS-CoV-2 nucleocapsid protein facilitates NF-ÎºB hyper-activation and inflammation. Signal Transduction and Targeted Therapy, 2021, 6, 167.	7.1	87
1204	Redundant and non-redundant cytokine-activated enhancers control Csn1s2b expression in the lactating mouse mammary gland. Nature Communications, 2021, 12, 2239.	5.8	9
1207	Sex-Specific Control of Human Heart Maturation by the Progesterone Receptor. Circulation, 2021, 143, 1614-1628.	1.6	42
1208	<i>Cis</i>-regulatory dissection of cone development reveals a broad role for Otx2 and Oc transcription factors. Development (Cambridge), 2021, 148, .	1.2	9
1209	Analysis of cell-type-specific chromatin modifications and gene expression in Drosophila neurons that direct reproductive behavior. PLoS Genetics, 2021, 17, e1009240.	1.5	9
1210	Hi-C analyses with GENOVA: a case study with cohesin variants. NAR Genomics and Bioinformatics, 2021, 3, lqab040.	1.5	59
1211	Genetic perturbation of PU.1 binding and chromatin looping at neutrophil enhancers associates with autoimmune disease. Nature Communications, 2021, 12, 2298.	5.8	32
1212	The 7SK/P-TEFb snRNP controls ultraviolet radiation-induced transcriptional reprogramming. Cell Reports, 2021, 35, 108965.	2.9	28
1213	The impact of cell type and context-dependent regulatory variants on human immune traits. Genome Biology, 2021, 22, 122.	3.8	32
1214	Deconvoluting global cytokine signaling networks in natural killer cells. Nature Immunology, 2021, 22, 627-638.	7.0	31
1215	Efficient and strand-specific profiling of replicating chromatin with enrichment and sequencing of protein-associated nascent DNA in mammalian cells. Nature Protocols, 2021, 16, 2698-2721.	5.5	8
1216	OTUD7B Deubiquitinates LSD1 to Govern Its Binding Partner Specificity, Homeostasis, and Breast Cancer Metastasis. Advanced Science, 2021, 8, e2004504.	5.6	27
1217	OCRDetector: Accurately Detecting Open Chromatin Regions via Plasma Cell-Free DNA Sequencing Data. International Journal of Molecular Sciences, 2021, 22, 5802.	1.8	4
1218	Dynamic methylation of histone H3K18 in differentiating Theileria parasites. Nature Communications, 2021, 12, 3221.	5.8	15

#	ARTICLE	IF	CITATIONS
1219	Induction of OCT2 contributes to regulate the gene expression program in human neutrophils activated via TLR8. Cell Reports, 2021, 35, 109143.	2.9	14
1220	The nuclear receptor HNF4 drives a brush border gene program conserved across murine intestine, kidney, and embryonic yolk sac. Nature Communications, 2021, 12, 2886.	5.8	24
1221	The AraC-Type Transcriptional Regulator GliR (PA3027) Activates Genes of Glycerolipid Metabolism in Pseudomonas aeruginosa. International Journal of Molecular Sciences, 2021, 22, 5066.	1.8	11
1222	Chromatin-associated MRN complex protects highly transcribing genes from genomic instability. Science Advances, 2021, 7, .	4.7	18
1223	Long noncoding RNA MIR4435-2HG enhances metabolic function of myeloid dendritic cells from HIV-1 elite controllers. Journal of Clinical Investigation, 2021, 131, .	3.9	27
1224	Core-binding factor leukemia hijacks the T-cellâ€“prone PU.1 antisense promoter. Blood, 2021, 138, 1345-1358.	0.6	12
1225	Glucocorticoid signaling in pancreatic islets modulates gene regulatory programs and genetic risk of type 2 diabetes. PLoS Genetics, 2021, 17, e1009531.	1.5	13
1226	Mouse totipotent stem cells captured and maintained through spliceosomal repression. Cell, 2021, 184, 2843-2859.e20.	13.5	108
1227	Multimodal analysis of cell-free DNA whole-genome sequencing for pediatric cancers with low mutational burden. Nature Communications, 2021, 12, 3230.	5.8	95
1228	Loss of EZH2-like or SU(VAR)3â€“9-like proteins causes simultaneous perturbations in H3K27 and H3K9 tri-methylation and associated developmental defects in the fungus Podospora anserina. Epigenetics and Chromatin, 2021, 14, 22.	1.8	18
1229	Discovery of first-in-class inhibitors of ASH1L histone methyltransferase with anti-leukemic activity. Nature Communications, 2021, 12, 2792.	5.8	17
1230	Functional mapping of androgen receptor enhancer activity. Genome Biology, 2021, 22, 149.	3.8	18
1231	JASMONATE-ZIM DOMAIN proteins engage Polycomb chromatin modifiers to modulate Jasmonate signaling in Arabidopsis. Molecular Plant, 2021, 14, 732-747.	3.9	21
1232	Reprogramming of the esophageal squamous carcinoma epigenome by SOX2 promotes ADAR1 dependence. Nature Genetics, 2021, 53, 881-894.	9.4	44
1233	Selective androgen receptor modulators activate the canonical prostate cancer androgen receptor program and repress cancer growth. Journal of Clinical Investigation, 2021, 131, .	3.9	23
1234	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
1236	Hippocampal glucocorticoid target genes associated with enhancement of memory consolidation. European Journal of Neuroscience, 2022, 55, 2666-2683.	1.2	20
1237	Histone demethylase complexes KDM3A and KDM3B cooperate with OCT4/SOX2 to define a pluripotency gene regulatory network. FASEB Journal, 2021, 35, e21664.	0.2	19

#	ARTICLE	IF	CITATIONS
1239	Reverse-transcribed SARS-CoV-2 RNA can integrate into the genome of cultured human cells and can be expressed in patient-derived tissues. Proceedings of the National Academy of Sciences of the United States of America, 2021, 118, .	3.3	175
1240	Cryo-EM structure of SETD2/Set2 methyltransferase bound to a nucleosome containing oncohistone mutations. Cell Discovery, 2021, 7, 32.	3.1	18
1241	MPP8 is essential for sustaining self-renewal of ground-state pluripotent stem cells. Nature Communications, 2021, 12, 3034.	5.8	35
1242	DNMT1 reads heterochromatic H4K20me3 to reinforce LINE-1 DNA methylation. Nature Communications, 2021, 12, 2490.	5.8	63
1243	Environmental Enrichment Induces Epigenomic and Genome Organization Changes Relevant for Cognition. Frontiers in Molecular Neuroscience, 2021, 14, 664912.	1.4	12
1248	Transcriptome Profiling of Embryonic Retinal Pigment Epithelium Reprogramming. Genes, 2021, 12, 840.	1.0	9
1249	Cell-surface SLC nucleoside transporters and purine levels modulate BRD4-dependent chromatin states. Nature Metabolism, 2021, 3, 651-664.	5.1	7
1250	Qki regulates myelinogenesis through Srebp2-dependent cholesterol biosynthesis. ELife, 2021, 10, .	2.8	13
1251	Long-read whole-genome methylation patterning using enzymatic base conversion and nanopore sequencing. Nucleic Acids Research, 2021, 49, e81-e81.	6.5	31
1252	Sarcomere function activates a p53-dependent DNA damage response that promotes polyploidization and limits inÂvivo cell engraftment. Cell Reports, 2021, 35, 109088.	2.9	11
1254	Balancing cohesin eviction and retention prevents aberrant chromosomal interactions, Polycomb-mediated repression, and X-inactivation. Molecular Cell, 2021, 81, 1970-1987.e9.	4.5	30
1255	Impact of chromatin context on Cas9-induced DNA double-strand break repair pathway balance. Molecular Cell, 2021, 81, 2216-2230.e10.	4.5	106
1256	The histone H3K9M mutation synergizes with H3K14 ubiquitylation to selectively sequester histone H3K9 methyltransferase Clr4 at heterochromatin. Cell Reports, 2021, 35, 109137.	2.9	8
1257	A dual role for H2A.Z.1 in modulating the dynamics of RNA polymerase II initiation and elongation. Nature Structural and Molecular Biology, 2021, 28, 435-442.	3.6	27
1258	The Zinc Finger Antiviral Protein ZAP Restricts Human Cytomegalovirus and Selectively Binds and Destabilizes Viral <i>UL4</i> / <i>UL5</i> Transcripts. MBio, 2021, 12, .	1.8	33
1259	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
1260	Cotranscriptional splicing efficiencies differ within genes and between cell types. Rna, 2021, 27, 829-840.	1.6	16
1261	The connectome of neural crest enhancers reveals regulatory features of signaling systems. Developmental Cell, 2021, 56, 1268-1282.e6.	3.1	16

#	Article	IF	Citations
1263	Chromatin accessibility and translational landscapes of tea plants under chilling stress. Horticulture Research, 2021, 8, 96.	2.9	28
1264	A termination-independent role of Rat1 in cotranscriptional splicing. Nucleic Acids Research, 2021, 49, 5520-5536.	6.5	3
1265	Integrated genomic analysis reveals key features of long undecoded transcript isoform-based gene repression. Molecular Cell, 2021, 81, 2231-2245.e11.	4.5	20
1267	The landscape of chromatin accessibility in skeletal muscle during embryonic development in pigs. Journal of Animal Science and Biotechnology, 2021, 12, 56.	2.1	20
1270	RAS mutations drive proliferative chronic myelomonocytic leukemia via a KMT2A-PLK1 axis. Nature Communications, 2021, 12, 2901.	5.8	44
1272	Two competing mechanisms of DNMT3A recruitment regulate the dynamics of de novo DNA methylation at PRC1-targeted CpG islands. Nature Genetics, 2021, 53, 794-800.	9.4	59
1274	Global Chromatin Changes Resulting from Single-Gene Inactivationâ€"The Role of SMARCB1 in Malignant Rhabdoid Tumor. Cancers, 2021, 13, 2561.	1.7	8
1277	KDM4 orchestrates epigenomic remodeling of senescent cells and potentiates the senescence-associated secretory phenotype. Nature Aging, 2021, 1, 454-472.	5.3	31
1278	Epigenetic Modulation of Radiation-Induced Diacylglycerol Kinase Alpha Expression Prevents Pro-Fibrotic Fibroblast Response. Cancers, 2021, 13, 2455.	1.7	8
1280	DNA methylation changes during long-term in vitro cell culture are caused by epigenetic drift. Communications Biology, 2021, 4, 598.	2.0	27
1281	Hox dosage contributes to flight appendage morphology in Drosophila. Nature Communications, 2021, 12, 2892.	5.8	30
1283	The human Î²â€globin enhancer LCR HS2 plays a role in forming a TAD by activating chromatin structure at neighboring CTCF sites. FASEB Journal, 2021, 35, e21669.	0.2	4
1284	The complement system drives local inflammatory tissue priming by metabolic reprogramming of synovial fibroblasts. Immunity, 2021, 54, 1002-1021.e10.	6.6	106
1288	Human placental cytotrophoblast epigenome dynamics over gestation and alterations in placental disease. Developmental Cell, 2021, 56, 1238-1252.e5.	3.1	29
1289	Mechanism for DPY30 and ASH2L intrinsically disordered regions to modulate the MLL/SET1 activity on chromatin. Nature Communications, 2021, 12, 2953.	5.8	21
1290	Multiple roles of H2A.Z in regulating promoter chromatin architecture in human cells. Nature Communications, 2021, 12, 2524.	5.8	22
1295	The nuclear periphery is a scaffold for tissue-specific enhancers. Nucleic Acids Research, 2021, 49, 6181-6195.	6.5	28
1296	Single-PanIN-seq unveils that ARID1A deficiency promotes pancreatic tumorigenesis by attenuating KRAS-induced senescence. ELife, 2021, 10, .	2.8	5

#	ARTICLE	IF	CITATIONS
1297	Arabidopsis RPD3-like histone deacetylases form multiple complexes involved in stress response. Journal of Genetics and Genomics, 2021, 48, 369-383.	1.7	18
1298	Epigenome editing of the CFTR-locus for treatment of cystic fibrosis. Journal of Cystic Fibrosis, 2022, 21, 164-171.	0.3	3
1299	A multi-gene knockdown approach reveals a new role for Pax6 in controlling organ number in Drosophila. Development (Cambridge), 2021, 148, .	1.2	6
1300	The SWI/SNF chromatin remodeling complex helps resolve R-loop-mediated transcriptionâ€"replication conflicts. Nature Genetics, 2021, 53, 1050-1063.	9.4	85
1301	Pathogenic LMNA variants disrupt cardiac lamina-chromatin interactions and de-repress alternative fate genes. Cell Stem Cell, 2021, 28, 938-954.e9.	5.2	61
1302	POINT technology illuminates the processing of polymerase-associated intact nascent transcripts. Molecular Cell, 2021, 81, 1935-1950.e6.	4.5	52
1303	Dynamic imaging of nascent RNA reveals general principles of transcription dynamics and stochastic splice site selection. Cell, 2021, 184, 2878-2895.e20.	13.5	89
1304	The double-stranded DNA-binding proteins TEBP-1 and TEBP-2 form a telomeric complex with POT-1. Nature Communications, 2021, 12, 2668.	5.8	12
1305	Genome-wide profiling reveals functional interplay of DNA sequence composition, transcriptional activity, and nucleosome positioning in driving DNA supercoiling and helix destabilization in <i>C. elegans</i>. Genome Research, 2021, 31, 1187-1202.	2.4	7
1306	NF-Î°B dynamics determine the stimulus specificity of epigenomic reprogramming in macrophages. Science, 2021, 372, 1349-1353.	6.0	91
1307	Fever supports CD8 ⁺ effector T cell responses by promoting mitochondrial translation. Proceedings of the National Academy of Sciences of the United States of America, 2021, 118, .	3.3	28
1309	Translation and codon usage regulate Argonaute slicer activity to trigger small RNA biogenesis. Nature Communications, 2021, 12, 3492.	5.8	24
1310	Differential chromatin accessibility landscape of gain-of-function mutant p53 tumours. BMC Cancer, 2021, 21, 669.	1.1	2
1311	CD44 alternative splicing senses intragenic DNA methylation in tumors via direct and indirect mechanisms. Nucleic Acids Research, 2021, 49, 6213-6237.	6.5	12
1312	AP-1 is a temporally regulated dual gatekeeper of reprogramming to pluripotency. Proceedings of the National Academy of Sciences of the United States of America, 2021, 118, .	3.3	19
1313	JAK inhibitors dampen activation of interferon-stimulated transcription of ACE2 isoforms in human airway epithelial cells. Communications Biology, 2021, 4, 654.	2.0	18
1315	Successful ATAC-Seq From Snap-Frozen Equine Tissues. Frontiers in Genetics, 2021, 12, 641788.	1.1	8
1317	AP-1 activity is a major barrier of human somatic cell reprogramming. Cellular and Molecular Life Sciences, 2021, 78, 5847-5863.	2.4	4

#	ARTICLE	IF	CITATIONS
1318	DET1-mediated COP1 regulation avoids HY5 activity over second-site gene targets to tune plant photomorphogenesis. Molecular Plant, 2021, 14, 963-982.	3.9	27
1319	A convolutional neural network-based regression model to infer the epigenetic crosstalk responsible for CG methylation patterns. BMC Bioinformatics, 2021, 22, 341.	1.2	0
1322	Comprehensive interactome profiling of the human Hsp70 network highlights functional differentiation of J domains. Molecular Cell, 2021, 81, 2549-2565.e8.	4.5	47
1323	STAG2 loss rewires oncogenic and developmental programs to promote metastasis in Ewing sarcoma. Cancer Cell, 2021, 39, 827-844.e10.	7.7	49
1324	mSWI/SNF promotes Polycomb repression both directly and through genome-wide redistribution. Nature Structural and Molecular Biology, 2021, 28, 501-511.	3.6	50
1325	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
1326	HIRA stabilizes skeletal muscle lineage identity. Nature Communications, 2021, 12, 3450.	5.8	17
1327	A KMT2A-AFF1 gene regulatory network highlights the role of core transcription factors and reveals the regulatory logic of key downstream target genes. Genome Research, 2021, 31, 1159-1173.	2.4	16
1331	Chromatin accessibility profiling in Neurospora crassa reveals molecular features associated with accessible and inaccessible chromatin. BMC Genomics, 2021, 22, 459.	1.2	13
1333	C/EBPÎ´ drives key endocrine signals in the human amnion at parturition. Clinical and Translational Medicine, 2021, 11, e416.	1.7	14
1337	Reproducible and accessible analysis of transposon insertion sequencing in Galaxy for qualitative essentiality analyses. BMC Microbiology, 2021, 21, 168.	1.3	1
1339	Nuclear ADP-ribosylation drives IFNÎ³-dependent STAT1Î± enhancer formation in macrophages. Nature Communications, 2021, 12, 3931.	5.8	20
1340	Elongation factor ELOF1 drives transcription-coupled repair and prevents genome instability. Nature Cell Biology, 2021, 23, 608-619.	4.6	41
1341	A protocol for rapid degradation of endogenous transcription factors in mammalian cells and identification of direct regulatory targets. STAR Protocols, 2021, 2, 100530.	0.5	8
1342	ChIP-seq protocol for sperm cells and embryos to assess environmental impacts and epigenetic inheritance. STAR Protocols, 2021, 2, 100602.	0.5	7
1343	Unrestrained poly-ADP-ribosylation provides insights into chromatin regulation and human disease. Molecular Cell, 2021, 81, 2640-2655.e8.	4.5	52
1344	LINE-1 transcription in round spermatids is associated with accretion of 5-carboxylcytosine in their open reading frames. Communications Biology, 2021, 4, 691.	2.0	8
1347	Lasp1 regulates adherens junction dynamics and fibroblast transformation in destructive arthritis. Nature Communications, 2021, 12, 3624.	5.8	16

#	Article	IF	Citations
1348	Loss of histone methyltransferase ASH1L in the developing mouse brain causes autistic-like behaviors. Communications Biology, 2021, 4, 756.	2.0	19
1349	A role for condensin in mediating transcriptional adaptation to environmental stimuli. Life Science Alliance, 2021, 4, e202000961.	1.3	3
1350	Genome Scale Analysis Reveals IscR Directly and Indirectly Regulates Virulence Factor Genes in Pathogenic Yersinia. MBio, 2021, 12, e0063321.	1.8	4
1351	IP3-mediated Ca2+ signals regulate larval to pupal transition under nutrient stress through the H3K36 methyltransferase Set2. Development (Cambridge), 2021, 148, .	1.2	1
1352	HMGB1 coordinates SASPâ€related chromatin folding and RNA homeostasis on the path to senescence. Molecular Systems Biology, 2021, 17, e9760.	3.2	31
1354	Impaired stem cell differentiation and somatic cell reprogramming in DIDO3 mutants with altered RNA processing and increased R-loop levels. Cell Death and Disease, 2021, 12, 637.	2.7	8
1355	BRN2 is a non-canonical melanoma tumor-suppressor. Nature Communications, 2021, 12, 3707.	5.8	10
1356	A disproportionate impact of G9a methyltransferase deficiency on the X chromosome. Genes and Development, 2021, 35, 1035-1054.	2.7	4
1357	Generation of gene-level resolution chromosome contact maps in bacteria and archaea. STAR Protocols, 2021, 2, 100512.	0.5	7
1358	Correct dosage of X chromosome transcription is controlled by a nuclear pore component. Cell Reports, 2021, 35, 109236.	2.9	12
1359	Combined epigenetic and metabolic treatments overcome differentiation blockade in acute myeloid leukemia. IScience, 2021, 24, 102651.	1.9	4
1362	Enzymatic methyl sequencing detects DNA methylation at single-base resolution from picograms of DNA. Genome Research, 2021, 31, 1280-1289.	2.4	170
1363	NANOS2 is a sequence-specific mRNA-binding protein that promotes transcript degradation in spermatogonial stem cells. IScience, 2021, 24, 102762.	1.9	11
1368	Repeat to gene expression ratios in leukemic blast cells can stratify risk prediction in acute myeloid leukemia. BMC Medical Genomics, 2021, 14, 166.	0.7	8
1369	Contribution of genetic and epigenetic changes to escape from X-chromosome inactivation. Epigenetics and Chromatin, 2021, 14, 30.	1.8	11
1370	Halobacterium salinarum and Haloferax volcanii Comparative Transcriptomics Reveals Conserved Transcriptional Processing Sites. Genes, 2021, 12, 1018.	1.0	5
1372	Prdm16-mediated H3K9 methylation controls fibro-adipogenic progenitors identity during skeletal muscle repair. Science Advances, 2021, 7, .	4.7	30
1373	Temporal evolution of cellular heterogeneity during the progression to advanced AR-negative prostate cancer. Nature Communications, 2021, 12, 3372.	5.8	45

#	Article	IF	Citations
1374	Phase separation drives aberrant chromatin looping and cancer development. Nature, 2021, 595, 591-595.	13.7	197
1375	RUNX1-mediated alphaherpesvirus-host trans-species chromatin interaction promotes viral transcription. Science Advances, 2021, 7, .	4.7	11
1376	DNA G-Quadruplexes Contribute to CTCF Recruitment. International Journal of Molecular Sciences, 2021, 22, 7090.	1.8	15
1377	BMI1 maintains the Treg epigenomic landscape to prevent inflammatory bowel disease. Journal of Clinical Investigation, 2021, 131, .	3.9	10
1378	The global and promoter-centric 3D genome organization temporally resolved during a circadian cycle. Genome Biology, 2021, 22, 162.	3.8	21
1379	Deep and accurate detection of m6A RNA modifications using miCLIP2 and m6Aboost machine learning. Nucleic Acids Research, 2021, 49, e92-e92.	6.5	50
1380	Putative Causal Variants Are Enriched in Annotated Functional Regions From Six Bovine Tissues. Frontiers in Genetics, 2021, 12, 664379.	1.1	20
1383	Intergenerational effect of short-term spaceflight in mice. IScience, 2021, 24, 102773.	1.9	7
1384	Orphan CpG islands amplify poised enhancer regulatory activity and determine target gene responsiveness. Nature Genetics, 2021, 53, 1036-1049.	9.4	56
1385	Genome-wide detection of enhancer-hijacking events from chromatin interaction data in rearranged genomes. Nature Methods, 2021, 18, 661-668.	9.0	70
1386	A unified atlas of CD8 TÂcell dysfunctional states in cancer and infection. Molecular Cell, 2021, 81, 2477-2493.e10.	4.5	57
1388	Multifaceted regulation of hepatic lipid metabolism by YY1. Life Science Alliance, 2021, 4, e202000928.	1.3	13
1391	Chemical profiling of DNA G-quadruplex-interacting proteins in live cells. Nature Chemistry, 2021, 13, 626-633.	6.6	82
1394	Polycomb-dependent differential chromatin compartmentalization determines gene coregulation in <i>Arabidopsis</i>. Genome Research, 2021, 31, 1230-1244.	2.4	36
1395	A methionine-Mettl3-N-methyladenosine axis promotes polycystic kidney disease. Cell Metabolism, 2021, 33, 1234-1247.e7.	7.2	52
1396	Bromodomain-containing proteins BRD1, BRD2, and BRD13 are core subunits of SWI/SNF complexes and vital for their genomic targeting in Arabidopsis. Molecular Plant, 2021, 14, 888-904.	3.9	25
1397	MBD5 and MBD6 couple DNA methylation to gene silencing through the J-domain protein SILENZIO. Science, 2021, 372, 1434-1439.	6.0	38
1398	Enhancer Hijacking Drives Oncogenic <i>BCL11B</i> Expression in Lineage-Ambiguous Stem Cell Leukemia. Cancer Discovery, 2021, 11, 2846-2867.	7.7	83

#	ARTICLE	IF	CITATIONS
1399	MeCP2 is a microsatellite binding protein that protects CA repeats from nucleosome invasion. Science, 2021, 372, .	6.0	36
1401	The major mechanism of melanoma mutations is based on deamination of cytosine in pyrimidine dimers as determined by circle damage sequencing. Science Advances, 2021, 7, .	4.7	23
1402	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
1403	Genome-wide mapping of human DNA replication by optical replication mapping supports a stochastic model of eukaryotic replication. Molecular Cell, 2021, 81, 2975-2988.e6.	4.5	57
1404	Pax7 pioneer factor action requires both paired and homeo DNA binding domains. Nucleic Acids Research, 2021, 49, 7424-7436.	6.5	14
1405	Loss of Setd2 associates with aberrant microRNA expression and contributes to inflammatory bowel disease progression in mice. Genomics, 2021, 113, 2441-2454.	1.3	2
1410	Histone H3K4me1 and H3K27ac play roles in nucleosome eviction and eRNA transcription, respectively, at enhancers. FASEB Journal, 2021, 35, e21781.	0.2	31
1413	Oncogenic enhancers drive esophageal squamous cell carcinogenesis and metastasis. Nature Communications, 2021, 12, 4457.	5.8	27
1414	Genome-Wide Transcriptomic Analysis Reveals the Gene Regulatory Network Controlled by SRL1 in Regulating Rice Leaf Rolling. Journal of Plant Growth Regulation, 2022, 41, 2292-2304.	2.8	1
1416	RNA helicase, DDX3X, is actively recruited to sites of DNA damage in live cells. DNA Repair, 2021, 103, 103137.	1.3	12
1417	COMPASS functions as a module of the INO80 chromatin remodeling complex to mediate histone H3K4 methylation in Arabidopsis. Plant Cell, 2021, 33, 3250-3271.	3.1	17
1419	Hydroxycarbamide effects on DNA methylation and gene expression in myeloproliferative neoplasms. Genome Research, 2021, 31, 1381-1394.	2.4	3
1421	Comparative Analysis of Promoters and Enhancers in the Pituitary Glands of the Bama Xiang and Large White Pigs. Frontiers in Genetics, 2021, 12, 697994.	1.1	3
1425	Neuronal activity-induced BRG1 phosphorylation regulates enhancer activation. Cell Reports, 2021, 36, 109357.	2.9	11
1429	Chromatin states shaped by an epigenetic code confer regenerative potential to the mouse liver. Nature Communications, 2021, 12, 4110.	5.8	12
1433	Improving distance measures between genomic tracks with mutual proximity. Briefings in Bioinformatics, 2021, 22, .	3.2	2
1434	Pervasive transcription of the mitochondrial genome in <i>Candida albicans</i> is revealed in mutants lacking the mtEXO RNase complex. RNA Biology, 2021, 18, 303-317.	1.5	3
1435	Systematic dissection of transcriptional regulatory networks by genome-scale and single-cell CRISPR screens. Science Advances, 2021, 7, .	4.7	19

#	Article	IF	Citations
1436	Establishment, maintenance, and recall of inflammatory memory. Cell Stem Cell, 2021, 28, 1758-1774.e8.	5.2	98
1437	An integrated functional and clinical genomics approach reveals genes driving aggressive metastatic prostate cancer. Nature Communications, 2021, 12, 4601.	5.8	18
1438	Distinct mechanisms mediate X chromosome dosage compensation in <i>Anopheles</i> and <i>Drosophila</i>. Life Science Alliance, 2021, 4, e202000996.	1.3	13
1440	Simultaneous disruption of PRC2 and enhancer function underlies histone H3.3-K27M oncogenic activity in human hindbrain neural stem cells. Nature Genetics, 2021, 53, 1221-1232.	9.4	36
1441	The Drosophila HP1 family is associated with active gene expression across chromatin contexts. Genetics, 2021, 219, .	1.2	8
1442	Complete loss of H3K9 methylation dissolves mouse heterochromatin organization. Nature Communications, 2021, 12, 4359.	5.8	41
1443	Whole genome sequencing of two human rhinovirus A types (A101 and A15) detected in Kenya, 2016-2018. Wellcome Open Research, 2021, 6, 178.	0.9	5
1444	CoBRA: Containerized Bioinformatics Workflow for Reproducible ChIP/ATAC-seq Analysis. Genomics, Proteomics and Bioinformatics, 2021, 19, 652-661.	3.0	18
1445	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
1446	Harmful R-loops are prevented via different cell cycle-specific mechanisms. Nature Communications, 2021, 12, 4451.	5.8	32
1447	Sensitivity of cohesinâ€“chromatin association to high-salt treatment corroborates non-topological mode of loop extrusion. Epigenetics and Chromatin, 2021, 14, 36.	1.8	4
1448	A functional map of genomic HIF1Î±-DNA complexes in the eye lens revealed through multiomics analysis. BMC Genomics, 2021, 22, 497.	1.2	6
1449	SMARCA4 deficient tumours are vulnerable to KDM6A/UTX and KDM6B/JMJD3 blockade. Nature Communications, 2021, 12, 4319.	5.8	22
1452	The histone chaperone HIR maintains chromatin states to control nitrogen assimilation and fungal virulence. Cell Reports, 2021, 36, 109406.	2.9	10
1453	Reprogramming of bivalent chromatin states in NRAS mutant melanoma suggests PRC2 inhibition as a therapeutic strategy. Cell Reports, 2021, 36, 109410.	2.9	17
1454	Massively parallel in vivo CRISPR screening identifies RNF20/40 as epigenetic regulators of cardiomyocyte maturation. Nature Communications, 2021, 12, 4442.	5.8	27
1456	Nuclear Organization during Hepatogenesis in Zebrafish Requires Uhrf1. Genes, 2021, 12, 1081.	1.0	4
1458	HP1Î³ binding preâ€·mRNA intronic repeatsÂmodulates RNA splicing decisions. EMBO Reports, 2021, 22, e52320.	2.0	12

#	ARTICLE	IF	CITATIONS
1459	Nascent RNA antagonizes the interaction of a set of regulatory proteins with chromatin. Molecular Cell, 2021, 81, 2944-2959.e10.	4.5	19
1460	Metabolically controlled histone H4K5 acylation/acetylation ratio drives BRD4 genomic distribution. Cell Reports, 2021, 36, 109460.	2.9	27
1461	Multiple CTCF sites cooperate with each other to maintain a TAD for enhancerâ€“promoter interaction in the Î²â€globin locus. FASEB Journal, 2021, 35, e21768.	0.2	5
1462	Transcription factor RFX7 governs a tumor suppressor network in response to p53 and stress. Nucleic Acids Research, 2021, 49, 7437-7456.	6.5	17
1463	Stromal induction of BRD4 phosphorylation Results in Chromatin Remodeling and BET inhibitor Resistance in Colorectal Cancer. Nature Communications, 2021, 12, 4441.	5.8	49
1464	Interplay and cooperation between SREBF1 and master transcription factors regulate lipid metabolism and tumor-promoting pathways in squamous cancer. Nature Communications, 2021, 12, 4362.	5.8	50
1465	Maternally inherited piRNAs direct transient heterochromatin formation at active transposons during early Drosophila embryogenesis. ELife, 2021, 10, .	2.8	26
1466	Distinct nuclear compartment-associated genome architecture in the developing mammalian brain. Nature Neuroscience, 2021, 24, 1235-1242.	7.1	28
1468	Whole-genome sequencing of H3K4me3 and DNA methylation in human sperm reveals regions of overlap linked to fertility and development. Cell Reports, 2021, 36, 109418.	2.9	25
1469	Chemotherapy-induced transposable elements activate MDA5 to enhance haematopoietic regeneration. Nature Cell Biology, 2021, 23, 704-717.	4.6	40
1471	A ChIP-exo screen of 887 Protein Capture Reagents Program transcription factor antibodies in human cells. Genome Research, 2021, 31, 1663-1679.	2.4	9
1472	A Genome Doubling Event Reshapes Rice Morphology and Products by Modulating Chromatin Signatures and Gene Expression Profiling. Rice, 2021, 14, 72.	1.7	6
1473	Interplay between CTCF boundaries and a super enhancer controls cohesin extrusion trajectories and gene expression. Molecular Cell, 2021, 81, 3082-3095.e6.	4.5	29
1474	Transcriptional reprogramming by oxidative stress occurs within a predefined chromatin accessibility landscape. Free Radical Biology and Medicine, 2021, 171, 319-331.	1.3	6
1475	Pim kinase inhibitor co-treatment decreases alternative non-homologous end-joining DNA repair and genomic instability induced by topoisomerase 2 inhibitors in cells with FLT3 internal tandem duplication. Oncotarget, 2021, 12, 1763-1779.	0.8	2
1478	m6A RNA methylation regulates promoter- proximal pausing of RNA polymerase II. Molecular Cell, 2021, 81, 3356-3367.e6.	4.5	47
1479	DNA features beyond the transcription factor binding site specify target recognition by plant MYC2-related bHLH proteins. Plant Communications, 2021, 2, 100232.	3.6	18
1480	AtHDA6 functions as an H3K18ac eraser to maintain pericentromeric CHG methylation in Arabidopsis thaliana. Nucleic Acids Research, 2021, 49, 9755-9767.	6.5	6

#	Article	IF	Citations
1481	Epigenomic and transcriptional profiling identifies impaired glyoxylate detoxification in NAFLD as a risk factor for hyperoxaluria. Cell Reports, 2021, 36, 109526.	2.9	22
1484	Formation of artificial chromosomes in <i>Caenorhabditis elegans</i> and analyses of their segregation in mitosis, DNA sequence composition and holocentromere organization. Nucleic Acids Research, 2021, 49, 9174-9193.	6.5	13
1485	Altered chromatin states drive cryptic transcription in aging mammalian stem cells. Nature Aging, 2021, 1, 684-697.	5.3	26
1486	A TALE/HOX code unlocks WNT signalling response towards paraxial mesoderm. Nature Communications, 2021, 12, 5136.	5.8	10
1487	Structural Variations in the Genome of Potato Varieties of the Ural Selection. Agronomy, 2021, 11, 1703.	1.3	4
1489	Transovarial transmission of a core virome in the Chagas disease vector Rhodnius prolixus. PLoS Pathogens, 2021, 17, e1009780.	2.1	7
1490	Targeting enhancer reprogramming to mitigate MEK inhibitor resistance in preclinical models of advanced ovarian cancer. Journal of Clinical Investigation, 2021, 131, .	3.9	6
1491	CdrS Is a Global Transcriptional Regulator Influencing Cell Division in Haloferax volcanii. MBio, 2021, 12, e0141621.	1.8	14
1495	ATG5 and ATG7 Expression Levels Are Reduced in Cutaneous Melanoma and Regulated by NRF1. Frontiers in Oncology, 2021, 11, 721624.	1.3	15
1496	Loss of grand histone H3 lysine 27 trimethylation domains mediated transcriptional activation in esophageal squamous cell carcinoma. Npj Genomic Medicine, 2021, 6, 65.	1.7	7
1497	Evidence of pioneer factor activity of an oncogenic fusion transcription factor. IScience, 2021, 24, 102867.	1.9	22
1500	NF1 regulates mesenchymal glioblastoma plasticity and aggressiveness through the AP-1 transcription factor FOSL1. ELife, 2021, 10, .	2.8	41
1502	Su(Hw) primes 66D and 7F Drosophila chorion genes loci for amplification through chromatin decondensation. Scientific Reports, 2021, 11, 16963.	1.6	7
1503	Mutational bias in spermatogonia impacts the anatomy of regulatory sites in the human genome. Genome Research, 2021, 31, 1994-2007.	2.4	4
1504	Visualizing and Annotating Hi-C Data. Methods in Molecular Biology, 2022, 2301, 97-132.	0.4	0
1505	Integrative Epigenome Map of the Normal Human Prostate Provides Insights Into Prostate Cancer Predisposition. Frontiers in Cell and Developmental Biology, 2021, 9, 723676.	1.8	5
1506	Molecular phenotyping reveals the identity of Barrettâ€™s esophagus and its malignant transition. Science, 2021, 373, 760-767.	6.0	99
1508	Histone crotonylation regulates neural stem cell fate decisions by activating bivalent promoters. EMBO Reports, 2021, 22, e52023.	2.0	21

#	ARTICLE	IF	CITATIONS
1512	Uncovering Divergence in Gene Expression Regulation in the Adaptation of Yeast to Nitrogen Scarcity. MSystems, 2021, 6, e0046621.	1.7	10
1513	Binary pan-cancer classes with distinct vulnerabilities defined by pro- or anti-cancer YAP/TEAD activity. Cancer Cell, 2021, 39, 1115-1134.e12.	7.7	86
1514	Cell-free DNA ultra-low-pass whole genome sequencing to distinguish malignant peripheral nerve sheath tumor (MPNST) from its benign precursor lesion: A cross-sectional study. PLoS Medicine, 2021, 18, e1003734.	3.9	35
1515	Diagnostic Validation of a Clinical Laboratory-Oriented Targeted RNA Sequencing System for Detecting Gene Fusions in Hematologic Malignancies. Journal of Molecular Diagnostics, 2021, 23, 1015-1029.	1.2	1
1517	Mesomelic dysplasias associated with the HOXD locus are caused by regulatory reallocations. Nature Communications, 2021, 12, 5013.	5.8	14
1521	Acute depletion of CTCF rewires genome-wide chromatin accessibility. Genome Biology, 2021, 22, 244.	3.8	29
1523	TERA-Seq: true end-to-end sequencing of native RNA molecules for transcriptome characterization. Nucleic Acids Research, 2021, 49, e115-e115.	6.5	18
1524	Chromatin and transcriptomic profiling uncover dysregulation of the Tip60 HAT/HDAC2 epigenomic landscape in the neurodegenerative brain. Epigenetics, 2022, 17, 786-807.	1.3	5
1528	Methyltransferase-like 3 Modulates Severe Acute Respiratory Syndrome Coronavirus-2 RNA N6-Methyladenosine Modification and Replication. MBio, 2021, 12, e0106721.	1.8	53
1529	A custom capture sequence approach for oculocutaneous albinism identifies structural variant alleles at the <i>OCA2</i> locus. Human Mutation, 2021, 42, 1239-1253.	1.1	7
1533	RAC1 plays an essential role in estrogen receptor alpha function in breast cancer cells. Oncogene, 2021, 40, 5950-5962.	2.6	8
1534	Genetic and epigenetic orchestration of Gfi1aa-Lsd1-<i>cebpÎ±</i> in zebrafish neutrophil development. Development (Cambridge), 2021, 148, .	1.2	3
1535	Targeted protein degradation reveals a direct role of SPT6 in RNAPII elongation and termination. Molecular Cell, 2021, 81, 3110-3127.e14.	4.5	38
1540	Cell-type-specific Hox regulatory strategies orchestrate tissue identity. Current Biology, 2021, 31, 4246-4255.e4.	1.8	40
1541	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
1542	Genome accessibility dynamics in response to phosphate limitation is controlled by the PHR1 family of transcription factors in <i>Arabidopsis</i>. Proceedings of the National Academy of Sciences of the United States of America, 2021, 118, .	3.3	38
1543	Intragenic tRNA-promoted R-loops orchestrate transcription interference for plant oxidative stress responses. Plant Cell, 2021, 33, 3574-3591.	3.1	11
1546	Mutations in the transcription factor FOXO1 mimic positive selection signals to promote germinal center B cell expansion and lymphomagenesis. Immunity, 2021, 54, 1807-1824.e14.	6.6	12

#	ARTICLE	IF	CITATIONS
1547	Nhp2 is a reader of H2AQ105me and part of aÂnetwork integrating metabolism with rRNA synthesis. EMBO Reports, 2021, 22, e52435.	2.0	5
1548	Co-transcriptional RNA cleavage by Drosha homolog Pac1 triggers transcription termination in fission yeast. Nucleic Acids Research, 2021, 49, 8610-8624.	6.5	2
1550	CTCF is a barrier for 2C-like reprogramming. Nature Communications, 2021, 12, 4856.	5.8	38
1552	Activation of bivalent factor DLX5 cooperates with master regulator TP63 to promote squamous cell carcinoma. Nucleic Acids Research, 2021, 49, 9246-9263.	6.5	13
1553	A cascade of transcriptional repression determines sexual commitment and development in <i>Plasmodium falciparum</i>. Nucleic Acids Research, 2021, 49, 9264-9279.	6.5	36
1554	H4K20me3 marks distal intergenic and repetitive regions in human mature spermatozoa. Development (Cambridge), 2021, 148, .	1.2	6
1555	PPARÎ³-Induced Global H3K27 Acetylation Maintains Osteo/Cementogenic Abilities of Periodontal Ligament Fibroblasts. International Journal of Molecular Sciences, 2021, 22, 8646.	1.8	9
1556	Porcine Reproductive and Respiratory Syndrome Virus Infection Upregulates Negative Immune Regulators and T-Cell Exhaustion Markers. Journal of Virology, 2021, 95, e0105221.	1.5	13
1557	Stochastic gene expression drives mesophyll protoplast regeneration. Science Advances, 2021, 7, .	4.7	44
1558	CHIPIN: ChIP-seq inter-sample normalization based on signal invariance across transcriptionally constant genes. BMC Bioinformatics, 2021, 22, 407.	1.2	8
1559	Connection of core and tail Mediator modules restrains transcription from TFIID-dependent promoters. PLoS Genetics, 2021, 17, e1009529.	1.5	9
1561	Polyamine metabolism is a central determinant of helper TÂcell lineage fidelity. Cell, 2021, 184, 4186-4202.e20.	13.5	121
1562	A Y-linked anti-MÃ¼llerian hormone type-II receptor is the sex-determining gene in ayu, Plecoglossus altivelis. PLoS Genetics, 2021, 17, e1009705.	1.5	25
1563	Copy number variation detection using single cell sequencing data. , 2021, , .		0
1564	Brg1 Supports B Cell Proliferation and Germinal Center Formation Through Enhancer Activation. Frontiers in Immunology, 2021, 12, 705848.	2.2	8
1565	The establishment of variant surface glycoprotein monoallelic expression revealed by single-cell RNA-seq of Trypanosoma brucei in the tsetse fly salivary glands. PLoS Pathogens, 2021, 17, e1009904.	2.1	29
1566	BAP1 enhances Polycomb repression by counteracting widespread H2AK119ub1 deposition and chromatin condensation. Molecular Cell, 2021, 81, 3526-3541.e8.	4.5	46
1567	Joint changes in RNA, RNA polymerase II, and promoter activity through the cell cycle identify non-coding RNAs involved in proliferation. Scientific Reports, 2021, 11, 18952.	1.6	7

#	Article	IF	Citations
1568	CTCF knockout in zebrafish induces alterations in regulatory landscapes and developmental gene expression. Nature Communications, 2021, 12, 5415.	5.8	27
1569	H3K4 di-methylation governs smooth muscle lineage identity and promotes vascular homeostasis by restraining plasticity. Developmental Cell, 2021, 56, 2765-2782.e10.	3.1	21
1570	SWO1 modulates cell wall integrity under salt stress by interacting with importin É‘ in Arabidopsis. Stress Biology, 2021, 1, 1.	1.5	6
1571	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
1572	Reshaping of the androgen-driven chromatin landscape in normal prostate cells by early cancer drivers and effect on therapeutic sensitivity. Cell Reports, 2021, 36, 109625.	2.9	22
1573	An inferred functional impact map of genetic variants in rice. Molecular Plant, 2021, 14, 1584-1599.	3.9	48
1575	Nascent RNA scaffolds contribute to chromosome territory architecture and counter chromatin compaction. Molecular Cell, 2021, 81, 3509-3525.e5.	4.5	63
1576	The leukemic oncogene EVI1 hijacks a MYC super-enhancer by CTCF-facilitated loops. Nature Communications, 2021, 12, 5679.	5.8	31
1578	The folate antagonist methotrexate diminishes replication of the coronavirus SARS-CoV-2 and enhances the antiviral efficacy of remdesivir in cell culture models. Virus Research, 2021, 302, 198469.	1.1	28
1579	ZMYND8-regulated IRF8 transcription axis is an acute myeloid leukemia dependency. Molecular Cell, 2021, 81, 3604-3622.e10.	4.5	32
1580	Release of Notch activity coordinated by IL-1Î² signalling confers differentiation plasticity of airway progenitors via Fosl2 during alveolar regeneration. Nature Cell Biology, 2021, 23, 953-966.	4.6	37
1581	A bacterial bile acid metabolite modulates Treg activity through the nuclear hormone receptor NR4A1. Cell Host and Microbe, 2021, 29, 1366-1377.e9.	5.1	111
1582	Deficiency of PolÎ· in Saccharomyces cerevisiae reveals the impact of transcription on damage-induced cohesion. PLoS Genetics, 2021, 17, e1009763.	1.5	0
1584	The histone acetyltransferase HBO1 promotes efficient tip cell sprouting during angiogenesis. Development (Cambridge), 2021, 148, .	1.2	4
1585	Epigenetic Regulation by <i>Suv4-20h1</i> in Cardiopulmonary Progenitor Cells Is Required to Prevent Pulmonary Hypertension and Chronic Obstructive Pulmonary Disease. Circulation, 2021, 144, 1042-1058.	1.6	9
1586	The zinc-finger protein OEF-1 stabilizes histone modification patterns and promotes efficient splicing in the <i>Caenorhabditis elegans</i> germline. G3: Genes, Genomes, Genetics, 2021, 11, .	0.8	3
1587	Chromatin accessibility associates with protein-RNA correlation in human cancer. Nature Communications, 2021, 12, 5732.	5.8	18
1588	MAX mutant small-cell lung cancers exhibit impaired activities of MGA-dependent noncanonical polycomb repressive complex. Proceedings of the National Academy of Sciences of the United States of America, 2021, 118, e2024824118.	3.3	9

#	ARTICLE	IF	CITATIONS
1589	Metagenomic Analysis of Biochemical Passive Reactors During Acid Mine Drainage Bioremediation Reveals Key Co-selected Metabolic Functions. Microbial Ecology, 2022, 84, 465-472.	1.4	2
1590	The concurrence of DNA methylation and demethylation is associated with transcription regulation. Nature Communications, 2021, 12, 5285.	5.8	29
1591	Chromatin and transcription factor profiling in rare stem cell populations using CUT&Tag. STAR Protocols, 2021, 2, 100751.	0.5	5
1594	<i>Smarca4</i> Inactivation Promotes Lineage-Specific Transformation and Early Metastatic Features in the Lung. Cancer Discovery, 2022, 12, 562-585.	7.7	48
1595	Fused in sarcoma regulates DNA replication timing and kinetics. Journal of Biological Chemistry, 2021, 297, 101049.	1.6	7
1597	SPT5 stabilizes RNA polymerase II, orchestrates transcription cycles, and maintains the enhancer landscape. Molecular Cell, 2021, 81, 4425-4439.e6.	4.5	51
1598	Chronic stress primes innate immune responses in mice and humans. Cell Reports, 2021, 36, 109595.	2.9	53
1599	Systematic evaluation of chromosome conformation capture assays. Nature Methods, 2021, 18, 1046-1055.	9.0	108
1600	Profiling of chromatin accessibility identifies transcription factor binding sites across the genome of Aspergillus species. BMC Biology, 2021, 19, 189.	1.7	10
1601	InÂvivo CRISPR screens identify the E3 ligase Cop1 as a modulator of macrophage infiltration and cancer immunotherapy target. Cell, 2021, 184, 5357-5374.e22.	13.5	79
1602	High-resolution breakpoint junction mapping of proximally extended D4Z4 deletions in FSHD1 reveals evidence for a founder effect. Human Molecular Genetics, 2022, 31, 748-760.	1.4	8
1603	Anterior patterning genes induced by Zic1 are sensitive to retinoic acid and its metabolite, <scp>4â€oxoâ€RA</scp>. Developmental Dynamics, 2022, 251, 498-512.	0.8	2
1604	<i>De novo</i> genome assembly and <i>in natura</i> epigenomics reveal salinityâ€induced DNA methylation in the mangrove tree <i>Bruguiera gymnorhiza</i>. New Phytologist, 2022, 233, 2094-2110.	3.5	25
1606	Î²-actin dependent chromatin remodeling mediates compartment level changes in 3D genome architecture. Nature Communications, 2021, 12, 5240.	5.8	31
1607	Gene expression profiling of epidermal cell types in <i>C. elegans</i> using Targeted DamID. Development (Cambridge), 2021, 148, .	1.2	11
1608	STL-seq reveals pause-release and termination kinetics for promoter-proximal paused RNA polymerase II transcripts. Molecular Cell, 2021, 81, 4398-4412.e7.	4.5	16
1609	Histone H3K27 demethylase KDM6A is an epigenetic gatekeeper of mTORC1 signalling in cancer. Gut, 2021, , gutjnl-2021-325405.	6.1	15
1610	Parallel characterization of cis-regulatory elements for multiple genes using CRISPRpath. Science Advances, 2021, 7, eabi4360.	4.7	16

#	Article	IF	Citations
1611	Characterizing the molecular composition and diagnostic potential of Mycobacterium tuberculosis urinary cell-free DNA using next-generation sequencing. International Journal of Infectious Diseases, 2021, 112, 330-337.	1.5	3
1613	The Th1 cell regulatory circuitry is largely conserved between human and mouse. Life Science Alliance, 2021, 4, e202101075.	1.3	1
1615	Transcription and chromatin-based surveillance mechanism controls suppression of cryptic antisense transcription. Cell Reports, 2021, 36, 109671.	2.9	3
1616	SPT5 stabilization of promoter-proximal RNA polymerase II. Molecular Cell, 2021, 81, 4413-4424.e5.	4.5	46
1619	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
1620	ATAD2 controls chromatin-bound HIRA turnover. Life Science Alliance, 2021, 4, e202101151.	1.3	9
1621	Hybrid Stomach-Intestinal Chromatin States Underlie Human Barrettâ€™s Metaplasia. Gastroenterology, 2021, 161, 924-939.e11.	0.6	18
1622	Sequential actions of EOMES and T-BET promote stepwise maturation of natural killer cells. Nature Communications, 2021, 12, 5446.	5.8	38
1623	Selection on Accessible Chromatin Regions in<i>Capsella grandiflora</i>. Molecular Biology and Evolution, 2021, 38, 5563-5575.	3.5	6
1624	Infections by Transovarially Transmitted DMelSV in Drosophila Have No Impact on Ovarian Transposable Element Transcripts but Increase Their Amounts in the Soma. Genome Biology and Evolution, 2021, 13, .	1.1	1
1626	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
1627	Interplay Between BALL and CREB Binding Protein Maintains H3K27 Acetylation on Active Genes in Drosophila. Frontiers in Cell and Developmental Biology, 2021, 9, 740866.	1.8	3
1628	A modified CUT&RUN protocol and analysis pipeline to identify transcription factor binding sites in human cell lines. STAR Protocols, 2021, 2, 100750.	0.5	7
1632	Mechanistic dissection of dominant AIRE mutations in mouse models reveals AIRE autoregulation. Journal of Experimental Medicine, 2021, 218, .	4.2	18
1634	Reproducible, scalable, and shareable analysis pipelines with bioinformatics workflow managers. Nature Methods, 2021, 18, 1161-1168.	9.0	83
1635	Whole genome sequencing of two human rhinovirus A types (A101 and A15) detected in Kenya, 2016-2018. Wellcome Open Research, 2021, 6, 178.	0.9	3
1637	The ETS transcription factor ERF controls the exit from the naÃ¯ve pluripotent state in a MAPK-dependent manner. Science Advances, 2021, 7, eabg8306.	4.7	6
1638	Multi-omic analysis of altered transcriptome and epigenetic signatures in the UV-induced DNA damage response. DNA Repair, 2021, 106, 103172.	1.3	8

#	ARTICLE	IF	CITATIONS
1639	Enhancer-associated H3K4 methylation safeguards in vitro germline competence. Nature Communications, 2021, 12, 5771.	5.8	20
1640	Productive visualization of high-throughput sequencing data using the SeqCode open portable platform. Scientific Reports, 2021, 11, 19545.	1.6	9
1642	The bromodomain inhibitor JQ1+ reduces calcium-sensing receptor activity in pituitary cell lines. Journal of Molecular Endocrinology, 2021, 67, 83-94.	1.1	1
1643	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
1644	Effects of glufosinate-ammonium on male reproductive health: Focus on epigenome and transcriptome in mouse sperm. Chemosphere, 2022, 287, 132395.	4.2	5
1645	GATA2 regulates mast cell identity and responsiveness to antigenic stimulation by promoting chromatin remodeling at super-enhancers. Nature Communications, 2021, 12, 494.	5.8	28
1646	Chromatin accessibility profiling methods. Nature Reviews Methods Primers, 2021, 1, .	11.8	95
1647	Architectural Mediator subunits are differentially essential for global transcription in <i>Saccharomyces cerevisiae</i>. Genetics, 2021, 217, .	1.2	7
1648	Genome-wide mapping of binding sites of the transposase-derived SETMAR protein in the human genome. Computational and Structural Biotechnology Journal, 2021, 19, 4032-4041.	1.9	3
1649	A protease-mediated mechanism regulates the cytochrome <i>c</i> ₆ /plastocyanin switch in <i>Synechocystis</i> sp. PCC 6803. Proceedings of the National Academy of Sciences of the United States of America, 2021, 118, .	3.3	18
1651	Different mutant RUNX1 oncoproteins program alternate haematopoietic differentiation trajectories. Life Science Alliance, 2021, 4, e202000864.	1.3	15
1652	Transcription shapes genome-wide histone acetylation patterns. Nature Communications, 2021, 12, 210.	5.8	84
1653	p53 expression confers sensitivity to 5â€'fluorouracil via distinct chromatin accessibility dynamics in human colorectal cancer. Oncology Letters, 2021, 21, 226.	0.8	4
1654	De novo DNA methyltransferase activity in colorectal cancer is directed towards H3K36me3 marked CpG islands. Nature Communications, 2021, 12, 694.	5.8	24
1656	NADPH levels affect cellular epigenetic state by inhibiting HDAC3â€"Ncor complex. Nature Metabolism, 2021, 3, 75-89.	5.1	35
1657	BET bromodomain inhibitor JQ1 regulates spermatid development by changing chromatin conformation in mouse spermatogenesis. Genes and Diseases, 2022, 9, 1062-1073.	1.5	1
1659	VELCRO-IP RNA-seq reveals ribosome expansion segment function in translation genome-wide. Cell Reports, 2021, 34, 108629.	2.9	10
1660	Transcriptome of nasopharyngeal samples from COVID-19 patients and a comparative analysis with other SARS-CoV-2 infection models reveal disparate host responses against SARS-CoV-2. Journal of Translational Medicine, 2021, 19, 32.	1.8	44

#	ARTICLE	IF	CITATIONS
1662	Linkage-specific deubiquitylation by OTUD5 defines an embryonic pathway intolerant to genomic variation. Science Advances, 2021, 7, .	4.7	25
1663	Accessible chromatin regions and their functional interrelations with gene transcription and epigenetic modifications in sorghum genome. Plant Communications, 2021, 2, 100140.	3.6	15
1664	Simultaneous Tagmentation-Based Detection of ChIP/ATAC Signal with Sequencing. Methods in Molecular Biology, 2021, 2351, 337-352.	0.4	1
1665	The Hox Transcription Factor Ubx Ensures Somatic Myogenesis by Suppressing the Mesodermal Master Regulator Twist. Cell Reports, 2021, 34, 108577.	2.9	8
1666	A Polycomb repressive complex is required for RNAi-mediated heterochromatin formation and dynamic distribution of nuclear bodies. Nucleic Acids Research, 2021, 49, 5407-5425.	6.5	27
1667	Promoter-proximal CTCF binding promotes distal enhancer-dependent gene activation. Nature Structural and Molecular Biology, 2021, 28, 152-161.	3.6	172
1668	Interrogating the Accessible Chromatin Landscape of Eukaryote Genomes Using ATAC-seq. Methods in Molecular Biology, 2021, 2243, 183-226.	0.4	13
1669	Bioinformatics Research Methodology of Non-coding RNAs in Cardiovascular Diseases. Advances in Experimental Medicine and Biology, 2020, 1229, 49-64.	0.8	9
1670	Genetic variants drive altered epigenetic regulation of endotoxin response in BTBR macrophages. Brain, Behavior, and Immunity, 2020, 89, 20-31.	2.0	4
1671	SETD5-Coordinated Chromatin Reprogramming Regulates Adaptive Resistance to Targeted Pancreatic Cancer Therapy. Cancer Cell, 2020, 37, 834-849.e13.	7.7	48
1672	Metabolic Regulation of the Epigenome Drives Lethal Infantile Ependymoma. Cell, 2020, 181, 1329-1345.e24.	13.5	79
1673	The Methyltransferase DOT1L Controls Activation and Lineage Integrity in CD4+ T Cells during Infection and Inflammation. Cell Reports, 2020, 33, 108505.	2.9	23
1674	CDK8 Fine-Tunes IL-6 Transcriptional Activities by Limiting STAT3 Resident Time at the Gene Loci. Cell Reports, 2020, 33, 108545.	2.9	26
1675	RTEL1 Regulates G4/R-Loops to Avert Replication-Transcription Collisions. Cell Reports, 2020, 33, 108546.	2.9	38
1676	The INO80 Complex Regulates Epigenetic Inheritance of Heterochromatin. Cell Reports, 2020, 33, 108561.	2.9	17
1677	KAP1 Is a Chromatin Reader that Couples Steps of RNA Polymerase II Transcription to Sustain Oncogenic Programs. Molecular Cell, 2020, 78, 1133-1151.e14.	4.5	26
1678	Synthetic Lethal and Resistance Interactions with BET Bromodomain Inhibitors in Triple-Negative Breast Cancer. Molecular Cell, 2020, 78, 1096-1113.e8.	4.5	114
1679	Opposing Functions of BRD4 Isoforms in Breast Cancer. Molecular Cell, 2020, 78, 1114-1132.e10.	4.5	95

#	ARTICLE	IF	CITATIONS
1680	Protein arginine methyltransferase 5 represses tumor suppressor miRNAs that down-regulate CYCLIN D1 and c-MYC expression in aggressive B-cell lymphoma. Journal of Biological Chemistry, 2020, 295, 1165-1180.	1.6	21
1681	Small-RNA-mediated transgenerational silencing of histone genes impairs fertility in piRNA mutants. Nature Cell Biology, 2020, 22, 235-245.	4.6	64
1682	Decoding myofibroblast origins in human kidney fibrosis. Nature, 2021, 589, 281-286.	13.7	380
1683	Differentiation of human pluripotent stem cells into neurons or cortical organoids requires transcriptional co-regulation by UTX and 53BP1. Nature Neuroscience, 2019, 22, 362-373.	7.1	33
1684	Three-dimensional genome restructuring across timescales of activity-induced neuronal gene expression. Nature Neuroscience, 2020, 23, 707-717.	7.1	99
1685	A quest for coordination among activities at the replisome. Biochemical Society Transactions, 2019, 47, 1067-1075.	1.6	5
1686	Chromatin structure restricts origin utilization when quiescent cells re-enter the cell cycle. Nucleic Acids Research, 2021, 49, 864-878.	6.5	10
1687	The human ZC3H3 and RBM26/27 proteins are critical for PAXT-mediated nuclear RNA decay. Nucleic Acids Research, 2020, 48, 2518-2530.	6.5	50
1688	Two interacting ethylene response factors regulate heat stress response. Plant Cell, 2021, 33, 338-357.	3.1	72
1902	A Chromodomain-Helicase-DNA-Binding Factor Functions in Chromatin Modification and Gene Regulation. Plant Physiology, 2020, 183, 1035-1046.	2.3	14
1903	A latent lineage potential in resident neural stem cells enables spinal cord repair. Science, 2020, 370, .	6.0	89
1904	CIC is a critical regulator of neuronal differentiation. JCI Insight, 2020, 5, .	2.3	21
1905	Chromatin remodeling ATPase BRG1 and PTEN are synthetic lethal in prostate cancer. Journal of Clinical Investigation, 2019, 129, 759-773.	3.9	56
1906	N-Mycâ€"mediated epigenetic reprogramming drives lineage plasticity in advanced prostate cancer. Journal of Clinical Investigation, 2019, 129, 3924-3940.	3.9	115
1907	IRF4 instructs effector Treg differentiation and immune suppression in human cancer. Journal of Clinical Investigation, 2020, 130, 3137-3150.	3.9	103
1908	A stress-responsive enhancer induces dynamic drug resistance in acute myeloid leukemia. Journal of Clinical Investigation, 2020, 130, 1217-1232.	3.9	26
1909	HiCHap: a package to correct and analyze the diploid Hi-C data. BMC Genomics, 2020, 21, 746.	1.2	6
1910	Biparental contributions of the H2A.B histone variant control embryonic development in mice. PLoS Biology, 2020, 18, e3001001.	2.6	13

#	Article	IF	Citations
1911	The INO80 chromatin remodeler sustains metabolic stability by promoting TOR signaling and regulating histone acetylation. PLoS Genetics, 2018, 14, e1007216.	1.5	23
1912	Opposing functions of Fng1 and the Rpd3 HDAC complex in H4 acetylation in Fusarium graminearum. PLoS Genetics, 2020, 16, e1009185.	1.5	24
1913	TDP-43 mutations link Amyotrophic Lateral Sclerosis with R-loop homeostasis and R loop-mediated DNA damage. PLoS Genetics, 2020, 16, e1009260.	1.5	54
1914	Analysis of chromatin accessibility in human epidermis identifies putative barrier dysfunction-sensing enhancers. PLoS ONE, 2017, 12, e0184500.	1.1	8
1915	Termination of nonâ€coding transcription in yeast relies on both an RNA Pol II CTD interaction domain and a CTDâ€mimicking region in Sen1. EMBO Journal, 2020, 39, e101548.	3.5	23
1916	A small targeting domain in Ty1 integrase is sufficient to direct retrotransposon integration upstream of tRNA genes. EMBO Journal, 2020, 39, e104337.	3.5	23
1917	A genetic memory initiates the epigenetic loop necessary to preserve centromere position. EMBO Journal, 2020, 39, e105505.	3.5	26
1918	Integrator is recruited to promoterâ€proximally paused RNA Pol II to generate <i>Caenorhabditis elegans</i> piRNA precursors. EMBO Journal, 2021, 40, e105564.	3.5	25
1919	<scp>LSD</scp>1 inhibition induces differentiation and cell death in Merkel cell carcinoma. EMBO Molecular Medicine, 2020, 12, e12525.	3.3	41
1920	Loss of p53-inducible long non-coding RNA LINC01021 increases chemosensitivity. Oncotarget, 2017, 8, 102783-102800.	0.8	13
1923	Prevention of Chromatin Destabilization by FACT Is Crucial for Malignant Transformation. SSRN Electronic Journal, 0, , .	0.4	1
1924	Activation of the SARS-CoV-2 Receptor <i>Ace2</i> by Cytokines Through Pan JAK-STAT Enhancers. SSRN Electronic Journal, 2020, , 3601827.	0.4	5
1925	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
1926	Optimized ChIP-seq method facilitates transcription factor profiling in human tumors. Life Science Alliance, 2019, 2, e201800115.	1.3	41
1927	TAF-ChIP: an ultra-low input approach for genome-wide chromatin immunoprecipitation assay. Life Science Alliance, 2019, 2, e201900318.	1.3	12
1928	Endogenous epitope-tagging of <i>Tet1</i>, <i>Tet2</i> and <i>Tet3</i> identifies TET2 as a naÃ¯ve pluripotency marker. Life Science Alliance, 2019, 2, e201900516.	1.3	13
1929	Essential role of the<i>Crk</i>family-dosage in DiGeorge-like anomaly and metabolic homeostasis. Life Science Alliance, 2020, 3, e201900635.	1.3	7
1930	Tet2 and Tet3 cooperate with B-lineage transcription factors to regulate DNA modification and chromatin accessibility. ELife, 2016, 5, .	2.8	121

#	ARTICLE	IF	CITATIONS
1931	Landscape of histone modifications in a sponge reveals the origin of animal cis-regulatory complexity. ELife, 2017, 6, .	2.8	51
1932	Cooperation between a hierarchical set of recruitment sites targets the X chromosome for dosage compensation. ELife, 2017, 6, .	2.8	28
1933	lncRNA requirements for mouse acute myeloid leukemia and normal differentiation. ELife, 2017, 6, .	2.8	54
1934	Cooperative interactions enable singular olfactory receptor expression in mouse olfactory neurons. ELife, 2017, 6, .	2.8	90
1935	cAMP signaling regulates DNA hydroxymethylation by augmenting the intracellular labile ferrous iron pool. ELife, 2017, 6, .	2.8	31
1936	BRG1 governs glucocorticoid receptor interactions with chromatin and pioneer factors across the genome. ELife, 2018, 7, .	2.8	59
1937	Systematic perturbation of retroviral LTRs reveals widespread long-range effects on human gene regulation. ELife, 2018, 7, .	2.8	146
1938	Species and cell-type properties of classically defined human and rodent neurons and glia. ELife, 2018, 7, .	2.8	66
1939	Parvovirus minute virus of mice interacts with sites of cellular DNA damage to establish and amplify its lytic infection. ELife, 2018, 7, .	2.8	31
1940	Rif1 inhibits replication fork progression and controls DNA copy number in Drosophila. ELife, 2018, 7, .	2.8	40
1941	Affinity capture of polyribosomes followed by RNAseq (ACAPseq), a discovery platform for protein-protein interactions. ELife, 2018, 7, .	2.8	12
1942	ASH1-catalyzed H3K36 methylation drives gene repression and marks H3K27me2/3-competent chromatin. ELife, 2018, 7, .	2.8	50
1943	Beta-catenin signaling regulates barrier-specific gene expression in circumventricular organ and ocular vasculatures. ELife, 2019, 8, .	2.8	74
1944	Amplification of a broad transcriptional program by a common factor triggers the meiotic cell cycle in mice. ELife, 2019, 8, .	2.8	78
1945	TERRA regulate the transcriptional landscape of pluripotent cells through TRF1-dependent recruitment of PRC2. ELife, 2019, 8, .	2.8	37
1946	Density-dependent resistance protects Legionella pneumophila from its own antimicrobial metabolite, HGA. ELife, 2019, 8, .	2.8	11
1947	Evidence for DNA-mediated nuclear compartmentalization distinct from phase separation. ELife, 2019, 8, .	2.8	222
1948	piRNA-guided co-transcriptional silencing coopts nuclear export factors. ELife, 2019, 8, .	2.8	60

#	ARTICLE	IF	CITATIONS
1949	Repressive H3K9me2 protects lifespan against the transgenerational burden of COMPASS activity in C. elegans. ELife, 2019, 8, .	2.8	47
1950	Dynamic regulation of chromatin accessibility by pluripotency transcription factors across the cell cycle. ELife, 2019, 8, .	2.8	61
1951	The MADS-box transcription factor PHERES1 controls imprinting in the endosperm by binding to domesticated transposons. ELife, 2019, 8, .	2.8	73
1952	Herpes simplex viral nucleoprotein creates a competitive transcriptional environment facilitating robust viral transcription and host shut off. ELife, 2019, 8, .	2.8	53
1953	A genome-wide view of the de-differentiation of central nervous system endothelial cells in culture. ELife, 2020, 9, .	2.8	41
1954	Analysis of zebrafish periderm enhancers facilitates identification of a regulatory variant near human KRT8/18. ELife, 2020, 9, .	2.8	23
1955	Loss of Kat2a enhances transcriptional noise and depletes acute myeloid leukemia stem-like cells. ELife, 2020, 9, .	2.8	26
1956	Sphingosine 1-phosphate-regulated transcriptomes in heterogenous arterial and lymphatic endothelium of the aorta. ELife, 2020, 9, .	2.8	34
1957	Keratin 14-dependent disulfides regulate epidermal homeostasis and barrier function via 14-3-3Ïƒ and YAP1. ELife, 2020, 9, .	2.8	41
1958	The histone modification reader ZCWPW1 links histone methylation to PRDM9-induced double-strand break repair. ELife, 2020, 9, .	2.8	34
1959	Condensin I subunit Cap-G is essential for proper gene expression during the maturation of post-mitotic neurons. ELife, 2020, 9, .	2.8	13
1960	Umbilical cord blood-derived ILC1-like cells constitute a novel precursor for mature KIR+NKG2A- NK cells. ELife, 2020, 9, .	2.8	25
1961	Cardiac endothelial cells maintain open chromatin and expression of cardiomyocyte myofibrillar genes. ELife, 2020, 9, .	2.8	26
1962	Trait-associated noncoding variant regions affect TBX3 regulation and cardiac conduction. ELife, 2020, 9, .	2.8	7
1963	Repurposing of KLF5 activates a cell cycle signature during the progression from a precursor state to oesophageal adenocarcinoma. ELife, 2020, 9, .	2.8	14
1964	The testis protein ZNF165 is a SMAD3 cofactor that coordinates oncogenic TGFÎ² signaling in triple-negative breast cancer. ELife, 2020, 9, .	2.8	21
1965	The nucleosome DNA entry-exit site is important for transcription termination and prevention of pervasive transcription. ELife, 2020, 9, .	2.8	11
1966	Genome duplication in Leishmania major relies on persistent subtelomeric DNA replication. ELife, 2020, 9, .	2.8	17

#	ARTICLE	IF	CITATIONS
1967	Damage-responsive, maturity-silenced enhancers regulate multiple genes that direct regeneration in Drosophila. ELife, 2020, 9, .	2.8	41
1968	Spatial inter-centromeric interactions facilitated the emergence of evolutionary new centromeres. ELife, 2020, 9, .	2.8	31
1969	Establishment and maintenance of motor neuron identity via temporal modularity in terminal selector function. ELife, 2020, 9, .	2.8	24
1970	Arrayed CRISPRi and quantitative imaging describe the morphotypic landscape of essential mycobacterial genes. ELife, 2020, 9, .	2.8	50
1971	Genome-wide alterations of uracil distribution patterns in human DNA upon chemotherapeutic treatments. ELife, 2020, 9, .	2.8	13
1972	Sustained TNF-Î± stimulation leads to transcriptional memory that greatly enhances signal sensitivity and robustness. ELife, 2020, 9, .	2.8	21
1973	Dimerisation of the PICTS complex via LC8/Cut-up drives co-transcriptional transposon silencing in Drosophila. ELife, 2021, 10, .	2.8	28
1974	Genome-wide analysis of 8-oxo-7,8-dihydro-2'-deoxyguanosine at single-nucleotide resolution unveils reduced occurrence of oxidative damage at G-quadruplex sites. Nucleic Acids Research, 2021, 49, 12252-12267.	6.5	23
1975	SigTools: exploratory visualization for genomic signals. Bioinformatics, 2022, 38, 1126-1128.	1.8	2
1976	proChIPdb: a chromatin immunoprecipitation database for prokaryotic organisms. Nucleic Acids Research, 2022, 50, D1077-D1084.	6.5	9
1977	Chromatin loading of MCM hexamers is associated with di-/tri-methylation of histone H4K20 toward SÂphase entry. Nucleic Acids Research, 2021, 49, 12152-12166.	6.5	12
1980	The adeno-associated virus 2 genome and Rep 68/78 proteins interact with cellular sites of DNA damage. Human Molecular Genetics, 2022, 31, 985-998.	1.4	8
1981	Satb2 acts as a gatekeeper for major developmental transitions during early vertebrate embryogenesis. Nature Communications, 2021, 12, 6094.	5.8	9
1983	Single-cell epigenomics reveals mechanisms of human cortical development. Nature, 2021, 598, 205-213.	13.7	154
1984	A global screening identifies chromatin-enriched RNA-binding proteins and the transcriptional regulatory activity of QKI5 during monocytic differentiation. Genome Biology, 2021, 22, 290.	3.8	13
1985	BACH1, the master regulator of oxidative stress, has a dual effect on CFTR expression. Biochemical Journal, 2021, 478, 3741-3756.	1.7	11
1986	Histone H4 lysine 16 acetylation controls central carbon metabolism and diet-induced obesity in mice. Nature Communications, 2021, 12, 6212.	5.8	16
1989	Longitudinal clonal tracking in humanized mice reveals sustained polyclonal repopulation of gene-modified human-HSPC despite vector integration bias. Stem Cell Research and Therapy, 2021, 12, 528.	2.4	0

#	ARTICLE	IF	CITATIONS
1990	Pig genome functional annotation enhances the biological interpretation of complex traits and human disease. Nature Communications, 2021, 12, 5848.	5.8	70
1991	PRC1 drives Polycomb-mediated gene repression by controlling transcription initiation and burst frequency. Nature Structural and Molecular Biology, 2021, 28, 811-824.	3.6	62
1992	Epithelial NELF guards intestinal barrier function to ameliorate colitis by maintaining junctional integrity. Mucosal Immunology, 2022, 15, 279-288.	2.7	6
1994	Oestrogen engages brain MC4R signalling to drive physical activity in female mice. Nature, 2021, 599, 131-135.	13.7	59
1995	Comparative cellular analysis of motor cortex in human, marmoset and mouse. Nature, 2021, 598, 111-119.	13.7	361
1996	KDM5B promotes immune evasion by recruiting SETDB1 to silence retroelements. Nature, 2021, 598, 682-687.	13.7	117
1997	Pervasive 3â€²-UTR Isoform Switches During Mouse Oocyte Maturation. Frontiers in Molecular Biosciences, 2021, 8, 727614.	1.6	5
1998	Dual detection of chromatin accessibility and DNA methylation using ATAC-Me. Nature Protocols, 2021, 16, 5377-5397.	5.5	10
1999	RNF2 ablation reprograms the tumor-immune microenvironment and stimulates durable NK and CD4+ T-cell-dependent antitumor immunity. Nature Cancer, 2021, 2, 1018-1038.	5.7	11
2001	Proximal-end bias from in-vitro reconstituted nucleosomes and the result on downstream data analysis. PLoS ONE, 2021, 16, e0258737.	1.1	1
2003	Characterization of chromatin accessibility in psoriasis. Frontiers of Medicine, 2021, , 1.	1.5	1
2004	Hybrid Sequencing in Different Types of Goat Skeletal Muscles Reveals Genes Regulating Muscle Development and Meat Quality. Animals, 2021, 11, 2906.	1.0	4
2005	NRF1 association with AUTS2-Polycomb mediates specific gene activation in the brain. Molecular Cell, 2021, 81, 4663-4676.e8.	4.5	23
2006	A Polycomb domain found in committed cells impairs differentiation when introduced into PRC1 in pluripotent cells. Molecular Cell, 2021, 81, 4677-4691.e8.	4.5	20
2007	Epigenetic dynamics shaping melanophore and iridophore cell fate in zebrafish. Genome Biology, 2021, 22, 282.	3.8	8
2008	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
2010	DNA methylation signatures reveal that distinct combinations of transcription factors specify human immune cell epigenetic identity. Immunity, 2021, 54, 2465-2480.e5.	6.6	31
2012	The chromatin-remodeling enzyme Smarca5 regulates erythrocyte aggregation via Keap1-Nrf2 signaling. ELife, 2021, 10, .	2.8	9

#	Article	IF	Citations
2013	Genome-Wide Identification of Ralstonia solanacearum Genes Required for Survival in Tomato Plants. MSystems, 2021, 6, e0083821.	1.7	13
2014	eccDNAs are apoptotic products with high innate immunostimulatory activity. Nature, 2021, 599, 308-314.	13.7	121
2015	DREAM represses distinct targets by cooperating with different THAP domain proteins. Cell Reports, 2021, 37, 109835.	2.9	6
2016	Atypical molecular features of RNA silencing against the phloem-restricted polerovirus TuYV. Nucleic Acids Research, 2021, 49, 11274-11293.	6.5	10
2018	Identification of chromatin states during zebrafish gastrulation using <scp>CUT</scp>&<scp>RUN</scp> and <scp>CUT</scp>&Tag. Developmental Dynamics, 2022, 251, 729-742.	0.8	10
2020	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
2022	Single-cell analysis reveals androgen receptor regulates the ER-to-Golgi trafficking pathway with CREB3L2 to drive prostate cancer progression. Oncogene, 2021, 40, 6479-6493.	2.6	10
2023	Metabolic remodelling during early mouse embryo development. Nature Metabolism, 2021, 3, 1372-1384.	5.1	45
2025	Embryonic LTR retrotransposons supply promoter modules to somatic tissues. Genome Research, 2021, 31, 1983-1993.	2.4	7
2026	Increased ACTL6A occupancy within mSWI/SNF chromatin remodelers drives human squamous cell carcinoma. Molecular Cell, 2021, 81, 4964-4978.e8.	4.5	19
2028	Sequence features of retrotransposons allow for epigenetic variability. ELife, 2021, 10, .	2.8	9
2029	Transcription and splicing dynamics during early <i>Drosophila</i> development. Rna, 2022, 28, 139-161.	1.6	11
2030	Automated CUT&Tag profiling of chromatin heterogeneity in mixed-lineage leukemia. Nature Genetics, 2021, 53, 1586-1596.	9.4	42
2031	Neurotransmitter signaling regulates distinct phases of multimodal human interneuron migration. EMBO Journal, 2021, 40, e108714.	3.5	16
2033	BRCA1-BARD1 regulates transcription through modulating topoisomerase IIÎ². Open Biology, 2021, 11, 210221.	1.5	9
2036	Multilayer omics analysis reveals a non-classical retinoic acid signaling axis that regulates hematopoietic stem cell identity. Cell Stem Cell, 2022, 29, 131-148.e10.	5.2	40
2038	SARS-CoV-2 whole-genome sequencing using reverse complement PCR: For easy, fast and accurate outbreak and variant analysis.. Journal of Clinical Virology, 2021, 144, 104993.	1.6	18
2059	PBRM1 Regulates the Stress Response in Epithelial Cells. SSRN Electronic Journal, 0, , .	0.4	0

#	ARTICLE	IF	CITATIONS
2061	ChIP-seq Experiment and Data Analysis in the Cyanobacterium Synechocystis sp. PCC 6803. Bio-protocol, 2018, 8, e2895.	0.2	0
2062	Activation of Oncogenic Super-Enhancers Is Coupled with DNA Repair by RAD51. SSRN Electronic Journal, 0, , .	0.4	0
2103	Specific Contributions of Cohesin-SA1 and Cohesin-SA2 to TADs and Polycomb Domains in Embryonic Stem Cells. SSRN Electronic Journal, 0, , .	0.4	0
2105	ModHMM: A Modular Supra-Bayesian Genome Segmentation Method. Lecture Notes in Computer Science, 2019, , 35-50.	1.0	2
2106	Genomic Resolution of DLX-Orchestrated Transcriptional Circuits Driving Development of Forebrain GABAergic Neurons. SSRN Electronic Journal, 0, , .	0.4	0
2107	Deconstructing Stepwise Fate Conversion of Human Fibroblasts to Neurons by MicroRNAs. SSRN Electronic Journal, 0, , .	0.4	0
2179	Genome-wide identification of imprinted genes in pigs and their different imprinting status compared with other mammals. Zoological Research, 2020, 41, 721-725.	0.9	9
2251	Accurate Quantification of Overlapping Herpesvirus Transcripts from RNA Sequencing Data. Journal of Virology, 2022, 96, JVI0163521.	1.5	6
2252	Mitochondrial metabolism coordinates stage-specific repair processes in macrophages during wound healing. Cell Metabolism, 2021, 33, 2398-2414.e9.	7.2	89
2253	The role of MORC3 in silencing transposable elements in mouse embryonic stem cells. Epigenetics and Chromatin, 2021, 14, 49.	1.8	9
2254	Sequential in <i>cis</i> mutagenesis in vivo reveals various functions for CTCF sites at the mouse <i>HoxD</i> cluster. Genes and Development, 2021, 35, 1490-1509.	2.7	29
2255	Comprehensive understanding of Tn5 insertion preference improves transcription regulatory element identification. NAR Genomics and Bioinformatics, 2021, 3, lqab094.	1.5	8
2258	Paraspeckle Protein NONO Promotes TAZ Phase Separation in the Nucleus to Drive the Oncogenic Transcriptional Program. Advanced Science, 2021, 8, e2102653.	5.6	24
2260	Inner nuclear protein Matrin-3 coordinates cell differentiation by stabilizing chromatin architecture. Nature Communications, 2021, 12, 6241.	5.8	25
2262	p21 produces a bioactive secretome that places stressed cells under immunosurveillance. Science, 2021, 374, eabb3420.	6.0	112
2263	Reprogramming CBX8-PRC1 function with a positive allosteric modulator. Cell Chemical Biology, 2022, 29, 555-571.e11.	2.5	12
2264	Small RNA F6 Provides Mycobacterium smegmatis Entry into Dormancy. International Journal of Molecular Sciences, 2021, 22, 11536.	1.8	4
2266	Depletion of m⁶A reader protein YTHDC1 induces dilated cardiomyopathy by abnormal splicing of <i>Titin</i>. Journal of Cellular and Molecular Medicine, 2021, 25, 10879-10891.	1.6	21

#	ARTICLE	IF	CITATIONS
2268	Hepatocyte nuclear factor HNF1A is a potential regulator in shaping the superâ€enhancer landscape in colorectal cancer liver metastasis. FEBS Letters, 2021, 595, 3056-3071.	1.3	4
2270	A nuclear pore sub-complex restricts the propagation of Ty retrotransposons by limiting their transcription. PLoS Genetics, 2021, 17, e1009889.	1.5	4
2277	Requirement of DNMT1 to orchestrate epigenomic reprogramming for NPM-ALKâ€“driven lymphomagenesis. Life Science Alliance, 2021, 4, e202000794.	1.3	6
2284	Epigenetic Analysis in Ewing Sarcoma. Methods in Molecular Biology, 2021, 2226, 285-302.	0.4	1
2287	Loss of Epigenetic Information as a Cause of Mammalian Aging. SSRN Electronic Journal, 0, , .	0.4	0
2288	Unusual nucleosome formation and transcriptome influence by the histone H3mm18 variant. Nucleic Acids Research, 2022, 50, 72-91.	6.5	7
2289	Bioinformatic tools for research in CRC. , 2022, , 231-247.		0
2295	Promoter Repression and 3D-Restructuring Resolves Divergent Developmental Gene Expression in TADs. SSRN Electronic Journal, 0, , .	0.4	3
2296	ChIP-Seq from Limited Starting Material of K562 Cells and Drosophila Neuroblasts Using Tagmentation Assisted Fragmentation Approach. Bio-protocol, 2020, 10, e3520.	0.2	0
2302	<i>In vivo</i> CRISPR Screens Identify E3 Ligase <i>Cop1</i> as a Modulator of Macrophage Infiltration and Cancer Immunotherapy Target. SSRN Electronic Journal, 0, , .	0.4	0
2316	Histone H3K27 Methylation Perturbs Transcriptional Robustness and Underpins Dispensability of Highly Conserved Genes in Fungi. Molecular Biology and Evolution, 2022, 39, .	3.5	4
2325	Modeling population size independent tissue epigenomes by ChILâ€seq with single thin sections. Molecular Systems Biology, 2021, 17, e10323.	3.2	1
2329	Local chromatin fiber folding represses transcription and loop extrusion in quiescent cells. ELife, 2021, 10, .	2.8	18
2330	Integrator enforces the fidelity of transcriptional termination at protein-coding genes. Science Advances, 2021, 7, eabe3393.	4.7	23
2333	Sumoylation of the human histone H4 tail inhibits p300-mediated transcription by RNA polymerase II in cellular extracts. ELife, 2021, 10, .	2.8	12
2335	Mouse strain-specific polymorphic provirus functions as cis-regulatory element leading to epigenomic and transcriptomic variations. Nature Communications, 2021, 12, 6462.	5.8	4
2336	Identification of the sex-determining factor in the liverwort Marchantia polymorpha reveals unique evolution of sex chromosomes in a haploid system. Current Biology, 2021, 31, 5522-5532.e7.	1.8	36
2337	Opponent vesicular transporters regulate the strength of glutamatergic neurotransmission in a C. elegans sensory circuit. Nature Communications, 2021, 12, 6334.	5.8	6

#	Article	IF	Citations
2339	Acute depletion of the ARID1A subunit of SWI/SNF complexes reveals distinct pathways for activation and repression of transcription. Cell Reports, 2021, 37, 109943.	2.9	23
2340	Demethylating therapy increases anti-CD123 CAR T cell cytotoxicity against acute myeloid leukemia. Nature Communications, 2021, 12, 6436.	5.8	45
2341	preciseTAD: a transfer learning framework for 3D domain boundary prediction at base-pair resolution. Bioinformatics, 2022, 38, 621-630.	1.8	4
2343	Spatial and Functional Organization of Human Papillomavirus Replication Foci in the Productive Stage of Infection. MBio, 2021, 12, e0268421.	1.8	10
2345	Xist nucleates local protein gradients to propagate silencing across the X chromosome. Cell, 2021, 184, 6174-6192.e32.	13.5	62
2346	Inherent genomic properties underlie the epigenomic heterogeneity of human induced pluripotent stem cells. Cell Reports, 2021, 37, 109909.	2.9	14
2347	Identification of LZTFL1 as a candidate effector gene at a COVID-19 risk locus. Nature Genetics, 2021, 53, 1606-1615.	9.4	93
2348	Control of osteocyte dendrite formation by Sp7 and its target gene osteocrin. Nature Communications, 2021, 12, 6271.	5.8	41
2349	The RNA recognition motifâ€containing protein UBA2c prevents early flowering by promoting transcription of the flowering repressor <i>FLM</i> in Arabidopsis. New Phytologist, 2022, 233, 751-765.	3.5	5
2350	Identification of high-confidence human poly(A) RNA isoform scaffolds using nanopore sequencing. Rna, 2022, 28, 162-176.	1.6	12
2351	FGFR-inhibitor-mediated dismissal of SWI/SNF complexes from YAP-dependent enhancers induces adaptive therapeutic resistance. Nature Cell Biology, 2021, 23, 1187-1198.	4.6	21
2352	NSD2 dimethylation at H3K36 promotes lung adenocarcinoma pathogenesis. Molecular Cell, 2021, 81, 4481-4492.e9.	4.5	42
2353	rRNA biogenesis regulates mouse 2C-like state by 3D structure reorganization of peri-nucleolar heterochromatin. Nature Communications, 2021, 12, 6365.	5.8	24
2354	The transposable element-rich genome of the cereal pest Sitophilus oryzae. BMC Biology, 2021, 19, 241.	1.7	40
2361	Egr2 and 3 control inflammation, but maintain homeostasis, of PD-1^{high} memory phenotype CD4 T cells. Life Science Alliance, 2020, 3, e202000766.	1.3	7
2395	Landscape of active enhancers developed de novo in cirrhosis and conserved in hepatocellular carcinoma. American Journal of Cancer Research, 2020, 10, 3157-3178.	1.4	8
2396	Regulatory Elements Inserted into AAVs Confer Preferential Activity in Cortical Interneurons. ENeuro, 2020, 7, .	0.9	4
2398	Coordinated glucocorticoid receptor and MAFB action induces tolerogenesis and epigenome remodeling in dendritic cells. Nucleic Acids Research, 2022, 50, 108-126.	6.5	17

#	ARTICLE	IF	CITATIONS
2399	DNA methylation-calling tools for Oxford Nanopore sequencing: a survey and human epigenome-wide evaluation. Genome Biology, 2021, 22, 295.	3.8	87
2400	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
2401	The Histone H3 K4me3, K27me3, and K27ac Genome-Wide Distributions Are Differently Influenced by Sex in Brain Cortexes and Gastrocnemius of the Alzheimerâ€™s Disease PSAPP Mouse Model. Epigenomes, 2021, 5, 26.	0.8	3
2404	25-Hydroxycholesterol Inhibits Kaposiâ€™s Sarcoma Herpesvirus and Epstein-Barr Virus Infections and Activates Inflammatory Cytokine Responses. MBio, 2021, 12, e0290721.	1.8	11
2405	Chromatin and regulatory differentiation between bundle sheath and mesophyll cells in maize. Plant Journal, 2022, 109, 675-692.	2.8	16
2409	Reprogramming of H3K9bhb at regulatory elements is a key feature of fasting in the small intestine. Cell Reports, 2021, 37, 110044.	2.9	22
2410	Comparing the epigenetic landscape in myonuclei purified with a PCM1 antibody from a fast/glycolytic and a slow/oxidative muscle. PLoS Genetics, 2021, 17, e1009907.	1.5	12
2413	Heat shock factor 1 (HSF1) cooperates with estrogen receptor Î± (ERÎ±) in the regulation of estrogen action in breast cancer cells. ELife, 2021, 10, .	2.8	12
2414	ZHX2 promotes HIF1Î± oncogenic signaling in triple-negative breast cancer. ELife, 2021, 10, .	2.8	21
2415	Comprehensive determination of transcription start sites derived from all RNA polymerases using ReCappable-seq. Genome Research, 2022, 32, 162-174.	2.4	14
2417	A growth factorâ€"expressing macrophage subpopulation orchestrates regenerative inflammation via GDF-15. Journal of Experimental Medicine, 2022, 219, .	4.2	31
2418	Regulation of translation by site-specific ribosomal RNA methylation. Nature Structural and Molecular Biology, 2021, 28, 889-899.	3.6	51
2420	The miRNome function transitions from regulating developmental genes to transposable elements during pollen maturation. Plant Cell, 2022, 34, 784-801.	3.1	17
2421	Master lineage transcription factors anchor trans mega transcriptional complexes at highly accessible enhancer sites to promote long-range chromatin clustering and transcription of distal target genes. Nucleic Acids Research, 2021, 49, 12196-12210.	6.5	7
2422	Mitochondrial DNA Content May Not Be a Reliable Screening Biomarker for Live Birth After Single Euploid Blastocyst Transfer. Frontiers in Endocrinology, 2021, 12, 762976.	1.5	4
2424	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
2425	Runx3 is required for oncogenic Myc upregulation in p53-deficient osteosarcoma. Oncogene, 2022, 41, 683-691.	2.6	14
2426	MicroRNA-29 specifies age-related differences in the CD8+ TÂcell immune response. Cell Reports, 2021, 37, 109969.	2.9	3

#	ARTICLE	IF	CITATIONS
2427	Interrogation of the microenvironmental landscape in spinal ependymomas reveals dual functions of tumor-associated macrophages. Nature Communications, 2021, 12, 6867.	5.8	19
2429	Six1 promotes skeletal muscle thyroid hormone response through regulation of the MCT10 transporter. Skeletal Muscle, 2021, 11, 26.	1.9	5
2430	Genome surveillance by HUSH-mediated silencing of intronless mobile elements. Nature, 2022, 601, 440-445.	13.7	64
2431	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
2432	Persistence and plasticity in bacterial gene regulation. Nature Methods, 2021, 18, 1499-1505.	9.0	23
2433	Chromatin Accessibility Predetermines Odontoblast Terminal Differentiation. Frontiers in Cell and Developmental Biology, 2021, 9, 769193.	1.8	3
2434	recount3: summaries and queries for large-scale RNA-seq expression and splicing. Genome Biology, 2021, 22, 323.	3.8	103
2435	Recurrent integration of human papillomavirus genomes at transcriptional regulatory hubs. Npj Genomic Medicine, 2021, 6, 101.	1.7	28
2437	Genome-wide cancer-specific chromatin accessibility patterns derived from archival processed xenograft tumors. Genome Research, 2021, 31, 2327-2339.	2.4	3
2439	UBR7 acts as a histone chaperone for postâ€nucleosomal histone H3. EMBO Journal, 2021, 40, e108307.	3.5	12
2440	Mutant p53 elicits context-dependent pro-tumorigenic phenotypes. Oncogene, 2022, 41, 444-458.	2.6	13
2441	Coordinated maintenance of H3K36/K27 methylation by histone demethylases preserves germ cell identity and immortality. Cell Reports, 2021, 37, 110050.	2.9	4
2442	Temporal transitions in the post-mitotic nervous system of Caenorhabditis elegans. Nature, 2021, 600, 93-99.	13.7	27
2444	Single cell multi-omic analysis identifies a Tbx1-dependent multilineage primed population in murine cardiopharyngeal mesoderm. Nature Communications, 2021, 12, 6645.	5.8	31
2445	ecDNA hubs drive cooperative intermolecular oncogene expression. Nature, 2021, 600, 731-736.	13.7	123
2446	JAK2-STAT Epigenetically Regulates Tolerized Genes in Monocytes in the First Encounter With Gram-Negative Bacterial Endotoxins in Sepsis. Frontiers in Immunology, 2021, 12, 734652.	2.2	13
2447	Mammalian SWI/SNF chromatin remodeler is essential for reductional meiosis in males. Nature Communications, 2021, 12, 6581.	5.8	9
2448	Harnessing natural variation to identify cis regulators of sex-biased gene expression in a multi-strain mouse liver model. PLoS Genetics, 2021, 17, e1009588.	1.5	5

#	Article	IF	Citations
2449	Long Non-Coding RNAs Associated with Ribosomes in Human Adipose-Derived Stem Cells: From RNAs to Microproteins. Biomolecules, 2021, 11, 1673.	1.8	5
2450	Landscape of transcription termination in Arabidopsis revealed by single-molecule nascent RNA sequencing. Genome Biology, 2021, 22, 322.	3.8	13
2451	Stem cells expand potency and alter tissue fitness by accumulating diverse epigenetic memories. Science, 2021, 374, eabh2444.	6.0	56
2452	Autocrine vitamin D signaling switches off pro-inflammatory programs of TH1 cells. Nature Immunology, 2022, 23, 62-74.	7.0	105
2453	Cell-type specialization is encoded by specific chromatin topologies. Nature, 2021, 599, 684-691.	13.7	112
2455	High-throughput single-cell epigenomic profiling by targeted insertion of promoters (TIP-seq). Journal of Cell Biology, 2021, 220, .	2.3	19
2456	Genome annotation with long RNA reads reveals new patterns of gene expression and improves single-cell analyses in an ant brain. BMC Biology, 2021, 19, 254.	1.7	11
2457	Epsteinâ€“Barr virus nuclear antigen 2 extensively rewires the human chromatin landscape at autoimmune risk loci. Genome Research, 2021, 31, 2185-2198.	2.4	24
2458	Histone variant H2A.Z regulates zygotic genome activation. Nature Communications, 2021, 12, 7002.	5.8	24
2459	Effects of the noncoding subgenomic RNA of red clover necrotic mosaic virus in virus infection. Journal of Virology, 2021, , JVI0181521.	1.5	5
2461	Jpx RNA regulates CTCF anchor site selection and formation of chromosome loops. Cell, 2021, 184, 6157-6173.e24.	13.5	35
2462	Ezh2 is essential for the generation of functional yolk sac derived erythro-myeloid progenitors. Nature Communications, 2021, 12, 7019.	5.8	8
2464	Histone H1 prevents non-CG methylation-mediated small RNA biogenesis in Arabidopsis heterochromatin. ELife, 2021, 10, .	2.8	23
2465	SPEN is required for Xist upregulation during initiation of X chromosome inactivation. Nature Communications, 2021, 12, 7000.	5.8	16
2466	Twist2-Driven Chromatin Remodeling Governs the Postnatal Maturation of Dermal Fibroblasts. SSRN Electronic Journal, 0, , .	0.4	0
2467	A Multi-Omics Atlas of the Human Retina at Single-Cell Resolution. SSRN Electronic Journal, 0, , .	0.4	1
2468	Modulated termination of non-coding transcription partakes in the regulation of gene expression. Nucleic Acids Research, 2022, 50, 1430-1448.	6.5	4
2469	The Polycomb Protein Bmi1 is a Key Effector of the H3.3 K27m Oncohistone. SSRN Electronic Journal, 0, , .	0.4	0

#	Article	IF	Citations
2470	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
2471	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
2472	Waves of sumoylation support transcription dynamics during adipocyte differentiation. Nucleic Acids Research, 2022, 50, 1351-1369.	6.5	8
2473	YAP1 and PRDM14 converge to promote cell survival and tumorigenesis. Developmental Cell, 2022, 57, 212-227.e8.	3.1	9
2474	H3K9me2 genome-wide distribution in the holocentric insect Spodoptera frugiperda (Lepidoptera:) Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50	1.3	1
2475	A test of the pioneer factor hypothesis using ectopic liver gene activation. ELife, 2022, 11, .	2.8	35
2476	Alleleâ€aware chromosomeâ€scale assembly of the allopolyploid genome of hexaploid Ma bamboo (<i>Dendrocalamus latiflorus</i> Munro). Journal of Integrative Plant Biology, 2022, 64, 649-670.	4.1	24
2478	Computational modeling of chromatin accessibility identified important epigenomic regulators. BMC Genomics, 2022, 23, 19.	1.2	1
2479	HDAC8 suppresses the epithelial phenotype and promotes EMT in chemotherapy-treated basal-like breast cancer. Clinical Epigenetics, 2022, 14, 7.	1.8	16
2480	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
2481	Advanced genomics identifies growth effectors for proteotoxic ER stress recovery in Arabidopsis thaliana. Communications Biology, 2022, 5, 16.	2.0	11
2482	The CLASSY family controls tissue-specific DNA methylation patterns in Arabidopsis. Nature Communications, 2022, 13, 244.	5.8	35
2484	ATRX loss in glioma results in dysregulation of cell-cycle phase transition and ATM inhibitor radio-sensitization. Cell Reports, 2022, 38, 110216.	2.9	32
2485	Regulatory Elements Inserted into AAVs Confer Preferential Activity in Cortical Interneurons. ENeuro, 2020, 7, ENEURO.0211-20.2020.	0.9	12
2486	SALL1 regulates commitment of odontoblast lineages by interacting with RUNX2 to remodel open chromatin regions. Stem Cells, 2021, 39, 196-209.	1.4	13
2488	Single-cell-resolved dynamics of chromatin architecture delineate cell and regulatory states in zebrafish embryos. Cell Genomics, 2022, 2, 100083.	3.0	8
2489	The histone H4 lysine 20 demethylase DPY-21 regulates the dynamics of condensin DC binding. Journal of Cell Science, 2022, 135, .	1.2	6
2491	Bacon: a comprehensive computational benchmarking framework for evaluating targeted chromatin conformation capture-specific methodologies. Genome Biology, 2022, 23, 30.	3.8	7

#	ARTICLE	IF	CITATIONS
2492	Identification of Drug Transporter Genomic Variants and Inhibitors That Protect Against Doxorubicin-Induced Cardiotoxicity. Circulation, 2022, 145, 279-294.	1.6	46
2493	SPARCLE, a p53-induced lncRNA, controls apoptosis after genotoxic stress by promoting PARP-1 cleavage. Molecular Cell, 2022, 82, 785-802.e10.	4.5	24
2495	Glufosinate-Ammonium Induced Aberrant Histone Modifications in Mouse Sperm Are Concordant With Transcriptome in Preimplantation Embryos. Frontiers in Physiology, 2021, 12, 819856.	1.3	4
2496	piRNAs initiate transcriptional silencing of spermatogenic genes during C.Âelegans germline development. Developmental Cell, 2022, 57, 180-196.e7.	3.1	25
2497	Proximity labeling identifies a repertoire of site-specific R-loop modulators. Nature Communications, 2022, 13, 53.	5.8	49
2498	Decoding gene regulation in the fly brain. Nature, 2022, 601, 630-636.	13.7	102
2501	Establishment of developmental gene silencing by ordered polycomb complex recruitment in early zebrafish embryos. ELife, 2022, 11, .	2.8	13
2502	Rapid factor depletion highlights intricacies of nucleoplasmic RNA degradation. Nucleic Acids Research, 2022, 50, 1583-1600.	6.5	15
2503	Patient-specific MDS-RS iPSCs define the mis-spliced transcript repertoire and chromatin landscape of <i>SF3B1</i>-mutant HSPCs. Blood Advances, 2022, 6, 2992-3005.	2.5	7
2504	Epigenomics analysis of miRNA cis-regulatory elements in pig muscle and fat tissues. Genomics, 2022, 114, 110276.	1.3	7
2507	Coordinated post-transcriptional control of oncogene-induced senescence by UNR/CSDE1. Cell Reports, 2022, 38, 110211.	2.9	7
2509	Loss of the transcription repressor ZHX3 induces senescence-associated gene expression and mitochondrial-nucleolar activation. PLoS ONE, 2022, 17, e0262488.	1.1	3
2510	A comprehensive long-read isoform analysis platform and sequencing resource for breast cancer. Science Advances, 2022, 8, eabg6711.	4.7	30
2512	DNMT1 regulates the timing of DNA methylation by DNMT3 in an enzymatic activity-dependent manner in mouse embryonic stem cells. PLoS ONE, 2022, 17, e0262277.	1.1	5
2514	Metabolic remodeling maintains a reducing environment for rapid activation of the yeast DNA replication checkpoint. EMBO Journal, 2022, 41, e108290.	3.5	8
2516	Glucose starvation induces a switch in the histone acetylome for activation of gluconeogenic and fat metabolism genes. Molecular Cell, 2022, 82, 60-74.e5.	4.5	43
2520	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
2521	The transcriptional elongation factor CTR9 demarcates PRC2-mediated H3K27me3 domains by altering PRC2 subtype equilibrium. Nucleic Acids Research, 2022, 50, 1969-1992.	6.5	6

#	Article	IF	Citations
2523	Gene-selective transcription promotes the inhibition of tissue reparative macrophages by TNF. Life Science Alliance, 2022, 5, e202101315.	1.3	10
2524	Selective translation of epigenetic modifiers affects the temporal pattern and differentiation of neural stem cells. Nature Communications, 2022, 13, 470.	5.8	20
2525	Identification and functional characterization of transcriptional activators in human cells. Molecular Cell, 2022, 82, 677-695.e7.	4.5	64
2526	Chromatin alterations during the epididymal maturation of mouse sperm refine the paternally inherited epigenome. Epigenetics and Chromatin, 2022, 15, 2.	1.8	11
2527	The three-dimensional structure of Epstein-Barr virus genome varies by latency type and is regulated by PARP1 enzymatic activity. Nature Communications, 2022, 13, 187.	5.8	30
2528	Coordinated repression of pro-differentiation genes via P-bodies and transcription maintains Drosophila intestinal stem cell identity. Current Biology, 2022, 32, 386-397.e6.	1.8	14
2529	N4-acetyldeoxycytosine DNA modification marks euchromatin regions in Arabidopsis thaliana. Genome Biology, 2022, 23, 5.	3.8	14
2530	Developmental and Injury-induced Changes in DNA Methylation in Regenerative versus Non-regenerative Regions of the Vertebrate Central Nervous System. BMC Genomics, 2022, 23, 2.	1.2	8
2531	Disruption of piRNA machinery by deletion of ASZ1/GASZ results in the expression of aberrant chimeric transcripts in gonocytes. Journal of Reproduction and Development, 2022, 68, 125-136.	0.5	2
2532	Comprehensive characterization of the epigenetic landscape in Multiple Myeloma. Theranostics, 2022, 12, 1715-1729.	4.6	10
2534	Down-syndrome-induced senescence disrupts the nuclear architecture of neural progenitors. Cell Stem Cell, 2022, 29, 116-130.e7.	5.2	41
2536	A chromosomal loop anchor mediates bacterial genome organization. Nature Genetics, 2022, 54, 194-201.	9.4	17
2537	Genome-wide analysis and functional annotation of chromatin-enriched noncoding RNAs in rice during somatic cell regeneration. Genome Biology, 2022, 23, 28.	3.8	13
2538	Multimodal regulatory elements within a hormone-specific super enhancer control a heterogeneous transcriptional response. Molecular Cell, 2022, 82, 803-815.e5.	4.5	14
2539	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
2541	Nanopore Sequencing and Data Analysis for Base-Resolution Genome-Wide 5-Methylcytosine Profiling. Methods in Molecular Biology, 2022, 2458, 75-94.	0.4	2
2542	InÂvivo CRISPR screening identifies BAZ2 chromatin remodelers as druggable regulators of mammalian liver regeneration. Cell Stem Cell, 2022, 29, 372-385.e8.	5.2	18
2544	<i>Caenorhabditis elegans</i> transposable elements harbor diverse transcription factor DNA-binding sites. G3: Genes, Genomes, Genetics, 2022, 12, .	0.8	0

#	ARTICLE	IF	CITATIONS
2546	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
2547	A reproducible and sensitive method for generating highâ€quality transcriptomes from single whitefly salivary glands and other lowâ€input tissues. Insect Science, 2022, , .	1.5	0
2551	Genome-wide sequencing analysis of Sgs1, Exo1, Rad51, and Srs2 in DNA repair by homologous recombination. Cell Reports, 2022, 38, 110201.	2.9	3
2552	Pre-configuring chromatin architecture with histone modifications guides hematopoietic stem cell formation in mouse embryos. Nature Communications, 2022, 13, 346.	5.8	11
2553	Zebrafish transposable elements show extensive diversification in age, genomic distribution, and developmental expression. Genome Research, 2022, 32, 1408-1423.	2.4	29
2554	The PCY-SAG14 phytocyanin module regulated by PIFs and miR408 promotes dark-induced leaf senescence in <i>Arabidopsis</i>. Proceedings of the National Academy of Sciences of the United States of America, 2022, 119, .	3.3	17
2556	Histone deacetylase 3 contributes to the antiviral innate immunity of macrophages by interacting with FOXK1 to regulate STAT1/2 transcription. Cell Reports, 2022, 38, 110302.	2.9	18
2558	Polycomb Repressive Complex 2 in Eukaryotesâ€"An Evolutionary Perspective. Epigenomes, 2022, 6, 3.	0.8	15
2559	Epigenomic priming of immune genes implicates oligodendroglia in multiple sclerosis susceptibility. Neuron, 2022, 110, 1193-1210.e13.	3.8	36
2561	Recursive splicing is a rare event in the mouse brain. PLoS ONE, 2022, 17, e0263082.	1.1	2
2562	The DNA dioxygenase Tet1 regulates H3K27 modification and embryonic stem cell biology independent of its catalytic activity. Nucleic Acids Research, 2022, 50, 3169-3189.	6.5	27
2563	Endogenous retroviruses co-opted as divergently transcribed regulatory elements shape the regulatory landscape of embryonic stem cells. Nucleic Acids Research, 2022, 50, 2111-2127.	6.5	12
2564	PHOSPHATE STARVATION RESPONSE transcription factors enable arbuscular mycorrhiza symbiosis. Nature Communications, 2022, 13, 477.	5.8	81
2565	Spt5 histone binding activity preserves chromatin during transcription by RNA polymerase II. EMBO Journal, 2022, 41, e109783.	3.5	14
2566	Profiling and functional characterization of maternal mRNA translation during mouse maternal-to-zygotic transition. Science Advances, 2022, 8, eabj3967.	4.7	52
2567	Impaired KDM2B-mediated PRC1 recruitment to chromatin causes defective neural stem cell self-renewal and ASD/ID-like behaviors. IScience, 2022, 25, 103742.	1.9	7
2568	Manipulation of RNA polymerase III by Herpes Simplex Virus-1. Nature Communications, 2022, 13, 623.	5.8	15
2569	Progesterone Inhibits the Establishment of Activation-Associated Chromatin During TH1 Differentiation. Frontiers in Immunology, 2022, 13, 835625.	2.2	7

#	ARTICLE	IF	CITATIONS
2570	Optimization of enzymatic fragmentation is crucial to maximize genome coverage: a comparison of library preparation methods for Illumina sequencing. BMC Genomics, 2022, 23, 92.	1.2	4
2572	CECR2 drives breast cancer metastasis by promoting NF-Î°B signaling and macrophage-mediated immune suppression. Science Translational Medicine, 2022, 14, eabf5473.	5.8	51
2574	UALCAN: An update to the integrated cancer data analysis platform. Neoplasia, 2022, 25, 18-27.	2.3	666
2575	The novel activity of Argonautes in intron splicing: A transcriptome-wide survey in plants. Journal of Plant Physiology, 2022, 270, 153632.	1.6	3
2576	Role of the cellular factor CTCF in the regulation of bovine leukemia virus latency and three-dimensional chromatin organization. Nucleic Acids Research, 2022, 50, 3190-3202.	6.5	5
2577	High Stability of the Epigenome in<i>Drosophila</i>Interspecific Hybrids. Genome Biology and Evolution, 2022, 14, .	1.1	2
2580	Chemical-induced chromatin remodeling reprograms mouse ESCs to totipotent-like stem cells. Cell Stem Cell, 2022, 29, 400-418.e13.	5.2	68
2581	H3K27ac chromatin acetylation and gene expression analysis reveal sex- and situs-related differences in developing chicken gonads. Biology of Sex Differences, 2022, 13, 6.	1.8	7
2582	METTL16 exerts an m6A-independent function to facilitate translation and tumorigenesis. Nature Cell Biology, 2022, 24, 205-216.	4.6	143
2583	Pluripotency factors determine gene expression repertoire at zygotic genome activation. Nature Communications, 2022, 13, 788.	5.8	9
2584	Targeted DamID in <i>C. elegans</i> reveals a direct role for LIN-22 and NHR-25 in antagonizing the epidermal stem cell fate. Science Advances, 2022, 8, eabk3141.	4.7	9
2585	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
2586	Bryostatin Activates CAR T-Cell Antigen-Non-Specific Killing (CTAK), and CAR-T NK-Like Killing for Pre-B ALL, While Blocking Cytolysis of a Burkitt Lymphoma Cell Line. Frontiers in Immunology, 2022, 13, 825364.	2.2	6
2588	The Coxiella burnetii T4SS effector protein AnkG hijacks the 7SK small nuclear ribonucleoprotein complex for reprogramming host cell transcription. PLoS Pathogens, 2022, 18, e1010266.	2.1	12
2589	Bivalent-histone-marked immediate-early gene regulation is vital for VEGF-responsive angiogenesis. Cell Reports, 2022, 38, 110332.	2.9	11
2590	Integrative analysis reveals multiple modes of LXR transcriptional regulation in liver. Proceedings of the National Academy of Sciences of the United States of America, 2022, 119, .	3.3	11
2592	Dynamic Runx1 chromatin boundaries affect gene expression in hematopoietic development. Nature Communications, 2022, 13, 773.	5.8	10
2593	PRDM paralogs antagonistically balance Wnt/Î²-catenin activity during craniofacial chondrocyte differentiation. Development (Cambridge), 2022, 149, .	1.2	13

#	Article	IF	Citations
2595	ADAR1-mediated RNA editing links ganglioside catabolism to glioblastoma stem cell maintenance. Journal of Clinical Investigation, 2022, 132, .	3.9	27
2598	Functional annotation of regulatory elements in cattle genome reveals the roles of extracellular interaction and dynamic change of chromatin states in rumen development during weaning. Genomics, 2022, 114, 110296.	1.3	4
2599	Autism risk gene POGZ promotes chromatin accessibility and expression of clustered synaptic genes. Cell Reports, 2021, 37, 110089.	2.9	38
2600	Focal disruption of DNA methylation dynamics at enhancers in IDH-mutant AML cells. Leukemia, 2022, 36, 935-945.	3.3	18
2601	Cell-type-specific chromatin occupancy by the pioneer factor Zelda drives key developmental transitions in Drosophila. Nature Communications, 2021, 12, 7153.	5.8	18
2602	Connecting the Dots: PHF13 and Cohesin Promote Polymer-Polymer Phase Separation of Chromatin Into Chromosomes. SSRN Electronic Journal, 0, , .	0.4	0
2603	OUP accepted manuscript. Nucleic Acids Research, 2022, , .	6.5	14
2604	Decoding Human Genome Regulatory Features That Influence HIV-1 Proviral Expression and Fate Through an Integrated Genomics Approach. Bioinformatics and Biology Insights, 2022, 16, 117793222110723.	1.0	1
2605	Ptbp1-Activateded Co-Transcriptional Splicing Controls Epigenetic Status of Pluripotent Stem Cells. SSRN Electronic Journal, 0, , .	0.4	0
2606	Bacterial N4-methylcytosine as an epigenetic mark in eukaryotic DNA. Nature Communications, 2022, 13, 1072.	5.8	27
2608	Induction of senescence-associated secretory phenotype underlies the therapeutic efficacy of PRC2 inhibition in cancer. Cell Death and Disease, 2022, 13, 155.	2.7	14
2609	Hydrop enables droplet-based single-cell ATAC-seq and single-cell RNA-seq using dissolvable hydrogel beads. ELife, 2022, 11, .	2.8	37
2610	TLR4 is a regulator of trained immunity in a murine model of Duchenne muscular dystrophy. Nature Communications, 2022, 13, 879.	5.8	22
2612	H2B.V demarcates divergent strand-switch regions, some tDNA loci, and genome compartments in Trypanosoma cruzi and affects parasite differentiation and host cell invasion. PLoS Pathogens, 2022, 18, e1009694.	2.1	15
2613	EZH2 noncanonically binds cMyc and p300 through a cryptic transactivation domain to mediate gene activation and promote oncogenesis. Nature Cell Biology, 2022, 24, 384-399.	4.6	88
2614	The widespread nature of Pack-TYPE transposons reveals their importance for plant genome evolution. PLoS Genetics, 2022, 18, e1010078.	1.5	3
2615	The SWI/SNF subunit BRG1 affects alternative splicing by changing RNA binding factor interactions with nascent RNA. Molecular Genetics and Genomics, 2022, 297, 463-484.	1.0	11
2616	Histone H3 Lysine 4 and 27 Trimethylation Landscape of Human Alzheimerâ€™s Disease. Cells, 2022, 11, 734.	1.8	10

#	ARTICLE	IF	CITATIONS
2617	Global and context-specific transcriptional consequences of oncogenic Fbw7 mutations. ELife, 2022, 11, .	2.8	6
2618	Decrease in RNase HII and Accumulation of lncRNAs/DNA Hybrids: A Causal Implication in Psoriasis?. Biomolecules, 2022, 12, 368.	1.8	7
2619	Mosaic cis-regulatory evolution drives transcriptional partitioning of HERVH endogenous retrovirus in the human embryo. ELife, 2022, 11, .	2.8	31
2622	Rap1 regulates TIP60 function during fate transition between two-cell-like and pluripotent states. Genes and Development, 2022, 36, 313-330.	2.7	6
2624	A comparison of experimental assays and analytical methods for genome-wide identification of active enhancers. Nature Biotechnology, 2022, 40, 1056-1065.	9.4	28
2625	The antiâ€aging protein Klotho affects early postnatal myogenesis by downregulating Jmjd3 and the canonical Wnt pathway. FASEB Journal, 2022, 36, e22192.	0.2	5
2626	CRP-Like Transcriptional Regulator MrpC Curbs c-di-GMP and 3â€²,3â€²-cGAMP Nucleotide Levels during Development in Myxococcus xanthus. MBio, 2022, 13, e0004422.	1.8	8
2627	The Pet127 protein is a mitochondrial 5â€²-to-3â€² exoribonuclease from the PD-(D/E)XK superfamily involved in RNA maturation and intron degradation in yeasts. Rna, 2022, 28, 711-728.	1.6	3
2629	A genome-scale CRISPR screen reveals PRMT1 as a critical regulator of androgen receptor signaling in prostate cancer. Cell Reports, 2022, 38, 110417.	2.9	17
2630	Unraveling Microbial Volatile Elicitors Using a Transparent Methodology for Induction of Systemic Resistance and Regulation of Antioxidant Genes at Expression Levels in Chili against Bacterial Wilt Disease. Antioxidants, 2022, 11, 404.	2.2	28
2634	The cAMP signaling pathway regulates Epe1 protein levels and heterochromatin assembly. PLoS Genetics, 2022, 18, e1010049.	1.5	6
2635	Panoramix SUMOylation on chromatin connects the piRNA pathway to the cellular heterochromatin machinery. Nature Structural and Molecular Biology, 2022, 29, 130-142.	3.6	19
2636	Separable roles for RNAi in regulation of transposable elements and viability in the fission yeast Schizosaccharomyces japonicus. PLoS Genetics, 2022, 18, e1010100.	1.5	7
2637	Simultaneous cellular and molecular phenotyping of embryonic mutants using single-cell regulatory trajectories. Developmental Cell, 2022, 57, 496-511.e8.	3.1	3
2639	Epigenetic reprogramming by TET enzymes impacts co-transcriptional R-loops. ELife, 2022, 11, .	2.8	15
2643	Dicer promotes genome stability via the bromodomain transcriptional co-activator BRD4. Nature Communications, 2022, 13, 1001.	5.8	10
2644	A cattle graph genome incorporating global breed diversity. Nature Communications, 2022, 13, 910.	5.8	35
2645	Promoters of ASCL1â€•and NEUROD1â€dependent genes are specific targets of lurbinectedin in SCLC cells. EMBO Molecular Medicine, 2022, 14, e14841.	3.3	14

#	Article	IF	Citations
2646	Reversible phase separation of HSF1 is required for an acute transcriptional response during heat shock. Nature Cell Biology, 2022, 24, 340-352.	4.6	60
2647	The histone H3.1 variant regulates TONSOKU-mediated DNA repair during replication. Science, 2022, 375, 1281-1286.	6.0	33
2648	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
2649	Regulation of chromatin accessibility by hypoxia and HIF. Biochemical Journal, 2022, 479, 767-786.	1.7	19
2650	The genome organization of <i>Neurospora crassa</i> at high resolution uncovers principles of fungal chromosome topology. G3: Genes, Genomes, Genetics, 2022, , .	0.8	11
2651	Phased polyploid genomes provide deeper insight into the multiple origins of domesticated Saccharomyces cerevisiae beer yeasts. Current Biology, 2022, 32, 1350-1361.e3.	1.8	19
2652	The BTB transcription factors ZBTB11 and ZFP131 maintain pluripotency by repressing pro-differentiation genes. Cell Reports, 2022, 38, 110524.	2.9	7
2655	Integrative epigenomic and transcriptomic analyses reveal metabolic switching by intermittent fasting in brain. GeroScience, 2022, 44, 2171-2194.	2.1	10
2657	A single-cell regulatory map of postnatal lung alveologenesis in humans and mice. Cell Genomics, 2022, 2, 100108.	3.0	13
2658	The control of transcriptional memory by stable mitotic bookmarking. Nature Communications, 2022, 13, 1176.	5.8	26
2660	Whole-genome profiling of DNA methylation and hydroxymethylation identifies distinct regulatory programs among innate lymphocytes. Nature Immunology, 2022, 23, 619-631.	7.0	14
2661	ZFP541 maintains the repression of pre-pachytene transcriptional programs and promotes male meiosis progression. Cell Reports, 2022, 38, 110540.	2.9	11
2662	CREBBP/EP300 acetyltransferase inhibition disrupts FOXA1-bound enhancers to inhibit the proliferation of ER+ breast cancer cells. PLoS ONE, 2022, 17, e0262378.	1.1	5
2663	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
2664	GATA4/5/6 family transcription factors are conserved determinants of cardiac versus pharyngeal mesoderm fate. Science Advances, 2022, 8, eabg0834.	4.7	14
2665	Starvation causes changes in the intestinal transcriptome and microbiome that are reversed upon refeeding. BMC Genomics, 2022, 23, 225.	1.2	10
2669	H3K56 deacetylation and H2A.Z deposition are required for aberrant heterochromatin spreading. Nucleic Acids Research, 2022, 50, 3852-3866.	6.5	8
2671	A near-chromosome level genome assembly of the European hoverfly, Sphaerophoria rueppellii (Diptera: Syrphidae), provides comparative insights into insecticide resistance-related gene family evolution. BMC Genomics, 2022, 23, 198.	1.2	2

#	ARTICLE	IF	CITATIONS
2672	Reorganization of 3D genome architecture across wild boar and Bama pig adipose tissues. Journal of Animal Science and Biotechnology, 2022, 13, 32.	2.1	6
2673	Presence of H3K4me3 on Paternally Expressed Genes of the Paternal Genome From Sperm to Implantation. Frontiers in Cell and Developmental Biology, 2022, 10, 838684.	1.8	4
2674	Systematic mapping of nuclear domain-associated transcripts reveals speckles and lamina as hubs of functionally distinct retained introns. Molecular Cell, 2022, 82, 1035-1052.e9.	4.5	31
2675	HiCuT: An efficient and low input method to identify protein-directed chromatin interactions. PLoS Genetics, 2022, 18, e1010121.	1.5	9
2676	CUT&Tag2for1: a modified method for simultaneous profiling of the accessible and silenced regulome in singleÂcells. Genome Biology, 2022, 23, 81.	3.8	30
2677	Inhibition of cGAS-STING by JQ1 alleviates oxidative stress-induced retina inflammation and degeneration. Cell Death and Differentiation, 2022, 29, 1816-1833.	5.0	33
2678	m6A RNA modifications are measured at single-base resolution across the mammalian transcriptome. Nature Biotechnology, 2022, 40, 1210-1219.	9.4	115
2679	CRISPR-Mediated Synergistic Epigenetic and Transcriptional Control. CRISPR Journal, 2022, 5, 264-275.	1.4	13
2680	Oncogenic gene expression and epigenetic remodeling of cis-regulatory elements in ASXL1-mutant chronic myelomonocytic leukemia. Nature Communications, 2022, 13, 1434.	5.8	17
2683	A hidden layer of structural variation in transposable elements reveals potential genetic modifiers in human disease-risk loci. Genome Research, 2022, 32, 656-670.	2.4	13
2686	An optimized ChIPâ€Seq framework for profiling histone modifications in <i>Chromochloris zofingiensis</i>. Plant Direct, 2022, 6, e392.	0.8	0
2688	Despite its sequence identity with canonical H4, Drosophila H4r product is enriched at specific chromatin regions. Scientific Reports, 2022, 12, 5007.	1.6	1
2690	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
2691	Broad domains of histone marks in the highly compact <i>Paramecium</i> macronuclear genome. Genome Research, 2022, 32, 710-725.	2.4	7
2692	Convergence of case-specific epigenetic alterations identify a confluence of genetic vulnerabilities tied to opioid overdose. Molecular Psychiatry, 2022, 27, 2158-2170.	4.1	9
2693	SUMOylation of Jun fine-tunes the Drosophila gut immune response. PLoS Pathogens, 2022, 18, e1010356.	2.1	3
2694	Wt1 transcription factor impairs cardiomyocyte specification and drives a phenotypic switch from myocardium to epicardium. Development (Cambridge), 2022, 149, .	1.2	5
2695	Transcriptional, epigenetic and metabolic signatures in cardiometabolic syndrome defined by extreme phenotypes. Clinical Epigenetics, 2022, 14, 39.	1.8	6

#	Article	IF	Citations
2696	Reducing N6AMT1-mediated 6mA DNA modification promotes breast tumor progression via transcriptional repressing cell cycle inhibitors. Cell Death and Disease, 2022, 13, 216.	2.7	8
2697	Highly enriched BEND3 prevents the premature activation of bivalent genes during differentiation. Science, 2022, 375, 1053-1058.	6.0	38
2698	The VIL gene CRAWLING ELEPHANT controls maturation and differentiation in tomato via polycomb silencing. PLoS Genetics, 2022, 18, e1009633.	1.5	2
2699	Bioorthogonal Chemical Epigenetic Modifiers Enable Dose-Dependent CRISPR Targeted Gene Activation in Mammalian Cells. ACS Synthetic Biology, 2022, 11, 1397-1407.	1.9	3
2700	Anatomic position determines oncogenic specificity in melanoma. Nature, 2022, 604, 354-361.	13.7	44
2701	Loops, topologically associating domains, compartments, and territories are elastic and robust to dramatic nuclear volume swelling. Scientific Reports, 2022, 12, 4721.	1.6	14
2702	Genome-wide cis-decoding for expression design in tomato using cistrome data and explainable deep learning. Plant Cell, 2022, 34, 2174-2187.	3.1	10
2704	Telomerase RNA TERC and the PI3K-AKT pathway form a positive feedback loop to regulate cell proliferation independent of telomerase activity. Nucleic Acids Research, 2022, 50, 3764-3776.	6.5	10
2705	A new technique for genome-wide mapping of nucleotide excision repair without immunopurification of damaged DNA. Journal of Biological Chemistry, 2022, 298, 101863.	1.6	2
2706	FOXC1 Binds Enhancers and Promotes Cisplatin Resistance in Bladder Cancer. Cancers, 2022, 14, 1717.	1.7	5
2708	Transcription factor protein interactomes reveal genetic determinants in heart disease. Cell, 2022, 185, 794-814.e30.	13.5	39
2710	Facultative heterochromatin formation in rDNA is essential for cell survival during nutritional starvation. Nucleic Acids Research, 2022, 50, 3727-3744.	6.5	9
2711	Identification of the global miR-130a targetome reveals a role for TBL1XR1 in hematopoietic stem cell self-renewal and t(8;21) AML. Cell Reports, 2022, 38, 110481.	2.9	4
2712	The PAF1 complex promotes 3â€² processing of pervasive transcripts. Cell Reports, 2022, 38, 110519.	2.9	17
2713	A robust mechanism for resetting juvenility during each generation in Arabidopsis. Nature Plants, 2022, 8, 257-268.	4.7	17
2714	Dynamic control of chromatin-associated m6A methylation regulates nascent RNA synthesis. Molecular Cell, 2022, 82, 1156-1168.e7.	4.5	69
2715	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
2717	Epigenetic patterns in a complete human genome. Science, 2022, 376, eabj5089.	6.0	118

#	ARTICLE	IF	CITATIONS
2718	Lamin B1 deletion in myeloid neoplasms causes nuclear anomaly and altered hematopoietic stem cell function. Cell Stem Cell, 2022, 29, 577-592.e8.	5.2	13
2719	The histone variant macroH2A1.1 regulates RNA polymerase II-paused genes within defined chromatin interaction landscapes. Journal of Cell Science, 2022, 135, .	1.2	9
2720	Multi-omics protein-coding units as massively parallel Bayesian networks: Empirical validation of causality structure. IScience, 2022, 25, 104048.	1.9	5
2721	Activation of WNT/CTNNB1/TCF7L2 in Epsteinâ€Barr virusâ€"positive gastric cancer regulates epithelial mesenchymal transition. Biochemical and Biophysical Research Communications, 2022, 609, 54-61.	1.0	1
2722	H3K36 dimethylation shapes the epigenetic interaction landscape by directing repressive chromatin modifications in embryonic stem cells. Genome Research, 2022, , gr.276383.121.	2.4	17
2723	From telomere to telomere: The transcriptional and epigenetic state of human repeat elements. Science, 2022, 376, eabk3112.	6.0	146
2724	Elevated ASCL1 activity creates de novo regulatory elements associated with neuronal differentiation. BMC Genomics, 2022, 23, 255.	1.2	15
2725	Transcriptional states and chromatin accessibility during bovine myoblasts proliferation and myogenic differentiation. Cell Proliferation, 2022, 55, e13219.	2.4	8
2726	Downregulation of CHCHD2 may Contribute to Parkinsonâ€™s Disease by Reducing Expression of NFE2L2 and RQCD1. Current Neurovascular Research, 2022, 19, .	0.4	0
2728	Maf regulates the overexpression of CYP307A1, which is involved in the fitness advantage of bistrifluron-resistant Spodoptera litura (Fab.) (Noctuidae: Lepidoptera). Ecotoxicology and Environmental Safety, 2022, 234, 113425.	2.9	2
2729	Elastic dosage compensation by X-chromosome upregulation. Nature Communications, 2022, 13, 1854.	5.8	18
2730	STAG2 regulates interferon signaling in melanoma via enhancer loop reprogramming. Nature Communications, 2022, 13, 1859.	5.8	21
2732	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
2733	Single-cell profiling of transcriptome and histone modifications with EpiDamID. Molecular Cell, 2022, 82, 1956-1970.e14.	4.5	28
2734	Oct4 dependent chromatin activation is required for chicken primordial germ cell migration. Stem Cell Reviews and Reports, 2022, 18, 2535-2546.	1.7	7
2735	Promoter and enhancer RNAs regulate chromatin reorganization and activation of miR-10b/HOXD locus, and neoplastic transformation in glioma. Molecular Cell, 2022, 82, 1894-1908.e5.	4.5	15
2736	Altered BAF occupancy and transcription factor dynamics in PBAF-deficient melanoma. Cell Reports, 2022, 39, 110637.	2.9	12
2737	The Highly Repeat-Diverse (Peri) Centromeres of White Lupin (Lupinus albus L.). Frontiers in Plant Science, 2022, 13, 862079.	1.7	1

#	ARTICLE	IF	CITATIONS
2738	Coordinated regulation of RNA polymerase II pausing and elongation progression by PAF1. Science Advances, 2022, 8, eabm5504.	4.7	18
2739	TOX4 facilitates promoter-proximal pausing and C-terminal domain dephosphorylation of RNA polymerase II in human cells. Communications Biology, 2022, 5, 300.	2.0	6
2740	HIRA-dependent boundaries between H3 variants shape early replication in mammals. Molecular Cell, 2022, 82, 1909-1923.e5.	4.5	12
2741	CTCF functions as an insulator for somatic genes and a chromatin remodeler for pluripotency genes during reprogramming. Cell Reports, 2022, 39, 110626.	2.9	22
2742	Chromatin interactionâ€"aware gene regulatory modeling with graph attention networks. Genome Research, 2022, , .	2.4	15
2743	Dynamics of estrogen-induced ROS and DNA strand break generation in estrogen receptor Î±-positive breast cancer. Biochemical and Biophysical Research Communications, 2022, 602, 170-178.	1.0	6
2744	Eukaryotic Initiation Factor 5A2 Regulates Expression of Antiviral Genes. Journal of Molecular Biology, 2022, 434, 167564.	2.0	5
2745	Safeguard DCL2-Dependent 22-nt siRNA generation by DCL1. Biochemical and Biophysical Research Communications, 2022, 605, 97-103.	1.0	0
2746	DNA N6-Adenine methylation in HBV-related hepatocellular carcinoma. Gene, 2022, 822, 146353.	1.0	6
2747	Sperm histone H3 lysine 4 tri-methylation serves as a metabolic sensor of paternal obesity and is associated with the inheritance of metabolic dysfunction. Molecular Metabolism, 2022, 59, 101463.	3.0	40
2748	Cross-talk between enhancers, structural elements and activating transcription factors maintains the 3D architecture and expression of the CFTR gene. Genomics, 2022, 114, 110350.	1.3	6
2749	KrÃ¼ppel-Like Factor 5 Regulates CFTR Expression Through Repression by Maintaining Chromatin Architecture Coupled with Direct Enhancer Activation. Journal of Molecular Biology, 2022, 434, 167561.	2.0	5
2750	The accessible promoter-mediated supplementary effect of host factors provides new insight into the tropism of SARS-CoV-2. Molecular Therapy - Nucleic Acids, 2022, 28, 249-258.	2.3	2
2752	Characteristics, origin, and potential for cancer diagnostics of ultrashort plasma cell-free DNA. Genome Research, 2022, 32, 215-227.	2.4	41
2754	Single-Cell Analysis Identify Transcription Factor BACH1 as a Master Regulator Gene in Vascular Cells During Aging. Frontiers in Cell and Developmental Biology, 2021, 9, 786496.	1.8	8
2755	Analysis of long and short enhancers in melanoma cell states. ELife, 2021, 10, .	2.8	18
2756	Arabidopsis CHROMATIN REMODELING 19 acts as a transcriptional repressor and contributes to plant pathogen resistance. Plant Cell, 2022, 34, 1100-1116.	3.1	13
2757	Enhancer RNA Expression in Response to Glucocorticoid Treatment in Murine Macrophages. Cells, 2022, 11, 28.	1.8	7

#	Article	IF	Citations
2758	Integrative RNA-Seq and ATAC-Seq Analysis Reveals the Migration-Associated Genes Involved in Antitumor Effects of Herbal Medicine Feiyanning on Lung Cancer Cells. Frontiers in Genetics, 2021, 12, 799099.	1.1	4
2759	Profiling of open chromatin in developing pig (<i>Sus scrofa</i>) muscle to identify regulatory regions. G3: Genes, Genomes, Genetics, 2022, 12, .	0.8	13
2760	An Evolutionary Perspective on Hox Binding Site Preferences in Two Different Tissues. Journal of Developmental Biology, 2021, 9, 57.	0.9	3
2761	Profiling of H3K4me3 and H3K27me3 and Their Roles in Gene Subfunctionalization in Allotetraploid Cotton. Frontiers in Plant Science, 2021, 12, 761059.	1.7	8
2765	MAL2 mediates the formation of stable HER2 signaling complexes within lipid raft-rich membrane protrusions in breast cancer cells. Cell Reports, 2021, 37, 110160.	2.9	12
2766	TET deficiency perturbs mature B cell homeostasis and promotes oncogenesis associated with accumulation of G-quadruplex and R-loop structures. Nature Immunology, 2022, 23, 99-108.	7.0	33
2767	A predominant enhancer co-amplified with the SOX2 oncogene is necessary and sufficient for its expression in squamous cancer. Nature Communications, 2021, 12, 7139.	5.8	12
2768	Transcriptome-wide N6-Methyladenosine Methylome Profiling Reveals m6A Regulation of Skeletal Myoblast Differentiation in Cattle (Bos taurus). Frontiers in Cell and Developmental Biology, 2021, 9, 785380.	1.8	10
2769	ChIP-AP: an integrated analysis pipeline for unbiased ChIP-seq analysis. Briefings in Bioinformatics, 2022, 23, .	3.2	6
2770	cLoops2: a full-stack comprehensive analytical tool for chromatin interactions. Nucleic Acids Research, 2022, 50, 57-71.	6.5	24
2772	GIP: an open-source computational pipeline for mapping genomic instability from protists to cancer cells. Nucleic Acids Research, 2022, 50, e36-e36.	6.5	5
2773	5-Hydroxymethylcytosine-mediated active demethylation is required for mammalian neuronal differentiation and function. ELife, 2021, 10, .	2.8	21
2774	Chromatin-contact atlas reveals disorder-mediated protein interactions and moonlighting chromatin-associated RBPs. Nucleic Acids Research, 2021, 49, 13092-13107.	6.5	9
2775	Depletion of central memory CD8+ T cells might impede the antitumor therapeutic effect of Mogamulizumab. Nature Communications, 2021, 12, 7280.	5.8	11
2776	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
2778	Pan-AMPK activator O304 prevents gene expression changes and remobilisation of histone marks in islets of diet-induced obese mice. Scientific Reports, 2021, 11, 24410.	1.6	6
2780	Reprogramming of RNA silencing triggered by cucumber mosaic virus infection in Arabidopsis. Genome Biology, 2021, 22, 340.	3.8	17
2783	<i>BCOR</i> and <i>BCORL1</i> Mutations Drive Epigenetic Reprogramming and Oncogenic Signaling by Unlinking PRC1.1 from Target Genes. Blood Cancer Discovery, 2022, 3, 116-135.	2.6	18

#	ARTICLE	IF	CITATIONS
2784	R-loop proximity proteomics identifies a role of DDX41 in transcription-associated genomic instability. Nature Communications, 2021, 12, 7314.	5.8	64
2786	Sex-specific chromatin remodelling safeguards transcription in germ cells. Nature, 2021, 600, 737-742.	13.7	24
2787	Locus-specific chromatin profiling of evolutionarily young transposable elements. Nucleic Acids Research, 2022, 50, e33-e33.	6.5	9
2789	ENAP1 retrains seed germination via H3K9 acetylation mediated positive feedback regulation of ABI5. PLoS Genetics, 2021, 17, e1009955.	1.5	5
2790	Suppression of MYC transcription activators by the immune cofactor NPR1 fine-tunes plant immune responses. Cell Reports, 2021, 37, 110125.	2.9	41
2791	Nuclear pore protein NUP210 depletion suppresses metastasis through heterochromatin-mediated disruption of tumor cell mechanical response. Nature Communications, 2021, 12, 7216.	5.8	19
2792	Locus-specific induction of gene expression from heterochromatin loci during cellular senescence. Nature Aging, 2022, 2, 31-45.	5.3	12
2796	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
2797	MOJITOO: a fast and universal method for integration of multimodal single-cell data. Bioinformatics, 2022, 38, i282-i289.	1.8	6
2798	A Moonlighting Function of Aldh18a1 Supports Pausing RNA Polymerase II in Promoter-Proximal Regions. SSRN Electronic Journal, 0, , .	0.4	0
2799	MeConcord: a new metric to quantitatively characterize DNA methylation heterogeneity across reads and CpG sites. Bioinformatics, 2022, 38, i307-i315.	1.8	2
2800	SETDB1 fuels the lung cancer phenotype by modulating epigenome, 3D genome organization and chromatin mechanical properties. Nucleic Acids Research, 2022, 50, 4389-4413.	6.5	18
2801	Non-coding RNA LEVER sequestration of PRC2 can mediate long range gene regulation. Communications Biology, 2022, 5, 343.	2.0	2
2804	Sequential enhancer state remodelling defines human germline competence and specification. Nature Cell Biology, 2022, 24, 448-460.	4.6	27
2807	Uncovering N4-Acetylcytidine-Related mRNA Modification Pattern and Landscape of Stemness and Immunity in Hepatocellular Carcinoma. Frontiers in Cell and Developmental Biology, 2022, 10, 861000.	1.8	9
2808	STAT3 is a biologically relevant therapeutic target in H3K27M-mutant diffuse midline glioma. Neuro-Oncology, 2022, 24, 1700-1711.	0.6	13
2811	Genome-wide H3K9 acetylation level increases with age-dependent senescence of flag leaf in rice. Journal of Experimental Botany, 2022, 73, 4696-4715.	2.4	9
2812	A chromatin accessibility landscape during early adipogenesis of human adipose-derived stem cells. Adipocyte, 2022, 11, 239-249.	1.3	4

#	ARTICLE	IF	CITATIONS
2814	A Stage-Specific OTX2 Regulatory Network and Maturation-Associated Gene Programs Are Inherent Barriers to RPE Neural Competency. Frontiers in Cell and Developmental Biology, 2022, 10, 875155.	1.8	5
2815	Dynamics of CTCF- and cohesin-mediated chromatin looping revealed by live-cell imaging. Science, 2022, 376, 496-501.	6.0	190
2816	The Putative Bromodomain Protein PfBDP7 of the Human Malaria Parasite Plasmodium Falciparum Cooperates With PfBDP1 in the Silencing of Variant Surface Antigen Expression. Frontiers in Cell and Developmental Biology, 2022, 10, 816558.	1.8	10
2817	CDYL1-dependent decrease in lysine crotonylation at DNA double-strand break sites functionally uncouples transcriptional silencing and repair. Molecular Cell, 2022, 82, 1940-1955.e7.	4.5	12
2818	Unleashing Cell-Intrinsic Inflammation as a Strategy to Kill AML Blasts. Cancer Discovery, 2022, 12, 1760-1781.	7.7	15
2821	Cavî²1 regulates T cell expansion and apoptosis independently of voltage-gated Ca2+ channel function. Nature Communications, 2022, 13, 2033.	5.8	18
2822	High-quality genome and methylomes illustrate features underlying evolutionary success of oaks. Nature Communications, 2022, 13, 2047.	5.8	30
2823	A leukemia-protective germline variant mediates chromatin module formation via transcription factor nucleation. Nature Communications, 2022, 13, 2042.	5.8	6
2824	Inhibition of nonalcoholic fatty liver disease in mice by selective inhibition of mTORC1. Science, 2022, 376, eabf8271.	6.0	61
2825	The nuclear lamina binds the EBV genome during latency and regulates viral gene expression. PLoS Pathogens, 2022, 18, e1010400.	2.1	6
2827	An adult-stage transcriptional program for survival of serotonergic connectivity. Cell Reports, 2022, 39, 110711.	2.9	8
2829	SETD2 Haploinsufficiency Enhances Germinal Centerâ€“Associated AICDA Somatic Hypermutation to Drive B-cell Lymphomagenesis. Cancer Discovery, 2022, 12, 1782-1803.	7.7	14
2830	Jasmonates and Histone deacetylase 6 activate Arabidopsis genome-wide histone acetylation and methylation during the early acute stress response. BMC Biology, 2022, 20, 83.	1.7	5
2831	Chromatin remodeling complexes regulate genome architecture in Arabidopsis. Plant Cell, 2022, 34, 2638-2651.	3.1	24
2832	Genome-wide CRISPR screen identifies PRC2 and KMT2D-COMPASS as regulators of distinct EMT trajectories that contribute differentially to metastasis. Nature Cell Biology, 2022, 24, 554-564.	4.6	53
2834	An Extracytoplasmic Function Sigma Factor Required for Full Virulence in Xanthomonas citri pv. citri. Journal of Bacteriology, 2022, , e0062421.	1.0	0
2836	A computational pipeline to visualize DNA-protein binding states using dSMF data. STAR Protocols, 2022, 3, 101299.	0.5	0
2837	Nuclear transfer system for the direct induction of embryonic transcripts from intra- and cross-species nuclei using mouse 4-cell embryos. STAR Protocols, 2022, 3, 101284.	0.5	0

#	ARTICLE	IF	CITATIONS
2885	Profiling m6A RNA Modifications in Low Amounts of Plant Cells Using Maize Meiocytes. Methods in Molecular Biology, 2022, 2484, 313-331.	0.4	0
2886	Identifying small RNAs and Analyzing Their Association with Gene Expression Using IsolatedÂArabidopsis Male Meiocytes. Methods in Molecular Biology, 2022, 2484, 23-41.	0.4	0
2887	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
2888	R-loops at microRNA encoding loci promote co-transcriptional processing of pri-miRNAs in plants. Nature Plants, 2022, 8, 402-418.	4.7	47
2889	Population genomics confirms acquisition of drug-resistant Aspergillus fumigatus infection by humans from the environment. Nature Microbiology, 2022, 7, 663-674.	5.9	82
2890	Screening of ETO2-GLIS2â€“induced Super Enhancers identifies targetable cooperative dependencies in acute megakaryoblastic leukemia. Science Advances, 2022, 8, eabg9455.	4.7	9
2891	FoxP3 associates with enhancer-promoter loops to regulate T-specific gene expression.. Science Immunology, 2022, 7, eabj9836.	5.6	12
2893	Comprehensive bioinformatic analysis reveals oncogenic role of H2A.Z isoforms in cervical cancer progression.. Iranian Journal of Basic Medical Sciences, 2021, 24, 1470-1481.	1.0	0
2894	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
2895	A functional screen of RNA binding proteins identifies genes that promote or limit the accumulation of CD138+ plasma cells. ELife, 2022, 11, .	2.8	5
2896	Species-Specific Rewiring of Definitive Endoderm Developmental Gene Activation via Endogenous Retroviruses Through TET1 Mediated Demethylation. SSRN Electronic Journal, 0, , .	0.4	0
2897	Ryanodine receptor 2 (RYR2) dysfunction activates the unfolded protein response and perturbs cardiomyocyte maturation. Cardiovascular Research, 2023, 119, 221-235.	1.8	5
2898	Canonical PRC1 Recruitment Is Promoted by EZH1-PRC2 Independent of H3K27me3 in Quiescent Cells. SSRN Electronic Journal, 0, , .	0.4	0
2899	circRIP: an accurate tool for identifying circRNAâ€“RBP interactions. Briefings in Bioinformatics, 2022, 23, .	3.2	13
2900	<i>Stella</i> Regulates the Development of Female Germline Stem Cells by Modulating Chromatin Structure and DNA Methylation. International Journal of Biological Sciences, 2022, 18, 3006-3018.	2.6	6
2902	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
2904	Antisense-mediated repression of SAGA-dependent genes involves the HIR histone chaperone. Nucleic Acids Research, 2022, 50, 4515-4528.	6.5	4
2905	EWSR1-ATF1 dependent 3D connectivity regulates oncogenic and differentiation programs in Clear Cell Sarcoma. Nature Communications, 2022, 13, 2267.	5.8	18

#	ARTICLE	IF	CITATIONS
2906	A MYC inhibitor selectively alters the MYC and MAX cistromes and modulates the epigenomic landscape to regulate target gene expression. Science Advances, 2022, 8, eabh3635.	4.7	21
2908	Phosphorylation of the FACT histone chaperone subunit SPT16 affects chromatin at RNA polymerase II transcriptional start sites in <i>Arabidopsis</i>. Nucleic Acids Research, 2022, 50, 5014-5028.	6.5	9
2909	RPAP2 regulates a transcription initiation checkpoint by inhibiting assembly of pre-initiation complex. Cell Reports, 2022, 39, 110732.	2.9	5
2910	ASCL1 activates neuronal stem cell-like lineage programming through remodeling of the chromatin landscape in prostate cancer. Nature Communications, 2022, 13, 2282.	5.8	34
2916	Identification of crucial factors involved in Cynoglossus semilaevis sexual size dimorphism by GWAS and demonstration of zbed1 regulatory network by DAP-seq. Genomics, 2022, 114, 110376.	1.3	4
2917	Mitochondrial base editor induces substantial nuclear off-target mutations. Nature, 2022, 606, 804-811.	13.7	62
2918	VHL Ser65 mutations enhance HIF2Î± signaling and promote epithelial-mesenchymal transition of renal cancer cells. Cell and Bioscience, 2022, 12, 52.	2.1	4
2919	Aberrant H3K4me3 modification of epiblast genes of extraembryonic tissue causes placental defects and implantation failure in mouse IVF embryos. Cell Reports, 2022, 39, 110784.	2.9	12
2920	ISL2 is a putative tumor suppressor whose epigenetic silencing reprograms the metabolism of pancreatic cancer. Developmental Cell, 2022, 57, 1331-1346.e9.	3.1	9
2921	Intracellular infection and immune system cues rewire adipocytes to acquire immune function. Cell Metabolism, 2022, 34, 747-760.e6.	7.2	21
2922	FTO mediates LINE1 m ⁶ A demethylation and chromatin regulation in mESCs and mouse development. Science, 2022, 376, 968-973.	6.0	97
2924	The disordered N-terminal domain of DNMT3A recognizes H2AK119ub and is required for postnatal development. Nature Genetics, 2022, 54, 625-636.	9.4	31
2925	The investigation of sexâ€differential open chromatin in liver, spleen and gonads in <i>Larimichthys crocea</i> through <scp>ATAC</scp> â€seq. Aquaculture Research, 0, , .	0.9	0
2926	Gene regulation by gonadal hormone receptors underlies brainÂsex differences. Nature, 2022, 606, 153-159.	13.7	71
2928	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
2929	MEF2C opposes Notch in lymphoid lineage decision and drives leukemia in the thymus. JCI Insight, 2022, 7, .	2.3	7
2930	ASC proneural factors are necessary for chromatin remodeling during neuroectodermal to neuroblast fate transition to ensure the timely initiation of the neural stem cell program. BMC Biology, 2022, 20, 107.	1.7	0
2931	Dual role of specific promoter tandem repeats integrating epigenetic silencing with heat response. Physiologia Plantarum, 2022, 174, e13694.	2.6	2

#	Article	IF	Citations
2933	Stable inheritance of H3.3-containing nucleosomes during mitotic cell divisions. Nature Communications, 2022, 13, 2514.	5.8	11
2934	Polycomb contraction differentially regulates terminal human hematopoietic differentiation programs. BMC Biology, 2022, 20, 104.	1.7	5
2936	SAMS-1 coordinates HLH-30/TFEB and PHA-4/FOXA activities through histone methylation to mediate dietary restriction-induced autophagy and longevity. Autophagy, 2023, 19, 224-240.	4.3	3
2937	H3K4me3 recognition by the COMPASS complex facilitates the restoration of this histone mark following DNA replication. Science Advances, 2022, 8, eabm6246.	4.7	14
2938	Sox2 levels regulate the chromatin occupancy of WNT mediators in epiblast progenitors responsible for vertebrate body formation. Nature Cell Biology, 2022, 24, 633-644.	4.6	35
2940	Chromosomal rearrangements with stable repertoires of genes and transposable elements in an invasive forest-pathogenic fungus. , 0, 2, .		1
2941	The â€˜Alu-omeâ€™Âshapes the epigenetic environment of regulatory elements controlling cellular defense. Nucleic Acids Research, 2022, 50, 5095-5110.	6.5	2
2942	Decoding the dynamic H3K9cr landscapes during neural commitment of P19 embryonal carcinoma cells. Biochemical and Biophysical Research Communications, 2022, 613, 187-192.	1.0	1
2943	Prioritization of autoimmune disease-associated genetic variants that perturb regulatory element activity in T cells. Nature Genetics, 2022, 54, 603-612.	9.4	15
2944	NSD1 mediates antagonism between SWI/SNF and polycomb complexes and is required for transcriptional activation upon EZH2 inhibition. Molecular Cell, 2022, 82, 2472-2489.e8.	4.5	18
2946	A multiplex platform for small RNA sequencing elucidates multifaceted tRNA stress response and translational regulation. Nature Communications, 2022, 13, 2491.	5.8	21
2947	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
2948	Meis1 supports leukemogenesis through stimulation of ribosomal biogenesis and Myc. Haematologica, 2022, 107, 2601-2616.	1.7	4
2949	A genome-wide CRISPR-Cas9 knockout screen identifies essential and growth-restricting genes in human trophoblast stem cells. Nature Communications, 2022, 13, 2548.	5.8	25
2950	MafB, WDR77, and ÃŸ-catenin interact with each other and have similar genome association profiles. PLoS ONE, 2022, 17, e0264799.	1.1	0
2951	Sorghum root epigenetic landscape during limiting phosphorus conditions. Plant Direct, 2022, 6, .	0.8	5
2952	Mouse Chd4-NURD is required for neonatal spermatogonia survival and normal gonad development. Epigenetics and Chromatin, 2022, 15, 16.	1.8	5
2953	Th1 cytokines synergize to change gene expression and promote corticosteroid insensitivity in pediatric airway smooth muscle. Respiratory Research, 2022, 23, 126.	1.4	4

#	Article	IF	Citations
2954	A conserved YAP/Notch/REST network controls the neuroendocrine cell fate in the lungs. Nature Communications, 2022, 13, 2690.	5.8	19
2955	Mpe1 senses the binding of pre-mRNA and controls 3â€² end processing by CPF. Molecular Cell, 2022, 82, 2490-2504.e12.	4.5	9
2956	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
2957	Twist2-driven chromatin remodeling governs the postnatal maturation of dermal fibroblasts. Cell Reports, 2022, 39, 110821.	2.9	12
2958	H3-K27M-mutant nucleosomes interact with MLL1 to shape the glioma epigenetic landscape. Cell Reports, 2022, 39, 110836.	2.9	16
2959	Transcriptional competition shapes proteotoxic ER stress resolution. Nature Plants, 2022, 8, 481-490.	4.7	7
2960	miR778 mediates gene expression, histone modification, and DNA methylation during cyst nematode parasitism. Plant Physiology, 2022, 189, 2432-2453.	2.3	4
2961	Dynamic Interplay between Structural Variations and 3D Genome Organization in Pancreatic Cancer. Advanced Science, 2022, 9, e2200818.	5.6	10
2962	Assessing and assuring interoperability of a genomics file format. Bioinformatics, 2022, 38, 3327-3336.	1.8	3
2963	OCA-T1 and OCA-T2 are coactivators of POU2F3 in the tuft cell lineage. Nature, 2022, 607, 169-175.	13.7	35
2964	BMP4 drives primed to naÃ¯ve transition through PGC-like state. Nature Communications, 2022, 13, 2756.	5.8	2
2965	Interferon regulatory factor 1 (IRF1) controls the metabolic programmes of low-grade pancreatic cancer cells. Gut, 2023, 72, 109-128.	6.1	2
2966	Local chromatin context regulates the genetic requirements of the heterochromatin spreading reaction. PLoS Genetics, 2022, 18, e1010201.	1.5	6
2967	TFAP2 paralogs facilitate chromatin access for MITF at pigmentation and cell proliferation genes. PLoS Genetics, 2022, 18, e1010207.	1.5	13
2968	DNA methylation-mediated expression of zinc finger protein 615 affects embryonic development in <i>Bombyx</i> <i>mori</i>. Zoological Research, 2022, 43, 552-565.	0.9	6
2974	N6-methyladenosine regulates maternal RNA maintenance in oocytes and timely RNA decay during mouse maternal-to-zygotic transition. Nature Cell Biology, 2022, 24, 917-927.	4.6	28
2975	Localization of a TORC1-eIF4F translation complex during CD8+ TÂcell activation drives divergent cell fate. Molecular Cell, 2022, 82, 2401-2414.e9.	4.5	14
2976	Large-scale chromatin reorganization reactivates placenta-specific genes that drive cellular aging. Developmental Cell, 2022, 57, 1347-1368.e12.	3.1	32

#	ARTICLE	IF	CITATIONS
2979	BioViz Connect: Web Application Linking CyVerse Cloud Resources to Genomic Visualization in the Integrated Genome Browser. Frontiers in Bioinformatics, 2022, 2, .	1.0	0
2982	A cancer-associated RNA polymerase III identity drives robust transcription and expression of snaR-A noncoding RNA. Nature Communications, 2022, 13, .	5.8	12
2986	Identification of Robust and Key Differentially Expressed Genes during C2C12 Cell Myogenesis Based on Multiomics Data. International Journal of Molecular Sciences, 2022, 23, 6002.	1.8	7
2987	UvKmt2-Mediated H3K4 Trimethylation Is Required for Pathogenicity and Stress Response in Ustilaginoidea virens. Journal of Fungi (Basel, Switzerland), 2022, 8, 553.	1.5	3
2996	Divergent transcriptional and transforming properties of PAX3-FOXO1 and PAX7-FOXO1 paralogs. PLoS Genetics, 2022, 18, e1009782.	1.5	4
2997	Chromatin profiles classify castration-resistant prostate cancers suggesting therapeutic targets. Science, 2022, 376, .	6.0	75
2999	Alcohol induced increases in sperm Histone H3 lysine 4 trimethylation correlate with increased placental CTCF occupancy and altered developmental programming. Scientific Reports, 2022, 12, .	1.6	13
3000	Replication protein<scp>RPA2A</scp>regulates floral transition by cooperating with<scp>PRC2</scp>in<i>Arabidopsis</i>. New Phytologist, 2022, 235, 2439-2453.	3.5	4
3001	Use of CRISPR/Cas9 with homology-directed repair to silence the human topoisomerase IIÎ± intron-19 5â€™ splice site: Generation of etoposide resistance in human leukemia K562 cells. PLoS ONE, 2022, 17, e0265794.	1.1	3
3002	p63 Directs Subtype-Specific Gene Expression in HPV+ Head and Neck Squamous Cell Carcinoma. Frontiers in Oncology, 0, 12, .	1.3	3
3006	Dual function NFI factors control fetal hemoglobin silencing in adult erythroid cells. Nature Genetics, 2022, 54, 874-884.	9.4	13
3008	RNA inhibits dMi-2/CHD4 chromatin binding and nucleosome remodeling. Cell Reports, 2022, 39, 110895.	2.9	5
3009	The androgen receptor is a therapeutic target in desmoplastic small round cell sarcoma. Nature Communications, 2022, 13, .	5.8	14
3013	Chemoenzymatic labeling of DNA methylation patterns for single-molecule epigenetic mapping. Nucleic Acids Research, 2022, 50, e92-e92.	6.5	16
3015	Epigenomic analysis reveals prevalent contribution of transposable elements to <i>cis</i>-regulatory elements, tissue-specific expression, and alternative promoters in zebrafish. Genome Research, 2022, 32, 1424-1436.	2.4	7
3016	Snake venom gene expression is coordinated by novel regulatory architecture and the integration of multiple co-opted vertebrate pathways. Genome Research, 2022, 32, 1058-1073.	2.4	14
3017	Condensates induced by transcription inhibition localize active chromatin to nucleoli. Molecular Cell, 2022, 82, 2738-2753.e6.	4.5	19
3018	Nuclear Vav3 is required for polycomb repression complex-1 activity in B-cell lymphoblastic leukemogenesis. Nature Communications, 2022, 13, .	5.8	3

#	ARTICLE	IF	CITATIONS
3019	A TRIM66/DAX1/Dux axis suppresses the totipotent 2-cell-like state in murine embryonic stem cells. Cell Stem Cell, 2022, 29, 948-961.e6.	5.2	15
3020	Dietary intervention preserves Î² cell function in mice through CTCF-mediated transcriptional reprogramming. Journal of Experimental Medicine, 2022, 219, .	4.2	16
3021	A systems biology approach identifies candidate drugs to reduce mortality in severely ill patients with COVID-19. Science Advances, 2022, 8, .	4.7	14
3022	Recapitulation of endogenous 4R tau expression and formation of insoluble tau in directly reprogrammed human neurons. Cell Stem Cell, 2022, 29, 918-932.e8.	5.2	20
3023	Open chromatin analysis in Trypanosoma cruzi life forms highlights critical differences in genomic compartments and developmental regulation at tDNA loci. Epigenetics and Chromatin, 2022, 15, .	1.8	7
3026	Nuclear RIPK1 promotes chromatin remodeling to mediate inflammatory response. Cell Research, 2022, 32, 621-637.	5.7	18
3027	An essential role for <scp>PTIP</scp> in mediating Hox gene regulation along <scp>PcG</scp> and <scp>trxG</scp> pathways. FEBS Journal, 2022, 289, 6324-6341.	2.2	0
3028	Identification of aberrant transcription termination at specific gene loci with DNA hypomethylated transcription termination sites caused by DNA methyltransferase deficiency. Genes and Genetic Systems, 2022, 97, 139-152.	0.2	2
3029	Bioinformatics Methods for ChIP-seq Histone Analysis. Methods in Molecular Biology, 2022, , 267-293.	0.4	0
3031	Chromatin accessibility analysis from fresh and cryopreserved human ovarian follicles. Molecular Human Reproduction, 2022, 28, .	1.3	2
3033	Structural variant-based pangenome construction has low sensitivity to variability of haplotype-resolved bovine assemblies. Nature Communications, 2022, 13, .	5.8	19
3034	LncRNA <i>RUS</i> shapes the gene expression program towards neurogenesis. Life Science Alliance, 2022, 5, e202201504.	1.3	5
3035	Context-dependent enhancer function revealed by targeted inter-TAD relocation. Nature Communications, 2022, 13, .	5.8	8
3036	Hyaluronic acidâ€"GPRC5C signalling promotes dormancy in haematopoietic stem cells. Nature Cell Biology, 2022, 24, 1038-1048.	4.6	24
3038	Cell fate roadmap of human primed-to-naive transition reveals preimplantation cell lineage signatures. Nature Communications, 2022, 13, .	5.8	10
3039	Chromatin structure can introduce systematic biases in genome-wide analyses of Plasmodium falciparum. Open Research Europe, 0, 2, 75.	2.0	0
3040	Recapitulating early human development with 8C-like cells. Cell Reports, 2022, 39, 110994.	2.9	26
3041	Histone Deacetylase 6 Inhibitor JS28 Prevents Pathological Gene Expression in Cardiac Myocytes. Journal of the American Heart Association, 2022, 11, .	1.6	3

#	Article	IF	Citations
3042	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
3044	Integrated multi-omics reveal polycomb repressive complex 2 restricts human trophoblast induction. Nature Cell Biology, 2022, 24, 858-871.	4.6	30
3045	STAT5 does not drive steroid resistance in T-cell acute lymphoblastic leukemia despite the activation of <i>BCL2</i> and <i>BCLXL</i> following glucocorticoid treatment. Haematologica, 0, , .	1.7	3
3046	Increased gene dosage and mRNA expression from chromosomal duplications in <i>Caenorhabditis elegans</i>. G3: Genes, Genomes, Genetics, 2022, 12, .	0.8	2
3047	Comparative interactome analysis of the PRE DNA-binding factors: purification of the Combgap-, Zeste-, Psq-, and Adf1-associated proteins. Cellular and Molecular Life Sciences, 2022, 79, .	2.4	9
3049	Oncofusion-driven de novo enhancer assembly promotes malignancy in Ewing sarcoma via aberrant expression of the stereociliary protein LOXHD1. Cell Reports, 2022, 39, 110971.	2.9	6
3050	ARID1A loss derepresses a group of human endogenous retrovirus-H loci to modulate BRD4-dependent transcription. Nature Communications, 2022, 13, .	5.8	7
3051	Comparative parallel multi-omics analysis during the induction of pluripotent and trophectoderm states. Nature Communications, 2022, 13, .	5.8	4
3052	Integrating chromatin accessibility states in the design of targeted sequencing panels for liquid biopsy. Scientific Reports, 2022, 12, .	1.6	2
3053	Genomic analysis of Rad26 and Rad1â€“Rad10 reveals differences in their dependence on Mediator and RNA polymerase II. Genome Research, 2022, 32, 1516-1528.	2.4	1
3054	Defining pervasive transcription units usingÂchromatinÂRNA-sequencing data. STAR Protocols, 2022, 3, 101442.	0.5	1
3055	Machine-learning-optimized Cas12a barcoding enables the recovery of single-cell lineages and transcriptional profiles. Molecular Cell, 2022, 82, 3103-3118.e8.	4.5	14
3057	Identification of mechanism of cancer-cell-specific reactivation of <i>hTERT</i> offers therapeutic opportunities for blocking telomerase specifically in human colorectal cancer. Nucleic Acids Research, 2023, 51, 1-16.	6.5	10
3062	EZH2 endorses cell plasticity to non-small cell lung cancer cells facilitating mesenchymal to epithelial transition and tumour colonization. Oncogene, 2022, 41, 3611-3624.	2.6	6
3064	Sex-specific variation in R-loop formation in Drosophila melanogaster. PLoS Genetics, 2022, 18, e1010268.	1.5	3
3065	Thymic epithelial cells co-opt lineage-defining transcription factors to eliminate autoreactive TÂcells. Cell, 2022, 185, 2542-2558.e18.	13.5	63
3067	SMARCE1 deficiency generates a targetable mSWI/SNF dependency in clear cell meningioma. Nature Genetics, 2022, 54, 861-873.	9.4	16
3068	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

#	Article	IF	Citations
3070	ZFP281-BRCA2 prevents R-loop accumulation during DNA replication. Nature Communications, 2022, 13, .	5.8	12
3071	Transcriptomic and epigenomic analyses explore the potential role of H3K4me3 in neomycin-induced cochlear Lgr5+â€‰progenitor cell regeneration of hair cells. Human Cell, 2022, 35, 1030-1044.	1.2	3
3073	Foxa2 and Pet1 Direct and Indirect Synergy Drive Serotonergic Neuronal Differentiation. Frontiers in Neuroscience, 0, 16, .	1.4	1
3074	Nucleome programming is required for the foundation of totipotency in mammalian germline development. EMBO Journal, 2022, 41, .	3.5	9
3075	Dynamic profiling and functional interpretation of histone lysine crotonylation and lactylation during neural development. Development (Cambridge), 2022, 149, .	1.2	30
3076	SpyChIP identifies cell type-specific transcription factor occupancy from complex tissues. Proceedings of the National Academy of Sciences of the United States of America, 2022, 119, .	3.3	1
3078	Epstein-Barr Virus (EBV) Is Mostly Latent and Clonal in Angioimmunoblastic T Cell Lymphoma (AITL). Cancers, 2022, 14, 2899.	1.7	4
3079	Genomic Profiling of HIV-1 Integration in Microglia Cells Links Viral Integration to TAD Organization. SSRN Electronic Journal, 0, , .	0.4	0
3081	A novel SNF2 ATPase complex in Trypanosoma brucei with a role in H2A.Z-mediated chromatin remodelling. PLoS Pathogens, 2022, 18, e1010514.	2.1	7
3082	Genes Possessing the Most Frequent DNA DSBs Are Highly Associated with Development and Cancers, and Essentially Overlap with the rDNA-Contacting Genes. International Journal of Molecular Sciences, 2022, 23, 7201.	1.8	2
3083	Drug-Induced Epigenomic Plasticity Reprograms Circadian Rhythm Regulation to Drive Prostate Cancer toward Androgen Independence. Cancer Discovery, 2022, 12, 2074-2097.	7.7	22
3084	Coordinated Transcriptional and Catabolic Programs Support Iron-Dependent Adaptation to RASâ€“MAPK Pathway Inhibition in Pancreatic Cancer. Cancer Discovery, 2022, 12, 2198-2219.	7.7	32
3087	ChIP-seq Analysis of Histone H3K27ac and H3K27me3 Showing Different Distribution Patterns in Chromatin. Biomedical Science Letters, 2022, 28, 109-119.	0.0	0
3090	<scp>TRIM33</scp> drives prostate tumor growth by stabilizing androgen receptor from Skp2â€mediated degradation. EMBO Reports, 2022, 23, .	2.0	9
3091	GoPeaks: histone modification peak calling for CUT&Tag. Genome Biology, 2022, 23, .	3.8	9
3092	The megabase-scale crossover landscape is largely independent of sequence divergence. Nature Communications, 2022, 13, .	5.8	25
3093	Epigenetic modulators of B cell fate identified through coupled phenotype-transcriptome analysis. Cell Death and Differentiation, 2022, 29, 2519-2530.	5.0	5
3095	The additional <scp>PRC2</scp> subunit and Sin3 histone deacetylase complex are required for the normal distribution of <scp>H3K27me3</scp> occupancy and transcriptional silencing in <i>Magnaporthe oryzae</i>. New Phytologist, 2022, 236, 576-589.	3.5	8

#	ARTICLE	IF	CITATIONS
3096	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
3097	An integrated model for termination of RNA polymerase III transcription. Science Advances, 2022, 8, .	4.7	14
3098	KHSRP combines transcriptional and posttranscriptional mechanisms to regulate monocytic differentiation. Blood Science, 0, Publish Ahead of Print, .	0.4	1
3099	<scp>ASCL1</scp> regulates superâ€enhancerâ€associated <scp>miRNAs</scp> to define molecular subtypes of small cell lung cancer. Cancer Science, 2022, 113, 3932-3946.	1.7	8
3100	A de novo genome assembly of <i>Solanum verrucosum</i> Schlechtendal, a Mexican diploid species geographically isolated from other diploid A-genome species of potato relatives. G3: Genes, Genomes, Genetics, 0, , .	0.8	2
3101	NF-ÎºB signaling controls H3K9me3 levels at intronic LINE-1 and hematopoietic stem cell genes in cis. Journal of Experimental Medicine, 2022, 219, .	4.2	4
3102	Temporal resolution of gene derepression and proteome changes upon PROTAC-mediated degradation of BCL11A protein in erythroid cells. Cell Chemical Biology, 2022, 29, 1273-1287.e8.	2.5	14
3103	Kinetic principles underlying pioneer function of GAGA transcription factor in live cells. Nature Structural and Molecular Biology, 2022, 29, 665-676.	3.6	35
3104	Sox9 directs divergent epigenomic states in brain tumor subtypes. Proceedings of the National Academy of Sciences of the United States of America, 2022, 119, .	3.3	6
3105	Distinct p53 isoforms code for opposing transcriptional outcomes. Developmental Cell, 2022, 57, 1833-1846.e6.	3.1	5
3106	<scp>PGE₂â€EP3</scp> axis promotes brown adipose tissue formation through stabilization of <scp>WTAP RNA</scp> methyltransferase. EMBO Journal, 2022, 41, .	3.5	9
3108	Genome-wide identification of functional enhancers and their potential roles in pig breeding. Journal of Animal Science and Biotechnology, 2022, 13, .	2.1	3
3109	Transition to a mesenchymal state in neuroblastoma confers resistance to anti-GD2 antibody via reduced expression of ST8SIA1. Nature Cancer, 2022, 3, 976-993.	5.7	23
3110	Comparison of chromatin accessibility landscapes during early development of prefrontal cortex between rhesus macaque and human. Nature Communications, 2022, 13, .	5.8	7
3112	Potent Stimulation of the Androgen Receptor Instigates a Viral Mimicry Response in Prostate Cancer. Cancer Research Communications, 2022, 2, 706-724.	0.7	3
3113	Cis-regulatory chromatin loops analysis identifies GRHL3 as a master regulator of surface epithelium commitment. Science Advances, 2022, 8, .	4.7	3
3115	H3K27me3 shapes DNA methylome by inhibiting UHRF1-mediated H3 ubiquitination. Science China Life Sciences, 2022, 65, 1685-1700.	2.3	4
3116	Z-DNA is remodelled by ZBTB43 in prospermatogonia to safeguard the germline genome and epigenome. Nature Cell Biology, 2022, 24, 1141-1153.	4.6	8

#	ARTICLE	IF	CITATIONS
3119	ALBA proteins confer thermotolerance through stabilizing HSF messenger RNAs in cytoplasmic granules. Nature Plants, 2022, 8, 778-791.	4.7	24
3120	Determination of human DNA replication origin position and efficiency reveals principles of initiation zone organisation. Nucleic Acids Research, 2022, 50, 7436-7450.	6.5	18
3121	RPA1 controls chromatin architecture and maintains lipid metabolic homeostasis. Cell Reports, 2022, 40, 111071.	2.9	6
3123	Dissecting the treatment-naive ecosystem of human melanoma brain metastasis. Cell, 2022, 185, 2591-2608.e30.	13.5	62
3124	Recruitment of the CoREST transcription repressor complexes by Nerve Growth factor IB-like receptor (Nurr1/NR4A2) mediates silencing of HIV in microglial cells. PLoS Pathogens, 2022, 18, e1010110.	2.1	9
3130	PHF20 is crucial for epigenetic control of starvation-induced autophagy through enhancer activation. Nucleic Acids Research, 2022, 50, 7856-7872.	6.5	6
3133	Dynamic reprogramming of H3K9me3 at hominoid-specific retrotransposons during human preimplantation development. Cell Stem Cell, 2022, 29, 1031-1050.e12.	5.2	34
3135	Epigenomics of conventional type-I dendritic cells depicted preferential control of TLR9 versus TLR3 response by NCoR1 through differential IRF3 activation. Cellular and Molecular Life Sciences, 2022, 79, .	2.4	2
3136	Plasma contains ultrashort single-stranded DNA in addition to nucleosomal cell-free DNA. IScience, 2022, 25, 104554.	1.9	18
3138	TGFÎ² reprograms TNF stimulation of macrophages towards a non-canonical pathway driving inflammatory osteoclastogenesis. Nature Communications, 2022, 13, .	5.8	21
3139	IRF8 deficiency induces the transcriptional, functional, and epigenetic reprogramming of cDC1 into the cDC2 lineage. Immunity, 2022, 55, 1431-1447.e11.	6.6	16
3140	Rearrangement with the <i>nkd2</i> promoter contributed to allelic diversity of the <i>r1</i> gene in maize (<i>Zea mays</i>). Plant Journal, 0, , .	2.8	0
3141	TFEB induces mitochondrial itaconate synthesis to suppress bacterial growth in macrophages. Nature Metabolism, 2022, 4, 856-866.	5.1	35
3142	Polycomb-lamina antagonism partitions heterochromatin at the nuclear periphery. Nature Communications, 2022, 13, .	5.8	8
3144	The transcriptional repressors VAL1 and VAL2 mediate genome-wide recruitment of the CHD3 chromatin remodeler PICKLE in Arabidopsis. Plant Cell, 2022, 34, 3915-3935.	3.1	6
3146	Identification of candidate enhancers controlling the transcriptome during the formation of interphalangeal joints. Scientific Reports, 2022, 12, .	1.6	2
3147	Chromatin accessibility shapes meiotic recombination in mouse primordial germ cells through assisting double-strand breaks and loop formation. Biochimica Et Biophysica Acta - Gene Regulatory Mechanisms, 2022, , 194844.	0.9	0
3150	The BASP1 transcriptional corepressor modifies chromatin through lipid-dependent and lipid-independent mechanisms. IScience, 2022, 25, 104796.	1.9	5

#	Article	IF	Citations
3152	Robertsonian Fusion and Centromere Repositioning Contributed to the Formation of Satellite-free Centromeres During the Evolution of Zebras. Molecular Biology and Evolution, 2022, 39, .	3.5	7
3154	Human 5-lipoxygenase regulates transcription by association to euchromatin. Biochemical Pharmacology, 2022, 203, 115187.	2.0	6
3156	SUPT3H-less SAGA coactivator can assemble and function without significantly perturbing RNA polymerase II transcription in mammalian cells. Nucleic Acids Research, 2022, 50, 7972-7990.	6.5	2
3157	Convergent biological pathways underlying the Kallmann syndrome-linked genes <i>Hs6st1</i> and <i>Fgfr1</i>. Human Molecular Genetics, 2022, 31, 4207-4216.	1.4	5
3158	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
3159	Enrichment of centromeric DNA from human cells. PLoS Genetics, 2022, 18, e1010306.	1.5	2
3161	Global and precise identification of functional <scp>miRNA</scp> targets in <scp>mESCs</scp> by integrative analysis. EMBO Reports, 2022, 23, .	2.0	5
3162	Parasitic plant small RNA analyses unveil parasite-specific signatures of microRNA retention, loss, and gain. Plant Physiology, 2022, 190, 1242-1259.	2.3	7
3163	Extensive co-binding and rapid redistribution of NANOG and GATA6 during emergence of divergent lineages. Nature Communications, 2022, 13, .	5.8	19
3164	Systematic histone H4 replacement in <i>Arabidopsis thaliana</i> reveals a role for H4R17 in regulating flowering time. Plant Cell, 2022, 34, 3611-3631.	3.1	8
3165	MPST sulfurtransferase maintains mitochondrial protein import and cellular bioenergetics to attenuate obesity. Journal of Experimental Medicine, 2022, 219, .	4.2	14
3167	Limitations of mouse models for sickle cell disease conferred by their human globin transgene configurations. DMM Disease Models and Mechanisms, 2022, 15, .	1.2	9
3168	SOX9 reprograms endothelial cells by altering the chromatin landscape. Nucleic Acids Research, 2022, 50, 8547-8565.	6.5	12
3170	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
3171	Structural variation turnovers and defective genomes: key drivers for the in vitro evolution of the large double-stranded DNA koi herpesvirus (KHV). , 0, 2, .		2
3172	MPP6 stimulates both RRP6 and DIS3 to degrade a specified subset of MTR4-sensitive substrates in the human nucleus. Nucleic Acids Research, 2022, 50, 8779-8806.	6.5	3
3173	CDK9 activity switch associated with AFF1 and HEXIM1 controls differentiation initiation from epidermal progenitors. Nature Communications, 2022, 13, .	5.8	7
3174	The HDAC7â€“TET2 epigenetic axis is essential during early B lymphocyte development. Nucleic Acids Research, 2022, 50, 8471-8490.	6.5	4

#	ARTICLE	IF	CITATIONS
3175	Leishmania parasites exchange drug-resistance genes through extracellular vesicles. Cell Reports, 2022, 40, 111121.	2.9	28
3176	Bilineage embryo-like structure from EPS cells can produce live mice with tetraploid trophectoderm. Protein and Cell, 0, , .	4.8	3
3180	High enhancer activity is an epigenetic feature of HPV negative atypical head and neck squamous cell carcinoma. Frontiers in Cell and Developmental Biology, 0, 10, .	1.8	1
3181	Asymmetric subgenomic chromatin architecture impacts on gene expression in resynthesized and natural allopolyploid Brassica napus. Communications Biology, 2022, 5, .	2.0	0
3182	Multi-omics profiling of the cold tolerant Monoraphidium minutum 26B-AM in response to abiotic stress. Algal Research, 2022, 66, 102794.	2.4	3
3184	PRC2-mediated repression is essential to maintain identity and function of differentiated dopaminergic and serotonergic neurons. Science Advances, 2022, 8, .	4.7	8
3186	Context-dependent tumor-suppressive BMP signaling in diffuse intrinsic pontine glioma regulates stemness through epigenetic regulation of CXXC5. Nature Cancer, 2022, 3, 1105-1122.	5.7	14
3187	Rif1 interacts with non-canonical polycomb repressive complex PRC1.6 to regulate mouse embryonic stem cells fate potential. Cell Regeneration, 2022, 11, .	1.1	4
3188	A comparative investigation on H3K27ac enhancer activities in the brain and liver tissues between wild boars and domesticated pigs. Evolutionary Applications, 2022, 15, 1281-1290.	1.5	2
3190	Characterization and perturbation of CTCF-mediated chromatin interactions for enhancing myogenic transdifferentiation. Cell Reports, 2022, 40, 111206.	2.9	10
3193	SOX transcription factors direct TCF-independent WNT/Î²-catenin responsive transcription to govern cell fate in human pluripotent stem cells. Cell Reports, 2022, 40, 111247.	2.9	21
3194	CK2-induced cooperation of HHEX with the YAP-TEAD4 complex promotes colorectal tumorigenesis. Nature Communications, 2022, 13, .	5.8	13
3195	<scp>CDK9</scp> and <scp>PP2A</scp> regulate <scp>RNA</scp> polymerase <scp>II</scp> transcription termination and coupled <scp>RNA</scp> maturation. EMBO Reports, 2022, 23, .	2.0	15
3197	<scp>Lintâ€O</scp> cooperates with L(3)mbt in target gene suppression to maintain homeostasis in fly ovary and brain. EMBO Reports, 2022, 23, .	2.0	2
3199	Histone H3K36me2 and H3K36me3 form a chromatin platform essential for DNMT3A-dependent DNA methylation in mouse oocytes. Nature Communications, 2022, 13, .	5.8	21
3200	Characterization of Transposon-Derived Accessible Chromatin Regions in Rice (Oryza Sativa). International Journal of Molecular Sciences, 2022, 23, 8947.	1.8	2
3201	Paternally inherited H3K27me3 affects chromatin accessibility in mouse embryos produced by round spermatid injection. Development (Cambridge), 2022, 149, .	1.2	8
3202	Comprehensive Analysis of Chromatin Accessibility and Transcriptional Landscape Identified BRCA1 Repression as a Potential Pathological Factor for Keloid. Polymers, 2022, 14, 3391.	2.0	0

#	Article	IF	Citations
3203	Repeat-based holocentromeres influence genome architecture and karyotype evolution. Cell, 2022, 185, 3153-3168.e18.	13.5	52
3204	dbEmbryo multi-omics database for analyses of synergistic regulation in early mammalian embryo development. Genome Research, 2022, 32, 1612-1625.	2.4	2
3205	Maternal H3K36 and H3K27 HMTs protect germline development via regulation of the transcription factor LIN-15B. ELife, 0, 11, .	2.8	6
3208	Temporal analysis of enhancers during mouse cerebellar development reveals dynamic and novel regulatory functions. ELife, 0, 11, .	2.8	7
3210	A complex epigenome-splicing crosstalk governs epithelial-to-mesenchymal transition in metastasis and brain development. Nature Cell Biology, 2022, 24, 1265-1277.	4.6	11
3211	The landscape of Chlamydomonas histone <scp>H3</scp> lysine 4 methylation reveals both constant features and dynamic changes during the diurnal cycle. Plant Journal, 2022, 112, 352-368.	2.8	3
3212	PRC1-mediated epigenetic programming is required to generate the ovarian reserve. Nature Communications, 2022, 13, .	5.8	9
3214	Neonatal BCG vaccination is associated with a long-term DNA methylation signature in circulating monocytes. Science Advances, 2022, 8, .	4.7	29
3217	STAG2 promotes the myelination transcriptional program in oligodendrocytes. ELife, 0, 11, .	2.8	7
3218	Distinct, opposing functions for CFIm59 and CFIm68 in mRNA alternative polyadenylation of <i>Pten</i> and in the PI3K/Akt signalling cascade. Nucleic Acids Research, 2022, 50, 9397-9412.	6.5	3
3221	The mismatch-repair proteins MSH2 and MSH6 interact with the imprinting control regions through the ZFP57-KAP1 complex. Epigenetics and Chromatin, 2022, 15, .	1.8	0
3222	Xist exerts gene-specific silencing during XCI maintenance and impacts lineage-specific cell differentiation and proliferation during hematopoiesis. Nature Communications, 2022, 13, .	5.8	9
3223	Clostridium autoethanogenum isopropanol production via native plasmid pCA replicon. Frontiers in Bioengineering and Biotechnology, 0, 10, .	2.0	1
3225	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
3226	The SWI/SNF chromatin remodeling factor DPF3 regulates metastasis of ccRCC by modulating TGF-Î² signaling. Nature Communications, 2022, 13, .	5.8	9
3227	Selective TnsC recruitment enhances the fidelity of RNA-guided transposition. Nature, 2022, 609, 384-393.	13.7	34
3228	Nascent transcriptome reveals orchestration of zygotic genome activation in early embryogenesis. Current Biology, 2022, 32, 4314-4324.e7.	1.8	7
3229	Chromatin conformation of human oral epithelium can identify orofacial cleft missing functional variants. International Journal of Oral Science, 2022, 14, .	3.6	4

#	Article	IF	Citations
3230	<scp>Genomeâ€wide</scp> prediction of activating regulatory elements in rice by combining <scp>STARR</scp>â€seq with <scp>FACS</scp>. Plant Biotechnology Journal, 2022, 20, 2284-2297.	4.1	8
3233	CTCF DNA-binding domain undergoes dynamic and selective proteinâ€“protein interactions. IScience, 2022, 25, 105011.	1.9	6
3235	ATRX histone binding and helicase activities have distinct roles in neuronal differentiation. Nucleic Acids Research, 2022, 50, 9162-9174.	6.5	4
3236	Direct chemical reprogramming of human cord blood erythroblasts to induced megakaryocytes that produce platelets. Cell Stem Cell, 2022, 29, 1229-1245.e7.	5.2	5
3237	Mitotic DNA synthesis is caused by transcription-replication conflicts in BRCA2-deficient cells. Molecular Cell, 2022, 82, 3382-3397.e7.	4.5	17
3238	Identification of putative enhancer-like elements predicts regulatory networks active in planarian adult stem cells. ELife, 0, 11, .	2.8	9
3239	Phenotypic heterogeneity driven by plasticity of the intermediate EMT state governs disease progression and metastasis in breast cancer. Science Advances, 2022, 8, .	4.7	55
3240	Warburg-like metabolic transformation underlies neuronal degeneration in sporadic Alzheimerâ€™s disease. Cell Metabolism, 2022, 34, 1248-1263.e6.	7.2	55
3241	SPT6 functions in transcriptional pause/release via PAF1C recruitment. Molecular Cell, 2022, 82, 3412-3423.e5.	4.5	22
3242	PDS5A and PDS5B differentially affect gene expression without altering cohesin localization across the genome. Epigenetics and Chromatin, 2022, 15, .	1.8	1
3243	<scp>m6A</scp> is required for resolving progenitor identity during planarian stem cell differentiation. EMBO Journal, 2022, 41, .	3.5	11
3245	Relationships between genome-wide R-loop distribution and classes of recurrent DNA breaks in neural stem/progenitor cells. Scientific Reports, 2022, 12, .	1.6	4
3246	SUPPRESSOR OF PHYTOCHROME B-4Â#3 reduces the expression of PIF-activated genes and increases expression of growth repressors to regulate hypocotyl elongation in short days. BMC Plant Biology, 2022, 22, .	1.6	0
3247	Competitive binding of TET1 and DNMT3A/B cooperates the DNA methylation pattern in human embryonic stem cells. Biochimica Et Biophysica Acta - Gene Regulatory Mechanisms, 2022, 1865, 194861.	0.9	2
3250	S1-END-seq reveals DNA secondary structures in human cells. Molecular Cell, 2022, 82, 3538-3552.e5.	4.5	16
3251	Rvb1/Rvb2 proteins couple transcription and translation during glucose starvation. ELife, 0, 11, .	2.8	2
3253	Distinct Cell Adhesion Signature Defines Glioblastoma Myeloid-Derived Suppressor Cell Subsets. Cancer Research, 2022, 82, 4274-4287.	0.4	11
3254	Macrophage TGF-Î² signaling is critical for wound healing with heterotopic ossification after trauma. JCI Insight, 2022, 7, .	2.3	9

#	Article	IF	Citations
3255	Homeodomain Proteins Hierarchically Specify Neuronal Diversity and Synaptic Connectivity. SSRN Electronic Journal, 0, , .	0.4	0
3256	The synergistic interaction landscape of chromatin regulators reveals their epigenetic regulation mechanisms across five cancer cell lines. Computational and Structural Biotechnology Journal, 2022, 20, 5028-5039.	1.9	1
3257	Psychiatric risk gene transcription factor 4 preferentially regulates cortical interneuron neurogenesis during early brain development. Journal of Biomedical Research, 2022, 36, 242.	0.7	2
3258	GenoREC: A Recommendation System for Interactive Genomics Data Visualization. IEEE Transactions on Visualization and Computer Graphics, 2023, 29, 570-580.	2.9	5
3259	THOC5 Complexes With DDX5, DDX17 and CDK12 Are Essential in Primitive Cell Survival to Regulate R Loop Structures and Transcription Elongation Rate. SSRN Electronic Journal, 0, , .	0.4	1
3262	GRHL2 Enhances Phosphorylated Estrogen Receptor (ER) Chromatin Binding and Regulates ER-Mediated Transcriptional Activation and Repression. Molecular and Cellular Biology, 2022, 42, .	1.1	3
3265	NODULIN HOMEOBOX is required for heterochromatin homeostasis in Arabidopsis. Nature Communications, 2022, 13, .	5.8	5
3266	Npas3 deficiency impairs cortical astrogenesis and induces autistic-like behaviors. Cell Reports, 2022, 40, 111289.	2.9	4
3267	SMNDC1 links chromatin remodeling and splicing to regulate pancreatic hormone expression. Cell Reports, 2022, 40, 111288.	2.9	4
3268	Mapping of promoter usage QTL using RNA-seq data reveals their contributions to complex traits. PLoS Computational Biology, 2022, 18, e1010436.	1.5	2
3269	RBM45 is an m6A-binding protein that affects neuronal differentiation and the splicing of a subset of mRNAs. Cell Reports, 2022, 40, 111293.	2.9	13
3271	Changes in chromatin accessibility are not concordant with transcriptional changes for singleâ€factor perturbations. Molecular Systems Biology, 2022, 18, .	3.2	22
3275	Novel viral splicing events and open reading frames revealed by long-read direct RNA sequencing of adenovirus transcripts. PLoS Pathogens, 2022, 18, e1010797.	2.1	7
3276	PRC2-indepdendent actions of H3.3K27M in embryonic stem cell differentiation. Nucleic Acids Research, 0, , .	6.5	3
3277	Repression and 3D-restructuring resolves regulatory conflicts in evolutionarily rearranged genomes. Cell, 2022, 185, 3689-3704.e21.	13.5	25
3280	Widespread association of the Argonaute protein AGO2 with meiotic chromatin suggests a distinct nuclear function in mammalian male reproduction. Genome Research, 2022, 32, 1655-1668.	2.4	7
3282	Single-cell sequencing reveals activation of core transcription factors in PRC2-deficient malignant peripheral nerve sheath tumor. Cell Reports, 2022, 40, 111363.	2.9	4
3284	RNA Polymerase II â€œPauseâ€•Prepares Promoters for Upcoming Transcription during Drosophila Development. International Journal of Molecular Sciences, 2022, 23, 10662.	1.8	1

#	ARTICLE	IF	CITATIONS
3285	RSC and GRFs confer promoter directionality by restricting divergent noncoding transcription. Life Science Alliance, 2022, 5, e202201394.	1.3	3
3286	Architecture, Chromatin and Gene Organization of Toxoplasma gondii Subtelomeres. Epigenomes, 2022, 6, 29.	0.8	8
3287	Genomeâ€wide analysis of bivalent histone modifications during <i>Drosophila</i> embryogenesis. Genesis, 0, , .	0.8	0
3288	Target-enriched nanopore sequencing and de novo assembly reveals co-occurrences of complex on-target genomic rearrangements induced by CRISPR-Cas9 in human cells. Genome Research, 0, , .	2.4	9
3290	DNA methylation landscapes from pigâ€™s limbic structures underline regulatory mechanisms relevant for brain plasticity. Scientific Reports, 2022, 12, .	1.6	0
3291	Sir2 and Reb1 antagonistically regulate nucleosome occupancy in subtelomeric X-elements and repress TERRAs by distinct mechanisms. PLoS Genetics, 2022, 18, e1010419.	1.5	2
3293	Prenatal immune stress blunts microglia reactivity, impairing neurocircuitry. Nature, 2022, 610, 327-334.	13.7	30
3294	Genome-wide analysis of the FOXA1 transcriptional regulatory network identifies super enhancer associated LncRNAs in tamoxifen resistance. Frontiers in Genetics, 0, 13, .	1.1	3
3295	Mitochondrial stress induces AREG expression and epigenomic remodeling through c-JUN and YAP-mediated enhancer activation. Nucleic Acids Research, 2022, 50, 9765-9779.	6.5	5
3298	Functional genomics uncovers the transcription factor BNC2 as required for myofibroblastic activation in fibrosis. Nature Communications, 2022, 13, .	5.8	11
3299	Genome-scale RNA interference profiling of Trypanosoma brucei cell cycle progression defects. Nature Communications, 2022, 13, .	5.8	7
3300	The <scp>AraC</scp> â€type transcription factor <scp>TagK</scp> is a new player in the signaling cascade that induces the antiâ€eukaryotic <scp>T6SS</scp> of <i>Xanthomonas citri</i>. Molecular Microbiology, 0, , .	1.2	0
3301	Distinct role of subunits of the Arabidopsis RNA polymerase II elongation factor PAF1C in transcriptional reprogramming. Frontiers in Plant Science, 0, 13, .	1.7	6
3302	MYPT1-PP1Î² phosphatase negatively regulates both chromatin landscape and co-activator recruitment for beige adipogenesis. Nature Communications, 2022, 13, .	5.8	3
3304	ER stress transforms random olfactory receptor choice into axon targeting precision. Cell, 2022, 185, 3896-3912.e22.	13.5	15
3306	Dynamical modeling of the H3K27 epigenetic landscape in mouse embryonic stem cells. PLoS Computational Biology, 2022, 18, e1010450.	1.5	7
3307	DNA replication timing directly regulates the frequency of oncogenic chromosomal translocations. Science, 2022, 377, .	6.0	15
3308	Dual genome-wide coding and lncRNA screens in neural induction of induced pluripotent stem cells. Cell Genomics, 2022, 2, 100177.	3.0	10

#	ARTICLE	IF	CITATIONS
3309	Ectopic expression of meiotic cohesin generates chromosome instability in cancer cell line. Proceedings of the National Academy of Sciences of the United States of America, 2022, 119, .	3.3	6
3314	Microtubule integrity regulates budding yeast RAM pathway gene expression. Frontiers in Cell and Developmental Biology, 0, 10, .	1.8	1
3315	Variant Polycomb complexes in <i>Drosophila</i> consistent with ancient functional diversity. Science Advances, 2022, 8, .	4.7	12
3316	A direct comparison between AML1-ETO and ETO2-GLIS2 leukemia fusion proteins reveals context-dependent binding and regulation of target genes and opposite functions in cell differentiation. Frontiers in Cell and Developmental Biology, 0, 10, .	1.8	1
3318	BAF60c prevents abdominal aortic aneurysm formation through epigenetic control of vascular smooth muscle cell homeostasis. Journal of Clinical Investigation, 2022, 132, .	3.9	10
3320	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
3321	DNA methylation underpins the epigenomic landscape regulating genome transcription in Arabidopsis. Genome Biology, 2022, 23, .	3.8	20
3322	The nucleolus is the site for inflammatory RNA decay during infection. Nature Communications, 2022, 13, .	5.8	6
3323	Architecture of the yeast Pol III pre-termination complex and pausing mechanism on poly(dT) termination signals. Cell Reports, 2022, 40, 111316.	2.9	11
3325	Negative supercoils regulate meiotic crossover patterns in budding yeast. Nucleic Acids Research, 2022, 50, 10418-10435.	6.5	3
3326	Chromatin structure can introduce systematic biases in genome-wide analyses of Plasmodium falciparum. Open Research Europe, 0, 2, 75.	2.0	1
3328	A pan-cancer mycobiome analysis reveals fungal involvement in gastrointestinal and lung tumors. Cell, 2022, 185, 3807-3822.e12.	13.5	114
3329	Nitrogen starvation induces genomeâ€wide activation of transposable elements in <i>Arabidopsis</i>. Journal of Integrative Plant Biology, 2022, 64, 2374-2384.	4.1	5
3330	The chromatin accessibility landscape of pistils and anthers in rice. Plant Physiology, 2022, 190, 2797-2811.	2.3	1
3331	Transcriptional dynamics of transposable elements in the type I IFN response in Myotis lucifugus cells. Mobile DNA, 2022, 13, .	1.3	3
3332	Suppression of ACE2 SUMOylation protects against SARS-CoV-2 infection through TOLLIP-mediated selective autophagy. Nature Communications, 2022, 13, .	5.8	22
3335	RNA m6A regulates transcription via DNA demethylation and chromatin accessibility. Nature Genetics, 2022, 54, 1427-1437.	9.4	49
3338	Regulation of human cortical interneuron development by the chromatin remodeling protein CHD2. Scientific Reports, 2022, 12, .	1.6	1

#	Article	IF	Citations
3339	CTCF acetylation at lysine 20 is required for the early cardiac mesoderm differentiation of embryonic stem cells. Cell Regeneration, 2022, 11, .	1.1	1
3340	EBF1 primes B-lymphoid enhancers and limits the myeloid bias in murine multipotent progenitors. Journal of Experimental Medicine, 2022, 219, .	4.2	8
3341	Epigenetic activation of the FLT3 gene by ZNF384 fusion confers a therapeutic susceptibility in acute lymphoblastic leukemia. Nature Communications, 2022, 13, .	5.8	4
3342	Mettl3-dependent m6A modification attenuates the brain stress response in Drosophila. Nature Communications, 2022, 13, .	5.8	17
3343	Structural insights into molecular mechanism for N6-adenosine methylation by MT-A70 family methyltransferase METTL4. Nature Communications, 2022, 13, .	5.8	18
3344	Acquired semi-squamatization during chemotherapy suggests differentiation as a therapeutic strategy for bladder cancer. Cancer Cell, 2022, 40, 1044-1059.e8.	7.7	18
3345	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
3346	An LKB1â€"mitochondria axis controls TH17 effector function. Nature, 2022, 610, 555-561.	13.7	24
3348	<scp><i>MtING2</i></scp> encodes an <scp>ING</scp> domain <scp>PHD</scp> finger protein which affects Medicago growth, flowering, global patterns of <scp>H3K4me3</scp>, and gene expression. Plant Journal, 2022, 112, 1029-1050.	2.8	3
3350	Regulation of cohesinâ€mediated chromosome folding by <scp>PDS5</scp> in mammals. EMBO Reports, 0, , .	2.0	1
3351	Regulatory chromatin rewiring promotes metabolic switching during adaptation to oncogenic receptor tyrosine kinase inhibition. Oncogene, 2022, 41, 4808-4822.	2.6	2
3352	EWS/FLI mediated reprogramming of 3D chromatin promotes an altered transcriptional state in Ewing sarcoma. Nucleic Acids Research, 2022, 50, 9814-9837.	6.5	17
3353	The conservation of human functional variants and their effects across livestock species. Communications Biology, 2022, 5, .	2.0	6
3354	Slow RNAPII Transcription Elongation Rate, Low Levels of RNAPII Pausing, and Elevated Histone H1 Content at Promoters Associate with Higher m6A Deposition on Nascent mRNAs. Genes, 2022, 13, 1652.	1.0	1
3355	Non-coding RNAs associated with Praderâ€"Willi syndrome regulate transcription of neurodevelopmental genes in human induced pluripotent stem cells. Human Molecular Genetics, 2023, 32, 608-620.	1.4	5
3358	Epigenetic remodeling by vitamin C potentiates plasma cell differentiation. ELife, 0, 11, .	2.8	7
3359	Functional characterization of enhancer activity during a long terminal repeat's evolution. Genome Research, 0, , .	2.4	4
3360	MYC oncogene elicits tumorigenesis associated with embryonic, ribosomal biogenesis, and tissue-lineage dedifferentiation gene expression changes. Oncogene, 2022, 41, 4960-4970.	2.6	8

#	ARTICLE	IF	CITATIONS
3361	Translatome and transcriptome co-profiling reveals a role of TPRXs in human zygotic genome activation. Science, 2022, 378, .	6.0	46
3362	p300/CBP sustains Polycomb silencing by non-enzymatic functions. Molecular Cell, 2022, 82, 3580-3597.e9.	4.5	9
3363	HITS-CLIP analysis of human ALKBH8 reveals interactions with fully processed substrate tRNAs and with specific noncoding RNAs. Rna, 0, , rna.079421.122.	1.6	1
3364	Type 1 and Type 2 Epstein-Barr viruses induce proliferation, and inhibit differentiation, in infected telomerase-immortalized normal oral keratinocytes. PLoS Pathogens, 2022, 18, e1010868.	2.1	2
3365	The TRIPLE PHD FINGERS proteins are required for SWI/SNF complex-mediatedÂ+1 nucleosome positioning and transcription start site determination in Arabidopsis. Nucleic Acids Research, 2022, 50, 10399-10417.	6.5	19
3366	The Drosophila ZAD zinc finger protein Kipferl guides Rhino to piRNA clusters. ELife, 0, 11, .	2.8	25
3368	Cooperative ETS transcription factors enforce adult endothelial cell fate and cardiovascular homeostasis. , 2022, 1, 882-899.		5
3369	A noncoding single-nucleotide polymorphism at 8q24 drives <i>IDH1</i> -mutant glioma formation. Science, 2022, 378, 68-78.	6.0	20
3370	Dissection of the MEF2D-IRF8 transcriptional circuit dependency in acute myeloid leukemia. IScience, 2022, 25, 105139.	1.9	1
3371	Bacterial Transcription Factors Bind to Coding Regions and Regulate Internal Cryptic Promoters. MBio, 2022, 13, .	1.8	4
3373	Profiling RNA at chromatin targets in situ by antibody-targeted tagmentation. Nature Methods, 2022, 19, 1383-1392.	9.0	9
3374	The inÂvivo Interaction Landscape of Histones H3.1 and H3.3. Molecular and Cellular Proteomics, 2022, 21, 100411.	2.5	6
3375	Chromatin architectural alterations due to null mutation of a major CG methylase in rice. Journal of Integrative Plant Biology, 2022, 64, 2396-2410.	4.1	4
3376	Progression of prostate cancer reprograms MYC-mediated lipid metabolism via lysine methyltransferase 2A. Discover Oncology, 2022, 13, .	0.8	2
3377	The human mitochondrial genome contains a second light strand promoter. Molecular Cell, 2022, 82, 3646-3660.e9.	4.5	16
3379	Cross-lineage potential of Ascl1 uncovered by comparing diverse reprogramming regulatomes. Cell Stem Cell, 2022, 29, 1491-1504.e9.	5.2	19
3380	Genome-Wide Analysis Reveals that PhoP Regulates Pathogenicity in Riemerella anatipestifer. Microbiology Spectrum, 2022, 10, .	1.2	3
3381	CTCFâ€“CTCF loops and intra-TAD interactions show differential dependence on cohesin ring integrity. Nature Cell Biology, 2022, 24, 1516-1527.	4.6	22

#	ARTICLE	IF	CITATIONS
3383	Enhancer reprogramming promotes the activation of cancer-associated fibroblasts and breast cancer metastasis. Theranostics, 2022, 12, 7491-7508.	4.6	3
3385	Uncovering the Relationship between Tissue-Specific TF-DNA Binding and Chromatin Features through a Transformer-Based Model. Genes, 2022, 13, 1952.	1.0	5
3387	<scp>CBP</scp>/p300 and <scp>HDAC</scp> activities regulate <scp>H3K27</scp> acetylation dynamics and zygotic genome activation in mouse preimplantation embryos. EMBO Journal, 2022, 41, .	3.5	28
3388	A FOXO1-dependent transcription network is a targetable vulnerability of mantle cell lymphomas. Journal of Clinical Investigation, 2022, 132, .	3.9	8
3389	Barley FASCIATED EAR genes determine inflorescence meristem size and yield traits. Crop Journal, 2023, 11, 679-691.	2.3	4
3390	The m6A reader IGF2BP2 regulates glutamine metabolism and represents a therapeutic target in acute myeloid leukemia. Cancer Cell, 2022, 40, 1566-1582.e10.	7.7	58
3391	Rescue of deficits by Brwd1 copy number restoration in the Ts65Dn mouse model of Down syndrome. Nature Communications, 2022, 13, .	5.8	7
3392	Population genomics of an icefish reveals mechanisms of glacier-driven adaptive radiation in Antarctic notothenioids. BMC Biology, 2022, 20, .	1.7	5
3393	A quantitative metric of pioneer activity reveals that HNF4A has stronger in vivo pioneer activity than FOXA1. Genome Biology, 2022, 23, .	3.8	12
3394	<i>HIRA</i> loss transforms <i>FH</i> -deficient cells. Science Advances, 2022, 8, .	4.7	5
3395	Chromatin remodeling is required for <scp>sRNA</scp>â€guided <scp>DNA</scp> elimination in <i>Paramecium</i>. EMBO Journal, 2022, 41, .	3.5	8
3396	Deep cis-regulatory homology of the butterfly wing pattern ground plan. Science, 2022, 378, 304-308.	6.0	23
3397	An evolutionary trade-off between host immunity and metabolism drives fatty liver in male mice. Science, 2022, 378, 290-295.	6.0	17
3398	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
3399	Establishment of 3D chromatin structure after fertilization and the metabolic switch at the morula-to-blastocyst transition require CTCF. Cell Reports, 2022, 41, 111501.	2.9	13
3402	Polycomb group (PcG) proteins prevent the assembly of abnormal synaptonemal complex structures during meiosis. Proceedings of the National Academy of Sciences of the United States of America, 2022, 119, .	3.3	1
3404	Immediate Early Proteins of Herpes Simplex Virus Transiently Repress Viral Transcription before Subsequent Activation. Journal of Virology, 2022, 96, .	1.5	4
3405	Generation of mitochondria-rich kidney organoids from expandable intermediate mesoderm progenitors reprogrammed from human urine cells under defined medium. Cell and Bioscience, 2022, 12, .	2.1	4

#	ARTICLE	IF	CITATIONS
3407	Genome-wide chromatin accessibility analysis unveils open chromatin convergent evolution during polyploidization in cotton. Proceedings of the National Academy of Sciences of the United States of America, 2022, 119, .	3.3	13
3409	Characterizing and Targeting Genes Regulated by Transcription Factor MYBL2 in Lung Adenocarcinoma Cells. Cancers, 2022, 14, 4979.	1.7	3
3410	Base editor scanning charts the DNMT3A activity landscape. Nature Chemical Biology, 2023, 19, 176-186.	3.9	17
3412	GATA4 Regulates Developing Endocardium Through Interaction With ETS1. Circulation Research, 2022, 131, .	2.0	6
3413	BAF Complex Maintains Glioma Stem Cells in Pediatric H3K27M Glioma. Cancer Discovery, 0, , OF1-OF26.	7.7	8
3415	Exploring Epigenomic Datasets by ChIPseeker. Current Protocols, 2022, 2, .	1.3	75
3417	Alleleâ€specific expression and chromatin accessibility contribute to heterosis in tea plants (<i>Camellia sinensis</i>). Plant Journal, 2022, 112, 1194-1211.	2.8	17
3418	Multifactorial profiling of epigenetic landscapes at single-cell resolution using MulTI-Tag. Nature Biotechnology, 2023, 41, 708-716.	9.4	27
3419	Topoisomerases I and II facilitate condensin DC translocation to organize and repress X chromosomes in C.Âelegans. Molecular Cell, 2022, 82, 4202-4217.e5.	4.5	4
3421	Spatially resolved epigenomic profiling of single cells in complex tissues. Cell, 2022, 185, 4448-4464.e17.	13.5	60
3424	<scp>Cdt1</scp> overexpression drives colorectal carcinogenesis through origin overlicensing and <scp>DNA</scp> damage. Journal of Pathology, 2023, 259, 10-20.	2.1	3
3425	Distinct roles for CKMâ€"Mediator in controlling Polycomb-dependent chromosomal interactions and priming genes for induction. Nature Structural and Molecular Biology, 2022, 29, 1000-1010.	3.6	7
3426	The characteristics of mRNA m6A methylomes in allopolyploid <i>Brassica napus</i> and its diploid progenitors. Horticulture Research, 2023, 10, .	2.9	2
3428	Loss of CASZ1 tumor suppressor linked to oncogenic subversion of neuroblastoma core regulatory circuitry. Cell Death and Disease, 2022, 13, .	2.7	2
3429	Transcription start site signal profiling improves transposable element RNA expression analysis at locus-level. Frontiers in Genetics, 0, 13, .	1.1	4
3430	G9a Modulates Lipid Metabolism in CD4 T Cells to Regulate Intestinal Inflammation. Gastroenterology, 2023, 164, 256-271.e10.	0.6	6
3431	Epigenome Programming by H3.3K27M Mutation Creates a Dependence of Pediatric Glioma on SMARCA4. Cancer Discovery, 2022, 12, 2906-2929.	7.7	11
3432	Arctic introgression and chromatin regulation facilitated rapid Qinghai-Tibet Plateau colonization by an avian predator. Nature Communications, 2022, 13, .	5.8	9

#	Article	IF	Citations
3434	A critical developmental window for ELAV/Hu-dependent mRNA signatures at the onset of neuronal differentiation. Cell Reports, 2022, 41, 111542.	2.9	2
3436	Resident T _H 2 cells orchestrate adipose tissue remodeling at a site adjacent to infection. Science Immunology, 2022, 7, .	5.6	11
3439	<i>nudt7</i> gene depletion causes transcriptomic change in early development of zebrafish. Journal of Biochemistry, 2023, 173, 53-63.	0.9	0
3440	High-Altitude Stress Orchestrates mRNA Expression and Alternative Splicing of Ovarian Follicle Development Genes in Tibetan Sheep. Animals, 2022, 12, 2812.	1.0	4
3441	FOXA2 drives lineage plasticity and KIT pathway activation in neuroendocrine prostate cancer. Cancer Cell, 2022, 40, 1306-1323.e8.	7.7	33
3443	Involvement of the SAGA and TFIID coactivator complexes in transcriptional dysregulation caused by separation of core and tail Mediator modules. G3: Genes, Genomes, Genetics, 0, , .	0.8	0
3444	LncRNA CCTT-mediated RNA-DNA and RNA-protein interactions facilitate the recruitment of CENP-C to centromeric DNA during kinetochore assembly. Molecular Cell, 2022, 82, 4018-4032.e9.	4.5	9
3445	Temporal analysis suggests a reciprocal relationship between 3D chromatin structure and transcription. Cell Reports, 2022, 41, 111567.	2.9	19
3446	Hippo-Yap Signaling Maintains Sinoatrial Node Homeostasis. Circulation, 2022, 146, 1694-1711.	1.6	8
3447	Selective advantage of epigenetically disrupted cancer cells via phenotypic inertia. Cancer Cell, 2023, 41, 70-87.e14.	7.7	18
3448	The epigenetic state of IL-4-polarized macrophages enables inflammatory cistromic expansion and extended synergistic response to TLR ligands. Immunity, 2022, 55, 2006-2026.e6.	6.6	14
3449	Mechanisms governing target search and binding dynamics of hypoxia-inducible factors. ELife, 0, 11, .	2.8	20
3450	Activation of Pancreatic Acinar FXR Protects against Pancreatitis via Osgin1-Mediated Restoration of Efficient Autophagy. Research, 2022, 2022, .	2.8	5
3452	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
3453	Rearranged Endogenized Plant Pararetroviruses as Evidence of Heritable RNA-based Immunity. Molecular Biology and Evolution, 2023, 40, .	3.5	3
3454	Histone H2B.8 compacts flowering plant sperm through chromatin phase separation. Nature, 2022, 611, 614-622.	13.7	28
3455	Inducible transcriptional condensates drive 3D genome reorganization in the heat shock response. Molecular Cell, 2022, 82, 4386-4399.e7.	4.5	20
3456	GLH-1/Vasa represses neuropeptide expression and drives spermiogenesis in the C.Âelegans germline. Developmental Biology, 2022, 492, 200-211.	0.9	2

#	Article	IF	Citations
3457	InÂvivo, genome-wide profiling of endogenously tagged chromatin-binding proteins with spatial and temporal resolution using NanoDam in Drosophila. STAR Protocols, 2022, 3, 101788.	0.5	0
3458	Chicken chromatin accessibility atlas accelerates epigenetic annotation of birds and gene fine-mapping associated with growth traits. Zoological Research, 2023, 44, 53-62.	0.9	5
3459	<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
3460	Increased chromatin accessibility facilitates intron retention in specific cell differentiation states. Nucleic Acids Research, 2022, 50, 11563-11579.	6.5	8
3461	Therapeutic targeting the oncogenic driver EWSR1::FLI1 in Ewing sarcoma through inhibition of the FACT complex. Oncogene, 0, , .	2.6	4
3462	LACTB exerts tumor suppressor properties in epithelial ovarian cancer through regulation of Slug. Life Science Alliance, 2023, 6, e202201510.	1.3	0
3464	Replication collisions induced by de-repressed S-phase transcription are connected with malignant transformation of adult stem cells. Nature Communications, 2022, 13, .	5.8	1
3465	Characterization of MxiE- and H-NS-Dependent Expression of <i>ipaH7.8</i> , <i>ospC1</i> , <i>yccE</i> , and <i>yfdF</i> in Shigella flexneri. MSphere, 2022, 7, .	1.3	6
3466	Hi-TrAC reveals division of labor of transcription factors in organizing chromatin loops. Nature Communications, 2022, 13, .	5.8	16
3468	Repurposing the lineage-determining transcription factor Atoh1 without redistributing its genomic binding sites. Frontiers in Cell and Developmental Biology, 0, 10, .	1.8	3
3469	Genome-wide map of R-loops reveals its interplay with transcription and genome integrity during germ cell meiosis. Journal of Advanced Research, 2023, 51, 45-57.	4.4	2
3470	A giant virus genome is densely packaged by stable nucleosomes within virions. Molecular Cell, 2022, , .	4.5	7
3471	Somatic XIST activation and features of X chromosome inactivation in male human cancers. Cell Systems, 2022, 13, 932-944.e5.	2.9	7
3472	Histone chaperone ASF1 mediates H3.3-H4 deposition in Arabidopsis. Nature Communications, 2022, 13, .	5.8	8
3473	Mcm2 promotes stem cell differentiation via its ability to bind H3-H4. ELife, 0, 11, .	2.8	7
3474	High-affinity chromodomains engineered for improved detection of histone methylation and enhanced CRISPR-based gene repression. Nature Communications, 2022, 13, .	5.8	4
3475	Identification of transcription factors dictating blood cell development using a bidirectional transcription network-based computational framework. Scientific Reports, 2022, 12, .	1.6	6
3476	Histone H3 proline 16 hydroxylation regulates mammalian gene expression. Nature Genetics, 2022, 54, 1721-1735.	9.4	22

#	Article	IF	Citations
3477	Systematic discovery and functional dissection of enhancers needed for cancer cell fitness and proliferation. Cell Reports, 2022, 41, 111630.	2.9	10
3478	Brain molecular mechanisms in Rasmussen encephalitis. Epilepsia, 2023, 64, 218-230.	2.6	3
3479	Nucleoporins facilitate ORC loading onto chromatin. Cell Reports, 2022, 41, 111590.	2.9	9
3480	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
3482	Tcf12 is required to sustain myogenic genes synergism with MyoD by remodelling the chromatin landscape. Communications Biology, 2022, 5, .	2.0	4
3483	Evolution and function of developmentally dynamic pseudogenes in mammals. Genome Biology, 2022, 23, .	3.8	7
3484	Type 1 diabetes risk genes mediate pancreatic beta cell survival in response to proinflammatory cytokines. Cell Genomics, 2022, 2, 100214.	3.0	8
3485	TBX20 Improves Contractility and Mitochondrial Function During Direct Human Cardiac Reprogramming. Circulation, 2022, 146, 1518-1536.	1.6	19
3486	Mapping open chromatin by ATAC-seq in bread wheat. Frontiers in Plant Science, 0, 13, .	1.7	4
3487	PAX3-FOXO1 coordinates enhancer architecture, eRNA transcription, and RNA polymerase pause release at select gene targets. Molecular Cell, 2022, 82, 4428-4442.e7.	4.5	12
3488	Combinatorial depletions of G-protein coupled receptor kinases in immune cells identify pleiotropic and cell type-specific functions. Frontiers in Immunology, 0, 13, .	2.2	0
3489	QSER1 preserves the suppressive status of the pro-apoptotic genes to prevent apoptosis. Cell Death and Differentiation, 2023, 30, 779-793.	5.0	5
3490	SEGCOND predicts putative transcriptional condensate-associated genomic regions by integrating multi-omics data. Bioinformatics, 0, , .	1.8	0
3491	The 3D enhancer network of the developing T cell genome is shaped by SATB1. Nature Communications, 2022, 13, .	5.8	14
3494	A new CUT&RUN low volume-urea (LoV-U) protocol optimized for transcriptional co-factors uncovers Wnt/Î²-catenin tissue-specific genomic targets. Development (Cambridge), 2022, 149, .	1.2	12
3495	Acetate supplementation restores cognitive deficits caused by <scp>ARID1A</scp> haploinsufficiency in excitatory neurons. EMBO Molecular Medicine, 2022, 14, .	3.3	4
3497	Characterization of the promoter region of the murine <i>Catsper2</i> gene. FEBS Open Bio, 0, , .	1.0	2
3498	Coordinated regulation of microRNA genes in C19MC by SETDB1. Biochemical and Biophysical Research Communications, 2022, 637, 17-22.	1.0	2

#	Article	IF	Citations
3499	Computational workflow for integrative analyses of DNA replication timing, epigenomic, and transcriptomic data. STAR Protocols, 2022, 3, 101827.	0.5	0
3500	Efficient Generation of Genome-wide Libraries for Proteinâ€“ligand Screens Using Gibson Assembly. Bio-protocol, 2022, 12, .	0.2	5
3501	Mapping separase-mediated cleavage in situ. NAR Genomics and Bioinformatics, 2022, 4, .	1.5	0
3504	Unscheduled DNA replication in G1 causes genome instability and damage signatures indicative of replication collisions. Nature Communications, 2022, 13, .	5.8	6
3506	The Heterochromatin protein 1 is a regulator in RNA splicing precision deficient in ulcerative colitis. Nature Communications, 2022, 13, .	5.8	4
3508	Integrative analyses of maternal plasma cell-free DNA nucleosome footprint differences reveal chromosomal aneuploidy fetuses gene expression profile. Journal of Translational Medicine, 2022, 20, .	1.8	0
3510	Xrn2 substrate mapping identifies torpedo loading sites and extensive premature termination of RNA pol II transcription. Genes and Development, 2022, 36, 1062-1078.	2.7	14
3511	Nucleosome Patterns in Circulating Tumor DNA Reveal Transcriptional Regulation of Advanced Prostate Cancer Phenotypes. Cancer Discovery, 2023, 13, 632-653.	7.7	13
3512	A Myb enhancer-guided analysis of basophil and mast cell differentiation. Nature Communications, 2022, 13, .	5.8	5
3515	THOC5 complexes with DDX5, DDX17, and CDK12 to regulate R loop structures and transcription elongation rate. IScience, 2023, 26, 105784.	1.9	5
3516	TFIIS Is Crucial During Early Transcript Elongation for Transcriptional Reprogramming in Response to Heat Stress. Journal of Molecular Biology, 2023, 435, 167917.	2.0	4
3520	The mechanical regulation of RNA binding protein hnRNPC in the failing heart. Science Translational Medicine, 2022, 14, .	5.8	6
3521	Poly ADP-ribosylation of SET8 leads to aberrant H4K20 methylation in mammalian nuclear genome. Communications Biology, 2022, 5, .	2.0	2
3523	Regulome analysis in B-acute lymphoblastic leukemia exposes Core Binding Factor addiction as a therapeutic vulnerability. Nature Communications, 2022, 13, .	5.8	4
3525	ZMP recruits and excludes Pol IVâ€“mediated DNA methylation in a site-specific manner. Science Advances, 2022, 8, .	4.7	7
3526	Functional analysis of structural variants in single cells using Strand-seq. Nature Biotechnology, 2023, 41, 832-844.	9.4	14
3528	Knockdown of YY1 Inhibits XIST Expression and Enhances Cloned Pig Embryo Development. International Journal of Molecular Sciences, 2022, 23, 14572.	1.8	1
3529	MYB44-ENAP1/2 restricts HDT4 to regulate drought tolerance in Arabidopsis. PLoS Genetics, 2022, 18, e1010473.	1.5	15

#	ARTICLE	IF	CITATIONS
3530	Extensive androgen receptor enhancer heterogeneity in primary prostate cancers underlies transcriptional diversity and metastatic potential. Nature Communications, 2022, 13, .	5.8	8
3532	Chromatin dynamics associated with seed desiccation tolerance/sensitivity at early germination in Medicago truncatula. Frontiers in Plant Science, 0, 13, .	1.7	2
3534	TDP-43 safeguards the embryo genome from L1 retrotransposition. Science Advances, 2022, 8, .	4.7	9
3535	TERRA regulates DNA G-quadruplex formation and ATRX recruitment to chromatin. Nucleic Acids Research, 2022, 50, 12217-12234.	6.5	7
3536	The RNA-binding protein RBP33 dampens non-productive transcription in trypanosomes. Nucleic Acids Research, 2022, 50, 12251-12265.	6.5	2
3537	Contribution of variant subunits and associated factors to genome-wide distribution and dynamics of cohesin. Epigenetics and Chromatin, 2022, 15, .	1.8	5
3538	Global DNA and protein interactomes of FLT1P1 (Fms-related tyrosine kinase 1 pseudogene 1) revealed its molecular regulatory functions associated with preeclampsia. Molecular Biology Reports, 0, , .	1.0	0
3539	The noncoding RNA <i>HIDDEN TREASURE 1</i> promotes phytochrome B-dependent seed germination by repressing abscisic acid biosynthesis. Plant Cell, 2023, 35, 700-716.	3.1	8
3540	Breast cancer plasticity is restricted by a LATS1-NCOR1 repressive axis. Nature Communications, 2022, 13, .	5.8	5
3541	Essential role of MESP1-RING1A complex in cardiac differentiation. Developmental Cell, 2022, 57, 2533-2549.e7.	3.1	0
3542	Immunoâ€epigenomic analysis identifies attenuated interferon responses in naÃ¯ve <scp>CD4</scp> T cells of adolescents with peanut and multiâ€food allergy. Pediatric Allergy and Immunology, 2022, 33, .	1.1	3
3545	PCGF1-PRC1 links chromatin repression with DNA replication during hematopoietic cell lineage commitment. Nature Communications, 2022, 13, .	5.8	3
3546	The extrachromosomal circular DNAs of the rice blast pathogen Magnaporthe oryzae contain a wide variety of LTR retrotransposons, genes, and effectors. BMC Biology, 2022, 20, .	1.7	9
3547	Extensive germline-somatic interplay contributes to prostate cancer progression through HNF1B co-option of TMPRSS2-ERG. Nature Communications, 2022, 13, .	5.8	6
3549	Single-nucleus RNA-seq reveals that MBD5, MBD6, and SILENZIO maintain silencing in the vegetative cell of developing pollen. Cell Reports, 2022, 41, 111699.	2.9	13
3552	Prenatal inflammation perturbs murine fetal hematopoietic development and causes persistent changes to postnatal immunity. Cell Reports, 2022, 41, 111677.	2.9	15
3553	Generalized nuclear localization of retroelement transcripts. Mobile DNA, 2022, 13, .	1.3	1
3554	Histone H2Bub dynamics in the 5â€² region of active genes are tightly linked to the UV-induced transcriptional response. Computational and Structural Biotechnology Journal, 2023, 21, 614-629.	1.9	1

#	Article	IF	Citations
3556	DOT1L regulates chamber-specific transcriptional networks during cardiogenesis and mediates postnatal cell cycle withdrawal. Nature Communications, 2022, 13, .	5.8	5
3557	K27M in canonical and noncanonical H3 variants occurs in distinct oligodendroglial cell lineages in brain midline gliomas. Nature Genetics, 2022, 54, 1865-1880.	9.4	27
3558	The Sum of Two Halves May Be Different from the Wholeâ€"Effects of Splitting Sequencing Samples Across Lanes. Genes, 2022, 13, 2265.	1.0	0
3559	Classification and characterization of alternative promoters in 26 lung adenocarcinoma cell lines. Japanese Journal of Clinical Oncology, 0, , .	0.6	1
3560	Ikaros family proteins redundantly regulate temporal patterning in the developing mouse retina. Development (Cambridge), 2023, 150, .	1.2	9
3561	Exon junction complex shapes the m6A epitranscriptome. Nature Communications, 2022, 13, .	5.8	36
3565	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
3566	The PNUTS-PP1 complex acts as an intrinsic barrier to herpesvirus KSHV gene expression and replication. Nature Communications, 2022, 13, .	5.8	1
3568	Usp22 is an intracellular regulator of systemic emergency hematopoiesis. Science Immunology, 2022, 7, .	5.6	3
3571	A Natural Fungal Gene Drive Enacts Killing via DNA Disruption. MBio, 2023, 14, .	1.8	1
3572	PPARÎ³ and C/EBPÎ± response to acute cold stress in brown adipose tissue. IScience, 2023, 26, 105848.	1.9	1
3573	Asxl1 deletion disrupts MYC and RNA polymerase II function in granulocyte progenitors. Leukemia, 0, , .	3.3	1
3574	Active DNA demethylation promotes cell fate specification and the DNA damage response. Science, 2022, 378, 983-989.	6.0	39
3575	Activation of OSM-STAT3 Epigenetically Regulates Tumor-Promoting Transcriptional Programs in Cervical Cancer. Cancers, 2022, 14, 6090.	1.7	0
3576	Recruitment of <scp>TRIM33</scp> to cellâ€context specific <scp>PML</scp> nuclear bodies regulates nodal signaling in <scp>mESCs</scp>. EMBO Journal, 2023, 42, .	3.5	5
3578	Inferring Protein-DNA Binding Profiles at Interspersed Repeats Using HiChIP and PAtChER. Methods in Molecular Biology, 2023, , 199-214.	0.4	1
3579	PPM1D suppresses p53-dependent transactivation and cell death by inhibiting the Integrated Stress Response. Nature Communications, 2022, 13, .	5.8	9
3580	Transcription elongator SPT6L regulates the occupancies of the SWI2/SNF2 chromatin remodelers SYD/BRM and nucleosomes at transcription start sites in Arabidopsis. Nucleic Acids Research, 2022, 50, 12754-12767.	6.5	10

#	Article	IF	Citations
3581	Tup1 is critical for transcriptional repression in Quiescence in S. cerevisiae. PLoS Genetics, 2022, 18, e1010559.	1.5	5
3582	Chromatin Immunoprecipitation Approach to Determine How PARP1 Domains Affect Binding Pattern to Chromatin. Methods in Molecular Biology, 2023, , 297-313.	0.4	0
3584	Interplay Between the Histone Variant H2A.Z and the Epigenome in Pancreatic Cancer. Archives of Medical Research, 2022, 53, 840-858.	1.5	3
3585	DAP5 enables main ORF translation on mRNAs with structured and uORF-containing 5â€² leaders. Nature Communications, 2022, 13, .	5.8	15
3586	Cooperation of chromatin remodeling SWI/SNF complex and pioneer factor AP-1 shapes 3D enhancer landscapes. Nature Structural and Molecular Biology, 2023, 30, 10-21.	3.6	26
3587	Î²-hydroxybutyrate inhibits ferroptosis-mediated pancreatic damage in acute liver failure through the increase of H3K9bhb. Cell Reports, 2022, 41, 111847.	2.9	8
3588	Global dissection of the recombination landscape in soybean using a highâ€density <scp>600K SoySNP</scp> array. Plant Biotechnology Journal, 2023, 21, 606-620.	4.1	8
3589	Short-chain fatty acid-mediated epigenetic modulation of inflammatory T cells in vitro. Drug Delivery and Translational Research, 2023, 13, 1912-1924.	3.0	9
3591	<i>CHD8</i>suppression impacts on histone H3 lysine 36 trimethylation and alters RNA alternative splicing. Nucleic Acids Research, 2022, 50, 12809-12828.	6.5	9
3592	Comprehensive characterization of three classes of Arabidopsis SWI/SNF chromatin remodelling complexes. Nature Plants, 2022, 8, 1423-1439.	4.7	19
3593	Regulatory dynamics distinguishing desiccation tolerance strategies within resurrection grasses. Plant Direct, 2022, 6, .	0.8	2
3594	Transcriptional Effects of Rootstock on Scion after Drought: A Case Study of Using MdGH3 RNAi as the Rootstock. Horticulturae, 2022, 8, 1212.	1.2	0
3595	Zygotic genome activation by the totipotency pioneer factor Nr5a2. Science, 2022, 378, 1305-1315.	6.0	40
3596	Dephosphorylation of the pre-initiation complex is critical for origin firing. Molecular Cell, 2023, 83, 12-25.e10.	4.5	5
3598	Drosophila SUMM4 complex couples insulator function and DNA replication control. ELife, 0, 11, .	2.8	3
3599	A genetic disorder reveals a hematopoietic stem cell regulatory network co-opted in leukemia. Nature Immunology, 2023, 24, 69-83.	7.0	15
3600	Genetic variation in histone modifications and gene expression identifies regulatory variants in the mammary gland of cattle. BMC Genomics, 2022, 23, .	1.2	8
3601	Oncogene expression from extrachromosomal DNA is driven by copy number amplification and does not require spatial clustering in glioblastoma stem cells. ELife, 0, 11, .	2.8	10

#	ARTICLE	IF	CITATIONS
3603	Species-specific rewiring of definitive endoderm developmental gene activation via endogenous retroviruses through TET1-mediated demethylation. Cell Reports, 2022, 41, 111791.	2.9	6
3604	Chromatin-associated YTHDC1 coordinates heat-induced reprogramming of gene expression. Cell Reports, 2022, 41, 111784.	2.9	3
3607	Silent gene clusters encode magnetic organelle biosynthesis in a non-magnetotactic phototrophic bacterium. ISME Journal, 2023, 17, 326-339.	4.4	6
3608	Lhx2 is a progenitor-intrinsic modulator of Sonic Hedgehog signaling during early retinal neurogenesis. ELife, 0, 11, .	2.8	3
3610	Integrating extrusion complex-associated pattern to predict cell type-specific long-range chromatin loops. IScience, 2022, 25, 105687.	1.9	2
3611	ATACâ€seq exposes differences in chromatin accessibility leading to distinct leaf shapes in mulberry. Plant Direct, 2022, 6, .	0.8	1
3612	Modulation of RNA splicing enhances response to BCL2 inhibition in leukemia. Cancer Cell, 2023, 41, 164-180.e8.	7.7	15
3613	ONE-seq: epitranscriptome and gene-specific profiling of NAD-capped RNA. Nucleic Acids Research, 2023, 51, e12-e12.	6.5	9
3615	An ectopic enhancer restores CFTR expression through de novo chromatin looping. Gene Therapy, 2023, 30, 478-486.	2.3	2
3616	Effect of M2-like macrophages of the injured-kidney cortex on kidney cancer progression. Cell Death Discovery, 2022, 8, .	2.0	3
3618	NEDDylated Cullin 3 mediates the adaptive response to topoisomerase 1 inhibitors. Science Advances, 2022, 8, .	4.7	6
3619	LncRNA LENGA acts as a tumor suppressor in gastric cancer through BRD7/TP53 signaling. Cellular and Molecular Life Sciences, 2023, 80, .	2.4	1
3620	ERK1/2 signalling dynamics promote neural differentiation by regulating chromatin accessibility andÂthe polycomb repressive complex. PLoS Biology, 2022, 20, e3000221.	2.6	9
3621	A simple and robust method for isolating and analyzing chromatin-bound RNAs in Arabidopsis. Plant Methods, 2022, 18, .	1.9	1
3622	Integrated genomic analysis identifies novel low-frequency cis-regulatory variant rs2279658 associated with VSD risk in Chinese children. Frontiers in Cell and Developmental Biology, 0, 10, .	1.8	1
3623	Cell-type specific profiling of histone post-translational modifications in the adult mouse striatum. Nature Communications, 2022, 13, .	5.8	1
3624	Widespread transposon co-option in the <i>Caenorhabditis</i> germline regulatory network. Science Advances, 2022, 8, .	4.7	1
3625	spKAS-seq reveals R-loop dynamics using low-input materials by detecting single-stranded DNA with strand specificity. Science Advances, 2022, 8, .	4.7	10

#	ARTICLE	IF	CITATIONS
3626	A framework for clinical cancer subtyping from nucleosome profiling of cell-free DNA. Nature Communications, 2022, 13, .	5.8	27
3627	Reconstituting human somitogenesis in vitro. Nature, 2023, 614, 509-520.	13.7	40
3629	A metabolic associated fatty liver disease risk variant in MBOAT7 regulates toll like receptor induced outcomes. Nature Communications, 2022, 13, .	5.8	11
3630	Histone lactylation driven by mROS-mediated glycolytic shift promotes hypoxic pulmonary hypertension. Journal of Molecular Cell Biology, 2023, 14, .	1.5	10
3634	KMT2D deficiency drives lung squamous cell carcinoma and hypersensitivity to RTK-RAS inhibition. Cancer Cell, 2023, 41, 88-105.e8.	7.7	12
3635	G-quadruplexes sense natural porphyrin metabolites for regulation of gene transcription and chromatin landscapes. Genome Biology, 2022, 23, .	3.8	8
3636	Hepatic GATA4 regulates cholesterol and triglyceride homeostasis in collaboration with LXRs. Genes and Development, 0, , .	2.7	0
3637	Stable isotope tracing inÂvivo reveals a metabolic bridge linking the microbiota to host histone acetylation. Cell Reports, 2022, 41, 111809.	2.9	7
3639	A generalizable deep learning framework for inferring fine-scale germline mutation rate maps. Nature Machine Intelligence, 2022, 4, 1209-1223.	8.3	5
3640	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
3641	Elongation factor-specific capture of RNA polymerase II complexes. Cell Reports Methods, 2022, 2, 100368.	1.4	0
3642	Distinct binding pattern of EZH2 and JARID2 on RNAs and DNAs in hepatocellular carcinoma development. Frontiers in Oncology, 0, 12, .	1.3	1
3643	Architecture design of cucurbit crops for enhanced productivity by a natural allele. Nature Plants, 2022, 8, 1394-1407.	4.7	12
3644	SMAD9-MYCN positive feedback loop represents a unique dependency for MYCN-amplified neuroblastoma. Journal of Experimental and Clinical Cancer Research, 2022, 41, .	3.5	1
3645	Whole-genome functional characterization of RE1 silencers using a modified massively parallel reporter assay. Cell Genomics, 2023, 3, 100234.	3.0	0
3646	MLL3 loss drives metastasis by promoting a hybrid epithelialâ€“mesenchymal transition state. Nature Cell Biology, 2023, 25, 145-158.	4.6	16
3647	Inhibition of histone methyltransferase Smyd3 rescues NMDAR and cognitive deficits in a tauopathy mouse model. Nature Communications, 2023, 14, .	5.8	6
3648	Dysregulation of PRMT5 in chronic lymphocytic leukemia promotes progression with high risk of Richterâ€™s transformation. Nature Communications, 2023, 14, .	5.8	10

#	Article	IF	Citations
3649	Antagonistic action of GPS2 and KDM1A at enhancers governs alternative macrophage activation by interleukin 4. Nucleic Acids Research, 2023, 51, 1067-1086.	6.5	3
3652	Systematic evaluation of chromatin immunoprecipitation sequencing to study histone occupancy in dormancy transitions of grapevine buds. Tree Physiology, 0, , .	1.4	0
3654	A DNA methylation atlas of normal human cell types. Nature, 2023, 613, 355-364.	13.7	130
3655	PTBP1-activated co-transcriptional splicing controls epigenetic status of pluripotent stem cells. Molecular Cell, 2023, 83, 203-218.e9.	4.5	7
3657	Perturbed fatty-acid metabolism is linked to localized chromatin hyperacetylation, increased stress-response gene expression and resistance to oxidative stress. PLoS Genetics, 2023, 19, e1010582.	1.5	5
3658	Elongation factor 1 is a component of the <i>Arabidopsis</i>Â<scp>RNA</scp> polymerase <scp>II</scp> elongation complex and associates with a subset of transcribed genes. New Phytologist, 2023, 238, 113-124.	3.5	2
3659	ChIATAC is an efficient strategy for multi-omics mapping of 3D epigenomes from low-cell inputs. Nature Communications, 2023, 14, .	5.8	4
3660	Past history of obesity triggers persistent epigenetic changes in innate immunity and exacerbates neuroinflammation. Science, 2023, 379, 45-62.	6.0	39
3662	A novel active transposon creates allelic variation through altered translation rate to influence protein abundance. Nucleic Acids Research, 2023, 51, 595-609.	6.5	5
3663	Active enhancers strengthen insulation by RNA-mediated CTCF binding at chromatin domain boundaries. Genome Research, 0, , .	2.4	14
3664	The human pre-replication complex is an open complex. Cell, 2023, 186, 98-111.e21.	13.5	19
3665	Genome-wide measurement of DNA replication fork directionality and quantification of DNA replication initiation and termination with Okazaki fragment sequencing. Nature Protocols, 2023, 18, 1260-1295.	5.5	1
3667	Targetome Analysis of Malaria Sporozoite Transcription Factor AP2-Sp Reveals Its Role as a Master Regulator. MBio, 2023, 14, .	1.8	2
3669	Loss of epigenetic information as a cause of mammalian aging. Cell, 2023, 186, 305-326.e27.	13.5	184
3670	Human SMARCA5 is continuously required to maintain nucleosome spacing. Molecular Cell, 2023, 83, 507-522.e6.	4.5	11
3671	Stem cell plasticity, acetylation of H3K14, and de novo gene activation rely on KAT7. Cell Reports, 2023, 42, 111980.	2.9	3
3673	The landscape of expression and alternative splicing variation across human traits. Cell Genomics, 2023, 3, 100244.	3.0	9
3674	Î²â€Catenin activity induces an <scp>RNA</scp> biosynthesis program promoting therapy resistance in Tâ€cell acute lymphoblastic leukemia. EMBO Molecular Medicine, 2023, 15, .	3.3	3

#	ARTICLE	IF	CITATIONS
3675	ZFP462 safeguards neural lineage specification by targeting G9A/GLP-mediated heterochromatin to silence enhancers. Nature Cell Biology, 2023, 25, 42-55.	4.6	6
3676	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
3677	Diverse Partners of the Partitioning ParB Protein in Pseudomonas aeruginosa. Microbiology Spectrum, 2023, 11, .	1.2	2
3678	A Systemic and Integrated Analysis of p63-Driven Regulatory Networks in Mouse Oral Squamous Cell Carcinoma. Cancers, 2023, 15, 446.	1.7	1
3679	The Drosophila Fab-7 boundary modulates Abd-B gene activity by guiding an inversion of collinear chromatin organization and alternate promoter use. Cell Reports, 2023, 42, 111967.	2.9	3
3681	Clustered PHD domains in KMT2/MLL proteins are attracted by H3K4me3 and H3 acetylation-rich active promoters and enhancers. Cellular and Molecular Life Sciences, 2023, 80, .	2.4	3
3683	The homeodomain of Oct4 is a dimeric binder of methylated CpG elements. Nucleic Acids Research, 2023, 51, 1120-1138.	6.5	3
3685	Changes in PRC1 activity during interphase modulate lineage transition in pluripotent cells. Nature Communications, 2023, 14, .	5.8	1
3687	TGFÎ²1-Induced EMT in the MCF10A Mammary Epithelial Cell Line Model Is Executed Independently of SNAIL1 and ZEB1 but Relies on JUNB-Coordinated Transcriptional Regulation. Cancers, 2023, 15, 558.	1.7	5
3689	OKseqHMM: a genome-wide replication fork directionality analysis toolkit. Nucleic Acids Research, 2023, 51, e22-e22.	6.5	6
3690	HAND2 Assists MYCN Enhancer Invasion to Regulate a Noradrenergic Neuroblastoma Phenotype. Cancer Research, 2023, 83, 686-699.	0.4	4
3693	High-resolution mapping of mitotic DNA synthesis under conditions of replication stress in cultured cells. STAR Protocols, 2023, 4, 101970.	0.5	0
3694	Integrating Transcriptomic and ChIP-Seq Reveals Important Regulatory Regions Modulating Gene Expression in Myometrium during Implantation in Pigs. Biomolecules, 2023, 13, 45.	1.8	1
3696	Predicting cell type-specific effects of variants on TF-DNA binding by meta-learning. , 2022, , .		0
3698	Costâ€saving population genomic investigation of <i>Daphnia longispina</i> complex resting eggs using wholeâ€genome amplification and preâ€sequencing screening. Ecology and Evolution, 2022, 12, .	0.8	0
3699	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
3700	bulkAnalyseR: an accessible, interactive pipeline for analysing and sharing bulk multi-modal sequencing data. Briefings in Bioinformatics, 2023, 24, .	3.2	4
3701	Npl3 functions in mRNP assembly by recruitment of mRNP components to the transcription site and their transfer onto the mRNA. Nucleic Acids Research, 0, , .	6.5	5

#	ARTICLE	IF	CITATIONS
3702	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
3703	dU-adaptor-assembled Tn5-mediated strand-specific RNA-sequencing. Journal of Experimental Botany, 0, , .	2.4	1
3704	Disruption of the ATXN1-CIC complex reveals the role of additional nuclear ATXN1 interactors in spinocerebellar ataxia type 1. Neuron, 2023, 111, 481-492.e8.	3.8	7
3705	Enhancer remodeling drives MLL oncogene-dependent transcriptional dysregulation in leukemia stem cells. Blood Advances, 2023, 7, 2504-2519.	2.5	1
3706	The ETS transcription factor ETV6 constrains the transcriptional activity of EWSâ€“FLI to promote Ewing sarcoma. Nature Cell Biology, 0, , .	4.6	6
3707	Expansion of ventral foregut is linked to changes in the enhancer landscape for organ-specific differentiation. Nature Cell Biology, 2023, 25, 481-492.	4.6	2
3708	B1 SINE-binding ZFP266 impedes mouse iPSC generation through suppression of chromatin opening mediated by reprogramming factors. Nature Communications, 2023, 14, .	5.8	7
3709	Post-transcriptional control of a stemness signature by RNA-binding protein MEX3A regulates murine adult neurogenesis. Nature Communications, 2023, 14, .	5.8	3
3711	Centromeres as universal hotspots of DNA breakage, driving RAD51-mediated recombination during quiescence. Molecular Cell, 2023, 83, 523-538.e7.	4.5	19
3713	Genome-wide analysis of transcriptome and histone modifications in Brassica napus hybrid. Frontiers in Plant Science, 0, 14, .	1.7	1
3714	Oncogenic ERRB2 signals through the AP-1 transcription factor to control mesenchymal-like properties of oesophageal adenocarcinoma. NAR Cancer, 2023, 5, .	1.6	1
3715	STAT3 regulates CD8+ T cell differentiation and functions in cancer and acute infection. Journal of Experimental Medicine, 2023, 220, .	4.2	12
3716	ETV6 dependency in Ewing sarcoma by antagonism of EWS-FLI1-mediated enhancer activation. Nature Cell Biology, 0, , .	4.6	4
3717	<i>Lnc956</i> regulates mouse embryonic stem cell differentiation in response to DNA damage in a p53-independent pathway. Science Advances, 2023, 9, .	4.7	1
3718	Characteristics and functions of DNA N(6)-methyladenine in embryonic chicken muscle development. Poultry Science, 2023, 102, 102528.	1.5	2
3720	Psi promotes <i>Drosophila</i> wing growth via direct transcriptional activation of cell cycle targets and repression of growth inhibitors. Development (Cambridge), 2023, 150, .	1.2	0
3721	Genome-wide mapping of proteinâ€“DNA damage interaction by PADD-seq. Nucleic Acids Research, 2023, 51, e32-e32.	6.5	2
3722	Auxin-inducible degron 2 system deciphers functions of CTCF domains in transcriptional regulation. Genome Biology, 2023, 24, .	3.8	4

#	Article	IF	Citations
3724	HSFA1a modulates plant heat stress responses and alters the 3D chromatin organization of enhancer-promoter interactions. Nature Communications, 2023, 14, .	5.8	18
3725	Integration of chromatin accessibility and gene expression reveals new regulators of cold hardening to enhance freezing tolerance in<i>Prunus mume</i>. Journal of Experimental Botany, 2023, 74, 2173-2187.	2.4	4
3726	Dynamic changes in whole genome DNA methylation, chromatin and gene expression during mouse lens differentiation. Epigenetics and Chromatin, 2023, 16, .	1.8	7
3727	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
3728	Allosteric autoregulation of DNA binding via a DNA-mimicking protein domain: a biophysical study of ZNF410â€“DNA interaction using small angle X-ray scattering. Nucleic Acids Research, 2023, 51, 1674-1686.	6.5	5
3731	Genome-wide RNA polymerase stalling shapes the transcriptome during aging. Nature Genetics, 2023, 55, 268-279.	9.4	36
3733	PGC-1Î± senses the CBC of pre-mRNA to dictate the fate of promoter-proximally paused RNAPII. Molecular Cell, 2023, 83, 186-202.e11.	4.5	8
3736	scm6A-seq reveals single-cell landscapes of the dynamic m6A during oocyte maturation and early embryonic development. Nature Communications, 2023, 14, .	5.8	21
3738	Chromosome territory reorganization through artificial chromosome fusion is compatible with cell fate determination and mouse development. Cell Discovery, 2023, 9, .	3.1	2
3741	Human zygotic genome activation is initiated from paternal genome. Cell Discovery, 2023, 9, .	3.1	7
3742	Chem-map profiles drug binding to chromatin in cells. Nature Biotechnology, 2023, 41, 1265-1271.	9.4	10
3743	Chromatin Immunoprecipitation Experiments from Drosophila Ovaries. Methods in Molecular Biology, 2023, , 335-351.	0.4	0
3744	RNA mis-splicing drives viral mimicry response after DNMTi therapy in SETD2-mutant kidney cancer. Cell Reports, 2023, 42, 112016.	2.9	5
3745	Long-read genome assemblies reveal a <i>cis</i>-regulatory landscape associated with phenotypic divergence in two sister <i>Siniperca</i> fish species. Zoological Research, 2023, 44, 287-302.	0.9	1
3746	Assembly of the 81.6 Mb centromere of pea chromosome 6 elucidates the structure and evolution of metapolycentric chromosomes. PLoS Genetics, 2023, 19, e1010633.	1.5	6
3747	AN EMPIRICAL STUDY TO MEASURE EMPLOYEEâ€™S AWARENESS TOWARDS GREEN SUPPLY CHAIN MANAGEMENT PRACTICES IN INDIA. Towards Excellence, 0, , 574-582.	0.0	0
3748	Combined analysis of chromatin accessibility and gene expression profiles provide insight into Fucoxanthin biosynthesis in Isochrysis galbana under green light. Frontiers in Microbiology, 0, 14, .	1.5	0
3749	S-adenosylmethionine synthases specify distinct H3K4me3 populations and gene expression patterns during heat stress. ELife, 0, 12, .	2.8	4

#	ARTICLE	IF	CITATIONS
3752	TFIIIC as a Potential Epigenetic Modulator of Histone Acetylation in Human Stem Cells. International Journal of Molecular Sciences, 2023, 24, 3624.	1.8	2
3753	Pyruvate dehydrogenase fuels a critical citrate pool that is essential for Th17 cell effector functions. Cell Reports, 2023, 42, 112153.	2.9	7
3754	The conserved histone chaperone Spt6 is strongly required for DNA replication and genome stability. Cell Reports, 2023, 42, 112264.	2.9	4
3755	H4K20me1 plays a dual role in transcriptional regulation of regeneration and axis patterning in<i>Hydra</i>. Life Science Alliance, 2023, 6, e202201619.	1.3	2
3756	Cell context-dependent CFI-1/ARID3 functions control neuronal terminal differentiation. Cell Reports, 2023, 42, 112220.	2.9	1
3759	An efficient CRISPRâ€"Cas12a promoter editing system for crop improvement. Nature Plants, 2023, 9, 588-604.	4.7	31
3761	FIPRESCI: droplet microfluidics based combinatorial indexing for massive-scale 5â€²-end single-cell RNA sequencing. Genome Biology, 2023, 24, .	3.8	4
3762	DNA double-strand break end synapsis by DNA loop extrusion. Nature Communications, 2023, 14, .	5.8	6
3763	ETV4 mediates dosage-dependent prostate tumor initiation and cooperates with p53 loss to generate prostate cancer. Science Advances, 2023, 9, .	4.7	2
3765	Comprehensive characterization of the embryonic factor LEUTX. IScience, 2023, 26, 106172.	1.9	1
3768	Organization, genomic targeting, and assembly of three distinct SWI/SNF chromatin remodeling complexes in Arabidopsis. Plant Cell, 2023, 35, 2464-2483.	3.1	7
3770	Protocol for Bulk-ATAC sequencing in head and neck squamous cell carcinoma. STAR Protocols, 2023, 4, 102233.	0.5	0
3771	An analysis of differentially expressed and differentially m6A-modified transcripts in soybean roots treated with lead. Journal of Hazardous Materials, 2023, 453, 131370.	6.5	3
3772	DIS3L2 ribonuclease degrades terminal-uridylated RNA to ensure oocyte maturation and female fertility. Nucleic Acids Research, 2023, 51, 3078-3093.	6.5	2
3773	Annelid functional genomics reveal the origins of bilaterian life cycles. Nature, 2023, 615, 105-110.	13.7	34
3774	The endothelial-enriched lncRNA LINC00607 mediates angiogenic function. Basic Research in Cardiology, 2023, 118, .	2.5	6
3775	RNA exosome ribonuclease DIS3 degrades Pou6f1 to promote mouse pre-implantation cell differentiation. Cell Reports, 2023, 42, 112047.	2.9	4
3776	FAM122A Is Required for Mesendodermal and Cardiac Differentiation of Embryonic Stem Cells. Stem Cells, 2023, 41, 354-367.	1.4	1

#	ARTICLE	IF	CITATIONS
3779	Low-affinity CTCF binding drives transcriptional regulation whereas high-affinity binding encompasses architectural functions. IScience, 2023, 26, 106106.	1.9	4
3781	Threeâ€dimensional chromatin reâ€organization during muscle stem cell aging. Aging Cell, 2023, 22, .	3.0	5
3782	Centromere repositioning and shifts in wheat evolution. Plant Communications, 2023, 4, 100556.	3.6	16
3783	Lens Epithelial Explants Treated with Vitreous Humor Undergo Alterations in Chromatin Landscape with Concurrent Activation of Genes Associated with Fiber Cell Differentiation and Innate Immune Response. Cells, 2023, 12, 501.	1.8	4
3787	Simultaneous sequencing of genetic and epigenetic bases in DNA. Nature Biotechnology, 2023, 41, 1457-1464.	9.4	26
3789	Reactivation of Epstein-Barr Virus from Latency Involves Increased RNA Polymerase Activity at CTCF Binding Sites on the Viral Genome. Journal of Virology, 2023, 97, .	1.5	4
3793	<i>Mycobacterium tuberculosis</i>infection triggers epigenetic changes that are enriched in a type I IFN signature. MicroLife, 2023, 4, .	1.0	2
3795	Single-molecule footprinting identifies context-dependent regulation of enhancers by DNA methylation. Molecular Cell, 2023, 83, 787-802.e9.	4.5	31
3796	CTCF mediates CD8+ effector differentiation through dynamic redistribution and genomic reorganization. Journal of Experimental Medicine, 2023, 220, .	4.2	5
3798	Transcription factor SOX15 regulates stem cell pluripotency and promotes neural fate during differentiation by activating the neurogenic gene Hes5. Journal of Biological Chemistry, 2023, 299, 102996.	1.6	1
3799	Epigenomic variability is associated with ageâ€specific naÃ¯ve <scp>CD4</scp> T cell response to activation in infants and adolescents. Immunology and Cell Biology, 2023, 101, 397-411.	1.0	2
3800	An enhanced network of energy metabolism, lysine acetylation, and growth-promoting protein accumulation is associated with heterosis in elite hybrid rice. Plant Communications, 2023, 4, 100560.	3.6	3
3801	KDM8 epigenetically controls cardiac metabolism to prevent initiation of dilated cardiomyopathy. , 2023, 2, 174-191.		3
3803	H3.3 contributes to chromatin accessibility and transcription factor binding at promoter-proximal regulatory elements in embryonic stem cells. Genome Biology, 2023, 24, .	3.8	12
3804	Kupffer-cell-derived IL-6 is repurposed for hepatocyte dedifferentiation via activating progenitor genes from injury-specific enhancers. Cell Stem Cell, 2023, 30, 283-299.e9.	5.2	28
3805	Expanded Potential Stem Cells from Human Embryos Have an Open Chromatin Configuration with Enhanced Trophoblast Differentiation Ability. Advanced Science, 2023, 10, .	5.6	1
3806	Proteasome inhibition targets the KMT2A transcriptional complex in acute lymphoblastic leukemia. Nature Communications, 2023, 14, .	5.8	5
3808	Intra-Host Evolution Provides for the Continuous Emergence of SARS-CoV-2 Variants. MBio, 2023, 14, .	1.8	5

#	ARTICLE	IF	CITATIONS
3813	Genomic profiling of HIV-1 integration in microglia cells links viral integration to the topologically associated domains. Cell Reports, 2023, 42, 112110.	2.9	7
3817	The SAGA histone acetyltransferase module targets SMC5/6 to specific genes. Epigenetics and Chromatin, 2023, 16, .	1.8	4
3819	Sorting nexin 10 sustains PDGF receptor signaling in glioblastoma stem cells via endosomal protein sorting. JCI Insight, 2023, 8, .	2.3	3
3820	BRG1 HSA domain interactions with BCL7 proteins are critical for remodeling and gene expression. Life Science Alliance, 2023, 6, e202201770.	1.3	2
3821	Differential regulation of mRNA stability modulates transcriptional memory and facilitates environmental adaptation. Nature Communications, 2023, 14, .	5.8	3
3824	Proximity labeling reveals a new in vivo network of interactors for the histone demethylase KDM5. Epigenetics and Chromatin, 2023, 16, .	1.8	4
3825	Critical Role of the Transcription Factor AKNA in T-Cell Activation: An Integrative Bioinformatics Approach. International Journal of Molecular Sciences, 2023, 24, 4212.	1.8	0
3827	FLI1 and FRA1 transcription factors drive the transcriptional regulatory networks characterizing muscle invasive bladder cancer. Communications Biology, 2023, 6, .	2.0	4
3828	Phosphorylation of ATF2 promotes odontoblastic differentiation via intrinsic HAT activity. Journal of Genetics and Genomics, 2023, , .	1.7	0
3829	Detailed molecular and epigenetic characterization of the pig IPEC-J2 and chicken SL-29 cell lines. IScience, 2023, 26, 106252.	1.9	1
3830	A Satellite-Free Centromere in Equus przewalskii Chromosome 10. International Journal of Molecular Sciences, 2023, 24, 4134.	1.8	2
3831	Bat pluripotent stem cells reveal unusual entanglement between host and viruses. Cell, 2023, 186, 957-974.e28.	13.5	17
3832	A genome-wide map of DNA replication at single-molecule resolution in the malaria parasite<i>Plasmodium falciparum</i>. Nucleic Acids Research, 2023, 51, 2709-2724.	6.5	4
3833	Histone deacetylase OsHDA706 increases salt tolerance via H4K5/K8 deacetylation of <i>OsPP2C49</i> in rice. Journal of Integrative Plant Biology, 2023, 65, 1394-1407.	4.1	4
3835	Conserved reduction of m ⁶ A RNA modifications during aging and neurodegeneration is linked to changes in synaptic transcripts. Proceedings of the National Academy of Sciences of the United States of America, 2023, 120, .	3.3	20
3836	Evolutionarily distinct and sperm-specific supersized chromatin loops are marked by Helitron transposons in Xenopus tropicalis. Cell Reports, 2023, 42, 112151.	2.9	1
3837	Nanoparticle-mediated targeting of the fusion gene RUNX1/ETO in t(8;21)-positive acute myeloid leukaemia. Leukemia, 2023, 37, 820-834.	3.3	10
3838	Nutrient regulation of the islet epigenome controls adaptive insulin secretion. Journal of Clinical Investigation, 2023, 133, .	3.9	6

#	ARTICLE	IF	CITATIONS
3839	MacroH2A histone variants modulate enhancer activity to repress oncogenic programs and cellular reprogramming. Communications Biology, 2023, 6, .	2.0	6
3841	Retrospective analysis of enhancer activity and transcriptome history. Nature Biotechnology, 2023, 41, 1582-1592.	9.4	3
3844	An integrative epigenomic approach identifies <i>ELF3</i> as an oncogenic regulator in <i>ASCL1</i>â€positive neuroendocrine carcinoma. Cancer Science, 2023, 114, 2596-2608.	1.7	4
3845	Disruption of polyhomeotic polymerization decreases nucleosome occupancy and alters genome accessibility. Life Science Alliance, 2023, 6, e202201768.	1.3	1
3846	Translational landscape in human early neural fate determination. Development (Cambridge), 2023, 150, .	1.2	3
3852	Mapping Nucleosome Location Using FS-Seq. Methods in Molecular Biology, 2023, , 21-38.	0.4	0
3853	Measuring Inaccessible Chromatin Genome-Wide Using Protect-seq. Methods in Molecular Biology, 2023, , 53-61.	0.4	0
3854	ATAC-seq Data Processing. Methods in Molecular Biology, 2023, , 305-323.	0.4	1
3855	Determination of the Chromatin Openness in Bacterial Genomes. Methods in Molecular Biology, 2023, , 63-69.	0.4	0
3858	Distinct roles for canonical and variant histone H3 lysine-36 in Polycomb silencing. Science Advances, 2023, 9, .	4.7	10
3859	Functional annotation of the animal genomes: An integrated annotation resource for the horse. PLoS Genetics, 2023, 19, e1010468.	1.5	3
3860	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
3861	A CUT&RUN protocol to determine patterns of epigenetic marks in imaginal discs of Drosophila. STAR Protocols, 2023, 4, 101878.	0.5	1
3862	Apolipoprotein E induces pathogenic senescent-like myeloid cells in prostate cancer. Cancer Cell, 2023, 41, 602-619.e11.	7.7	19
3863	BACH1 deficiency prevents neointima formation and maintains the differentiated phenotype of vascular smooth muscle cells by regulating chromatin accessibility. Nucleic Acids Research, 2023, 51, 4284-4301.	6.5	5
3866	A gene regulatory network for neural induction. ELife, 0, 12, .	2.8	9
3867	Zeb2 DNA-Binding Sites in Neuroprogenitor Cells Reveal Autoregulation and Affirm Neurodevelopmental Defects, Including in Mowat-Wilson Syndrome. Genes, 2023, 14, 629.	1.0	2
3868	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

#	Article	IF	Citations
3870	A gene silencing screen uncovers diverse tools for targeted gene repression in Arabidopsis. Nature Plants, 2023, 9, 460-472.	4.7	13
3871	Single-cell chromatin accessibility and transcriptome atlas of mouse embryos. Cell Reports, 2023, 42, 112210.	2.9	9
3872	RGT: a toolbox for the integrative analysis of high throughput regulatory genomics data. BMC Bioinformatics, 2023, 24, .	1.2	3
3875	Antagonistic regulation of target genes by the SISTER OF TM3â€“JOINTLESS2 complex in tomato inflorescence branching. Plant Cell, 2023, 35, 2062-2078.	3.1	4
3876	Genome-wide profiling of histone H3 lysine 27 trimethylation and its modification in response to chilling stress in grapevine leaves. Horticultural Plant Journal, 2023, 9, 496-508.	2.3	2
3877	A Comprehensive and Integrative Approach to MeCP2 Disease Transcriptomics. International Journal of Molecular Sciences, 2023, 24, 5122.	1.8	1
3878	Immunomodulatory Microparticles Epigenetically Modulate T Cells and Systemically Ameliorate Autoimmune Arthritis. Advanced Science, 2023, 10, .	5.6	7
3879	Pharmacological disruption of mSWI/SNF complex activity restricts SARS-CoV-2 infection. Nature Genetics, 2023, 55, 471-483.	9.4	14
3881	Extensive sequence duplication in Arabidopsis revealed by pseudo-heterozygosity. Genome Biology, 2023, 24, .	3.8	13
3882	Identification of the viral and cellular microRNA interactomes during SARS-CoV-2 infection. Cell Reports, 2023, 42, 112282.	2.9	6
3883	Global loss of cellular m⁶A RNA methylation following infection with different SARS-CoV-2 variants. Genome Research, 2023, 33, 299-313.	2.4	8
3885	Different NIPBL requirements of cohesin-STAG1 and cohesin-STAG2. Nature Communications, 2023, 14, .	5.8	8
3888	Tnâ€seq identifies <i>Ralstonia solanacearum</i> genes required for tolerance of plant immunity induced by exogenous salicylic acid. Molecular Plant Pathology, 2023, 24, 536-548.	2.0	4
3890	Heterochromatin rewiring and domain disruption-mediated chromatin compaction during erythropoiesis. Nature Structural and Molecular Biology, 2023, 30, 463-474.	3.6	4
3891	A Genome-Scale Atlas Reveals Complex Interplay of Transcription and Translation in an Archaeon. MSystems, 2023, 8, .	1.7	4
3892	A combinatorial approach to uncover an additional Integrator subunit. Cell Reports, 2023, 42, 112244.	2.9	7
3893	The patterns and participants of parental histone recycling during DNA replication in Saccharomyces cerevisiae. Science China Life Sciences, 2023, 66, 1600-1614.	2.3	3
3894	Batf stabilizes Th17 cell development via impaired Stat5 recruitment of <scp>Ets1â€Runx1</scp> complexes. EMBO Journal, 2023, 42, .	3.5	4

#	ARTICLE	IF	CITATIONS
3896	Conservation and divergence of canonical and non-canonical imprinting in murids. Genome Biology, 2023, 24, .	3.8	7
3898	The plant response to high <scp>CO₂</scp> levels is heritable and orchestrated by <scp>DNA</scp> methylation. New Phytologist, 2023, 238, 2427-2439.	3.5	4
3899	Whole-genome doubling drives oncogenic loss of chromatin segregation. Nature, 2023, 615, 925-933.	13.7	10
3900	The tissue-specific chromatin accessibility landscape of Papaver somniferum. Frontiers in Genetics, 0, 14, .	1.1	2
3903	Hematopoietic/erythroid enhancers activate nearby target genes by extending histone <scp>H3K27ac</scp> and transcribing intergenic <scp>RNA</scp>. FASEB Journal, 2023, 37, .	0.2	1
3905	POSTRE: a tool to predict the pathological effects of human structural variants. Nucleic Acids Research, 2023, 51, e54-e54.	6.5	3
3906	SOCS1 regulates a subset of NFÎºB-target genes through direct chromatin binding and defines macrophage functional phenotypes. IScience, 2023, 26, 106442.	1.9	4
3907	TXNIP loss expands Myc-dependent transcriptional programs by increasing Myc genomic binding. PLoS Biology, 2023, 21, e3001778.	2.6	3
3908	Spt6 directly interacts with Cdc73 and is required for Paf1 complex occupancy at active genes in <i>Saccharomyces cerevisiae</i>. Nucleic Acids Research, 2023, 51, 4814-4830.	6.5	5
3910	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
3911	Stressâ€sensitive dynamics of miRNAs and Elba1 in <i>Drosophila</i> embryogenesis. Molecular Systems Biology, 2023, 19, .	3.2	2
3912	Highly efficient and rapid generation of human pluripotent stem cells by chemical reprogramming. Cell Stem Cell, 2023, 30, 450-459.e9.	5.2	21
3913	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
3914	Epigenetic dosage identifies two major and functionally distinct Î² cell subtypes. Cell Metabolism, 2023, 35, 821-836.e7.	7.2	12
3915	LINE-1 repression in Epsteinâ€"Barr virus-associated gastric cancer through viralâ€"host genome interaction. Nucleic Acids Research, 2023, 51, 4867-4880.	6.5	3
3916	Spontaneously evolved progenitor niches escape Yap oncogene addiction in advanced pancreatic ductal adenocarcinomas. Nature Communications, 2023, 14, .	5.8	1
3917	Nutrigenomic regulation of sensory plasticity. ELife, 0, 12, .	2.8	3
3918	<scp>PRâ€DUB</scp> safeguards Polycomb repression through <scp>H2AK119ub1</scp> restriction. Cell Proliferation, 0, , .	2.4	2

#	ARTICLE	IF	CITATIONS
3920	Detection of Z-DNA Structures in Supercoiled Genome. Methods in Molecular Biology, 2023, , 179-193.	0.4	0
3921	A multi-organoid platform identifies CIART as a key factor for SARS-CoV-2 infection. Nature Cell Biology, 2023, 25, 381-389.	4.6	9
3922	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
3923	Expression of down-regulated ERV LTR elements associates with immune activation in human small-cell lung cancers. Mobile DNA, 2023, 14, .	1.3	1
3924	Snapshot: a package for clustering and visualizing epigenetic history during cell differentiation. BMC Bioinformatics, 2023, 24, .	1.2	3
3925	Genomic rearrangements and evolutionary changes in 3D chromatin topologies in the cotton tribe (Gossypieae). BMC Biology, 2023, 21, .	1.7	2
3927	Rewired m6A epitranscriptomic networks link mutant p53 to neoplastic transformation. Nature Communications, 2023, 14, .	5.8	2
3928	Dynamics of histone acetylation during human early embryogenesis. Cell Discovery, 2023, 9, .	3.1	11
3929	Redistribution of the chromatin remodeler Brg1 directs smooth muscleâ€“derived adventitial progenitorâ€“toâ€“myofibroblast differentiation and vascular fibrosis. JCI Insight, 2023, 8, .	2.3	6
3930	Arabidopsis TRB proteins function in H3K4me3 demethylation by recruiting JMJ14. Nature Communications, 2023, 14, .	5.8	11
3931	Deep learning-based active contour technique with bagging and boosting algorithms hybrid approach for detecting bone Cancer from Mri scan images. Multimedia Tools and Applications, 2023, 82, 36363-36377.	2.6	1
3933	Transcriptomic and Chromatin Landscape Analysis Reveals That Involvement of Pituitary Level Transcription Factors Modulate Incubation Behaviors of Magang Geese. Genes, 2023, 14, 815.	1.0	2
3934	Targeted DNA integration in human cells without double-strand breaks using CRISPR-associated transposases. Nature Biotechnology, 2024, 42, 87-98.	9.4	27
3935	Phosphorylation stabilized TET1 acts as an oncoprotein and therapeutic target in B cell acute lymphoblastic leukemia. Science Translational Medicine, 2023, 15, .	5.8	3
3937	Epitranscriptic regulation of <i>HRAS</i> by <i>N</i> ⁶ -methyladenosine drives tumor progression. Proceedings of the National Academy of Sciences of the United States of America, 2023, 120, .	3.3	1
3938	RNA Polymerase II transcription independent of TBP in murine embryonic stem cells. ELife, 0, 12, .	2.8	5
3939	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
3940	Novel enhancers conferring compensatory transcriptional regulation of Nkx2-5 in heart development. IScience, 2023, 26, 106509.	1.9	1

#	Article	IF	Citations
3941	MYC reshapes CTCF-mediated chromatin architecture in prostate cancer. Nature Communications, 2023, 14, .	5.8	4
3942	Role of the RNA-binding protein ZC3H41 in the regulation of ribosomal protein messenger RNAs in trypanosomes. Parasites and Vectors, 2023, 16, .	1.0	0
3943	C ₄ gene induction during de-etiolation evolved through changes in cis to allow integration with ancestral C ₃ gene regulatory networks. Science Advances, 2023, 9, .	4.7	4
3944	A highly contiguous genome assembly reveals sources of genomic novelty in the symbiotic fungus <i>Rhizophagus irregularis</i>. G3: Genes, Genomes, Genetics, 2023, 13, .	0.8	5
3946	Regulation of human trophoblast gene expression by endogenous retroviruses. Nature Structural and Molecular Biology, 2023, 30, 527-538.	3.6	17
3947	Plasmodium falciparum gametocytes display global chromatin remodelling during sexual differentiation. BMC Biology, 2023, 21, .	1.7	5
3948	Titration-based normalization of antibody amount improves consistency of ChIP-seq experiments. BMC Genomics, 2023, 24, .	1.2	0
3949	Hypoxiaâ€mediated regulation of <scp>DDX5</scp> through decreased chromatin accessibility and postâ€translational targeting restricts Râ€loop accumulation. Molecular Oncology, 2023, 17, 1173-1191.	2.1	6
3950	The aryl hydrocarbon receptor regulates lipid mediator production in alveolar macrophages. Frontiers in Immunology, 0, 14, .	2.2	0
3952	Connectome and regulatory hubs of CAGE highly active enhancers. Scientific Reports, 2023, 13, .	1.6	1
3953	Genome-Wide Analysis of Hypoxia-Inducible Factor Binding Reveals Targets Implicated in Impaired Human Placental Syncytiotrophoblast Formation under Low Oxygen. American Journal of Pathology, 2023, 193, 846-865.	1.9	1
3954	RBBP4 is an epigenetic barrier for the induced transition of pluripotent stem cells into totipotent 2C-like cells. Nucleic Acids Research, 2023, 51, 5414-5431.	6.5	3
3955	Acetylation of histone H2B marks active enhancers and predicts CBP/p300 target genes. Nature Genetics, 2023, 55, 679-692.	9.4	9
3956	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
3957	Escape from oncogene-induced senescence is controlled by POU2F2 and memorized by chromatin scars. Cell Genomics, 2023, 3, 100293.	3.0	6
3958	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
3960	PRC2.1- and PRC2.2-specific accessory proteins drive recruitment of different forms of canonical PRC1. Molecular Cell, 2023, 83, 1393-1411.e7.	4.5	15
3961	Endothelial Brg1 fine-tunes Notch signaling during zebrafish heart regeneration. Npj Regenerative Medicine, 2023, 8, .	2.5	1

#	Article	IF	Citations
3964	Restraint of IFN-Î³ expression through a distal silencer CNSâ€“28 for tissue homeostasis. Immunity, 2023, 56, 944-958.e6.	6.6	3
3966	Optimal HSF1 activation in response to acute cold stress in BAT requires nuclear TXNIP. IScience, 2023, 26, 106538.	1.9	0
3967	Aberrant cell state plasticity mediated by developmental reprogramming precedes colorectal cancer initiation. Science Advances, 2023, 9, .	4.7	11
3968	MYC activation impairs cell-intrinsic IFNÎ³ signaling and confers resistance to anti-PD1/PD-L1 therapy in lung cancer. Cell Reports Medicine, 2023, 4, 101006.	3.3	3
3969	Histone H3K27 methyltransferase EZH2 regulates apoptotic and inflammatory responses in sepsis-induced AKI. Theranostics, 2023, 13, 1860-1875.	4.6	6
3970	A multi-omics atlas of the human retina at single-cell resolution. Cell Genomics, 2023, 3, 100298.	3.0	10
3972	Elevated enhancer-oncogene contacts and higher oncogene expression levels by recurrent CTCF inactivating mutations in acute TÂcell leukemia. Cell Reports, 2023, 42, 112373.	2.9	3
3973	Sequence-Based Platforms for Discovering Biomarkers in Liquid Biopsy of Non-Small-Cell Lung Cancer. Cancers, 2023, 15, 2275.	1.7	3
3974	SOX2 downregulation of PML increases HCMV gene expression and growth of glioma cells. PLoS Pathogens, 2023, 19, e1011316.	2.1	4
3975	Dynamic changes in P300 enhancers and enhancer-promoter contacts control mouse cardiomyocyte maturation. Developmental Cell, 2023, 58, 898-914.e7.	3.1	3
3977	Binding by the Polycomb complex component BMI1 and H2A monoubiquitination shape local and long-range interactions in the Arabidopsis genome. Plant Cell, 2023, 35, 2484-2503.	3.1	4
3978	Lamin B1 overexpression alters chromatin organization and gene expression. Nucleus, 2023, 14, .	0.6	4
3979	Transcriptome-wide profiling of RNA N4-cytidine acetylation in Arabidopsis thaliana and Oryza sativa. Molecular Plant, 2023, 16, 1082-1098.	3.9	2
3980	RNA degradome analysis reveals DNE1 endoribonuclease is required for the turnover of diverse mRNA substrates in Arabidopsis. Plant Cell, 2023, 35, 1936-1955.	3.1	4
3981	INTAC endonuclease and phosphatase modules differentially regulate transcription by RNA polymerase II. Molecular Cell, 2023, 83, 1588-1604.e5.	4.5	13
3982	Ovulatory signal-triggered chromatin remodeling in ovarian granulosa cells by HDAC2 phosphorylation activation-mediated histone deacetylation. Epigenetics and Chromatin, 2023, 16, .	1.8	0
3985	Transcriptional-translational conflict is a barrier to cellular transformation and cancer progression. Cancer Cell, 2023, 41, 853-870.e13.	7.7	6
3986	Proteomic discovery of chemical probes that perturb protein complexes in human cells. Molecular Cell, 2023, 83, 1725-1742.e12.	4.5	25

#	ARTICLE	IF	CITATIONS
3987	<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
3988	BMP4 triggers regulatory circuits specifying the cardiac mesoderm lineage. Development (Cambridge), 2023, 150, .	1.2	3
3990	NF-ÎºB/p52 augments ETS1 binding genome-wide to promote glioma progression. Communications Biology, 2023, 6, .	2.0	1
3991	Identification and analysis of the DNA content of small extracellular vesicles isolated from Leishmania parasites. STAR Protocols, 2023, 4, 102248.	0.5	1
4391	Regulation of gene editing using T-DNA concatenation. Nature Plants, 2023, 9, 1398-1408.	4.7	2
4424	Dissecting key regulators of transcriptome kinetics through scalable single-cell RNA profiling of pooled CRISPR screens. Nature Biotechnology, 0, , .	9.4	3
4827	Genetic Variability of the MAOA Gene among Aggressive Animals in a Noncanonical Behavioral Model of Neogale vison. Russian Journal of Genetics, 2023, 59, 632-635.	0.2	0
4898	MBD2 couples DNA methylation to transposable element silencing during male gametogenesis. Nature Plants, 2024, 10, 13-24.	4.7	1
4946	A practical guide for essential analyses of Hi-C data. , 2024, , 343-361.		0
4947	Best practices for ChIP-seq and its data analysis. , 2024, , 319-341.		0